

**GENETIC VARIABILITY, DIVERSITY
AND STABILITY STUDY IN NIGER**
(Guizotia abyssinica L.)

By

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FACULTY OF AGRICULTURE,
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November, 2021

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A thesis submitted to the

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(Agricultural University)
DIST. - RATNAGIRI (MAHARASHTRA), INDIA

In partial fulfillment of the requirements for the degree of

**DOCTOR OF PHILOSOPHY
(AGRICULTURE)**

In

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CERTIFICATE

This is to certify that, the thesis entitled “**GENETIC VARIABILITY, DIVERSITY AND STABILITY STUDY IN NIGER (*Guizotia abyssinica* L.)**” submitted to the Faculty of Agriculture, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, Dist. Ratnagiri, Maharashtra State in partial fulfillment of the requirement for the degree of **DOCTOR OF PHILOSOPHY (AGRICULTURE) in GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona-fide research carried out by **MR. BALAJI SHIVAJI THORAT** (Reg. No. ADPD/17/0266) under my guidance and supervision. No part of this thesis has been submitted for any other degree or diploma or published in other form. All the assistance and help received during this course of investigation and the sources of literature have been duly acknowledged by him.

Place: Dapoli

Date: /11/2021

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**DEPARTMENT OF AGRIL. BOTANY,
COLLEGE OF AGRICULTURE, DAPOLI**

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ABSTRACT

The present investigation entitled "Genetic variability, diversity and stability study in Niger (*Guizotia abyssinica* L.)" was undertaken at five environments *viz.*, ARS, Phondaghat (E1); ARS, Shirgaon (E2); Department of Agril. Botany, Dapoli (E3); RARS, Karjat (E4) and ARS, Palghar (E5) with research objectives (i.) To study the nature and extent of genetic variability in yield and yield contributing traits (ii.) To measure the divergence between different genotypes by D² statistics (iii.) To study the stability of Niger genotypes under different environments and (iv) To study the G x E interaction for yield and yield contributing traits. The material for the present study comprised of forty genotypes of Niger collected from all over Maharashtra state. Evaluation of these genotypes in Randomized Block Design with three replications was done during *Kharif*, 2018 and *Kharif*, 2019 with all recommended package of practices.

The observations were recorded on 13 characters *viz.*, days to 50 per cent flowering, plant height (cm), number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of capitula plant⁻¹, capitulum diameter (cm), number of seeds capitulum⁻¹, 1000 seed weight (g), seed yield plant⁻¹ (g), seed yield plot⁻¹ (g), days to maturity, oil content (%), protein content (%) etc.

From the present study it was concluded that the significant variation was present among the genotypes studied for all the traits except capitulum diameter and 1000 seed weight. Among all, G36, G24, G32, G40, G38, G10, G4 were recorded highest mean performance in most of the characters. The phenotypic coefficient of variation (PCV) was slightly more than genotypic coefficient of variation (GCV) for all the traits, indicating the role of environment in the expression of these traits.

Broad sense heritability was highest for days to 50 per cent flowering, number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of capitula plant⁻¹, capitulum diameter and days to maturity indicating these traits were least influenced by environments and selection for improvement of such characters may be useful. The highest genetic advance and genetic advance per cent mean was observed in seed yield plant⁻¹, seed yield plot⁻¹, number of capitula plant⁻¹ and number of seeds capitula⁻¹. These traits were governed by additive genes and selection for improvement is useful. The high heritability coupled with high genetic advance indicated preponderance of additive gene action in the inheritance of most of the yield contributing traits and these were used for future crop improvement.

As per inter and intra-cluster distance coupled with cluster means of different traits, the genotypes classified in clusters IV, V and III in E1; clusters III and IV in E2; clusters II and IV in E3; clusters VIII, III, VI and VII in E4, and III and IV in E5 were found to be superior and showing the wealth of genetic diversity for exploitation in future breeding programs. The genotypes, G1, G2, G4, G8, G9, G10, G24, G25, G26, G28, G32, G35, G36, G39 and G40 were identified as diverse in all tested environments as per D² statistics and these were suggested as potential parents in future crop improvement programme. The highest contributors towards the genetic divergence were days to 50 per cent flowering, number of primary and secondary branches plant⁻¹, number of capitula plant⁻¹ and capitulum diameter.

Combined analysis of variance was highly significant for genotype, environment and their interaction (GEI) for all the traits except capitulum

diameter and 1000 seed weight. Analysis of variance for AMMI model due to genotype, environment and their interaction (GEI), IPCA1, IPCA2 and IPCA3 were highly significant for all the characters, indicating environments were diverse and affects the performance potential of genotypes. Consideration of both Regression as well as AMMI stability model, among all, G36, G32, G24 and G10 were found most stable and ideal genotypes which indicating highest mean yield and maximum additive main effect (AMMI1) with least interaction between genotype x environment. The genotypes located on vertex of GGE biplot polygon (AMMI2), G25 and G1 were the best at E1; G8 was classiest at E2; G6 was the excellent at E3; G23 and G17 were the pre-eminent in E4, and G14 was the winning genotype at E5, suggesting highest interaction between genotype and environment for seed yield plot⁻¹. The genotypes, G6, G8, G22 and G28 were suitable for favorable/rich environments while G2, G4, G7, G23 and G31 for unfavorable/poor environments in most of the traits. The genotypes, G4, G17, G25 and G28 were best performers in some environments for few yield contributing traits. These genotypes behaved as a potential breeding materials stock for future crop improvement. AMMI GGE biplots were identified two different mega-environments (METs), the first MET consists E1, E3 and E4 which are potential, highly discriminating and representative, and would be used to identification of superior genotypes and second MET includes E2 and E5 were stable places for most of the characters.

On the basis of *per se* performance, genetic variability, genetic diversity and different stability parameters *viz.*, high mean, regression coefficient (bi), deviation from regression (S^2_{di}), IPCA1 scores, ASV, GSI revealed that the genotypes, G36, G32, G24 and G10 were found highly stable for yield and yield contributing traits over the seasons and over the environments. Therefore, these four genotypes were identified as candidate genotypes and are recommended for future investigations.

CHAPTER - I

INTRODUCTION

United Nations projections estimate that the world population will continue to grow from the 6 million to about 10 million by 2050 (Riley and Belayneh, 1989; and FAO, 1996). The increase in population and the subsequent rise in the demand for agricultural produce are expected to be greater in regions where production is already insufficient. The necessary increase in agricultural production represents a huge challenge to local farming system and must come mainly from increase yield unit⁻¹ area given the limited scope for extension of cultivated land worldwide (Rao, 2014). Humanity relies on a diverse range of cultivated species; at least 6000 such species are used for a variety of purposes (Hiremath and Murthy, 1988). Agricultural research has traditionally focused on few staples; while relatively little attention has been given to minor (neglected) crops like, Niger, in general and particularly by scientists in developed countries (Getinet and Sharma, 1996). Such crops have, therefore, generally failed to attract significant research funding's.

Niger (*Guizotia abyssinica* L.) is named after the French historian Guizot. The genus *Guizotia* belongs to the family of Compositae, tribe Heliantheae, subtribe Coreopsidinae (Dagne, 2001). A taxonomic revision of the genus based on the morphological traits was presented by Baagoe (1974) (Seegeler, 1983). The species of the genus *Guizotia* are diploid with $2n=30$ chromosomes (Richharia and Kalamkar 1938; Murthy 1990; Hiremath and Murthy 1992; Dagne 1994a, Dagne 1994b and Dagne *et. al.*, 2000). The genus *Guizotia* is small with only six species, which are all native of tropical Africa (Chavan, 1961 and Arora *et. al.*, 2003). From the place of origin, it was migrated to East Africa and India through the Persian Gulf traders along with other crops, which is popularly known as the 'Savannah complex' (Dagne, 2001). It is commonly known as ramtil, jagni or jatangi (Hindi), ramtal (Gujrati), karale or khurasani (Marathi), uhechellu (Kannada), payellu (Tamil), verrinuvvulu (Telugu), alashi (Oriya), sarguza (Bengali), ramtil (Punjabi) and sorguja (Assamese) in different parts of the country. Niger although considered a minor oilseed crop, is important in terms of its 32 to 40 per cent

content of quality oil with 18 to 24 per cent protein in the seed (Nagaraj and Patil, 2004; Ramteke *et. al.*, 2001; Dagne and Jonsson, 1997). Niger oil is slow drying, used in food, paint, soap, and as an illuminant. It is used as a substitute for olive oil. The oil from the seed is used to treat burns and in the treatment of scabies. The seed is eaten fried as a baby food (Chibto and litlit) and used as a condiment (Vles and Gottenbos, 1989). The press cake from oil extraction is used for livestock feed. Niger oil has good keeping quality and has < 70% unsaturated fatty acids free from toxins. The oil is considered good for health. It is premium oil because of high linoleic acid content (45-60 per cent) and oleic acid (13-39 per cent) (Dutta *et. al.*, 1994). Niger oil contains Omega 3 and Omega 6 fatty acids which are thought to help in reducing the risk of heart disease and also to promote healthy skin. They are also used along with diet and exercise to lower the levels of a certain blood fat (triglyceride) and to raise levels of good cholesterol (HDL) (Ramadan and Morsel, 2003 and Staughton, 2017). Whole plants are used as green manure in the pre flowering stage. Plants are used as a 'bee plant'. The crop is capable of giving better seed yield even under low soil fertility, moisture stress and poor crop management. Niger has an advantage of yielding oil and has good degree of tolerance to diseases, insects, pests and attack of wild animals. Niger has great potential for soil conservation. These attributes favour its cultivation on hilly areas, marginal and sub marginal lands in and around the forests. Niger is primarily grown on the denuded soils in the tribal pockets under input starved conditions in India. Further it is the life line of tribal agriculture and economy (Ranganatha, 2013).

Worlds occupies 5.60 lakh ha area under Niger cultivation with 1.52 MMT production and 271 kg/ha productivity (USDA, 2018-19). It is mainly grown in India, Ethiopia, Nepal, Germany, Switzerland, France, USSR, Sudan, Uganda, Tanzania, Malawi, Zimbabwe, Central and South Africa. India is the most important country accounting for more than 50 per cent of world Niger area with production. India tops in area, production and total export for Niger in the world. In India, Niger is grown on an area of 2.52 lakh ha. with the production of 0.85 MMT and 337 kg/ha productivity (FAO, 2018-19). India could earn the foreign

exchange of Rs. 100 crores by export of Niger seed and the milled oil. (Ranganatha *et. al.*, 2015). In Maharashtra, it is grown on an area of 28000 ha. with the production of 80000 MT with productivity of 286 kg/ha (Anonymous, 2018-19a) which is very low compared to the national average. The major Niger growing districts in Maharashtra are Palghar, Ratnagiri, Sindhudurg, Nashik, Dhule, Nandurbar, Jalgaon, Pune, Solapur, Ahmednagar, Satara, Kolhapur, Beed, Latur, Osmanabad, Nanded, Parbhani, Hingoli and some part of Akola, Buldhana, Washim, Amravati, Yavatmal, Bhandara and Chandrapur. In Konkan region, 1530 ha area is under Niger cultivation with 452 MT total production and 295 kg/ha productivity (Anonymous, 2018-19b).

Though Niger has nutritional and export value, very little work has been done on the improvement of Niger in India. Humanity relies on a diverse range of cultivated species. It is often stated that only a few staple crops produce the majority of the food supply. This might be correct but the important contribution of many minor species should not be underestimated. Agriculture research has traditionally focused on these staples; while relatively little attention has been given to minor crops, particularly by scientist in developed countries. Moreover, existing knowledge on the genetic potential of neglected crops is limited. This has resulted, frequently in un-coordinated research efforts for most of the neglected crops. Niger has problems in cultivation like low yield due to self-incompatibility, susceptibility to pest, diseases and biotic stresses. These leads to poor seed set resulting from protandrous self-incompatibility reinforced by insect pollination.

Poor yield of crop is attributable to its cultivation on marginal lands with negligible inputs and unavailability of suitable cultivar for diverse agro-climatic conditions. At present, local types are predominantly grown, which are having low productivity with longer durations. Niger being minor oil seed crops, very little attention has been paid with respect to genetic enhancement till now.

Since, the beginning of agriculture, cultivated crops has been subjected to intensive natural, human selections and the trend continues. This has resulted in huge collection of different crop species, land races and varieties distributed throughout the world, which comprises valuable germplasm collection. The

ultimate goal of every plant breeder is to develop superior varietal population through diverse types, generating variability and ultimately giving selection pressure to desirable ideal genotypes.

Selection is also effective when there is genetic variability among the individuals in a population. Hence, insight into the magnitude of genetic variability present in a population is of paramount importance to a plant breeder for starting a judicious breeding programme. Information regarding genetic variability present among the genotypes and estimates of heritability are prerequisites for designing an effective breeding programme for improvement of any crop. Therefore, it is necessary to collect, conserve and study the genetic diversity among the various crops in the form of germplasm for establishing the wide genetic base for the posterity.

Use of advanced, novel techniques of plant improvement is inevitable for the twenty first century, but; D² technique has been widely used in crops like maize, sorghum, pearl millet, wheat, linseed, cotton, tobacco, alfalfa and brassica (Murty and Arunachalan, 1965). D² statistics measure the forces of differentiation at intra and inter cluster levels and determine the relative contribution of each component trait to the total divergence. Its estimates are free from genetic assumptions and help to identify suitable germplasm for incorporation into plant breeding stocks.

Agricultural yield is strongly influenced by environmental conditions that generally lead to wide variations in yield, both among years in a location and among locations in a single year or even further, between locations and the years. Improving yield stability of an agricultural crop throughout production region is an important objective of breeding programmes. Stability is the ability of a genotype to have always the uniform yield regardless of environmental effects (Becker, 1981).

The lower productivity could be attributed mainly due to lack of stable and adaptable high yielding improved varieties of Niger. There are several stability parameters used in identifying high yielding genotypes for wide and specific environments. Also, G × E interaction is a critical factor in crop

improvement. Encountering the $G \times E$ interaction in study of genotype is a challenge to the plant breeders. A change in environment may have great effect in one genotype than the other. The occurrence of $G \times E$ interaction has long posed a major challenge to complete understanding of a genotype or hybrid. The location effect, seasonal fluctuations and their interaction highly had its influence in the performance of genotypes with its yield potential (Becker, 1981). Among different biometrical techniques are used to assess the $G \times E$ interactions, the model like linear regression is not adequate in treating the complex data of yield trials effectively (Zobel *et. al.*, 1988).

Therefore, the multivariate analyses *viz.*, AMMI and GGE models were powerful tools in assessing $G \times E$ interaction, stability and adaptability in multi environments. AMMI is hybrid model involving both additive and multiplicative effects had been applied for the data. They have substantial ability to partition a signal-rich model from a noise-rich discarded residual, thereby gaining accuracy (Gauch, 1988). The fundamental reason AMMI is appropriate for agricultural research is that the ANOVA part of AMMI can separate the genotype and environment main effects and the $G \times E$ interaction effects that present researchers with such vastly different problems and opportunities (Gauch *et. al.*, 2008). One of the greatest advantages of these models have ability to extract interaction PCA axes along which there is a maximum variation, thereby indicating the number of components necessary to explain the pattern in the interaction residual (Girma, 1999). AMMI offers better opportunities for graphically displaying of mega-environments and adaptive responses thereby identifying superior and stable varieties. In AMMI GGE biplot, if a genotype or an environment has a PCAI score around zero it has small interaction effect and are considered as stable variety over a wide range of environments. However, genotypes with high mean and high PCAI score are considered as having specific adaptability to the environments and shows maximum interaction between genotype and environment. The GGE biplot also view the discriminating and representativeness ability of environments to identify an environment that efficiently discernment the superior genotype in the tested environments. A long environmental

vector/spokes from origin showed a high capacity to discriminate genotype (Yan and Tinker, 2006).

Hence, the present investigation aims to collect the information on genetic variability, diversity and stability analysis in Niger. Keeping all the above-mentioned points in view, the present investigation was under taken using forty genotypes of Niger which are collected from all over the Maharashtra with following objectives,

1. To study the nature and extent of genetic variability in yield and yield contributing traits,
2. To measure the divergence between different genotypes by D^2 statistics,
3. To study the stability of Niger genotypes under different environments, and
4. To study the G x E interaction for yield and yield contributing traits.

CHAPTER II

REVIEW OF LITERATURE

The present investigation was undertaken to study the "**Genetic variability, diversity and stability study in Niger (*Guizotia abyssinica* L.)**." The biometrical studies so far carried out in India are mainly restricted to major oilseeds. Niger is categorised under the minor oilseeds. The literature on Niger is very scanty. The literature is available on genetic variability, diversity and stability in Niger is reviewed here. Some of the relevant evidences referred from other oilseed crops have also been quoted here section-wise.

2.1 Genetic Variability

2.2 Genetic Diversity

2.3 Stability Analysis and G x E Interaction

2.1. Genetic Variability

Nema and Singh (1965) reported 30.49 and 95.52 per cent heritability for earliness and grain yield, respectively. Branching, number of capitula plant⁻¹, number of seeds capitulum⁻¹ had moderate heritability. Phenotypic selection for head diameter, 1000 seed weight and oil content were found to be useful because of higher heritability values.

Bagari (1973) noticed the sufficient genetic variability for various studied characters except number of seeds capitulum⁻¹. Genotypic coefficient of variation was highest for number of branches plant⁻¹ while oil content had minimum genotypic coefficient of variation.

Nayakar (1976) observed high heritability for number of primary branches per plant, number of capitula plant⁻¹, 1000 seed weight and low heritability for yield plant⁻¹ in eighteen genotypes of Niger.

Adhanom (1985) reported good amount of genetic variability in Niger for all the 12 traits studied. He found a wide range of variation for the different plant characters *viz.*, days 50 per cent flowering, number of branches plant⁻¹, plant height and number of capitula plant⁻¹.

Goyal and Sudhir (1985) revealed a wide range of variation for all characters except for number of branches plant⁻¹ and seeds capitulum⁻¹ in thirty-

five indigenous genotypes of Niger. Heritability estimated moderately to high and genotypic coefficient of variation was equal to phenotypic coefficient of variation in most of the traits.

Channarayappa (1987) noticed the phenotypic variability was high for seed yield plot⁻¹, number of capitula plant⁻¹ and plant height and low for 1000 seed weight; whereas moderate for number of seeds capitulum⁻¹ and seed yield plant⁻¹. The genotypic coefficients of variation were high for seed plot⁻¹, number of capitula plant⁻¹ and plant height. Heritability and genetic advance over per cent of mean were high for plant height but oil content had moderate heritability with low genetic advance. Other characters had moderate heritability with high genetic advance.

Bilaiya (1987) observed high genetic variability for number of capitula plant⁻¹, number of seeds capitulum⁻¹, number of branches plant⁻¹ and at phenotypic level, days to maturity exhibited very low genetic variability. High heritability associated with high genetic advance were observed for number of capitula plant⁻¹, number of seeds plant⁻¹ and number of seeds capitulum⁻¹, however, days to 50 per cent flowering, days to maturity and oil content exhibited high heritability coupled with low genetic advance.

Payasi *et al.* (1987) studied 28 genotypes of Niger of five diverse Indian groups and reported high genotypic and phenotypic variation for 1000 seed weight and number of capitula plant⁻¹.

Abraham and Gupta (1989) observed high heritability for days to 50 per cent flowering, days to maturity and number of capitula plant⁻¹ and suggested use of these traits in selection for improving seed yield.

Mathur and Gupta (1993) reported high heritability and high genetic advance for grain yield plant⁻¹ and harvest index, suggesting the predominance of additive gene effects, while days to 50 per cent flowering, number of primary branches plant⁻¹, capitula plant⁻¹ and number of seeds capitulum⁻¹ exhibited moderate to high heritability and moderate genetic advance. Other traits showed low to high heritability but very low genetic gain indicating predominance of non-additive gene action.

Patel *et al.* (1993) reported high heritability along with high genetic advance for number of branches plant⁻¹ and 1000 seed weight indicating that predominance of additive gene action. Selection of these characters more effective for further hybridization programme.

Mishra (1995) evaluated ten genotypes of Niger for variability and observed greater variability for days to 50 per cent flowering, days to maturity, plant height, number of branches plant⁻¹ and number of seeds capitulum⁻¹ and reported low heritability for primary branches plant⁻¹, moderate for seed yield plant⁻¹ and high heritability for remaining characters studied.

Pradhan *et al.* (1995) studied seventeen promising local collection of Orissa and two national varieties. Highly significant differences were observed among the genotypes for all the characters except number of capitula plant⁻¹. High genotypic and phenotypic coefficient of variations for total number of seeds capitulum⁻¹ and moderately high values of genetic variability for yield indicates good amount of variability for these characters. Low heritability coupled with low genetic advance for number of branches plant⁻¹ and number of capitula plant⁻¹ indicates that selection for these characters would not be effective owing to greater environmental influence on the traits. The high heritability and moderate genetic advance for seed yield plant⁻¹ and 1000 seed weight showed the presence of both additive and non-additive gene action. High heritability coupled with high genetic advance for days to 50 per cent flowering, plant height and number of seeds capitulum⁻¹ suggested the role of additive gene action for these characters.

Borole and Patil (1997) reported maximum GCV for primary branches plant⁻¹ followed by number of capitula plant⁻¹. The difference between GCV and PCV were very low for all characters indicate that these characters governed due to genetic factors. The presence of high genetic variability is an indication of good scope for selection. High heritability coupled with high GA was observed for primary branches plant⁻¹ and number of seeds capitulum⁻¹, indicating predominance of additive gene action for these characters. High heritability coupled with low genetic advance was observed for days to 50 per cent flowering

and days to maturity, suggesting predominance of non-additive gene action. Low to moderate heritability coupled with low GA was observed for other traits indicating environment role in their expression.

Patil (1999) studied genotypic and phenotypic variability for fifteen genotypes of Niger. Significant variation was observed for the characters *viz*, number of capitula plant⁻¹, plant height and germination percentage. The 1000 seed weight showed maximum PCV and GCV. High heritability coupled with high genetic advance was noticed for the character number of capitula plant⁻¹, indicating the predominance of additive gene action.

Patil (2000) evaluated thirty genotypes of Niger (*Guizotia abyssinica*), significant positive genetic variability was observed for seven characters. Heritability estimate was low for primary branches plant⁻¹ and high for the remaining other characters. High heritability, along with high genetic advance was observed for number of capitula plant⁻¹ and plant height, indicating the predominance of additive gene action.

Kenjale *et al.* (2003) studied fifty genotypes of Niger, substantial genetic variability was observed for seven characters studied. Heritability estimate was high for all characters. The highest heritability observed for seed yield plant⁻¹.

Mehta *et al.* (2003) observed selection for number of branches plant⁻¹ and capitula plant⁻¹ is likely to increase the yield of Niger plant. But genetic variability and genetic advance for these characters low. Thus, more genetic variability for these characters created and selection should be based on these characters to improve yield. Therefore, the first cycle of selection should be based on number of seeds capitulum⁻¹ and thereafter more genetic variability for number of branches plant⁻¹ and number of capitula plant⁻¹ needs to be created for second cycle selection.

Ahmad *et al.* (2003) assessed forty-five genotypes of Niger for genetic association, heritability and genetic advance. The estimated broad sense heritability was greater for most of the characters except number of primary and secondary branches plant⁻¹. This may be due to the presence of greater genotypic variance. Moderate heritability was observed for plant height. Out of ten

characters maximum genetic gain was observed for number of seeds capitulum⁻¹ followed by plant height and least for capitula diameter. The moderate genetic gain was found for number of capitulum plant⁻¹, days to 50 per cent flowering and days to maturity.

Sreedhar (2003) reported maximum PCV and GCV for seed yield plant⁻¹, number of capitula plant⁻¹ and number of seeds capitulum⁻¹ had higher magnitude of difference between PCV and GCV value of number of capitulum plant⁻¹ was observed. High heritability coupled with high genetic advance was found for traits, seed yield plant⁻¹, number of capitula plant⁻¹, plant height and number of seeds capitulum⁻¹.

Patil and Duhoon (2005) studied 105 genotypes and noticed substantial variability for all characters studied. PCV was more or less equal to GCV. High to moderate heritability estimates were observed for all characters, except plant height. No linear relationship among GCV, heritability and genetic advance was noticed but seed yield plant⁻¹ and number of capitula plant⁻¹ were found to have high GCV along with high GA, suggesting predominant role of additive gene action. High heritability coupled with low GA was observed for days to 50 per cent flowering, days to maturity, number of seeds capitulum⁻¹, indicating non-additive gene action for these traits. A low heritability with low GA was observed for plant height, suggesting that environment had a major role in their expression.

Rani *et al.* (2010) reported high genotypic coefficient of variation for seed yield per plant (28.21), moderate variability in days to 50 per cent flowering (10.59) and plant height (11.79) was observed among the germplasm studied. Plant height expressed high heritability (95.4) coupled with high expected genetic advance (22.8) and days to 50 per cent flowering exhibited high heritability (95.7) with moderate expected genetic advance (10.8) indicating additive gene action for these characters may be useful in future population improvement of Niger.

Panda and Sial (2012) studied genotypic and phenotypic variability in eighteen Niger genotypes. Significant population differences existed among the genotypes for all the characters studied except number of branches plant⁻¹. High value of phenotypic coefficient of variability (PCV), genotypic coefficient of

variability (GCV), heritability and genetic advance as per cent of mean values indicated scope for improvement in days to 50 per cent flowering, plant height, number of capitula plant⁻¹ and number of seeds capitulum⁻¹. For maximizing the seed yield plant⁻¹ emphasis should be given in selection of characters such as days to 50 per cent flowering, plant height, number of capitula plant⁻¹, number of seeds capitulum⁻¹ and 1000 seed weight for future crop improvement.

Sangita *et al.* (2012) assessed 35 accessions of Niger for 1000 seed weight and oil quality parameters. High heritability (>90%) was recorded for all the oil parameters except for linoleic acid and 1000 seed weight.

Yadav *et al.* (2012) studied genotypic and phenotypic variability among 35 accessions of Niger (*Guizotia abyssinica* L.). Analysis of variance showed significant differences for 1000 seed weight and oil parameters. Most of the characters were found to have high GCV along with high GA, suggesting predominant role of additive gene action.

Ahmad *et al.* (2016) revealed the significant difference among the genotypes for all the traits. They observed the presence of sufficient variability among the genotypes for various traits under study. High estimate of genotypic and phenotypic coefficient of variation were observed for seed yield plant⁻¹, number of capitula plant⁻¹, primary branches plant⁻¹ and number of seeds capitulum⁻¹ indicated wider genetic variation for these traits. High value of heritability coupled with high expected genetic advance as per cent of mean were observed for the characters *viz.*, 1000 seed weight, number of capitulum plant⁻¹ and number of seeds capitulum⁻¹ indicated that selection may be effective for these characters. For maximizing the grain yield plant⁻¹ emphasis should be given in selection of characters such as number of branches plant⁻¹, number of capitula plant⁻¹, number of seeds capitulum⁻¹ and 1000 seed weight for future improvement of Niger crop.

Benelli *et al.* (2017) studied genotypic and phenotypic variability among 14 accessions of Niger. They observed significant positive GCV and PCV for the traits *viz.*, seed yield plant⁻¹, number of primary branches plant⁻¹, number of capitula plant⁻¹, number of seeds capitulum⁻¹ and plant height.

Dudhe *et al.* (2017) evaluated 32 sunflower germplasm accessions including three checks at three semi-arid dryland locations of Telangana and Maharashtra states. The magnitude of phenotypic coefficient of variation (PCV) values for all the traits were higher than the corresponding genotypic coefficient of variation (GCV) values indicating that all seven traits are under the influence of environmental effect. High heritability associated with high genetic advance as percent of mean were recorded for plant height, indicating less environmental influence on plant height and role of additive gene action.

Kusumlata *et al.* (2018) studied 53 genotypes/varieties of Niger during *Kharif*, 2017. The mean sum of square due to genotypes were highly significant for all the characters. High genotypic coefficient of variation and phenotypic coefficient of variation were observed for capitulum plant⁻¹ and seed yield plant⁻¹ (g). The high heritability was recorded for the trait days to maturity followed by days to 50 per cent flowering and oil content (%), plant height (cm), capitulum plant⁻¹, seed yield plant⁻¹ (g) seed capitulum⁻¹ and primary branches plant⁻¹. Genetic advance a percentage of mean recorded high for capitulum plant⁻¹, seed yield plant⁻¹ (g), seeds capitulum⁻¹, oil content (%), primary branches plant⁻¹ and plant height (cm).

Suryanarayana *et al.* (2018a) revealed the genetic variability parameters of twenty-eight Niger genotypes during *khariif*, 2011. Results were observed high estimates of genotypic coefficient of variation for grain yield and phenotypic coefficient of variation for number of capsules plant⁻¹. High heritability coupled with high genetic advance was observed for number of capsules plant⁻¹, number of seeds capsule⁻¹ and grain yield (q/ha) suggesting that they can be improved through direct selection due to predominant additive variation.

Fekadu (2020) carried out experiment to assess genetic variability. The results of combined analysis indicated that date of 50% flowering, date of 50% maturity, oil content and 1000 seed weight of studied traits of genotypes for yield and its related component traits were significantly different respectively. They revealed that there was a considerable magnitude of variability among the different genotypes for all the traits except for seed yield plot⁻¹, plant height and

oil yield. In genetic variability, Heritability, genetic advance genetic advance as per cent mean analysis seed yield plot⁻¹ (11388.054, 5574.22485), oil yield plot⁻¹ (1889.897, 898.38763), plant height (151.592, 0.062) showed high phenotypic and genotypic variances, respectively indicating that the genotypes could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these traits. The seed yield plot⁻¹ (48.948%), oil yield (47.536kg/ha) and oil percent (41.558%), exhibited high heritability estimates.

2.2 Genetic Diversity

Mahalanobis (1936b) described the concept of D² statistics as quantitative tool for estimating genetic divergence between the populations. Genetic divergence is the result of changes in the frequency of different population due to evolutionary forces.

Chatterjee (1983) observed the genetic diversity was not necessarily related to geographic distribution. He suggested that crossing programme involving distantly related cluster for seed yield improvement in Niger.

Sohan (1987) grouped 161 germplasm in 32 clusters irrespective of their origin. Geographic diversity though important but not solely responsible for genetic diversity. While selecting genotypes for hybridization from a particular cluster, the inter-cluster distance, cluster mean and *per se* performance should be considered.

Mehta (1989) studied genetic variability and diversity among forty genotypes of niger for eleven character *viz.*, days to 50 percent flowering, days to maturity, plant height, number of capitula plant⁻¹, number of seeds capitulum⁻¹, 1000 seed weight and seed yield plant⁻¹. The genotypes on the basis of D² estimate were grouped into seven clusters. Out of which four clusters were solitary.

Chatterjee and Khare (1991) evaluated 30 Niger genotypes from 5 Indian states for 11 yield and yield contributing traits for genetic divergence. Genotypes were grouped into 8 clusters on the basis of minimum generalized distance, using D² statistics. Clusters III and I contained genotypes with the highest seed yield plant⁻¹, with higher values for III due to longer growth period. An ideal genotype

would have an optimum growth period and more effective primary branches plant⁻¹ and number of capitula plant⁻¹.

Jagadev and Samal (1991) assessed the genetic diversity in fifteen cultivars of Niger using D² statistic for six developmental characters. Accordingly, fifteen genotypes of Niger grouped into seven clusters. Cluster II was largest with four cultivars, followed by cluster I with three cultivars and clusters III and V with two cultivars and cluster VI and VII with single cultivar each. Cluster II showed maximum distance from Cluster V, suggesting wider diversity between these groups. They observed maximum divergence was due to the days to 50 per cent flowering followed by days to maturity, 1000 seed weight and seed yield plant⁻¹. Four clusters consisting of nine cultivars have been judged as important for varietal improvement programme on the basis of their inter cluster distance and higher characters mean values for the aforesaid four characters. The magnitude of heterosis largely depends on the degree of genetic diversity in parental line. So, genotypes belonging to the distant cluster could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants. The highest contributors towards the divergence were days to 50 per cent flowering, days to maturity, 1000 seed weight and seed yield plant⁻¹; whereas the least contributor number of capitula plant⁻¹.

Biswas *et al.* (1993) studied genetic divergence in seventeen genotypes of Niger (*Guizotia abyssinica* (L. f.) Cass) using D² statistics for seven developmental characters. The genotypes were grouped into five clusters. The inter-group distance was much larger than the intra-group distance. Cluster III showed maximum genetic distance from cluster IV. Genotypes belonging to the cluster III, IV and V might be included in future hybridization programme for getting desirable segregants. The main characters contributing to the divergence were days to maturity, plant height, number of capitula plant⁻¹ and seed yield plant⁻¹.

Ravanappa (1994) evaluated 64 genotypes of Niger and these genotypes were grouped into 7 clusters based on D² analysis of 10 yield contributing traits. Information is tabulated on intra and inter-cluster D² values. The characters number of capitula plant⁻¹, 1000 seed weight, oil content and seed yield plant⁻¹

were most contributing to total divergence. The genotype cluster five recorded the highest cluster mean values for most of the economic character. Contribution of each character to the total divergence was estimated from the number of time that each character appeared in first rank, the highest contributor towards divergence was number of capitula plant⁻¹ (49.16%) followed by 1000 seed weight (23.06%), oil content (6.70) and seed yield plant⁻¹ (6.65%); while number of primary branches plant⁻¹ least contributor to the divergence.

Sohan and Kerketta (1998) studied 162 genotypes of Niger for nine quantitative traits. D² analysis used to rank characters and their contribution towards genetic divergence. The highest contribution towards divergence and rank total was expressed by 1000 seed weight followed by days to maturity. Ten genotypes expressing variation with respect to these two traits are identified for possible use as parent in hybrid crosses.

Kumar (1999) evaluated 25 germplasm lines for variability, association and genetic divergence. The studied genotypes were grouped into eight clusters of germplasm lines irrespective of their origin. Many genotypes based on cluster means and genetic diversity was identified as potential parents. Genotypes BNS-5, GA-23, Phule-5, and ONS-107 of cluster II and BNS-9, RCR-219 and RCR-234 of cluster VI were suggested as potential parents for crossing programme. Hybridization between genotypes of cluster II and VI was suggested for seed yield improvement. Days to maturity contributed more than 50 per cent flowering in genetic divergence, but the plant height and thousand seed weight also had recommendable role in genetic diversity.

Sreedhar *et al.* (2006) assessed 100 accessions of Niger for nature of genetic diversity by using D² statistics for ten characters. Plant height, days to 50 per cent flowering and days to maturity were observed to the major contributors to the genetic divergence. Grouping of genotypes in the clusters using Tocher's method resulted formation of seven clusters. Maximum intra-cluster distance was shown by cluster IV while cluster I and II showed highest inter-cluster distance.

Patil (2007) studied genetic divergence among sixty-seven genotypes of Niger (*Guizotia abyssinica* L.), the multivariate analysis of divergence was carried

out using Mahalanobis D^2 statistics. The analysis revealed significant differences among genotypes for all characters studied. These genotypes were grouped into fifteen clusters. Cluster - V was the largest containing twenty genotypes followed by cluster - I with eleven genotypes, clusters - II and IV with nine genotypes each and cluster - III with six genotypes. The remaining clusters *viz.*, cluster - VI to XV had only one or two genotypes. The clustering pattern indicated the absence of relationship between genetic diversity and geographical origin of genotypes. Number of seeds capitula⁻¹ contributed maximum divergence of 31.57% followed by seed yield plant⁻¹ (20.27%), days to maturity (20.05%) and capitula plant⁻¹ (14.50%).

Parmeshwarappa *et al.* (2009) grouped the fifty-two genotypes into seven clusters based on D^2 statistics. Inter cluster distance ranged from 54.01 to 187.36. The intra cluster distance showed range from (solitary cluster) to 35.82. The traits plant height, days to 50 per cent flowering and days to maturity contributed maximum to the total genetic divergence. Seed yield plant⁻¹ and harvest index made negligible contribution.

Parameshwarappa *et al.* (2011) grouped thirty-seven genotypes of Niger into seven cluster indicating wider genetic diversity in the germplasm of Niger. Out of seven cluster II was the largest with 28 genotypes, followed by cluster I with 18 genotypes. The maximum inter-cluster distance was observed between cluster I and V while lowest distance observed between cluster II and VI. Among seven characters studied seed yield plant⁻¹ contributed highest towards genetic divergence (71.17%) followed by number of capitula plant⁻¹ (27.03%), plant height (1.05%), number of branches plant⁻¹ and number of seeds capitulum⁻¹ (0.30%). Cluster IV exhibited highest mean for seed yield plant⁻¹ and number of seeds capitulum⁻¹. Cluster IV exhibited lowest mean for days to 50 per cent flowering, days to maturity and plant height. Cluster V exhibited highest mean for number of capitula plant⁻¹, seed yield plant⁻¹, days to maturity and plant height. The genotypes from cluster IV and V which have high cluster means for the majority characters should be utilized for hybridization programme to achieve novel recombinants.

Sangita *et al.* (2012) assessed 35 accessions of niger for 1000 seed weight and oil quality parameters. Analysis of variance showed significant differences for 1000 seed weight and oil parameters. Total oil content ranged from 35.16% to 40.47%. The oleic acid ranged from 23.52 to 53.3% of the total fatty acids while linoleic acid ranged from 32.03 to 58.28%. Cluster I included three accessions with highest linoleic acid (>53%), highest stearic acid (>8%), highest palmitic acid (>9%) and least oleic acid (<29%). The cluster III included 30 accessions and was divided into two sub-cluster *i.e.*, IIIA; with low linoleic acid (<43%) and high oleic acid (>40%); and IIIB; with high linoleic acid (>44%) and low oleic acid (<37%). Hybridization between accessions of different clusters will result in creation of wide spectrum of variability in subsequent segregating generations for future use in breeding programmes.

Goyal and Bisen (2017) found highly significant differences among the genotypes tested for all the traits. Cluster analysis revealed wide range of diversity in the genotypes grouped in eleven clusters. Out of eleven, Cluster II was the largest among all clusters followed by cluster I, cluster IX, cluster X, cluster VII, cluster XI and cluster IV. Cluster III, V, VI and VIII were monotypic. The highest intra cluster distance was recorded by cluster X followed by cluster IX, cluster XI, cluster IV, cluster VII, cluster II and Cluster I. The highest inter cluster distance was observed between the clusters VII and XI followed by clusters IV and XI and clusters VI and VII. The characters like seed yield plant⁻¹, 1000 seed weight and number of capitula plant⁻¹ exhibited major contribution towards the genetic divergence. On the basis of inter and intra-cluster distance coupled with cluster means of different traits, the genotypes classified in clusters IX, IV, XI, VII, II, VI and V were found to be superior and may be utilized in breeding programmes.

Misganaw and Abera (2017) studied 65 Ethiopian Niger accessions collected from diversified eco-geographic regions. The accessions were grouped into three major and six sub clusters, showing the wealth of genetic diversity for exploitation in future breeding programs.

Naik *et al.* (2018) grouped the sixty-one sunflower multi-head inbred lines into 7 clusters, among which the cluster I with 52 genotypes was the largest followed by cluster II with 4 genotypes. Maximum inter cluster distance was recorded between cluster II and VII (740.36) followed by clusters I and VII (426.99). Hence hybridizing between these divergent groups may lead to higher variation in segregating population. Among 7 clusters, IC-597575, EC-601938, EC-640337, IC-438395 and SS-2038 were most divergent lines compared to other and crosses may be affected among the genotypes of these clusters to get more heterosis among the hybrids. The study revealed that the characters *viz.*, plant height (cm), oil content (%), number of branches plant⁻¹ contributed more to the total genetic divergence in the genotypes.

Ram *et al.* (2018) evaluated thirty-two sunflower genotypes including two checks to study genetic divergence. The thirty-two genotypes were grouped into six cluster using Tocher method. The genotypes in cluster III and cluster IV, due to maximum inter cluster distance, exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization programme (transgressive breeding) for getting high yielding recombinants. Similar inter varietal crosses may be attempted in cluster V and cluster VI and cluster III and cluster V. On the basis of cluster mean values, the genotypes present in cluster VI was found early in terms of days to fifty per cent flowering and having highest volume weight and oil content. Genotypes present in cluster V have maximum harvest index and 1000 seed weight. Genotypes which are present in cluster III may be selected for minimum plant height and maximum biological yield while the genotypes present in cluster II was suitable for early in days to maturity. Based on cluster mean values for a given characters we can select highly divergent genotypes from the respective clusters and can be used in hybridization work.

Suryanarayana *et al.* (2018b) assessed 28 Niger genotypes by using Mahalanobis D² statistics for 7 characters. The genotypes were grouped into nine clusters. Cluster I was the largest with 14 genotypes followed by cluster II, III, IV, V, VI, VII with two genotypes in each cluster and cluster VIII and IX are solitary with single genotype in each cluster. The highest inter cluster distance was

observed between cluster VIII and cluster IX followed by cluster VI and VIII suggesting more variability in genetic makeup of the genotypes included in these clusters. Cluster VIII had highest mean values for plant height, number of branches plant⁻¹, number of capsules plant⁻¹, number of seeds capsule⁻¹ and grain yield ha⁻¹. Whereas, cluster IX had high mean value for days to 50 per cent flowering and low mean value for grain yield ha⁻¹. Cluster IV had highest value for days to maturity. The grain yield ha⁻¹ has contributed more towards the genetic divergence followed by number of capsules plant⁻¹.

Suryanarayana *et al.* (2019) estimated the genetic divergence of 30 genotypes by using D² statistics. The genotypes were grouped into seven clusters based on D² values for 7 characteristics indicating the presence of large amount of diversity among the genotypes. Maximum number of genotypes were grouped in cluster I (12) followed by cluster III (9), cluster IV (3), cluster V & cluster II with 2 genotypes in each cluster, whereas cluster VI and VII are solitary with single genotype in each cluster. The intra cluster distance ranged from 0.00 to 52.45. The highest intra cluster distance was observed for cluster III (52.45) followed by cluster IV (37.70), cluster I (27.20), cluster V (24.68), cluster II (3.22), cluster VI and cluster VII (0.0). The inter cluster D² values ranged from 17.11 to 200.17. The maximum inter cluster distance (200.17) was noticed between cluster VI and VII followed by cluster V and VI (167.08). Since the clusters VI and VII had a single genotype with maximum inter cluster distance indicated that the genotypes included in these clusters will give high heterotic response and better segregants.

2.3 Stability Analysis and G x E Interaction

Patil and Purkar (2000) studied the phenotypic stability of eight genotypes of Niger grown over seven locations in Maharashtra State for seed yield and five yield attributes. The variances due to genotypes, environments, G x E interaction, environment + (G x E) and environment linear were significant. On partitioning of G x E Interaction, both components were significant; however, linear component was larger in magnitude indicating its significance in the inheritance of studied traits. In the individual parameter of stability, it was observed that the genotype IGP-76 was found most responsive and stable for all

characters studied. The genotype Phule-4 was found stable for seed yield plant⁻¹ and number of capitula plant⁻¹, whereas, UN-4 observed below average stability for 1000 seed weight and number of seeds capitulum⁻¹.

Salah *et al.* (2008) observed highly significant differences of combined analysis of variance due to genotype for all characters. The genotype $\times$ season interaction was only significant for 1000 seed weight and seed yield ha⁻¹. The genotype $\times$ environment interaction was significant for 1000 seed weight, seed yield plant⁻¹ and seed yield ha⁻¹. The number of seeds head⁻¹ showed non-significant differences at the first and second order interactions. The highest yield hectare⁻¹ and plant⁻¹ averaged over the four environments was recorded for Hysun 33. The analysis of genotype $\times$ environment interaction for 1000 seed weight, seed yield plant⁻¹ and seed yield ha⁻¹ showed that the major part of the variance was due to non-linear components. The significant differences among the evaluated hybrids at the different interaction levels suggest that seed yield of sunflower is highly dependent upon the environmental conditions. Therefore, multilocation testing for several years is needed to identify high yielding stable hybrids.

Igor *et al.* (2010) assessed the effects of hybrids and planting dates as well as their interaction on oil yield in sunflower for three-year experiment. Oil yield was predominantly influenced by the year of growing (58.9%), then by planting date (12.9%) and by hybrid (10.7%). All interactions were significant. AMMI ANOVA showed high significance of both IPC1 and IPC2. The contribution of IPC1 was 77.5%. AMMI analysis of variance showed that both IPC axes (IPC1 and IPC2) were highly significant. The major part of variation belonged to IPC1 (77.5%). The hybrid, Miro showed the highest stability for oil yield. Hybrid Rimi, with the lowest mean value, was the most unstable for the examined character. Oil yield was higher in earlier than in later planting dates. Graphical presentation of AMMI1 in the form of biplot could facilitate the choice of stable hybrids and planting dates for desired characters in sunflower.

Marinkovic *et al.* (2011) tested stability performance of 25 new sunflower hybrid combinations for seed yield plant⁻¹ and oil content in seed by using AMMI

analysis compared against three standard hybrids in three locations. The tested combinations showed significant variations in seed yield plant⁻¹ (tons ha⁻¹) and oil content (%) from one location to another and within individual locations. Variations in seed yield plant⁻¹ were mostly due to the impact of location, while the variations in oil content were prevalently due to genotypic differences among the hybrids. The highest and lowest average total yields were obtained by the hybrids G20 and G1, respectively. The hybrids G17, G8, G2 and G21 showed the widest adaptability. Slightly narrower adaptability was exhibited by the hybrids G4, G7, G13, G14, etc. The hybrids G6, G16, G15 and G22 showed the narrowest adaptability, i.e., they were considerably affected by the analysed interactions. The highest and lowest average oil contents were recorded in the hybrids G23 and G28, respectively. The hybrids G7, G11 and G23 demonstrated the highest adaptability for oil content in seed. The lowest adaptability was demonstrated by the hybrids G1 and G16.

Tadesse and Abay (2011) reported combined analysis of variance for genotype, environment and their interaction (GEI) were significant ($p < 0.01$). Higher mean seed yield was obtained from genotype Col.sel.p#1 (629.7 kg ha⁻¹) followed by Acc-111-105 (599.7 kg ha⁻¹) and Acc-038-sel-1 (591.4 kg ha⁻¹). Based on high mean seed yield and ASV Col. Sel. p#1 and Acc-111-105 were the most stable genotypes. The significant G x E Interaction and the changes in the rank of genotypes across environments suggest for breeding strategy of specifically adapted genotypes in homogenously grouped environments and stable for wide adaptation. It is recommended that breeding should be carried out for specific adaptation based on selection in the target environments.

Hosseini (2012) assessed the G x E interaction and oil yield stability analysis of six sunflower cultivars in randomized complete block design with three replications. Several parametric and nonparametric stability analyses were investigated in this study regarding to mean yield, stability or both. They noticed both mean yield and stability parameters should be concerned in such analyses. They concluded none of the cultivars were stable for the all parameters under

investigation. Hybrids Hysun33 and Azargol with high mean oil yield were stable regarding to the measured parameters.

Milan *et al.* (2012) studied the performance of 25 new sunflower hybrids at three locations in Romania by using AMMI model. Seed yield plot⁻¹ was recorded on plants in middle rows to avoid edge effect. AMMI analysis showed that variations in seed yield were mostly due to main effects (74.07%), additive effects, genotype (32.45%) and environment (41.62%), but interaction effect (25.92%) was also not negligible. The largest part of the total variability that is explained by the first principal component (IPCA1), caused by the effect of genotype and eco-environment, was highly significant and makes 78.60% of the total interaction. The second principal component (IPCA2) which represents the rest of unexplained variance that remains after seclusion of the IPCA1 was also highly significant and made 21.40% of total interaction. The most productive hybrids with high yields and low values of interaction were NS-1, NS-2, NS-4, NS-5, NS-6, NS-9, NS-10, NS-11 and NS-16.

Igor *et al.* (2013) conducted the experiment on mega-environment analysis for the grain yield of 20 hybrids and 19 test locations during 2006, and 20 hybrids and 16 test locations during 2007 of sunflower. The analysis of variance components showed that hybrid by location interaction explained 2.74, 5.8, and 3.72 times more variation than hybrid for grain yield, for 2006, 2007 and combined data, respectively, and indicated potential mega-environment existence. Our results showed the existence of two mega-environments in Serbia sunflower growing region: (1) Kula Vitovnica, Aleksa Santic, Sombor and (2) Rimski Sancevi, Kikinda. They concluded that if they want promising sunflower hybrids to be optimally used, they should be cropped differently for the two determined mega-environments.

Muhammad *et al.* (2013) reported the variance due to GE interaction was highly significant for all the traits showing heritable variation among the genotypes. The linear component of G x E interaction was also significant for all traits except branches plant⁻¹. Pooled deviation was significant only for yield indicating the differential genotypic response across the locations. The significant

variance due to environment (linear) indicated that the performance of genotypes was under genetic control. The b-values of V-90005, T-89 and PARS-I was larger than unit regression; hence were suitable for favourable environments for yield. Whereas, V-III and Sanghar-1 were with b-values less than unity indicating their below average response. For branches plant⁻¹, Sanghar-1 and S-17 had regression coefficients less than one with negative sign making them suitable only for poor environment. Four genotypes had greater than unity and non-significant regression coefficients with high response towards better agronomic conditions and were stable due to low deviation from regression. Correlations of mean with b-value and S²d, for seed yield were highly significant and positive suggesting that average yield could be considered as a measure of response and stability.

Miroslav *et al.* (2013) observed seed yield, oil content and oil yield were significantly different at the tested locations and years. On average, for all investigated hybrids in seven environments, seed yield was recorded 3.30 tons ha⁻¹, oil content 47.48 % and oil yield 1.423 tons ha⁻¹. Significantly the highest seed and oil yield was achieved in an environment Os09 (4.220 and 1.831 tons ha⁻¹) and oil content in NG10 (50.59%). The highest grain yield, in seven environments, had a hybrid OS-H-4 (3.913 tons ha⁻¹). This hybrid had also the highest oil yield (1.721 tons ha⁻¹). The highest oil content in sunflower seed had a hybrid OS-H-1 (50.58%). By AMMI analysis of seed yield, oil content and oil yield, the first two IPCA components were significant at the 0.01 or 0.05 and explained 58.5, 73.7 and 60.5% of the total genotype x environment interaction. AMMI1 and AMMI2 biplots showed the hybrid with the largest seed and oil yield (OS-H-4), showed small interaction with the environment and had a great stability and hybrid that had the highest oil content (OS-H-1) had a great interaction with the environment and small stability. In addition, hybrids displayed a good stability for seed yield, oil content and oil yield. These hybrids had all three tested traits significantly better than the average of 7 environments.

Pourdad and Moghaddam (2013) found significant analysis of variance for the environmental variance compared to the genotype and GE interaction variances. The first two principal components (PC1 and PC2) together explained

68.2% of the total variability, so most of the information could be graphically displayed in the PC1 vs PC2 biplot. Polygon view of GGE biplot revealed that G3 was the inbred line with the highest seed yield in four out of six environments. The average environment coordinate (AEC) biplot showed that G3 with the highest mean yield was a highly stable inbred line as it was positioned close to the AEC abscissa. The second highest yielding and most stable inbred line was G10. The biplot of comparison of the sunflower inbred lines with the ideal genotype revealed that G3 was the closest inbred line to the ideal cultivar. Therefore, this inbred line seems to be widely adapted across several environments. According to the biplot of the ideal environment it was concluded that E1 was the closest to ideal environment and therefore the most desirable of all six environments. So, E1 is the most effective for the selection of superior inbred lines.

Abeya *et al.* (2014) observed the seed yields between 0.60 tons ha⁻¹ and 0.69 tons ha⁻¹ for Niger seed. Analysis of variance using additive main effects and multiplicative interactions (AMMI) model revealed significant differences ($p \leq 0.01$) for environment interaction for Niger seed. The percentage of variability due to IPCA1 and IPCA2 were 77.96% and 17.03% though IPC was not significant. Based on AMMI analysis, varieties, Shambu-1 and Esete-1 had comparable seed yield with moderately stable for the tested environments whereas Kuyu and local variety were unstable and not adopted to the testing environments. Additive main effects and multiplicative interaction (AMMI) model identified stable and adapted Niger seed varieties for specific and wide environments.

Patil *et al.* (2014) evaluated eleven elite genotypes of Niger over six seasons at Akola location of Vidrabha region at Maharashtra for seed yield, days to maturity, number of capsules per plant and number of branches per plant through six stability parameters. Genotype x environment interaction was found significant. On partitioning of it in to linear and nonlinear components, both were significant. However, linear component has its major share in inheritance of these characters; indicating that the prediction can be possible across the environment. With considering the individual adaptability parameter studied, the genotypes viz., JNS -10, IGPN 2005-10 and IGPN 2006-15 were found responsive and

adaptable for seed yield and the genotype JN-08-04 was found responsive and adaptable to specific favourable environment (below average stability). Whereas for remaining traits the genotype IGPN 2005-10 and PNS-6 were responsive and adaptable (average stability) to all traits.

Abate *et al.* (2015) reported combined analysis of variance highly significant ($P < 0.01$) difference between the varieties, environments and $G \times E$ interaction, suggesting differential response of varieties across testing environments and the need for stability analysis. Proportion of variance captured by environments were 1.43%, genotypes 91.5% and GEI 7.1% of the total variation, indicating less effect of environments on oil content as compared to the effect of genotypes. Stability analysis by AMMI and Joint-regression model were used to further shed light on the GEI of oil content. Two IPCA of AMMI were significant ($P < 0.01$) and captured the largest portion of variation of the total GEI, which indicated that the AMMI model was the best for the data set. The Joint regression analysis indicated that the linear regression (bi) did not deviate from unity for all varieties, suggesting that performance of the cultivars could not be predicted in a linear manner. The influence of environment is less prominent in the manifestation of oil content along the areas of Awash valleys. Season two is the best environment for growing the present set of genotypes for oil content. The variety, Adi was identified as the most stable variety across environments for oil content.

Mekonnen *et al.* (2015) observed highest seed yield from genotypes Acc. 00047, NN-0143 and Acc. 202-344 (712.8, 679.2 and 639.9 kg ha⁻¹), respectively. There was highly significant difference ($P < 0.01$) among genotypes, environments and genotype $\times$ environment interaction (GEI), indicating that genotypes performed differently across locations and the need for stability analysis. Based on stability models, genotype Borkena was stable genotype, but genotype Acc. 00047 had specific adaptability at potential environment (Kobo). In additive main effect and multiplicative interaction (AMMI) analysis, the proportion of variance captured by environment 51.2%, genotypes 12.9% and GEI 31.9% of the total variation. The interaction principal component axis 1 and 2 (IPCA1 and 2) of

AMMI model were highly significant ($P < 0.01$) and captured the largest portion of variation (74.7%) from the total GEL, indicated that the AMMI model 1 was the best for the data evaluated. AMMI 1 biplot graph showed that Shewarobit and Kobo were potential and favourable environments; Sirinka was an average, while Chefa and Jari were unfavourable environments and also Shewarobit and Chefa were the most discriminating environments, while local variety and genotype Acc.00047 were the most responsive genotypes.

Marisol *et al.* (2016) revealed the correlation between sunflower seed yield and oil content was positive in both groups (0.31 and 0.26). On the other hand, the correlation between sunflower seed yield and plant height was positive in the first group and negative in the second (0.27 and -0.10), the same occurred for the correlation between oil content and plant height (0.24 and -0.06). The best genotypes from group 2 according to high yield, acceptable height and adequate oil content and the best from group 1 on the basis of good oil content and reasonable yield and height would be G5, G18 (Group 2) and G13 (Group 1). In terms of specific environmental responses, G10 yields higher in environments like E1 and E7, while the reverse is true for G1 and G18. On the other hand, G13 has higher oil content in environments like E1 and E7.

Seyed *et al.* (2016) observed the considerable variation in seed yield. The results showed that the coefficient of variation for seed yield Nkarmoni and Brocar cultivars are biological stability and a high degree of flexibility. Terra, Vidoc and Alisson cultivars were stable respectively, according to the minimum variance Shukla, among varieties for seed yield. Based on the regression coefficient Fabiola and Arena cultivars were average yield stability and suitable adaptation. According to the graph AMMI1 of the function and stability Nkarmoni was higher than the other varieties. AMMI2 figures in the chart Euroflor, Alisson, Mas96a and Fabiola in Birjand place were identified yield stable part numbers and locations. GGE biplot method on seed yield was studied areas were divided into mega- environments, first mega- environments were included Isfahan and Sari places and second mega- environments were Birjand and Karaj places in terms of yield, Isfahan, Karaj and Birjand were varieties best.

Ali and Mohammadi (2017) assessed the adaptability and stability of twelve sunflower varieties in different climate conditions in randomized complete block designs with three replications. Analysis of additive main effects and multiplicative interaction effects revealed that the effect of environment and effect of genotype $\times$ environment interaction were significant and two first interaction principal components explained 84 per cent of the interaction sum squares. Biplot of first interaction principle and mean yield revealed that Progress genotype had adequate yield and lowest value for first principal component. Therefore, this genotype selected as a high yield and stable genotype; Record and Gabur genotypes were stable and high yield following Progress genotype. AMMI2 graph indicated that Progress, Master and Zargol in Arak and Karaj, Favorit, Record and Azargol in Shiraz, Gabur and SHF81-90 in Kashmar and Armaverski, Lakomka, Zaria and Sor in Birjand had specific adaptability. Among all genotypes, Zaria, Lakomka, SHF81-90, Gabur and Zargol had the highest general adaptability.

Bhavsar (2017) evaluated eight elite genotypes with two checks varieties of Niger for their yield performance over five locations. The sum of square due to genotypes and environment were significant, indicating presence of substantial genetic variability among the genotypes and seasons. The $G \times E$ interaction was observed significant. On partition of the same into linear and non-linear components both were found significant, suggesting their importance in the expression of seed yield in Niger. However, linear component was larger in magnitude, indicating that the prediction of performance across the environment is possible. This also confirm from overall ANOVA, where Linear is more than thrice over nonlinear. On examination of individual parameters, the genotypes IGPN 8007, IGPN 08-66 and Phule Karala were observed to be responsive and stable. Simultaneously the genotypes IGPN 8004 and IGPN 9001 was found to be suitable for poor environment conditions (below average stability). However, the genotypes IGPN 08-21, IGPN 08-26, IGPN 08-33 and IGP 76 suitable under rich environmental conditions (above average stability).

Boureima *et al.* (2017) evaluated ten sesame genotypes across locations and years for adaptability and stability. The seed yield of one environment ranged

from 722 kg ha⁻¹ to 1095 kg ha⁻¹ and seed yield of another environment ranged from 473 kg ha⁻¹ to 1414 kg ha⁻¹. The combined ANOVA for grain yield showed significant effects of the genotypes, environments and genotype x environment interaction. According to the genotype x environment interaction biplot (GGE biplot), genotypes 10 (SN403), 6 (SN-01-06) and 1 (38-1-7) were highly stable while the unstable genotype was 4 (HB168). The environment effect explained 81.09 % of the G+E+GE variation followed by the GEI (12.30 %) and the genotypes effects (6.60 %) Furthermore, the genotype main effects and GGE bi-plot showed Gou16 as the most discriminating and representative environment. The AMMI model analysis had partitioned the GEI into the first two significant interaction principal component axis (IPCA) with contributions of IPCA1 (29.27%) and IPCA2 (26.84 %) to GE sum of squares (SS). Together, they accounted for 56.11 % of GE interaction SS. The third IPCA explained 16.98 % of GE SS but this was not significant. Three different mega-environments (ME) were identified, the first ME containing Gou15, Haw15, Mai15 and Dad15 with DS01 as wining genotype; the second ME concern Mai16, Band16, Haw16, Band15 and Gou16 with GK01 as the best genotype and the third ME encompassing Dad16 with HB168 as wining genotype.

Baraki and Gebremariam (2018) determined the magnitude of Genotype x Environment Interaction (GEI). The highly significant ($p < 0.01$) oil content variation based on genotypes, environments and GEI resulting 26%, 42.7% and 30.9% of the total sum of squares for the oil content variation, respectively. The mean of the oil content was 53.9%, with genotypes G4 and G11 with the highest oil content (55.1%) each, and G8 with the lowest oil content (51.4%). G4 was the exceptional genotype with the highest oil content (55.1%) and oil yield (512.9 kg/ha). Based on the Environmental Index (EI) analysis, Environments, E4 and E5 were the favourable environments, while E1, E2 and E3 were unfavourable environments for oil production. According to the AMMI1 bi-plot, genotypes, G4, G13 and G10 with oil the content of 55.1%, 54.7% and 54.2% respectively, were stable genotypes. On the other hand, genotypes, G2, G8, G9, G3 and G1 were unstable genotypes in most of the environments. The AMMI2 bi-plot showed that,

genotypes, G2, G3 and G9, with long vector length, were specifically adaptable genotypes and genotypes, G10, G12, G4 and G7 with shorter vector length were widely adaptable in most of the environments for their oil content. Oil content varies highly both across years and locations.

Tadele *et. al.* (2018) revealed combined analysis of variance for mean grain yield was highly significant variation for year, environment, genotypes, and genotype by environment interaction. It revealed that 34.16% of the total variation was attributed to environment effect followed by genotypes 11.84%, and genotypes by environment interaction 2.97%. On the other hand, the AMMI analysis for the grain yield revealed that 69.75% of the variation was due to environment effect followed by Genotypes (24.18) and GE (6.07%). AMMI 1 component explained 61.64% of the total interaction sum squares whereas AMMI 2 accounted for 38.36% of the variation. Of the tested genotypes G5 and G11 showed consistent stability across the testing environments showing slop value close to unity and deviation from regression near to zero with high mean grain yield.

Baraki *et. al.* (2019) noticed significant effects in ANOVA of AMMI model for grain yield of the genotypes (37.3% sum of squares (SS)), environments (29.5% sum of squares) and Genotype x Environment interaction (25.9% SS). The AMMI model extracted five significant interaction principal component analysis (IPCA) with a total of 96.9% SS and 90.3% corresponding degrees of freedom. According to the total rank value (TR), G12, G11 and G4 were the furthestmost stable and widely adapted genotypes respectively, where as G8 and G9 were the furthestmost unstable genotypes. Grain yield was positively associated with all of the ranks of stability parameters at different significance levels. Grain yield (GY) had significant and positive correlations with YSI, Pi, S1 and CV. Regarding to the inter-parameter correlation coefficients, neither of the stability parameters were negatively correlated among each other. Environments E1, E2 and E4 were unfavourable environments; while E5, E6 and E7 were favourable environments and E3 was moderately favourable environment for most of the genotypes.

Abdelsatar *et. al.* (2020) found mean sum of squares due to environments, genotypes and their interaction were highly significant for seed yield and seed oil content. Most stability approaches revealed that high performing stable genotypes were L240 for seed yield and Sakha 53, L110 and L235 for seed oil content under divergent environments. Hence, these four stable genotypes could be behaved as good breeding materials stock for crop improvement.

Ansarifard *et. al.* (2020) revealed the analysis of variance due to the effect of location, year, location $\times$ year, genotype, and genotype $\times$ location was significant at 1% probability level. Results showed that the first and second principal components accounted 50.6% and 22.8%, respectively, and in total 73.4% of grain yield variance. The genotype, location, year, year $\times$ location, genotype $\times$ location, genotype $\times$ year, and genotype $\times$ year $\times$ location explained 2.75%, 17.36%, 5.47%, 17%, 10.8%, 1.04%, and 7.48% of total variance, respectively. they identified the top three genotypes and also three mega-environments. The genotype Zaria observed highest grain yield with high yield stability. Ranking the cultivars based on the ideal genotype introduced the genotype Zaria as the best genotype. The highest grain yield belonged to Zaria cultivar at 3.34 tons ha⁻¹ followed by Favorite with 3.23 tons ha⁻¹. Results obtained from ranking the environments based on the ideal environment introduced Kashmar and Birjand regions as the best environments. Examining the biplot figure for testing environments correlation confirms the positive correlation among Karaj, Birjand, and Kashmar. Correlation between Karaj with Arak, Karaj with Firooz-Abad, and Arak with Firooz-Abad was negative. Arak and Firooz-Abad were highly discriminating and representative and would be used to identification of superior genotypes.

Hosseini *et. al.* (2020) found significant differences in all sources of combined variance analysis. AMMI analysis of variance was divided into three parts, in which the interaction principal components IPC1 and IPC2 items justified about 85% of interactions. Also, IPC2 and residual were non-significant. They showed that the superior genotypes were G8 > G13 > G9 > G10 > G15 > G14 > G7. The labile locations were Karaj > Birjand > Arak > Shiraz. Furthermore, G4 > G8 >

G9 > G10 > G13 > G6 had the least GEI concerning IPC1 vs. grain yield (IPC1 vs. IPC2, respectively). They found genotypes for each region include G9, G2, G3 and G12 for Arak and Birjand; G7, G11 and G14 for Karaj; and G10, G8, G4 and G13 for Shiraz. According to the low environmental impact and the proximity of the IPC values of Shiraz, Arak and Birjand environments, Arak can be considered as the mega-environment for these three locations. The stable genotypes with higher general durability consisted of G4 > G6 > G1 > G2. Based on the AMMI stability value (ASV) and genotype selection index (GSI), Jirouf 13 (G4), Darab 14 (G8), Safi Abad 1 (G9), Ahwaz Local Cultivar (G10) and Isfahan Local Cultivar (G13) were superior genotypes about grain yield and GEI impact, and can be recommended for future investigations.

Chapter III

Materials and Methods

The present investigation entitled “**Genetic variability, diversity and stability study in Niger (*Guizotia abyssinica* L.)**” was undertaken during *kharif*, 2018 and *kharif*, 2019 to generate information on nature and magnitude of genetic variability, heritability, genetic advance, genetic advance per cent mean and gene action for yield and yield contributing traits. Also, to identify genetically diverse genotypes, G x E interaction and stable genotypes for yield and yield contributing traits. The details of material used, methods employed and statistical analysis followed, during the course of this investigation, are described below.

3.1. Planning of Research Programme

Experiment 1 (<i>Kharif</i> , 2018)	: Multi-location (Five) Research Trials
Experiment 2 (<i>Kharif</i> , 2019)	: Multi-location (Five) Research Trials

3.2. Experimental sites

The present investigation was carried out at the five locations *viz.*, Agriculture Research Station (ARS), Phondaghat (E1); Agriculture Research Station (ARS), Shirgaon (E2); Education and Research farm, Department of Agril. Botany, Dapoli (E3); Regional Agriculture Research Station (RARS), Karjat (E4) and Agriculture Research Station (ARS), Palghar (E5) during *kharif*, 2018 and *kharif*, 2019.

Geographically, ARS, Phondaghat (E1) is situated in the tropical region on the 16-22°35' North latitude and 73-47°18' East longitude having elevation of 145.10 meters above the mean sea level with warm and humid conditions throughout the year. The mean annual precipitation is 3500 mm. The soil of the experimental site is lateritic. ARS, Shirgaon (Ratnagiri) (E2) is situated in the western coast of India on the 17.45° North latitude and 73.62° East longitude having elevation of 75 meters above the mean sea level with humid conditions throughout the year. The mean annual precipitation is 3000 mm. The soil of the experimental site is lateritic. Education and Research farm, Department of Agril. Botany, Dapoli (E3) is situated in the western coast of India on the 17°45'32" North latitude and 73°11'8" East longitude having elevation of 243.84 meters above the

mean sea level with warm and humid conditions throughout the year. The mean annual precipitation is 4000 mm. The soil of the experimental site is lateritic. RARS, Karjat (E4) is situated in the tropical region on the 18°91" North latitude and 73°33" East longitude having elevation of 200 meters above the mean sea level with warm and humid conditions throughout the year. The mean annual precipitation is 3500 mm. The soil of the experimental site is medium black. ARS, Palghar (E5) is situated in the western coast of India on the 16.69° North latitude and 72.76° East longitude having elevation of 7 meters above the mean sea level with warm and humid conditions throughout the year. The mean annual precipitation is 2500 mm. The soil of the experimental site is medium black. The meteorological data during the period of experimentation was recorded at their meteorological observatory of respective research station. The details of the meteorological data is presented in Appendix I to X.

3.3. Experimental materials

The experimental material used for present study consists of forty genotypes of Niger (*Guizotia abyssinica* L.) which were collected from all over the Maharashtra state. The list of used genotypes for this investigation is given in the table 1.

3.4. Experimental details

The experiment was laid out in a Randomized Block Design with three replications. The experimental material consisting of forty genotypes of Niger were sown at 30 x 10 cm spacing with single seed per hill having plot size 3 x 2m. Spacing was maintained by cultural practices *viz.*, thinning and gap filling. Each genotype was represented by ten rows of 2m length in each replication. The timely application of FYM @ 12.5 tons and recommended fertilizers will be made @ 20 kg N₂O, 20 kg P₂O₅ and 10 kg K₂O and 15 kg sulphur hectare⁻¹. Entire quantity of all the fertilizers was applied at the time of sowing. Irrigation water was applied at planting to establish a good plant stand. Other cultural practices were carried out as per the recommendations.

Table 1: List of forty genotypes of Niger and their sources used in research programme.

Sr. No.	Genotype code	Name of Genotypes	Source	Sr. No.	Genotype code	Name of Genotypes	Source
1.	G1	GP-54	ZARS, Igatpuri	21.	G21	NMLT-12	ZARS, Igatpuri
2.	G2	GP-57	ZARS, Igatpuri	22.	G22	NMLT-13	ZARS, Igatpuri
3.	G3	IGPN 14-2	ZARS, Igatpuri	23.	G23	NMLT-14	ZARS, Igatpuri
4.	G4	IGPN 14-6	ZARS, Igatpuri	24.	G24	NMLT-15	ZARS, Igatpuri
5.	G5	IGPN 14-9	ZARS, Igatpuri	25.	G25	NGR -1	ARS, Shirgaon
6.	G6	IGPN 15-1	ZARS, Igatpuri	26.	G26	NGR -3	ARS, Shirgaon
7.	G7	IGPN 15-3	ZARS, Igatpuri	27.	G27	NGR -4	ARS, Shirgaon
8.	G8	IGPN 15-4	ZARS, Igatpuri	28.	G28	NGR -5	ARS, Shirgaon
9.	G9	IGPN 15-5	ZARS, Igatpuri	29.	G29	NGR -6	ARS, Shirgaon
10.	G10	NMLT-1	ZARS, Igatpuri	30.	G30	NGR -18	ARS, Shirgaon
11.	G11	NMLT-2	ZARS, Igatpuri	31.	G31	NGR -22	ARS, Shirgaon
12.	G12	NMLT-3	ZARS, Igatpuri	32.	G32	NGR -24	ARS, Shirgaon
13.	G13	NMLT-4	ZARS, Igatpuri	33.	G33	Devadi Local 2	Devadi, Solapur
14.	G14	NMLT-5	ZARS, Igatpuri	34.	G34	Devadi Local 3	Devadi, Solapur
15.	G15	NMLT-6	ZARS, Igatpuri	35.	G35	Devadi Local 4	Devadi, Solapur
16.	G16	NMLT-7	ZARS, Igatpuri	36.	G36	Devadi Local 5	Devadi, Solapur
17.	G17	NMLT-8	ZARS, Igatpuri	37.	G37	Modnimb Local 2	Modnimb, Solapur
18.	G18	NMLT-9	ZARS, Igatpuri	38.	G38	Sahyadri	ZARS, Igatpuri
19.	G19	NMLT-10	ZARS, Igatpuri	39.	G39	Phule Karala	ZARS, Igatpuri
20.	G20	NMLT-11	ZARS, Igatpuri	40.	G40	Phule Vaitrna	ZARS, Igatpuri

3.5. Observations recorded

The observations were recorded in each entry on five randomly selected competitive plants excluding border plants in each replication on following characters and averages were worked out for statistical analysis.

3.5.1. Days to 50 per cent flowering:

The days required from sowing to 50 per cent plants flowered in each genotype were recorded.

3.5.2. Days to maturity:

The days required for maturity of each genotype were recorded.

3.5.3. Plant height (cm):

The height of the plant from the ground surface to the tip was recorded in centimetre.

3.5.4. Number of primary branches plant⁻¹:

Total numbers of primary branches on the main stem were counted at maturity.

3.5.5. Number of secondary branches plant⁻¹:

Total numbers secondary of branches on the primary branches were counted at maturity.

3.5.6. Capitulum diameter (cm):

Diameter of capitulum was measured by using scale in centimetre.

3.5.7. Number of capitula plant⁻¹:

Total number of capitula of selected plants are counted and recorded.

3.5.8. Number of seeds capitulum⁻¹:

Total number of seeds are counted and recorded of capitulum of selected plants.

3.5.9. 1000 seed weight (g):

Determined from the average 1000 seeds at 12 per cent moisture content of the seed and expressed in grams.

3.5.10. Seed yield plant⁻¹ (g):

Dried plants were threshed separately and seeds obtained from them were weighted in grams.

3.5.11. Seed yield plot⁻¹ (g):

Dried all plants from whole plot were threshed separately and seeds obtained from them were weighted in grams.

3.5.12. Oil content (%):

Seeds from the five selected plants per genotype were bulked, out of these 100g of seeds per genotype were used for this analysis. Oil content was estimated on NMR facilities available at MPKV, Rahuri.

3.5.13. Protein content (%):

Seeds from the five selected plants per genotype were bulked, out of these 100g of seeds per genotype were used for this analysis. Protein content was estimated on NMR facilities available at MPKV, Rahuri.

3.6. Statistical analysis:

The data collected on genotypes of Niger with regards to the quantitative and qualitative characters of the five randomly selected plants in each genotype were averaged and the mean values obtained were subjected to statistical analysis of Randomized block design. Statistical analysis was carried out at Department of Agricultural Economics, College of Agriculture, Dapoli. The data for each trait was analysed by using standard statistical procedure (Panse and Sukhatme, 1985). Estimation of phenotypic and genotypic variances was calculated by using respective mean sum squares from variances table (Johnson *et al.*, 1955). Estimation of genetic parameter includes variance; coefficient of variance was done as per formula given by Burton and De Vane (1953). The analysis of divergence was carried out as per D^2 statistic of Mahalanobis (1936a) as described by Rao (1952). The mean data obtained for different observations was analysed by using AMMI Model (Gauch, 1992) with SAS programme.

3.6.1. Analysis of variance of genotypes:

Analysis of variance for all the characters under study was carried out as the formula given by Cochran and Cox (1957). For genetic variability and diversity analysis, first data was subjected to analysis of variance and for testing of significance of the genotypes and ANOVA was constructed.

Table 2: Analysis of variance of genotypes

Sr. No.	Sources of variation	D.F.	S.S.	M.S.S.	'F' value calculated
1	Replications	(r-1)	RSS	RSS/(r-1)	
2	Treatments	(t-1)	TrSS	TSS/(t-1)	
3	Error	(r-1) (t-1)	ESS	ESS/(r-1) (t-1)	

Where,

r = Number of replications

t = Number of treatments

The 'F' value is tested at error degrees of freedom of 5 per cent and 1 per cent level of significance.

As there is a significant difference between the treatments, the null hypothesis is rejected and further analysis is carried out.

3.6.2. Estimation of mean and range

Mean value of each character was worked out by dividing the total by corresponding number of observations.

$$\bar{X} = \frac{\sum Xi}{n}$$

Where,

$\bar{X}$ = Mean of observations

$\sum Xi$ = Sum of observations

n = Number of observations

Range: The lowest and highest values from the mean of each character were recorded as range.

$$\text{Coefficient of variation (C.V.)} = \frac{S.D.}{\bar{X}} \times 100$$

Where,

$$\text{Standard Deviation (S.D.)} = \sqrt{\frac{1}{n} \sum (X - \bar{X})^2}$$

3.6.3 Estimation of standard error of mean and standard error of difference

a) Standard error of mean:

$$SEm \pm = (\sigma^2 e / r)^{1/2}$$

b) Standard error of difference between two means was calculated as S.E. of difference of mean (SEd).

$$SEd = SEm \times \sqrt{2}$$

3.7. Estimation of genetic variability

3.7.1. Estimation of components of variation

The phenotypic ($\sigma^2 p$), genotypic ($\sigma^2 g$) variances and environmental ($\sigma^2 e$) were calculated as:

1. Genotypic variance

$$(\sigma^2 g) = \frac{GMS - EMS}{r}$$

2. Phenotypic variance

$$(\sigma^2_p) = (\sigma^2_g) + (\sigma^2_e)$$

3. Environmental variance

$$(\sigma^2_e) = \text{EMS}$$

Where,

GMS = Genotypic mean sum of squares

EMS = Error Mean squares

r = Number of replications

3.7.2. Estimation of coefficient of variation:

The genotypic and phenotypic coefficients of variation were calculated as per the formula given by Burton and De Vane (1953).

1. Genotypic coefficient of variation (GCV)

$$\text{GCV (\%)} = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$$

2. Phenotypic coefficient of variation (PCV)

$$\text{PCV (\%)} = \frac{\sqrt{\sigma^2_p}}{\bar{X}} \times 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

$\bar{X}$ = Mean of characters

3.7.3. Estimation of heritability

Heritability in broad sense estimated for various characters by using the formulae suggested by Lush (1949). It is estimated from total genetic variances.

$$H^2_b = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

Heritability in broad sense was estimated by method suggested by Robinson (1966) and Stansfield (1969), as given below.

Low	: 5 - 10 (%)
Moderate	: 10 - 30 (%)
High	: 30 - 60 (%)
Very high	: > 60 (%)

3.7.4. Estimation of genetic advance (GA)

Improvement in the mean genotypic value of selected plant over the parental population is known as genetic advance. The genetic variability is directly proportional to the genetic advance. The genetic advance is generally high with the characters having high heritability and vice versa. It is calculated in per cent by the formula suggested by Johnson *et al.* (1955).

1. Genetic advance

$$GA = \frac{\sigma^2_g}{\sigma^2_p} \times \sigma_p \times K$$

2. GA as per cent of mean

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where,

GA = Genetic advance

GAM = Genetic advance as per cent of mean

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

σ_p = Phenotypic standard deviation

K = Selection differential at 5% selection intensity

$\bar{X}$ = Mean of observations

3.7.5. Gene action

Heritability estimates along-with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. Estimates of heritability coupled with genetic advance give idea about the gene action involved in the expression of various polygenic traits (Robinson, 1966).

Sr. No.	Particular	Nature of gene action
1.	High heritability + High genetic advance	Additive
2.	High heritability + Low genetic advance	Non-additive
3.	Low heritability + High genetic advance	Additive
4.	Low heritability + Low genetic advance	Environmental effects

3.8. Estimation of genetic diversity:

The generalized distance between any two populations is defined as:

$$\Delta^2 = \sum \sum \lambda_{ij} \delta_i \delta_j$$

Where,

λ_{ij} is the reciprocal matrix other common dispersion matrix

σ^2 is the difference between the mean value of two populations from the j^{th} character.

The quantity is estimated by the D^2 statistics.

$$D^2 = \sum \sum \delta_{ij} \delta_i \delta_j$$

Where,

δ_{ij} is simple estimate of (λ_{ij}) and of the δ_i .

Since the formula for computation required the inversion of sixteen other determinants and then evaluation of $16(16-1)/2$ terms whose sum is D^2 transformation of the original correlated unstandardized character means to standardized uncorrelated variables was done.

3.8.1. Determination of group constellation

No rules can be laid down for finding the clusters, because a cluster is not well-defined term. The only criterion appeared to be that, any two groups belonging to the same, cluster should at least on the average showed a smaller D^2 value than those belonging to those of two different clusters. A simple device suggested by Tocher (Rao, 1952) was to start with two closely associated groups and find a third group which had smaller average D^2 value from first two. Similarly, the fourth was chosen to have smallest average D^2 value from first three and so on. If at any stage, the D^2 value of a group from those already listed, appeared to be higher than these groups did not fit with the former groups and was therefore taken to be outside the former cluster. The groups of the first cluster were then omitted and rest were treated similarly. It is also useful to calculate the change in average D^2 within cluster due to inclusion of an additional group. If the change was appreciable than the newly added group had to be considered as outside of cluster.

3.8.2. Average intra-cluster distance

Intra-cluster distance has to be calculated with the help of formula:

$$\Sigma D^2 i / n$$

Where,

ΣD^2 is the sum of distance between all possible combinations (n) of populations included in cluster.

3.8.3. Average inter-cluster distance

For computing the inter-cluster distance, the first step is to measure the distance between cluster I and II, between I and III and between I and IV and so on. Likewise, the clusters were taken one by one and the distance from the other clusters were calculated. The average inter-cluster distance was then calculated as

$$\Sigma D^2 i / (n_i n_j).$$

Where,

' n_i ' - number of populations in cluster i

' n_j ' - number of populations in cluster j.

3.8.4. Cluster diagram

With the help of D^2 values between the clusters, a diagram showing the relationship between different populations was drawn.

3.8.5. Cluster mean

The cluster mean for individual character was calculated on the basis of mean performance of the genotypes included in clusters.

3.9. Stability analysis and G x E Interaction:

The data collected for all the observations were analysed for all five environments. The pooled analysis was also carried out over environments for each character. Means of the various observations taken for phenotypic stability analysis were subjected to the following statistical analyses for drawing appropriate conclusions from the present investigation.

The combined analysis of variance was proceeded to look at $G \times E$ and stability of the genotypes across all environments. The AMMI model, which combines standard analysis of variance with IPC analysis (Zobel *et al.*, 1988), was used to investigate of $G \times E$ interaction. In AMMI model the contribution of each

genotype and each environment to the G x E interaction is assessed by use of the biplot graph display in which yield means are plotted against the scores of the IPCA 1 (Zobel *et. al.*, 1988).

The AMMI model is given below,

$$Y_{ijl} = \mu + G_i + E_j + (\sum \lambda_k \alpha_{ik} \gamma_{jk}) + e_{ijl}$$

Where,

Y_{ij} is the observed mean yield of the i^{th} genotype in j^{th} environment

μ is the general mean

G_i and E_j represent the effects of the genotype and environment

λ_k is the singular value of the k^{th} axis in the PCA

α_{ik} is the eigenvector of the i^{th} genotype for the k^{th} axis

γ_{jk} is the eigenvector of the j^{th} environment for the k^{th} axis

n is the number of principal components in the model

e_{ij} is the average of the corresponding random errors

The member of the AMMI family with IPCA 1 axis denoted AMMI 1; while AMMI 2 retains IPCA 2 retain IPCA 2 axes and so on. In general, AMMI N denotes the AMMI model with PCA axes 1 to N. AMMI 0 has no IPCA axes and is identically ANOVA. The full model with minimum (G-1, E-1) interaction principal component axes is denoted by AMMI E. The equation, except that it deletes the residual and error and that it stipulates a specific AMMI model rather than the entire AMMI family.

3.9.1. Analysis of variance of AMMI model

Environment wise analysis and pooled analysis of variance were conducted as per normal procedure.

If genotype, environment and G x E interaction are significant, the analysis may proceed further for AMMI analysis. If IPCA mean sum of square are significant and residual mean square is non- significant, the step may be conducted for development of bi plot. The AMMI bi plot developed by placing both genotype and environment mean value on X-axis and the respective IPCA axis eigenvector on the Y-axis.

Table 3: Analysis of Variance of AMMI model for stability analysis.

Sr. No.	Sources of variation	D.F.	S.S.	M.S.S.	'F' value calculated
1.	Treatments	(ge-1)	TrSS	MS 1	MS 1/MSE
2.	Genotypes	(g-1)	GSS	MS 2	MS 2/MSE
3.	Environments	(e-1)	EnSS	MS 3	MS 3/MSE
4.	G x E Interaction	(g-1) (e-1)	GESS	MS 4	MS 4/MSE
5.	IPCA 1	(G+E-1-2n)		MS 5	MS 5/MSE
6.	IPCA 2	(G+E-1-2n)		MS 6	MS 6/MSE
7.	IPCA N				
8.	Residual				
9.	Blocks	(r-1)	BSS		
10.	Total	(ger-1)	TSS		
11.	Error	(r-1) (ge-1)	ESS	MSE	

3.9.2. Estimation of stability parameters

The stability parameters which are estimated by different formulae.

3.9.2.1. Mean Value

The observations were recorded in each entry on five randomly selected competitive plants excluding border plants in each replication for all the environments and calculated its pooled mean. The highest mean is considered to find the stable genotypes.

3.9.2.2. Regression Coefficient (bi)

Regression coefficient (bi) was calculated as per stability model of Eberhart and Russell (1966). The regression coefficient (bi) which is the regression of the performance of each genotype under different environments on the environmental means over all the genotypes:

$$b_i = \sum_j Y_{ij} I_j / \sum_i I_j^2$$

Where,

$\sum_j Y_{ij} I_j$: Sum of the ith genotype x environmental index in jth environment

$\sum_i I_j^2$: as for environmental index

3.9.2.3. Line Deviation from Regression (S²di)

The deviation from regression line (S²di) was estimated as per stability model of Eberhart and Russell (1966). The performance of each genotype can be predicted by using estimate of parameter.

$$S^2 di = [\sum_j \sigma^2_{ij} / (e-2)] - (S^2_e / r)$$

Where,

$$\sum_j \sigma^2_{ij} : [\sum_j Y^2_{ij} - Y^2_i / g] - [(\sum_j Y_{ij} I_j)^2 / \sum_i I_j^2]$$

S²_e: Estimate of pooled error

3.9.2.4. AMMI stability value (ASV)

The AMMI stability value (ASV) as described by Purchase *et. al.* (2000) was calculated as follows:

$$ASV = \sqrt{\left\{ \frac{IPCA1\ SS}{IPCA2\ SS} \times (IPCA1\ score) \right\}^2 + (IPCA\ 2\ score)^2}$$

The larger the IPCA score, either negative or positive, the more specifically adapted a genotype is to certain environments. The smaller ASV scores indicate a more stable genotype across environments.

3.9.2.5. Genotypic selection index (GSI)

It is calculated by the formula suggested by (Farshadfar, 2003).

$$GSI = RASVi + RMi$$

Where,

RMi: Rank of mean of the corresponding trait of genotype across environments

RASVi: Rank of AMMI stability value

The low value of GSI with high mean yield shows desirable genotypes is stable (Farshadfar *et al.*, 2011). The AMMI stability value (low) and mean yield (high) with GSI (low) shows stability in a single criterion.

Those genotypes deviated non-significantly from zero (S^2_{di}), bi value near to unity, IPCA1 score close to zero, low value of ASV with less GSI index indicates these genotypes more stable across environments.

3.9.3. Interpretation of AMMI GGE bi-plot

In bi-plot displacement along the X-axis indicate differences in main effect, whereas displacement along the ordinate (Y-axis) indicate differences in interaction effect, for the points of different kinds, the AMMI model equation provides the expected yield value. The bi-plot has another important interpretation. The main effect for genotype reflects breeding advances. Similarly, the main effect for environment reflects overall comparison of environment.

In AMMI1 biplot, the genotypes with IPCA1 scores close to zero likely adapted to wide environment or less influenced by the environments and considered as stable variety over a wide range of environments. The larger scores

depict more specific adaptation in combination with environments of the same sign IPCA1 scores (Ebdon and Gauch, 2002). Furthermore, the relative magnitude and direction of genotypes along the abscissa and ordinate axis in biplot is also important to understand the response pattern of genotypes across environments and to differentiate high yielding and adaptable genotypes (Samonte *et. al.*, 2005).

In AMMI2 biplot, genotypes located on the vertices of the polygon performed either the best or the poorest in one or more environments (Yan and Kang, 2003). The equality lines divide the biplot into sectors, and the winning genotype for each sector is the one located on the respective vertex (Yan *et. al.*, 2007). The environmental scores were joined to the origin by site lines, site with short spokes didn't exert strong interactive forces, while those with long spokes exerted strong interaction. Genotypes or environments with large negative or positive IPCA scores have high interaction and those with IPCA scores near to zero have little interaction across environment and vice versa for environments (Crossa *et. al.*, 1990). The genotypes and environments that fall in the same sector interact positively. In contrast, if they fall in opposite sector interact negatively, if they fall into adjacent interaction is somewhat more complex. The GGE biplot also view the discriminating and representativeness ability of environments to identify an environment that efficiently discernment the superior genotype in the tested environments. A long environmental vector/spokes from origin showed a high capacity to discriminate genotype (Yan and Tinker, 2006).

CHAPTER – IV

EXPERIMENTAL RESULTS

The investigation entitled “**Genetic variability, diversity and stability study in Niger (*Guizotia abyssinica* L.)**” was undertaken with the view to study the genetic variability, genetic diversity, heritability, stability and G x E interaction. The research trials were carried out at five locations *viz.*, Experimental Research Farm of ARS, Phondaghat (E1); ARS, Shirgaon (E2); Department of Agril. Botany, Dapoli (E3); RARS, Karjat (E4) and ARS, Palghar (E5) during *kharif*, 2018 and *kharif*, 2019.

Forty Niger genotypes along with standard checks were grown in Randomized Block Design (RBD) in three replications under field conditions. The results of the experiment are presented in this chapter with the mean performance of all the genotypes pertaining to the genetic variability, heritability, gene action, genetic diversity, stability and G x E interaction for thirteen quantitative and qualitative traits. The season wise (*kharif*, 2018 and *kharif*, 2019) and environment wise (E1, E2, E3, E4 and E5) detailed results is presented in Appendix XI to XXIII.

4.1. Analysis of variance

Environment wise analysis of variance was computed for different characters studied and presented in Table no. 4. It is evident that, environment wise mean sum of squares among the genotypes was statistically significant for all the characters except capitulum diameter and 1000 seed weight. It showed that all these characters have significant variation. The genotype and error mean sum of squares were further used for analysis of genotypic and phenotypic variances.

4.2. Mean performance

The environment wise grand mean performance, grand pooled mean (GPM), over all mean, range, standard error and critical difference of forty genotypes of Niger for thirteen quantitative and qualitative characters were studied and presented in Table no. 5-11.

4.2.1. Days to 50 per cent flowering

The environment wise average variation in two seasons for days to 50 per cent flowering was ranged from 48 days (E5) to 52 days (E4) (Table 5).

Table 4: Environment wise analysis of variance for quantitative and qualitative traits in 40 genotypes of Niger.

Sr. No.	Characters	ARS, Phondaghat (E1)			ARS, Shirgaon (E2)			Dept. of Agril. Botany, Dapoli (E3)		
		Replication	Treatment	Error	Replication	Treatment	Error	Replication	Treatment	Error
	DF	2	39	78	2	39	78	2	39	78
1.	DFPF	11.56	20.67**	1.82	2.79	25.64**	2.21	2.10	37.84**	1.95
2.	PH (cm)	15.04	271.81**	34.21	6.50	113.62**	39.57	32.10	235.52**	44.21
3.	NPBPP	0.23	13.33**	0.99	0.63	9.62**	1.34	0.17	7.63**	0.92
4.	NSBPP	4.52	53.63**	3.49	2.18	30.00**	5.10	2.26	23.50**	3.29
5.	NCPP	0.23	404.45**	13.55	6.47	90.96**	19.30	7.94	170.62**	13.15
6.	CD (cm)	0.001	0.03	0.001	0.01	0.02	0.001	0.001	0.03	0.001
7.	NSPC	17.11	43.37**	10.27	1.79	32.33**	7.60	3.66	42.27**	9.16
8.	1000 SW (g)	0.04	0.05	0.02	0.03	0.06	0.02	0.02	0.10	0.03
9.	SYPP (g)	0.26	0.23**	0.08	0.03	0.23**	0.06	0.23	0.26**	0.09
10.	SYPP (g)	638.71	954.25**	317.14	612.87	1089.64**	326.21	2619.18	1543.62**	690.97
11.	DM	1.71	38.56**	2.99	0.01	24.60**	3.93	15.27	42.39**	10.13
12.	OC (%)	2.43	10.11**	4.80	4.31	7.44**	3.36	1.07	6.32**	2.88
13.	PC (%)	1.06	3.36*	0.66	2.76	3.71*	1.31	1.51	2.58*	0.66

*Significant at 5% level of significance

**Significant at 1% level of significance

DFPF: Days to 50 per cent flowering

NCPP: No. of capitula plant⁻¹

SYPP: Seed yield plant⁻¹

PC: Protein content

PH: Plant height

CD: Capitulum diameter

SYPP: Seed yield plot⁻¹

NPBPP: No. of primary branches plant⁻¹

NSPC: No. of seeds capitulum⁻¹

DM: Days to maturity

NSBPP: No. of secondary branches plant⁻¹

SW: Seed weight

OC: Oil content

(Table contd...)

Sr. No.	Characters	RARS, Karjat (E4)			ARS, Palghar (E5)		
		Replication	Treatment	Error	Replication	Treatment	Error
	DF	2	39	78	2	39	78
1.	DFPF	0.09	37.30**	2.13	3.39	33.47**	2.03
2.	PH (cm)	45.61	90.93**	30.45	11.82	144.00**	39.91
3.	NPBPP	0.64	12.48**	0.70	1.41	11.60**	1.09
4.	NSBPP	4.08	29.19**	2.50	13.58	30.90**	4.02
5.	NCPP	36.88	112.91**	10.22	3.70	109.77**	10.18
6.	CD (cm)	0.01	0.01	0.001	0.001	0.02	0.001
7.	NSPC	1.93	11.80**	4.41	5.26	30.96**	9.27
8.	1000 SW (g)	0.02	0.12*	0.06	0.07	0.09	0.05
9.	SYPP (g)	0.01	0.11*	0.04	0.06	0.16**	0.07
10.	SYPP (g)	128.34	550.26**	238.48	297.46	1054.34**	473.81
11.	DM	3.26	19.80**	4.05	7.39	45.24**	6.44
12.	OC (%)	2.13	8.29**	2.13	3.28	7.36**	2.78
13.	PC (%)	0.23	3.59*	1.31	6.00	3.08*	1.18

*Significant at 5% level of significance

**Significant at 1% level of significance

DFPF: Days to 50 per cent flowering

NCPP: No. of capitula plant⁻¹

SYPP: Seed yield plant⁻¹

PC: Protein content

PH: Plant height

CD: Capitulum diameter

SYPP: Seed yield plot⁻¹

NPBPP: No. of primary branches plant⁻¹

NSPC: No. of seeds capitulum⁻¹

DM: Days to maturity

NSBPP: No. of secondary branches plant⁻¹

SW: Seed weight

OC: Oil content

Among studied genotypes, the grand polled mean for this character over two seasons and five environments was varied from 42 days (G26) to 53 days (G35 and G37) with over all mean of 50 days.

In the present investigation, the overall mean performance for days to 50 per cent flowering was 50 days, 49 days, 49 days, 52 days and 48 days for the environments *viz.*, E1, E2, E3, E4 and E5, respectively. Among all, 15, 24, 22, 19 and 24 genotypes recorded more days to 50 per cent flowering than grand mean for different environments, *viz.*, E1, E2, E3, E4 and E5, respectively. While 18, 09, 14, 17 and 10 genotypes recorded less days to 50 per cent flowering than average for environments, *viz.*, E1, E2, E3, E4 and E5, respectively. The genotypes G26 & G3 (45 days) found less days for 50 per cent flowering followed by the genotypes, G11 (46 days), G10, G22, G24, G25 (47 days) and G6, G9, G17, G27, G28, G30, G31 (48 days) while genotype, G15 (55 days) observed maximum days for 50 per cent flowering followed by the genotypes, G2, G13, G14, G16, G21 (54 days), G4, G12, G32 (53 days) and G5, G8 (52 days) in E1. The genotype, G5 (54 days) recorded maximum days for 50 per cent flowering followed by the genotypes, G2 (53 days), G8, G15, G16, G21, G35, G37 (52 days) and G4, G9, G13, G14, G18, G31, G33 (51 days) while genotype, G26 (41 days) found early for 50 per cent flowering followed by the genotypes, G24, G25 (42 days) and G27 (45 days) in E2. The genotype, G25 (40 days) found less days for 50 per cent flowering followed by the genotype, G26 (41 days) and G27, G28, G29 (43 days) while genotypes G9 (54 days) recorded maximum days for 50 per cent flowering followed by the genotypes, G3, G4, (53 days) and G34, G35 (52 days) in E3. The genotype, G26 (44 days) found less days for 50 per cent flowering followed by the genotypes, G24, G25 (45 days) and G27 (47 days) while genotypes, G37, G35 (57 days) observed maximum days for 50 per cent flowering followed by the genotypes, G9, G17, G34 (56 days) and G18, G22, G33 (55 days) in E4. The genotypes, G24, G25, G26 (41 days) found less days for 50 per cent flowering followed by the genotypes, G27, G29 (42 days) and G28 (43 days) while genotypes, G2, G34, G35 (53 days) observed maximum days for 50 per cent flowering followed by the genotypes, G9, G33, G37 (52 days) and G4, G11, G36 (51 days) in E5.

Table 5: Environment wise pooled mean performance of two seasons for days to 50 per cent flowering and plant height in 40 genotypes of Niger.

S. No.	Genotype code	Days to 50 per cent flowering						Plant height (cm)					
		E1	E2	E3	E4	E5	GPM	E1	E2	E3	E4	E5	GPM
1	G 1	51	50	50	49	50	50	143	126	141	139	139	137
2	G 2	54	53	51	49	53	52	147	128	134	140	132	136
3	G 3	45	49	53	53	50	50	138	126	128	127	119	128
4	G 4	53	51	53	48	51	51	137	124	143	139	140	137
5	G 5	52	54	48	48	48	50	137	115	144	136	138	134
6	G 6	48	47	47	48	48	48	140	123	146	134	134	135
7	G 7	50	49	50	49	50	49	129	120	140	138	140	133
8	G 8	52	52	51	50	50	51	125	120	120	129	127	124
9	G 9	48	51	54	56	52	52	135	119	135	131	133	131
10	G 10	47	49	50	49	48	49	144	115	145	138	137	136
11	G 11	46	50	51	55	51	50	136	127	138	136	135	134
12	G 12	53	50	51	50	49	50	142	121	136	134	135	133
13	G 13	54	51	50	54	48	51	144	125	142	141	139	138
14	G 14	54	51	51	54	49	52	130	141	139	146	143	140
15	G 15	55	52	50	54	49	52	131	121	135	132	135	131
16	G 16	54	52	51	54	50	52	141	122	141	134	139	135
17	G 17	48	49	51	56	49	50	132	126	153	134	145	138
18	G 18	51	51	49	55	48	51	143	132	139	139	138	138
19	G 19	49	49	46	52	49	49	138	125	141	138	138	136
20	G 20	51	50	51	52	48	50	154	126	153	140	143	143
21	G 21	54	52	50	53	50	52	137	122	146	140	141	137
22	G 22	47	46	50	55	50	50	140	122	136	137	139	135
23	G 23	50	48	48	52	46	49	128	124	141	135	137	133
24	G 24	47	42	39	45	41	43	123	122	131	138	132	129
25	G 25	47	42	40	45	41	43	120	114	125	126	122	121
26	G 26	45	41	41	44	41	42	111	115	125	128	130	122
27	G 27	48	45	43	47	42	45	129	120	148	131	143	134
28	G 28	48	46	43	48	43	46	132	121	141	137	139	134
29	G 29	49	46	43	51	42	46	121	124	144	134	143	133
30	G 30	48	50	49	52	46	49	130	125	152	142	144	138
31	G 31	48	51	48	51	46	49	121	127	152	138	137	135
32	G 32	53	50	47	50	46	49	135	124	129	134	129	130
33	G 33	49	51	47	55	52	51	126	134	134	150	135	136
34	G 34	51	50	52	56	53	52	125	132	140	139	140	135
35	G 35	51	52	52	57	53	53	121	134	154	144	139	139
36	G 36	49	50	50	56	51	51	119	128	146	142	138	135
37	G 37	51	52	53	57	52	53	119	128	144	143	136	134
38	G 38	50	49	49	54	50	50	124	135	153	144	151	141
39	G 39	49	50	49	54	50	50	119	133	152	149	150	140
40	G 40	50	49	46	53	49	49	132	134	159	144	156	145
	GM	50	49	49	52	48	50	132	125	141	137	138	135
	Range	45-55	41-54	40-54	44-57	41-53	42-53	111-154	114-141	120-159	126-150	119-156	121-145
	S.E. $\pm$	1.10	1.21	1.14	1.19	1.16		4.78	5.14	5.43	4.51	5.16	
	C.D. (5%)	2.19	2.42	2.27	2.37	2.32		9.51	10.23	10.81	8.97	10.27	

Note: GM - Grand Mean & GPM - Grand Pooled Mean over the seasons and the environments

4.2.2. Plant height (cm):

The environment wise pooled mean of two seasons for plant height varied from 125 cm (E2) to 141 cm (E3) (Table 5). Among studied genotypes, the plant height in grand polled data over the seasons and the locations was ranged from 121 cm (G25) to 145 cm (G40) with over all mean of 135 cm.

The data pertaining to the plant height, the overall mean performance for height of the plant at maturity was recorded 132 cm, 125 cm, 141 cm, 137 cm and 138 cm for the environments *viz.*, E1, E2, E3, E4 and E5, respectively. Among all, 18, 17, 18, 22 and 19 genotypes observed more plant height than grand mean for the environments, *viz.*, E1, E2, E3, E4 and E5, respectively. While 19, 20, 15, 14 and 16 genotypes registered for less plant height at maturity than average for different environments, *viz.*, E1, E2, E3, E4 and E5, respectively. The genotype, G26 (111 cm) found short statured plant followed by the genotypes, G36, G37 (119 cm) and G25 (120 cm) while genotype, G20 (154 cm) recorded maximum height of the plant followed by G2 (147 cm) and G10, G13 (144 cm) in E1. The genotype, G14 (141 cm) registered for more plant height followed by G38 (135 cm) and G40, G33 (134 cm) while genotypes G25 (114 cm) found less heighted followed by G5, G10, G26 (115 cm) and G7, G8, G27 (120 cm) in E2. The genotype, G40 (159 cm) observed more plant height followed by G35 (154 days) and G17, G20, G38 (153 cm) while genotype, G8 (120 cm) observed lowest plant height followed by the genotypes, G25, G26 (125 cm) and G3 (128 cm) in E3. The genotype, G33 (150 cm) found maximum plant height at maturity followed by the genotypes, G39 (149cm), G14 (146 cm) and G35, G38, G40 (144 cm) while genotype, G25 (126 cm) observed minimum plant height followed by G3 (127 cm) and G26 (128 cm) in E4. The genotype, G3 (119 cm) registered for short plant stature followed by G25 (122 cm) and G8 (127 cm) while genotype, G40 (156 cm) found maximum plant height followed by G38 (151 cm) and G39 (150 cm) in E5.

4.2.3. Number of primary branches plant⁻¹:

The environment wise grand mean of two seasons for number of primary branches plant⁻¹ varied from 8 (E4) to 10 (E2) (Table 6). The grand pooled mean over the seasons and over the environments, the number of primary branches

plant⁻¹ ranged from 7 (G3, G5, G8, G15, G19, G21, G26, G28, G29 and G31) to 13 (G24) with over all mean of 9.

In the present investigation, the overall mean performance for number of primary branches plant⁻¹ was 9, 10, 9, 8 and 9 for the environments *viz.*, E1, E2, E3, E4 and E5, respectively. Among all, 17, 11, 14, 13 and 12 genotypes noticed greater number of primary branches plant⁻¹ than grand mean for the environments, *viz.*, E1, E2, E3, E4 and E5, respectively. The maximum number of primary branches plant⁻¹ noticed in genotypes, G36, G32, G24, G10 (13) followed by G1 (12) and G2, G9, G16, G40 (11) in E1. The genotypes, G4, G24, G32, G36, G8 (13) found higher number of primary branches plant⁻¹ followed by the genotypes, G10, G39, G40 (12) and G7, G33 (11) in E2. The genotype, G4 (12) had maximum number of primary branches plant⁻¹ followed by the genotypes, G1, G10, G24, G36, G40 (11) in E3. The genotype G24 (13) had a greater number of primary branches plant⁻¹ followed by G32 (12) and G36, G39, G40 (11) in E4. The genotypes, G24, G36 (14) had maximum number of primary branches plant⁻¹ followed by G4 (13) and G2, G10, G32 (12) in E5.

4.2.4. Number of secondary branches plant⁻¹:

The environment wise grand mean of two seasons for this trait ranged from 14 (E4) to 20 (E2) (Table 6). Among the genotypes studied, the grand polled mean over the seasons and over the environments were varied from 13 (G26) to 23 (G36) with over all mean of 17.

Data regards to the number of secondary branches plant⁻¹, the overall mean performance for number of secondary branches plant⁻¹ was 16, 20, 16, 14 and 17 for the environments *viz.*, E1, E2, E3, E4 and E5, respectively. Among all, 18, 17, 17, 16 and 14 genotypes observed greater number of secondary branches plant⁻¹ than grand mean for the environments, *viz.*, E1, E2, E3, E4 and E5, respectively. The genotype, G36 (25) recorded maximum number of secondary branches plant⁻¹ followed by G10 (24) and G32 (23) in E1. The genotype, G36 (28) found maximum number of secondary branches plant⁻¹ followed by the genotypes, G4, G24 (26) and G32, G40 (25) in E2. The genotype, G32 (22) observed maximum number of secondary branches plant⁻¹ followed by the genotypes, G24, G30 (21) and G10,

Table 6: Environment wise pooled mean performance of two seasons for number of primary and secondary branches plant⁻¹ in 40 genotypes of Niger.

S. No.	Genotype code	Number of primary branches plant ⁻¹						Number of secondary branches plant ⁻¹					
		E1	E2	E3	E4	E5	GPM	E1	E2	E3	E4	E5	GPM
1	G 1	12	10	11	9	11	11	21	21	21	15	14	18
2	G 2	11	10	12	10	12	11	21	24	19	17	19	20
3	G 3	7	8	6	6	8	7	12	18	12	12	17	14
4	G 4	10	13	12	10	13	11	18	26	18	16	20	20
5	G 5	7	8	8	6	8	7	12	21	16	11	14	15
6	G 6	9	8	10	8	10	9	17	18	14	15	15	16
7	G 7	8	11	10	7	6	8	14	21	13	14	14	15
8	G 8	8	7	8	6	7	7	13	18	18	12	16	15
9	G 9	11	9	8	7	9	9	18	18	16	12	19	17
10	G 10	13	12	11	8	12	11	24	22	20	18	19	21
11	G 11	8	10	9	8	8	8	13	17	14	12	15	14
12	G 12	7	9	9	6	9	8	15	19	14	13	18	16
13	G 13	10	8	10	5	7	8	18	16	16	11	14	15
14	G 14	9	9	8	8	8	8	14	18	18	13	14	15
15	G 15	8	9	6	6	7	7	13	17	13	13	15	14
16	G 16	11	9	8	6	9	9	20	19	17	12	16	17
17	G 17	8	7	9	6	9	8	13	15	18	12	17	15
18	G 18	10	8	8	6	7	8	22	16	15	12	13	15
19	G 19	8	9	6	6	7	7	17	21	12	12	13	15
20	G 20	10	9	8	8	8	9	21	20	14	15	16	17
21	G 21	8	9	8	5	8	7	13	19	15	11	16	15
22	G 22	9	8	7	6	8	8	13	19	13	13	14	14
23	G 23	8	10	8	7	7	8	13	21	13	14	14	15
24	G 24	13	13	11	13	14	13	16	26	21	23	25	22
25	G 25	7	9	8	8	9	8	11	18	14	16	18	15
26	G 26	5	9	6	6	8	7	9	19	13	11	16	13
27	G 27	6	9	7	7	8	8	11	18	17	13	15	15
28	G 28	6	8	8	7	8	7	10	17	16	12	13	14
29	G 29	6	8	8	7	8	7	11	16	15	13	13	14
30	G 30	8	10	9	6	8	8	13	23	21	12	12	16
31	G 31	6	9	7	5	9	7	12	20	15	13	16	15
32	G 32	13	13	10	12	12	12	23	25	22	22	21	22
33	G 33	10	11	7	10	9	9	15	21	14	16	18	17
34	G 34	10	10	9	9	9	9	16	20	14	15	16	16
35	G 35	10	13	10	9	11	11	18	24	19	15	21	19
36	G 36	13	13	11	11	14	12	25	28	20	21	24	23
37	G 37	8	8	8	10	8	8	13	17	14	14	17	15
38	G 38	10	13	10	9	10	10	20	24	18	17	20	20
39	G 39	9	12	10	11	11	10	20	22	18	19	22	20
40	G 40	11	12	11	11	11	11	22	25	19	20	23	22
	GM	9	10	9	8	9	9	16	20	16	14	17	17
	Range	5-13	7-13	6-12	5-13	6-14	7-13	9-25	15-28	12-22	11-23	12-25	13-23
	S.E. ±	0.81	0.94	0.78	0.68	0.85		1.53	1.84	1.48	1.29	1.54	
	C.D. (5%)	1.62	1.88	1.56	1.36	1.70		3.04	3.67	2.95	2.57	3.26	

Note: GM – Grand Mean & GPM – Grand Pooled Mean over the seasons and the environments

G36 (20) in E3. The genotype, G24 (23) observed maximum number of secondary branches plant⁻¹ followed by G32 (22) and G36 (21) in E4. The genotype, G24 (25) recorded maximum number of secondary branches plant⁻¹ followed by G36 (24) and G40 (23) in E5.

4.2.5. Number of capitula plant⁻¹:

The environment wise grand mean of two seasons for number of capitula plant⁻¹ varied from 36 (E5) to 41 (E3) (Table 7). Among the genotypes studied, the grand polled mean over two seasons and five environments, average number of capitula plant⁻¹ was ranged from 30 (G29) to 52 (G36) with over all mean of 38.

In the present investigation, the overall mean performance for number of capitula plant⁻¹ was 40, 37, 41, 37 and 36 for the environments *viz.*, E1, E2, E3, E4 and E5, respectively. Among all, a greater number of capitula plant⁻¹ observed in 15, 21, 20, 13 and 11 genotypes than grand mean for the environments, *viz.*, E1, E2, E3, E4 and E5, respectively. The genotype, G36 (67) had maximum number of capitula plant⁻¹ followed by G24 (58), G20, G32 (57) in E1. The genotype, G40 (47) recorded maximum number of capitula plant⁻¹ followed by the genotypes, G4, G35, G38 (46) and G24, G31 (44) in E2. The genotype, G2 (59) showed maximum number of capitula plant⁻¹ followed by the genotypes, G30, G40 (53), G38 (52) and G36 (51) in E3. The genotype, G24 (53) observed maximum number of capitula plant⁻¹ followed by G32 (51) and G2, G4 (47) in E4. The genotype, G36 (54) had maximum number of capitula plant⁻¹ followed by G24 (49) and G32, G40 (48) in E5.

4.2.6. Capitulum diameter (cm):

The environment wise grand mean performance of two seasons for capitulum diameter was ranged from 0.99 cm (E4) to 1.08 cm (E3 & E1) (Table 7). Among the studied genotypes, the grand polled mean over the seasons and over the environments was varied from 0.90 cm (G26) to 1.25 cm (G36) with over all mean of 1.04 cm.

As regards to the capitulum diameter, the overall mean performance for capitulum diameter was 1.08 cm, 1.05 cm, 1.08 cm, 0.99 cm and 1.01 cm for the environments *viz.*, E1, E2, E3, E4 and E5, respectively. Among all, 19, 20, 16, 16

Table 7: Environment wise pooled mean performance of two seasons for number of capitula plant⁻¹ and capitulum diameter (cm) in 40 genotypes of Niger

S. No.	Genotype code	Number of capitula plant ⁻¹						Capitulum diameter (cm)					
		E1	E2	E3	E4	E5	GPM	E1	E2	E3	E4	E5	GPM
1	G 1	49	43	48	45	44	46	1.15	1.20	1.10	0.95	1.00	1.08
2	G 2	38	42	59	47	34	44	1.05	1.03	1.12	1.08	1.00	1.06
3	G 3	34	36	37	34	32	35	1.07	1.13	1.08	1.07	0.98	1.07
4	G 4	36	46	45	47	43	43	1.23	1.03	1.07	1.03	1.02	1.08
5	G 5	29	40	37	38	33	35	1.00	0.92	1.12	0.97	1.03	1.01
6	G 6	29	34	39	36	33	34	1.13	1.08	1.08	0.97	0.93	1.04
7	G 7	32	39	41	34	31	35	0.95	0.92	0.97	0.95	0.95	0.95
8	G 8	27	36	35	34	35	33	1.17	1.15	0.98	0.95	0.90	1.03
9	G 9	53	31	43	40	35	40	1.02	1.08	1.00	0.97	0.97	1.01
10	G 10	62	40	44	48	44	47	1.05	1.05	1.07	1.00	0.97	1.03
11	G 11	29	34	36	35	32	33	1.12	1.05	0.98	0.98	0.97	1.02
12	G 12	34	34	37	36	36	35	1.17	1.12	0.97	0.95	0.93	1.03
13	G 13	50	28	49	31	31	38	1.07	1.07	0.98	0.95	1.00	1.01
14	G 14	39	35	46	36	33	38	1.13	1.10	1.00	0.93	0.95	1.02
15	G 15	34	40	28	37	34	35	1.15	1.15	1.08	1.10	1.08	1.11
16	G 16	43	34	42	32	33	37	1.18	1.08	1.05	0.93	0.93	1.04
17	G 17	32	34	48	29	30	35	1.02	1.02	1.12	0.95	1.02	1.02
18	G 18	59	34	36	33	34	39	1.08	1.07	1.00	1.02	0.92	1.02
19	G 19	45	40	36	33	30	36	1.02	0.98	1.07	1.05	1.05	1.03
20	G 20	57	40	43	33	37	42	1.00	1.00	0.95	1.00	0.87	0.96
21	G 21	37	41	37	30	33	36	1.00	0.97	1.13	0.95	1.02	1.01
22	G 22	33	33	34	29	31	32	1.12	1.22	1.08	1.00	1.02	1.09
23	G 23	31	38	32	36	33	34	1.07	0.97	1.03	0.95	0.92	0.99
24	G 24	58	44	47	53	49	50	0.95	1.07	1.22	1.03	1.05	1.06
25	G 25	27	32	29	36	36	32	0.93	1.00	1.00	0.90	0.92	0.95
26	G 26	24	34	29	31	35	31	0.88	0.90	0.92	0.95	0.85	0.90
27	G 27	30	33	34	32	34	32	0.93	0.88	1.05	0.90	1.00	0.95
28	G 28	27	26	41	30	30	31	0.93	0.93	1.12	0.87	1.05	0.98
29	G 29	28	25	33	30	33	30	0.98	0.97	1.08	0.95	1.05	1.01
30	G 30	32	36	53	32	30	36	1.10	1.05	1.15	0.97	1.00	1.05
31	G 31	28	44	43	32	32	36	1.10	1.15	1.15	0.97	1.03	1.08
32	G 32	57	43	44	51	48	48	1.07	1.07	1.07	0.93	1.02	1.03
33	G 33	38	39	32	34	32	35	1.10	1.00	1.20	0.97	1.05	1.06
34	G 34	38	38	33	37	34	36	1.10	0.97	1.12	1.00	1.12	1.06
35	G 35	48	46	47	39	37	43	1.17	1.08	1.23	1.07	1.08	1.13
36	G 36	67	42	51	43	54	52	1.27	1.23	1.32	1.18	1.25	1.25
37	G 37	31	34	43	33	33	35	1.00	0.92	1.02	0.98	1.00	0.98
38	G 38	42	46	52	39	40	44	1.18	1.12	1.27	1.13	1.17	1.17
39	G 39	51	41	48	42	44	45	1.18	1.08	1.20	1.08	1.17	1.14
40	G 40	53	47	53	43	48	49	1.20	1.20	1.25	1.15	1.23	1.21
	GM	40	37	41	37	36	38	1.08	1.05	1.08	0.99	1.01	1.04
	Range	24-67	25-47	28-59	29-53	30-54	30-52	0.88-1.27	0.88-1.23	0.92-1.32	0.87-1.18	0.85-1.25	0.90-1.25
	S.E. $\pm$	3.01	3.59	2.96	2.61	2.61		0.04	0.05	0.05	0.06	0.05	
	C.D. (5%)	5.98	7.14	5.89	5.20	5.19		0.07	0.10	0.10	0.11	0.10	

Note: GM - Grand Mean & GPM - Grand Pooled Mean over the seasons and the environments

and 19 genotypes recorded maximum capitulum diameter than grand mean for the environments, *viz.*, E1, E2, E3, E4 and E5, respectively. The genotype, G36 (1.27 cm) observed broader capitulum diameter followed by G40 (1.20 cm), G16, G38, G39 (1.18 cm) in E1. The genotype, G36 (1.23 cm) observed more far-flung capitulum diameter followed by G22 (1.22 cm) and G1 (1.20 cm) in E2. The genotype, G36 (1.32 cm) had large capitulum diameter followed by G38 (1.27 cm) and G40 (1.25 cm) in E3. The genotype, G36 (1.18 cm) had maximum capitulum diameter followed by G40 (1.15 cm) and G38 (1.13 cm) in E4. The genotype, G36 (1.25 cm) recorded more far-flung capitulum diameter followed by G40 (1.23 cm) and G38, G39 (1.17 cm) in E5.

4.2.7. Number of seeds capitulum⁻¹:

The environment wise grand mean of two seasons for number of seeds capitulum⁻¹ varied from 21 (E4) to 33 (E1) (Table 8). Among genotypes studied, the grand polled average number of seeds capitulum⁻¹ over the seasons and over the environments was ranged from 25 (G7, G17, G27 and G29) to 36 (G36) with over all mean of 28.

In the present investigation, the overall mean performance for number of seeds capitulum⁻¹ was 33, 30, 32, 21 and 25 for the environments *viz.*, E1, E2, E3, E4 and E5, respectively. Among all, 17, 17, 19, 16 and 14 genotypes recorded more number of seeds capitulum⁻¹ than grand mean for the environments, *viz.*, E1, E2, E3, E4 and E5, respectively. The genotypes, G36, G40 (42) recorded maximum number of seeds capitulum⁻¹ followed by G39 (40) and G35 (39) in E1. The genotype, G36 (39) observed maximum number of seeds capitulum⁻¹ followed by G40 (38) and G38 (37) in E2. The genotype, G36 (41) found maximum number of seeds capitulum⁻¹ followed by the genotypes, G24, G38, G40 (40) and G18 (36) in E3. The genotype, G36 (26) perceived maximum number of seeds capitulum⁻¹ followed by the genotypes, G40 (25), G2, G10, G38 (24) and G4, G5, G15 (23) in E4. The genotype, G36 (33) had maximum number of seeds capitulum⁻¹ followed by the genotypes, G32, G40 (31) and G38 (30) in E5.

Table 8: Environment wise pooled mean performance of two seasons for number of seeds capitulum⁻¹ and 1000 seed weight (g) in 40 genotypes of Niger.

S. No.	Genotype code	Number of seeds capitulum ⁻¹						1000 seed weight (g)					
		E1	E2	E3	E4	E5	GPM	E1	E2	E3	E4	E5	GPM
1	G 1	30	27	34	20	25	27	2.58	2.54	2.60	2.44	2.51	2.53
2	G 2	36	30	30	24	27	29	2.72	2.57	2.71	2.61	2.64	2.65
3	G 3	30	30	35	22	22	28	2.72	2.61	2.76	2.55	2.63	2.65
4	G 4	32	31	32	23	28	29	2.71	2.59	2.67	2.70	2.60	2.65
5	G 5	33	33	33	23	24	29	2.65	2.54	2.64	2.50	2.57	2.58
6	G 6	32	29	33	22	23	28	2.59	2.50	2.59	2.41	2.50	2.52
7	G 7	31	28	26	20	21	25	2.64	2.61	2.64	2.49	2.56	2.59
8	G 8	35	31	30	20	23	28	2.48	2.43	2.26	2.28	2.35	2.36
9	G 9	34	32	27	21	26	28	2.53	2.55	2.62	2.42	2.51	2.52
10	G 10	33	32	28	24	27	29	2.76	2.60	2.72	2.67	2.65	2.68
11	G 11	29	26	31	22	23	26	2.60	2.53	2.50	2.42	2.49	2.51
12	G 12	33	30	27	22	20	26	2.79	2.65	2.70	2.58	2.67	2.68
13	G 13	30	28	29	22	25	27	2.62	2.48	2.59	2.31	2.42	2.48
14	G 14	31	32	29	21	21	27	2.63	2.60	2.51	2.36	2.49	2.52
15	G 15	33	30	34	23	28	30	2.61	2.60	2.43	2.28	2.55	2.49
16	G 16	35	32	30	20	22	28	2.63	2.61	2.44	2.44	2.54	2.53
17	G 17	28	28	33	18	21	25	2.66	2.69	2.75	2.51	2.61	2.64
18	G 18	35	33	36	21	25	30	2.63	2.56	2.48	2.40	2.47	2.51
19	G 19	30	27	35	20	26	28	2.60	2.61	2.56	2.37	2.47	2.52
20	G 20	31	31	30	19	21	26	2.61	2.55	2.55	2.37	2.47	2.51
21	G 21	31	30	33	20	23	27	2.68	2.43	2.67	2.49	2.56	2.56
22	G 22	36	36	34	18	22	29	2.66	2.59	2.72	2.47	2.57	2.60
23	G 23	33	29	30	20	24	27	2.61	2.49	2.61	2.35	2.43	2.50
24	G 24	36	31	40	22	29	31	2.69	2.73	2.76	2.69	2.67	2.71
25	G 25	32	27	29	20	25	27	2.46	2.41	2.23	2.17	2.21	2.29
26	G 26	32	28	31	19	22	26	2.34	2.48	2.17	2.06	2.46	2.30
27	G 27	27	23	29	19	24	25	2.34	2.16	2.23	2.43	1.91	2.21
28	G 28	33	27	30	18	23	26	2.33	2.29	2.23	1.67	2.08	2.12
29	G 29	26	29	30	17	21	25	2.47	2.30	2.29	1.96	2.09	2.22
30	G 30	36	29	28	21	25	28	2.50	2.33	2.50	2.28	2.39	2.40
31	G 31	34	35	33	20	29	30	2.72	2.55	2.70	2.48	2.53	2.60
32	G 32	38	30	37	22	31	32	2.64	2.56	2.69	2.50	2.55	2.59
33	G 33	34	30	31	20	24	28	2.66	2.62	2.67	2.46	2.56	2.59
34	G 34	34	30	34	22	25	29	2.63	2.63	2.58	2.39	2.48	2.54
35	G 35	39	33	36	21	27	31	2.73	2.75	2.78	2.53	2.59	2.68
36	G 36	42	39	41	26	33	36	2.88	2.78	2.79	2.68	2.75	2.77
37	G 37	33	26	32	18	24	27	2.67	2.63	2.59	2.47	2.58	2.59
38	G 38	42	37	40	24	30	34	2.84	2.78	2.83	2.65	2.70	2.76
39	G 39	40	32	35	21	29	31	2.75	2.67	2.68	2.50	2.52	2.62
40	G 40	42	38	40	25	31	35	2.86	2.77	2.84	2.66	2.73	2.77
	GM	33	30	32	21	25	28	2.63	2.56	2.58	2.42	2.50	2.54
	Range	26-42	23-39	26-41	17-26	20-33	25-36	2.33-2.88	2.16-2.78	2.17-2.84	1.67-2.68	1.91-2.75	2.12-2.77
	S.E. ±	2.62	2.25	2.47	1.71	2.49		0.11	0.11	0.14	0.20	0.18	
	C.D. (5%)	5.21	4.48	4.92	3.41	4.95		0.23	0.21	0.28	0.39	0.36	

Note: GM – Grand Mean & GPM – Grand Pooled Mean over the seasons and the environments

4.2.8. 1000 seed weight (g):

The environment wise grand mean of two seasons for 1000 seed weight was ranged from 2.42g (E4) to 2.63g (E1) (Table 8). Among studied genotypes the grand polled mean over seasons and environments was varied from 2.12g (G28) to 2.77g (G36) with over all mean of 2.54g.

As regards to the 1000 seed weight, the overall mean performance for 1000 seed weight was 2.63 g, 2.56 g, 2.58 g, 2.42 g and 2.50 g for the environments *viz.*, E1, E2, E3, E4 and E5, respectively. Among all, 20, 20, 25, 24 and 24 genotypes observed more weight of 1000 seed than grand mean for the environments, *viz.*, E1, E2, E3, E4 and E5, respectively. While 16, 18, 14, 14 and 15 genotypes recorded less weight of 1000 seed than average for different environments, *viz.*, E1, E2, E3, E4 and E5, respectively. The genotype, G28 (2.33 g) found less weight of 1000 seed followed by G26, G27 (2.34 g) and G25 (2.46 g) while genotype, G36 (2.88 g) had maximum weight of 1000 seed followed by G40 (2.86 g) and G38 (2.84 g) in E1. The genotype G27 (2.16 g) found low weight of 1000 seed followed by G28 (2.29 g) and G29 (2.30 g) while genotypes, G36, G38 (2.78 g) recorded maximum weight of 1000 seed followed by G40 (2.77 g) and G35 (2.75 g) in E2. The genotype, G26 (2.17 g) recorded less weight of 1000 seed followed by the genotypes, G25, G27, G28 (2.23 g) and G29 (2.29 g) while genotype, G40 (2.84 g) noticed maximum 1000 seed weight followed by G38 (2.83 g) and G36 (2.79 g) in E3. The genotype, G28 (1.67 g) found less weight of 1000 seed followed by G29 (1.96 g) and G26 (2.06 g) while genotype, G36 (2.68 g) had maximum 1000 seed weight followed by G40 (2.66 g) and G38 (2.65 g) in E4. The genotype, G27 (1.91 g) found less weight of 1000 seed followed by G28 (2.08 g) and G29 (2.09 g) while genotype, G36 (2.75 g) recorded maximum weight of 1000 seed followed by G40 (2.73 g) and G38 (2.70 g) in E5.

4.2.9. Seed yield plant⁻¹ (g):

The environment wise grand mean of two seasons for seed yield plant⁻¹ was ranged from 2.40g (E4) to 3.47g (E3) (Table 59). The grand polled mean data over five locations and two seasons, the genotypic seed yield plant⁻¹ was varied from 2.48g (G28) to 3.48g (G36) with overall mean of 2.80g.

In the present investigation, the overall mean performance for seed yield plant⁻¹ was 2.70g, 2.82g, 3.47g, 2.40g and 2.57g for the environments *viz.*, E1, E2, E3, E4 and E5, respectively. Among all, 13, 10, 17, 17 and 20 genotypes observed more seed yield plant⁻¹ than grand mean for the environments, *viz.*, E1, E2, E3, E4 and E5, respectively. The genotype, G36 (3.57 g) recorded maximum seed yield plant⁻¹ followed by G32 (3.30 g) and G38 (2.23 g) in E1. The genotype, G36 (3.56 g) observed greater seed yield plant⁻¹ followed by G40 (3.41 g), G32 (3.40 g) and G24 (3.38 g) in E2. The maximum seed yield plant⁻¹ was recorded in genotype, G36 (4.18 g) followed by G24 (4.12 g) and G38 (4.11 g) in E3. The genotype G36 (2.85 g) was given maximum seed yield plant⁻¹ followed by G24 (2.78 g) and G32 (2.75 g) in E4. The genotype, G36 (3.17 g), G24 (3.08 g) recorded higher seed yield plant⁻¹ followed by G40 (2.97 g) in E5.

4.2.10. Seed yield plot⁻¹ (g):

The environment wise grand mean of two seasons for seed yield plot⁻¹ was ranged from 196g (E4) to 233g (E3) (Table 9). Among genotype studied, the grand polled data over two seasons and five environments, the seed yield plant⁻¹ was varied from 200g (G23) to 264g (G36) with over all mean of 221g.

Data regards to the seed yield plot⁻¹, the overall mean performance was 228g, 229g, 233g, 196g and 217g for the environments *viz.*, E1, E2, E3, E4 and E5, respectively. Among all, 15, 15, 19, 12 and 19 genotypes exhibited high seed yield plot⁻¹ than grand mean for the environments, *viz.*, E1, E2, E3, E4 and E5, respectively. The genotype, G36 (270g) had maximum seed yield plot⁻¹ followed by the genotypes, G24 (271g), G32 (267g) and G10 (266g) in E1. The genotype, G36 (275g) observed high seed yield plot⁻¹ followed by the genotypes, G24 (273g), G32 (272g) and G10 (267g) in E2. The genotype, G36 (285g) registered maximum seed yield plot⁻¹ followed by G10 (276g), G32 (274g) and G24 (270g) in E3. The genotype, G36 (231g) found high seed yield plot⁻¹ followed by G24 (227g), G10 (221g) and G32 (219g) in E4. The maximum seed yield plot⁻¹ recorded in genotype, G36 (263g) followed by G24 (261g), G10 (256g) and G4, G32 (253g) in E5.

Table 9: Environment wise pooled mean performance of two seasons for seed yield plant⁻¹ (g) and seed yield plot⁻¹ (g) in 40 genotypes of Niger.

S. No.	Genotype code	Seed yield plant ⁻¹						Seed yield plot ⁻¹					
		E1	E2	E3	E4	E5	GPM	E1	E2	E3	E4	E5	GPM
1	G 1	2.66	2.82	3.36	2.48	2.48	2.76	233	240	259	194	218	229
2	G 2	2.92	3.01	3.59	2.47	2.60	2.92	249	254	264	225	239	246
3	G 3	2.59	2.70	3.43	2.28	2.27	2.65	217	221	212	191	228	213
4	G 4	2.97	2.95	3.54	2.58	2.27	2.86	259	262	268	224	253	253
5	G 5	2.50	2.56	3.59	2.62	2.38	2.73	212	216	221	192	205	209
6	G 6	2.68	2.84	3.47	2.25	2.74	2.79	210	202	187	194	220	202
7	G 7	2.32	2.49	3.25	2.19	2.17	2.48	231	230	226	189	236	222
8	G 8	2.50	2.62	3.54	2.46	2.28	2.68	224	225	208	180	234	214
9	G 9	2.39	2.52	3.32	2.37	2.27	2.57	223	227	238	206	212	221
10	G 10	2.85	2.85	3.48	2.66	2.61	2.89	266	267	276	221	256	257
11	G 11	2.66	2.80	3.39	2.24	2.79	2.77	219	222	224	201	216	216
12	G 12	2.49	2.64	3.37	2.08	2.38	2.59	231	227	228	199	227	222
13	G 13	2.60	2.65	3.28	2.25	2.56	2.67	226	222	217	192	229	217
14	G 14	2.63	2.74	3.35	2.41	2.54	2.73	229	231	242	182	224	221
15	G 15	2.54	2.67	3.44	2.24	2.50	2.68	228	229	237	193	219	221
16	G 16	2.67	2.75	3.50	2.24	2.41	2.71	211	212	224	192	192	206
17	G 17	2.68	2.81	3.23	2.24	2.64	2.72	201	203	196	203	202	201
18	G 18	2.61	2.76	3.14	2.27	2.74	2.70	211	212	220	189	202	207
19	G 19	2.45	2.54	3.58	2.25	2.38	2.64	215	216	211	188	219	210
20	G 20	2.35	2.51	3.26	2.32	2.20	2.53	213	215	236	188	187	207
21	G 21	2.88	2.71	3.61	2.30	2.65	2.83	215	219	233	183	200	209
22	G 22	2.56	2.69	3.29	2.40	2.78	2.74	215	217	227	192	202	210
23	G 23	2.62	2.89	3.70	2.20	2.76	2.83	205	204	216	192	184	200
24	G 24	3.08	3.38	4.12	2.78	3.08	3.29	271	272	270	227	261	260
25	G 25	2.77	2.75	3.24	2.11	2.56	2.69	243	247	257	195	218	232
26	G 26	2.76	3.13	3.60	2.36	2.70	2.91	229	233	238	205	200	221
27	G 27	2.60	2.72	3.30	2.37	2.48	2.69	224	229	241	186	191	214
28	G 28	2.17	2.28	2.98	2.34	2.64	2.48	210	210	214	191	199	205
29	G 29	2.65	2.80	3.19	2.19	2.56	2.68	226	230	235	198	204	218
30	G 30	2.58	2.63	3.18	2.41	2.49	2.66	222	220	210	191	217	211
31	G 31	2.67	2.79	3.28	2.53	2.26	2.71	216	216	221	187	205	209
32	G 32	3.30	3.40	4.04	2.75	2.76	3.25	267	273	274	219	253	257
33	G 33	2.75	2.81	3.55	2.30	2.63	2.81	219	211	199	189	217	207
34	G 34	2.48	2.72	3.18	2.47	2.54	2.68	224	221	220	183	218	212
35	G 35	2.75	2.77	3.68	2.54	2.54	2.86	236	218	226	202	226	221
36	G 36	3.57	3.56	4.18	2.85	3.17	3.48	270	275	285	231	263	264
37	G 37	2.59	2.79	2.98	2.37	2.59	2.66	221	231	245	184	205	217
38	G 38	3.23	3.32	4.11	2.73	2.96	3.27	229	233	238	185	226	222
39	G 39	2.55	2.90	3.65	2.49	2.71	2.86	226	225	236	189	211	217
40	G 40	3.22	3.41	4.02	2.72	2.97	3.27	234	235	239	186	227	224
	GM	2.70	2.82	3.47	2.40	2.57	2.80	228	229	233	196	217	221
	Range	2.17-3.57	2.28-3.56	2.98-4.18	2.08-2.85	2.17-3.17	2.48-3.48	201-270	202-275	187-285	180-231	184-263	200-264
	S.E. ±	0.23	0.20	0.24	0.16	0.22		14.54	14.75	21.46	12.61	17.77	
	C.D. (5%)	0.45	0.39	0.48	0.31	0.44		28.95	29.36	42.73	25.10	35.38	

Note: GC - Genotype code, GM - Grand Mean & GPM - Grand Pooled Mean over the seasons and the environments

4.2.11. Days to maturity:

The environment wise variation in grand mean of two seasons for days to maturity varied from 81 days (E3) to 87 days (E4) (Table 10). The grand polled mean over two seasons and five environments, the mean days to maturity was varied from 75 days (G25) to 87 days (G9) with over all mean of 84 days.

In the present investigation, the overall mean performance for days to maturity was 84 days, 83 days, 81 days, 87 days and 83 days for the environments *viz.*, E1, E2, E3, E4 and E5, respectively. Among all, 26, 17, 21, 23 and 25 genotypes required more days to matured the crop than grand mean for the environments, *viz.*, E1, E2, E3, E4 and E5, respectively. While 11, 13, 13, 14 and 10 genotypes required less days to matured the crop than average for the environments, *viz.*, E1, E2, E3, E4 and E5, respectively. The genotype, G24 (75 days) found early matured followed by the genotypes, G25, G26 (76 days), G27, G28 (79 days) and G22 (81 days) while was genotypes, G5, G16 (90 days) reported maximum days for maturity of crop followed by G2 (89days) and G4, G8, G14, G15, G21 (88 days) in E1. The genotypes, G24, G25 (74 days) found early matured followed by G26 (77 days) and G19 (79 days) while genotypes, G2, G5 (87 days) observed maximum days to maturity followed by G8, G15, G21 (86 days) in E2. The genotypes, G24, G25 (71 days) found less days of crop maturity followed by G26 (75 days), G19 (76 days), G29 (77 days), G29 (78 days) and G28 (79 days) while genotype, G9 (87 days) observed late matured followed by the genotypes, G3, G34 (85 days) and G4, G8, G36 (84 days) in E3. The genotypes, G24, G26 (80 days) found early matured followed by G25 (81 days) and G27 (83 days) while genotype, G22 (92 days) reported maximum days for crop maturity followed by the genotypes, G9, G14, G17, G30 (90 days) in E4. The genotype, G26 (73 days) reported less days for crop maturity followed by the genotypes, G25 (74 days), G27, G29 (75 days), G28 (77 days) and G24 (78 days) while genotype, G8 (89 days) reported maximum days for maturity of crop followed by G8 (88 days) and G7, G11 (87 days) in E5.

4.2.12. Oil content (%):

The environment wise grand mean of two seasons for oil content was ranged from 37% (E1, E4 & E5) to 39% (E3) (Table 10). Among all the genotypes studied,

Table 10: Environment wise pooled mean performance of two seasons for days to maturity and oil content (%) in 40 genotypes of Niger.

S. No.	Genotype code	Days to maturity						Oil content (%)					
		E1	E2	E3	E4	E5	GPM	E1	E2	E3	E4	E5	GPM
1	G 1	87	84	82	85	83	84	38	40	38	38	37	38
2	G 2	89	87	83	86	84	86	37	39	40	38	37	38
3	G 3	86	84	85	87	84	85	37	38	38	36	37	37
4	G 4	88	85	84	86	88	86	38	39	40	37	38	38
5	G 5	90	87	81	86	85	85	38	39	39	38	37	38
6	G 6	83	82	81	88	85	84	38	39	40	38	38	38
7	G 7	85	83	82	87	87	85	38	39	38	38	38	38
8	G 8	88	86	84	89	88	87	38	39	38	37	38	38
9	G 9	86	84	87	90	89	87	39	39	39	38	37	38
10	G 10	86	83	82	88	85	85	39	40	42	39	39	40
11	G 11	85	83	82	88	87	85	38	39	40	37	38	38
12	G 12	86	83	82	89	86	85	34	35	37	36	36	36
13	G 13	87	84	82	89	85	85	38	39	38	38	38	38
14	G 14	88	83	83	90	86	86	33	35	40	34	34	35
15	G 15	88	86	81	88	86	86	35	37	39	36	35	37
16	G 16	90	85	83	89	85	86	38	39	37	37	38	38
17	G 17	84	80	82	90	84	84	37	38	40	37	37	38
18	G 18	87	83	80	88	85	84	35	37	40	36	37	37
19	G 19	82	79	76	88	84	82	37	38	38	36	37	37
20	G 20	85	81	81	88	84	84	35	37	38	36	36	36
21	G 21	88	86	81	88	86	86	36	38	38	37	36	37
22	G 22	81	80	83	92	85	84	36	38	37	35	37	36
23	G 23	84	83	80	89	81	83	34	35	40	35	36	36
24	G 24	75	74	71	80	78	76	40	40	42	40	40	40
25	G 25	76	74	71	81	74	75	35	37	40	35	37	37
26	G 26	76	77	75	80	73	76	36	37	39	35	36	37
27	G 27	79	81	78	83	75	79	35	36	40	36	37	37
28	G 28	79	82	79	86	77	80	36	37	38	36	36	37
29	G 29	83	81	77	88	75	81	34	36	39	35	35	36
30	G 30	84	85	80	90	80	84	36	38	37	35	36	36
31	G 31	85	82	69	89	79	81	36	38	40	37	38	38
32	G 32	87	82	80	85	80	83	39	40	42	40	40	40
33	G 33	85	85	78	89	84	84	36	38	40	36	37	37
34	G 34	85	84	85	87	85	85	35	36	40	36	35	36
35	G 35	85	83	83	88	85	85	36	37	40	36	38	37
36	G 36	85	85	84	87	83	85	41	41	43	41	41	41
37	G 37	85	84	83	89	85	85	34	35	40	36	35	36
38	G 38	82	84	82	85	83	83	38	40	41	39	39	39
39	G 39	83	83	81	86	83	83	39	41	41	40	40	40
40	G 40	85	83	82	84	83	84	40	40	42	40	41	40
	GM	84	83	81	87	83	84	37	38	39	37	37	38
	Range	75-90	74-87	71-87	80-92	73-89	75-87	33-41	35-41	37-43	34-41	34-41	35-41
	S.E. $\pm$	1.41	1.62	2.60	1.64	2.07		1.79	1.50	1.38	1.19	1.36	
	C.D. (5%)	2.81	3.22	5.17	3.27	4.13		3.56	2.98	2.76	2.37	2.71	

Note: GM - Grand Mean & GPM - Grand Pooled Mean over the seasons and the environments

the grand polled mean for oil content over two seasons and five environments was varied from 35% (G14) to 41% (G36) with over all mean of 38%.

In the present investigation, the overall mean performance for oil content was 37%, 38%, 39%, 37% and 37% for the environments *viz.*, E1, E2, E3, E4 and E5, respectively. Among all, 17, 18, 22, 12 and 16 genotypes recorded more oil content than grand mean for the environments, *viz.*, E1, E2, E3, E4 and E5, respectively. The genotype, G36 (41 %) observed maximum oil content followed by the genotypes, G24, G40 (40 %) and G9, G10, G32, G39 (39 %) in E1. The genotypes, G36, G39 (41 %) registered maximum oil content followed by the genotypes, G1, G10, G24, G32, G38, G40 (40 %) in E2. The genotype, G36 (43 %) observed maximum oil content followed by the genotypes, G10, G24, G32, G40 (42 %) and G38, G39 (41 %) in E3. The genotype, G36 (41 %) reported maximum oil content followed by the genotypes, G24, G32, G39, G40 (40 %) and G10, G38 (39 %) in E4. The genotypes, G36, G40 (41 %) noticed maximum oil content followed by the genotypes, G24, G32, G39 (40 %) and G10, G38 (39 %) in E5.

4.2.13. Protein content (%):

The environment wise grand mean performance of two seasons for protein content varied from 19% (E1, E2, E4 & E5) to 20% (E3) (Table 11). In grand polled mean, the genotypic protein content over two seasons and five environments was ranged from 18% (G1, G2, G14, G16, G17 and G27) to 22% (G36) with over all mean of 19%.

As regards to the protein content, the overall mean performance was 19%, 19%, 20%, 19% and 19% for the environments *viz.*, E1, E2, E3, E4 and E5, respectively. Among all, 08, 14, 09, 11 and 12 genotypes had more protein content than grand mean for the environments, *viz.*, E1, E2, E3, E4 and E5, respectively. The genotype, G36 (21%) observed maximum protein content followed by the genotypes, G4, G18, G24, G32, G35, G38, G40 (20%) in E1. The genotype, G36 (23%) required maximum protein content followed by G40 (22%) and G24, G32, G38, G39 (21%) in E2. The genotype, G36 (23%) showed maximum protein content followed by the genotypes, G24, G38, G40 (22%) and G6, G11, G32, G35, G39 (21%) in E3. The genotypes, G36, G24, G40 (22%) reported maximum protein

Table 11: Environment wise pooled mean performance of two seasons for protein content (%) in 40 genotypes of Niger.

S. No.	Genotype code	Protein content (%)					GPM
		E1	E2	E3	E4	E5	
1	G 1	17	18	19	19	17	18
2	G 2	19	18	19	19	17	18
3	G 3	18	19	19	19	19	19
4	G 4	20	19	19	20	19	19
5	G 5	16	19	20	19	20	19
6	G 6	19	18	21	19	19	19
7	G 7	18	18	20	20	18	19
8	G 8	17	19	20	18	19	19
9	G 9	19	19	20	19	19	19
10	G 10	19	20	20	20	20	20
11	G 11	19	19	21	20	18	19
12	G 12	19	19	20	19	19	19
13	G 13	18	20	20	19	20	19
14	G 14	17	18	20	18	18	18
15	G 15	18	19	19	19	18	19
16	G 16	18	18	20	18	18	18
17	G 17	18	18	20	18	18	18
18	G 18	20	19	20	19	19	19
19	G 19	19	19	20	19	19	19
20	G 20	19	19	20	18	19	19
21	G 21	19	20	20	19	19	19
22	G 22	19	19	20	19	19	19
23	G 23	18	19	20	18	19	19
24	G 24	20	21	22	22	20	21
25	G 25	19	18	20	18	19	19
26	G 26	18	20	19	18	20	19
27	G 27	17	18	19	18	19	18
28	G 28	17	20	19	19	19	19
29	G 29	18	20	20	18	19	19
30	G 30	18	19	19	19	19	19
31	G 31	19	18	19	19	18	19
32	G 32	20	21	21	21	21	21
33	G 33	19	19	20	19	19	19
34	G 34	19	20	20	20	20	20
35	G 35	20	20	21	19	20	20
36	G 36	21	23	23	22	22	22
37	G 37	18	19	20	19	19	19
38	G 38	20	21	22	20	20	21
39	G 39	19	21	21	21	20	20
40	G 40	20	22	22	22	21	21
	GM	19	19	20	19	19	19
	Range	16-21	18-23	19-23	18-22	17-22	18-22
	S.E. $\pm$	0.66	0.93	0.66	0.93	0.89	
	C.D. (5%)	1.32	1.86	1.32	1.86	1.76	

Note: GM - Grand Mean & GPM - Grand Pooled Mean over the seasons and the environments

content followed by the genotypes, G32, G39 (21%) and G4, G7, G10, G11, G34, G38 (20%) in E4. The genotype, G36 (22%) observed maximum protein content followed by the genotypes, G32, G40 (21%) and G5, G10, G13, G24, G34, G35, G38, G39 (20 %) in E5.

4.3. Genetic variability:

4.3.1. Component of variation

The total variation of the genotypes was partitioned into genotypic, phenotypic and environmental variance. In the present study, the estimates of variance due to these three components at each location over two seasons for thirteen quantitative and qualitative traits were given in Table no. 12.

On the basis of polled data, the environment wise phenotypic variances for various characters were ranged from 0.01 to 529.51 (E1), 0.01 to 580.68 (E2), 0.01 to 975.19 (E3), 0.01 to 342.40 (E4) and 0.01 to 667.32 (E5), respectively. The location wise range of genotypic variances for various characters from 0.01 to 212.37, 0.01 to 254.48, 0.01 to 284.22, 0.00 to 103.93 and 0.01 to 193.51 for E1, E2, E3, E4 and E5, respectively. The location wise environmental variances were ranged from 0.00 to 317.14 (E1), 0.00 to 326.21 (E2), 0.00 to 690.97 (E3), 0.00 to 238.48 (E4) and 0.00 to 473.81 (E5), respectively for various characters.

In pooled data at ARS, Phondaghat (Table 12), the phenotypic variance was maximum for seed yield plot⁻¹ (529.51) followed by number of capitulum plant⁻¹ (143.46) and plant height (113.21) while it was minimum for capitulum diameter (0.01) followed by 1000 seed weight (0.03) and seed yield plant⁻¹ (0.13). Similarly, the magnitude of genotypic variance was higher for seed yield plot⁻¹ (212.37) followed by number of capitulum plant⁻¹ (130.30) and plant height (79.20) while it was minimum for capitulum diameter (0.01) followed by 1000 seed weight (0.01), seed yield plant⁻¹ (0.05) and protein content (0.90). The magnitude for environmental variance was higher for seed yield plot⁻¹ (317.14) followed by plant height (34.21) and number of capitulum plant⁻¹ (13.55) while it was minimum for capitulum diameter (0.00) followed by 1000 seed weight (0.02) seed yield plant⁻¹ (0.08) protein content (0.66) and number of primary branches plant⁻¹ (0.99).

The phenotypic variance was maximum for seed yield plot⁻¹ (580.68) followed by plant height (64.26) and number of capitulum plant⁻¹ (43.18) while it was minimum for capitulum diameter (0.01) followed by 1000 seed weight (0.03) and seed yield plant⁻¹ (0.11). Similarly, the magnitude of genotypic variance was higher for seed yield plot⁻¹ (254.48) followed by number of capitulum plant⁻¹ (23.89) and plant height (24.68) while it was minimum for capitulum diameter (0.01) followed by 1000 seed weight (0.01), seed yield plant⁻¹ (0.06) and protein content (0.80). The magnitude for environmental variance was higher for seed yield plot⁻¹ (326.21) followed by plant height (39.57) and number of capitulum plant⁻¹ (19.30) while it was minimum for capitulum diameter (0.00) followed by 1000 seed weight (0.02) and seed yield plant⁻¹ (0.06) in case pooled results at ARS, Shirgaon (Table 19).

The pooled results of Department of Agril. Botany, Dapoli (Table 12) showed that, the phenotypic variance was maximum for seed yield plot⁻¹ (975.19) followed by plant height (107.98) and number of capitulum plant⁻¹ (65.64) while it was minimum for capitulum diameter (0.01) followed by 1000 seed weight (0.05) and seed yield plant⁻¹ (0.15). Similarly, the magnitude of genotypic variance was higher for seed yield plot⁻¹ (284.22) followed by plant height (63.77) and number of capitulum plant⁻¹ (52.49) while it was minimum for capitulum diameter (0.01) followed by 1000 seed weight (0.02) seed yield plant⁻¹ (0.06) and protein content (0.64). The magnitude for environmental variance was higher for seed yield plot⁻¹ (690.97) followed by plant height (44.21) and number of capitulum plant⁻¹ (13.15) while it was minimum for capitulum diameter (0.00) followed by 1000 seed weight (0.03) seed yield plant⁻¹ (0.09) and protein content (0.66).

In pooled data at RARS, Karjat (Table 12), the phenotypic variance was maximum for seed yield plot⁻¹ (342.40) followed by plant height (50.61) and number of capitulum plant⁻¹ (44.45) while it was minimum for capitulum diameter (0.01) followed by seed yield plant⁻¹ (0.06) and 1000 seed weight (0.08). Similarly, the magnitude of genotypic variance was higher for seed yield plot⁻¹ (103.93) followed by number of capitulum plant⁻¹ (34.23) and plant height (20.16) while it was minimum for capitulum diameter (0.00) followed by 1000 seed

Table 12: Environment wise components of variation of pooled data for quantitative and qualitative traits in 40 genotypes of Niger.

Sr. No.	Characters	ARS, Phondaghat (E1)			ARS, Shirgaon (E2)			Dept. of Agril. Botany, Dapoli (E3)			RARS, Karjat (E4)			ARS, Palghar (E5)		
		σ^2_p	σ^2_g	σ^2_e	σ^2_p	σ^2_g	σ^2_e	σ^2_p	σ^2_g	σ^2_e	σ^2_p	σ^2_g	σ^2_e	σ^2_p	σ^2_g	σ^2_e
1.	DFFP	8.10	6.28	1.82	10.02	7.81	2.21	13.91	11.96	1.95	12.51	10.48	2.03	13.86	11.72	2.13
2.	PH (cm)	113.41	79.20	34.21	64.26	24.68	39.57	107.98	63.77	44.21	74.61	34.70	39.91	50.61	20.16	30.45
3.	NPBPP	5.10	4.11	0.99	4.10	2.76	1.34	3.16	2.24	0.92	4.59	3.50	1.09	4.63	3.92	0.70
4.	NSBPP	20.21	16.71	3.49	13.40	8.30	5.10	10.03	6.74	3.29	12.98	8.96	4.02	11.40	8.90	2.50
5.	NCPP	143.85	130.30	13.55	43.18	23.89	19.30	65.64	52.49	13.15	43.38	33.20	10.18	44.45	34.23	10.22
6.	CD (cm)	0.01	0.01	0.00	0.01	0.01	0.00	0.01	0.01	0.00	0.01	0.01	0.00	0.01	0.00	0.00
7.	NSPC	21.30	11.03	10.27	15.84	8.24	7.60	20.20	11.04	9.16	16.50	7.23	9.27	6.87	2.47	4.41
8.	1000 SW (g)	0.03	0.01	0.02	0.03	0.01	0.02	0.05	0.02	0.03	0.06	0.01	0.05	0.08	0.02	0.06
9.	SYPP (g)	0.13	0.05	0.08	0.11	0.06	0.06	0.15	0.06	0.09	0.10	0.03	0.07	0.06	0.02	0.04
10.	SYPP (g)	529.51	212.37	317.14	580.68	254.48	326.21	975.19	284.22	690.97	667.32	193.51	473.81	342.40	103.93	238.48
11.	DM	14.85	11.86	2.99	10.82	6.89	3.93	20.88	10.75	10.13	19.37	12.93	6.44	9.30	5.25	4.05
12.	OC (%)	6.57	1.77	4.80	4.72	1.36	3.36	4.03	1.15	2.88	4.31	1.53	2.78	4.18	2.05	2.13
13.	PC (%)	1.56	0.90	0.66	2.11	0.80	1.31	1.30	0.64	0.66	1.81	0.63	1.18	2.07	0.76	1.31

σ^2_p : Phenotypic variance, σ^2_g : Genotypic variance and σ^2_e : Environmental variance

DFFP: Days to 50 per cent flowering

NCPP: No. of capitula plant⁻¹

SYPP: Seed yield plant⁻¹

PC: Protein content

PH: Plant height

CD: Capitulum diameter

SYPP: Seed yield plot⁻¹

NPBPP: No. of primary branches plant⁻¹

NSPC: No. of seeds capitulum⁻¹

DM: Days to maturity

NSBPP: No. of secondary branches plant⁻¹

SW: Seed weight

OC: Oil content

weight (0.02), seed yield plant⁻¹ (0.02) and protein content (0.76). The magnitude for environmental variance was higher for seed yield plot⁻¹ (238.48) followed by plant height (30.45) and number of capitulum plant⁻¹ (10.22) while it was minimum for capitulum diameter (0.00) followed by seed yield plant⁻¹ (0.04), 1000 seed weight (0.06) and number of primary branches plant⁻¹ (0.70).

The pooled results of ARS, Palghar (Table 12) showed that, the phenotypic variance was maximum for seed yield plot⁻¹ (667.32) followed by plant height (74.61) and number of capitulum plant⁻¹ (43.38) while it was minimum for capitulum diameter (0.01) followed by 1000 seed weight (0.06) and seed yield plant⁻¹ (0.10). Similarly, the magnitude of genotypic variance was higher for seed yield plot⁻¹ (193.51) followed by plant height (34.70) and number of capitulum plant⁻¹ (33.20) while it was minimum for capitulum diameter (0.01) followed by 1000 seed weight (0.01), seed yield plant⁻¹ (0.03) and protein content (0.63). The magnitude for environmental variance was higher for seed yield plot⁻¹ (473.81) followed by plant height (39.91) and number of capitulum plant⁻¹ (10.18) while it was minimum for capitulum diameter (0.00) followed by 1000 seed weight (0.05) and seed yield plant⁻¹ (0.07).

4.3.2. Coefficient of variation

The environment wise estimates of coefficient of variation over two seasons at phenotypic level and genotypic level was given in Table 13 and depicted in Fig. 1. The phenotypic coefficients of variation were greater in magnitude over the respective genotypic coefficient of variation for all the characters, locations, seasons and pooled data under study.

On the basis of pooled data, the environment wise phenotypic coefficient of variation for various characters were ranged from 4.56 to 30.20 (E1), 3.98 to 20.88 (E2), 5.10 to 20.51 (E3), 3.50 to 27.91 (E4) and 5.30 to 23.66 (E5), respectively. The location wise range of genotypic coefficient of variation for various characters was 3.62 to 28.75 (E1), 3.07 to 17.14 (E2), 2.72 to 17.69 (E3), 2.63 to 25.70 (E4) and 3.32 to 20.67 (E5), respectively.

In pooled data at ARS, Phondaghat (Table 13), the phenotypic coefficient of variation was maximum for number of capitulum plant⁻¹ (30.20), number of

secondary branches plant⁻¹ (28.18) and number of primary branches plant⁻¹ (25.46) while it was minimum for days to maturity (4.56), days to 50 per cent flowering (5.72) and 1000 seed weight (6.53). Similarly, the magnitude of genotypic coefficient of variation was higher for number of capitulum plant⁻¹ (28.75), number of secondary branches plant⁻¹ (25.63) and number of primary branches plant⁻¹ (22.85) while it was minimum for oil content (3.62), 1000 seed weight (3.81) and days to maturity (4.08).

The phenotypic coefficient of variation was maximum for number of primary branches plant⁻¹ (20.88), number of secondary branches plant⁻¹ (18.24) and number of capitulum plant⁻¹ (17.54) while it was minimum for days to maturity (3.98), oil content (5.72) and plant height (6.42). Similarly, the magnitude of genotypic coefficient of variation was higher for number of primary branches plant⁻¹ (17.14), number of secondary branches plant⁻¹ (14.35) and number of capitulum plant⁻¹ (13.05) while it was minimum for oil content (3.07), days to maturity (3.18) and plant height (3.98) in case pooled data of ARS, Shirgaon (Table 20).

The pooled results of Department of Agril. Botany, Dapoli (Table 13) showed that, the phenotypic coefficient of variation was maximum for number of primary branches plant⁻¹ (20.51), number of capitulum plant⁻¹ (19.78) and number of secondary branches plant⁻¹ (19.61) while it was minimum for oil content (5.10), days to maturity (5.67) and protein content (5.70). Similarly, the magnitude of genotypic coefficient of variation was higher for number of capitulum plant⁻¹ (17.69), number of primary branches plant⁻¹ (17.27) and number of secondary branches plant⁻¹ (16.08) while it was minimum for oil content (2.72), protein content (3.99) and days to maturity (4.07).

The pooled data of RARS, Karjat (Table 13), the phenotypic coefficient of variation was maximum for number of primary branches plant⁻¹ (27.91), number of secondary branches plant⁻¹ (23.54) and number of capitulum plant⁻¹ (18.20) while it was minimum for days to maturity (3.50), plant height (5.18) and oil content (5.54). Similarly, the magnitude of genotypic coefficient of variation was higher for number of primary branches plant⁻¹ (25.70) number of secondary

branches plant⁻¹ (20.80) and number of capitulum plant⁻¹ (15.97) while it was minimum for days to maturity (2.63), plant height (3.27) and oil content (3.88).

The pooled results of ARS, Palghar (Table 13) showed that, the phenotypic coefficient of variation was maximum for number of primary branches plant⁻¹ (23.66), number of secondary branches plant⁻¹ (21.51) and number of capitulum plant⁻¹ (18.35) while it was minimum for days to maturity (5.30), oil content (5.57) and plant height (6.27). Similarly, the magnitude of genotypic coefficient of variation was higher for number of primary branches plant⁻¹ (20.67) number of secondary branches plant⁻¹ (17.87) and number of capitulum plant⁻¹ (16.05) while it was minimum for oil content (3.32), protein content (4.20), plant height (4.28) and days to maturity (4.33).

4.4. Heritability

The environment wise estimation of heritability over two seasons for various traits was given in Table no. 13 and presented in Fig. 1.

On the basis of polled data, the environment wise heritability was ranged from 26.93 to 90.58 per cent (E1), 28.78 to 77.92 per cent (E2), 28.55 to 85.97 per cent (E3), 35.88 to 84.80 per cent (E4) and 35.02 to 83.78 per cent (E5), respectively.

The pooled results of ARS, Phondaghat (Table 20) showed that, very high heritability estimates were obtained for the character number of capitulum plant⁻¹ (90.58%) followed by number secondary branches plant⁻¹ (82.71%), capitulum diameter (80.82%), number primary branches plant⁻¹ (80.61%), days to 50 per cent flowering (77.55%), days to maturity (69.85%) and plant height (69.83). High heritability estimates were obtained for the characters, protein content (57.88%) followed by number seeds capitulum⁻¹ (51.79%), seed yield plot⁻¹ (40.11%), seed yield plant⁻¹ (39.90%) and 1000 seed weight (33.95%) and medium heritability was recorded in oil content (26.93%).

In pooled data at ARS, Shirgaon (Table 13), the highest heritability was exhibited for the characters, days to 50 per cent flowering (77.92%) followed by number primary branches plant⁻¹ (67.38%), days to maturity (63.70%) capitulum diameter (63.30%) and number secondary branches plant⁻¹ (61.94%). High heritability estimates were obtained for the characters total number of capitulum

plant⁻¹ (55.31%), followed by total number seeds capitulum⁻¹ (52.04%), seed yield plant⁻¹ (48.93%), seed yield plot⁻¹ (43.82%), 1000 seed weight (43.62%), plant height (38.41%) and protein content (37.96%) while medium heritability was obtained for oil content (28.78%).

The pooled results of Department of Agril. Botany, Dapoli (Table 13), very high heritability estimates were obtained for the character days to 50 per cent flowering (85.97%) followed by number of capitulum plant⁻¹ (79.97%) and number of primary branches plant⁻¹ (70.96%), capitulum diameter (67.39%), number of secondary branches plant⁻¹ (67.19%). High heritability estimates were obtained for the characters, plant height (59.06%), number seeds capitulum⁻¹ (54.65%), days to maturity (51.50%) protein content (49.15%), seed yield plot⁻¹ (49.14%), 1000 seed weight (42.56% and seed yield plant⁻¹ (40.13%) while medium heritability estimates were obtained for oil content (28.55%).

Highest heritability was exhibited in pooled data at RARS, Karjat (Table 13) for the characters, number of primary branches plant⁻¹ (84.80%) followed by days to 50 per cent flowering (84.60%), number of secondary branches plant⁻¹ (78.06%), number of capitulum plant⁻¹ (77.00%). High heritability estimates were obtained for the characters, plant height at maturity (59.06%), days to maturity (56.46%), oil content (49.09%), capitulum diameter (42.91%), seed yield plant⁻¹ (40.08%), seed yield plot⁻¹ (38.35%), protein content (36.74%), 1000 seed weight (36.64%) and number seeds capitulum⁻¹ (35.88%).

The pooled data at ARS, Palghar (Table 13), very high heritability estimates were obtained for the character days to 50 per cent flowering (83.78%) followed by number of capitulum plant⁻¹ (76.53%), number of primary branches plant⁻¹ (76.31%), number of secondary branches plant⁻¹ (69.02%), days to maturity (66.75%), capitulum diameter (63.30%). High heritability estimates were obtained for the characters, plant height (46.51%), number seeds capitulum⁻¹ (43.82%), seed yield plot⁻¹ (39.00%) seed yield plant⁻¹ (38.63%) and 1000 seed weight (38.07%) and medium heritability estimates were obtained for oil content (35.47%) and protein content (35.02%)

4.5. Genetic advance (GA) and genetic advance per cent mean (GAM)

The environment wise genetic advance and genetic advance per cent mean estimates over two seasons for various traits were presented in Table no. 13 and presented in Fig. 1.

On the basis of pooled data, the environment wise genetic advance was ranged from 0.16 to 22.38 per cent (E1), 0.14 to 21.75 per cent (E2), 0.15 to 18.75 per cent (E3), 0.08 to 11.57 per cent (E4) and 0.13 to 15.43 per cent (E5), respectively whereas genetic advance per cent mean was ranged from 3.87 to 56.36 per cent (E1), 3.39 to 28.99 per cent (E2), 3.00 to 32.59 per cent (E3), 4.07 to 48.75 per cent (E4) and 4.07 to 37.20 per cent (E5), respectively.

The pooled results of ARS, Phondaghat (Table 13) showed the highest estimates of genetic advance were noticed in character, number of capitula plant⁻¹ (22.38) followed by seed yield plot⁻¹ (19.01) and plant height (15.32) whereas lowest estimates of genetic advance was recorded in capitulum diameter (0.16). Other characters had genetic advance at the tune of 10.30 for seed yield plant⁻¹, 8.75 for total number of primary branches plant⁻¹, 7.66 for number of secondary branches plant⁻¹, 6.34 for days to maturity, 6.12 for 1000 seed weight, 4.92 for number of seeds capitulum⁻¹, 4.55 for days to 50 per cent flowering, 1.49 for protein content and 1.42 for oil content. The highest genetic advance as per cent of mean was reported by number of capitula plant⁻¹ (56.36%), followed by number of secondary branches plant⁻¹ (48.02%) and number of primary branches plant⁻¹ (42.27%) whereas the lowest genetic advance as per cent of mean was recorded by oil content (3.87%).

On the basis of pooled data of ARS, Shirgaon (Table 13) recorded the highest estimates of genetic advance were noticed in character, seed yield plot⁻¹ (21.75) followed by seed yield plant⁻¹ (10.34), 1000 seed weight (10.15) and number of primary branches plant⁻¹ (8.81) whereas lowest estimates of genetic advance was recorded in capitulum diameter (0.14). Other characters had genetic advance at the tune of 7.49 for number of capitula plant⁻¹ and 6.34 for plant height, 5.08 for days to 50 per cent flowering, 4.67 for number of secondary branches plant⁻¹, 4.32 for days to maturity, 4.27 for number of seeds capitulum⁻¹, 1.29 for oil content and

1.14 for protein content. The highest genetic advance as per cent of mean was reported by number of primary branches plant⁻¹ (28.99%) followed by number of secondary branches plant⁻¹ (23.27%) whereas the lowest genetic advance as per cent of mean was recorded by oil content (3.39%).

In pooled results at Department of Agril. Botany, Dapoli (Table 13), the highest estimates of genetic advance were noticed in character, seed yield plot⁻¹ (18.75) followed by number of capitula plant⁻¹ (13.35), plant height (12.64), seed yield plant⁻¹ (10.32) and 1000 seed weight (10.20) whereas lowest estimates of genetic advance was recorded in capitulum diameter (0.15). Other characters had genetic advance at the tune of 8.60 for number of primary branches plant⁻¹, 6.61 for days to 50 per cent flowering, 5.06 for number of seeds capitulum⁻¹, 4.85 for days to maturity, 4.38 for number of secondary branches plant⁻¹, 1.18 for oil content and 1.16 for protein content. The highest genetic advance as per cent of mean was reported by number of capitula plant⁻¹ (32.59%), followed by number of primary branches plant⁻¹ (29.98%) and number of primary branches plant⁻¹ (27.14%) whereas the lowest genetic advance as per cent of mean was recorded by oil content (3.00%).

In the investigation of pooled data at RARS, Karjat (Table 13) observed the highest estimates of genetic advance were noticed in character, seed yield plot⁻¹ (11.57) followed by number of capitula plant⁻¹ (10.58), seed yield plant⁻¹ (10.20) and 1000 seed weight (10.15) whereas lowest estimates of genetic advance was recorded in capitulum diameter (0.08). Other characters had genetic advance at the tune of 8.76 for number of primary branches plant⁻¹, 8.55 for days to maturity, 6.49 for days to 50 per cent flowering, 5.94 for number of seeds capitulum⁻¹, 5.84 for plant height, 5.43 for number of secondary branches plant⁻¹, 2.07 for oil content and 1.09 for protein content. The highest genetic advance as per cent of mean was reported by number of primary branches plant⁻¹ (48.75%), followed by number of secondary branches plant⁻¹ (37.85%) and number of capitula plant⁻¹ (28.87%) whereas the lowest genetic advance as per cent of mean was recorded by days to maturity (4.07%).

In pooled results at ARS, Palghar (Table 13), the highest estimates of genetic

Table 13: Environment wise estimates of genetic parameters of pooled data for quantitative and qualitative traits in 40 genotypes of Niger.

Sr. No.	Characters	ARS, Phondaghat (E1)						ARS, Shirgaon (E2)						Dept. of Agril. Botany, Dapoli (E3)					
		PCV	GCV	H ² b	GA	GAM	Ga	PCV	GCV	H ² b	GA	GAM	Ga	PCV	GCV	H ² b	GA	GAM	Ga
1.	DFPF	5.72	5.03	77.55	4.55	9.13	A	6.43	5.67	77.92	5.08	10.32	A	7.67	7.11	85.97	6.61	13.59	A
2.	PH (cm)	8.07	6.75	69.83	15.32	11.61	A	6.42	3.98	38.41	6.34	5.08	A	7.37	5.66	59.06	12.64	8.97	A
3.	NPBPP	25.46	22.85	80.61	8.75	42.27	A	20.88	17.14	67.38	8.81	28.99	A	20.51	17.27	70.96	8.60	29.98	A
4.	NSBPP	28.18	25.63	82.71	7.66	48.02	A	18.24	14.35	61.94	4.67	23.27	A	19.61	16.08	67.19	4.38	27.14	A
5.	NCP	30.20	28.75	90.58	22.38	56.36	A	17.54	13.05	55.31	7.49	19.99	A	19.78	17.69	79.97	13.35	32.59	A
6.	CD (cm)	9.20	8.27	80.82	0.16	15.31	NA	9.93	7.90	63.30	0.14	12.94	NA	9.75	8.00	67.39	0.15	13.54	NA
7.	NSPC	13.83	9.95	51.79	4.92	14.75	A	13.12	9.46	52.04	4.27	14.06	A	13.90	10.27	54.65	5.06	15.64	A
8.	1000 SW (g)	6.53	3.81	33.95	6.12	4.57	A	6.71	4.43	43.62	10.15	6.03	A	8.81	5.75	42.56	10.20	7.73	A
9.	SYPp (g)	13.37	8.45	39.90	10.30	10.99	A	12.02	8.41	48.93	10.34	12.12	A	11.00	6.97	40.13	10.32	9.09	A
10.	SYPP (g)	10.11	6.40	40.11	19.01	8.35	A	10.54	6.98	43.82	21.75	9.51	A	13.41	7.24	49.14	18.75	8.05	A
11.	DM	4.56	4.08	79.85	6.34	7.50	A	3.98	3.18	63.70	4.32	5.22	A	5.67	4.07	51.50	4.85	6.02	A
12.	OC (%)	6.98	3.62	26.93	1.42	3.87	NA	5.72	3.07	28.78	1.29	3.39	NA	5.10	2.72	28.55	1.18	3.00	NA
13.	PC (%)	6.74	5.13	57.88	1.49	8.04	NA	7.55	4.65	37.96	1.14	5.90	NA	5.70	3.99	49.15	1.16	5.77	NA

PCV: Phenotypic Coefficient of Variation

GCV: Genotypic Coefficient of Variation

H²b: Heritability (Broad Sense)

GA: Genetic Advance

GAM: Genetic Advance per cent Mean

Ga: Gene Action

NA: Non-Additive

A: Additive

DFPF: Days to 50 per cent flowering

PH: Plant height

NPBPP: No. of primary branches plant⁻¹

NSBPP: No. of secondary branches plant⁻¹

NCP: No. of capitula plant⁻¹

CD: Capitulum diameter

NSPC: No. of seeds capitulum⁻¹

SW: Seed weight

SYPp: Seed yield plant⁻¹

SYPP: Seed yield plot⁻¹

DM: Days to maturity

OC: Oil content

PC: Protein content

(Table Contd...)

Sr. No.	Characters	RARS, Karjat (E4)						ARS, Palghar (E5)					
		PCV	GCV	H ² b	GA	GAM	Ga	PCV	GCV	H ² b	GA	GAM	Ga
1.	DFPF	7.21	6.63	84.60	6.49	12.56	A	7.32	6.70	83.78	6.10	12.64	A
2.	PH (cm)	5.18	3.27	59.06	5.84	4.25	A	6.27	4.28	46.51	8.28	6.01	A
3.	NPBPP	27.91	25.70	84.80	8.76	48.75	A	23.66	20.67	76.31	8.37	37.20	A
4.	NSBPP	23.54	20.80	78.06	5.43	37.85	A	21.51	17.87	69.02	5.12	30.58	A
5.	NCPP	18.20	15.97	77.00	10.58	28.87	A	18.35	16.05	76.53	10.38	28.93	A
6.	CD (cm)	9.00	5.90	42.91	0.08	7.96	NA	10.05	7.99	63.30	0.13	13.10	NA
7.	NSPC	12.52	7.50	35.88	5.94	9.25	A	16.32	10.81	43.82	8.67	14.74	A
8.	1000 SW (g)	11.59	5.98	36.64	10.15	6.36	A	10.01	4.59	38.07	10.11	4.34	A
9.	SYPP (g)	10.32	6.53	40.08	10.20	8.52	A	12.48	6.68	38.63	10.19	7.36	A
10.	SYPP (g)	9.42	5.19	38.35	11.57	5.89	A	11.89	6.40	39.00	15.43	7.10	A
11.	DM	3.50	2.63	56.46	8.55	4.07	A	5.30	4.33	66.75	6.05	7.29	A
12.	OC (%)	5.54	3.88	49.09	2.07	5.60	NA	5.57	3.32	35.47	1.52	4.07	NA
13.	PC (%)	7.50	4.54	36.74	1.09	5.67	NA	7.09	4.20	35.02	0.97	5.11	NA

PCV: Phenotypic Coefficient of Variation

GCV: Genotypic Coefficient of Variation

H²b: Heritability (Broad Sense)

GA: Genetic Advance

GAM: Genetic Advance Per cent Mean

Ga: Gene Action

NA: Non-Additive

A: Additive

DFPF: Days to 50 per cent flowering

PH: Plant height

NPBPP: No. of primary branches plant⁻¹

NSBPP: No. of secondary branches plant⁻¹

NCPP: No. of capitula plant⁻¹

CD: Capitulum diameter

NSPC: No. of seeds capitulum⁻¹

SW: Seed weight

SYPP: Seed yield plant⁻¹

SYPP: Seed yield plot⁻¹

DM: Days to maturity

OC: Oil content

PC: Protein content

advance were noticed in character, seed yield plot⁻¹ (15.43) followed by number of capitula plant⁻¹ (10.38), seed yield plant⁻¹ (10.19), 1000 seed weight (10.11), number of seeds capitulum⁻¹ (8.67) and number of primary branches plant⁻¹ (8.37) whereas lowest estimates of genetic advance was recorded in capitulum diameter (0.13). Other characters had genetic advance at the tune of 8.28 for plant height, 6.10 for days to 50 per cent flowering, 6.05 for days to maturity, 5.12 for number of secondary branches plant⁻¹, 1.52 for oil content and 0.97 for protein content. The highest genetic advance as per cent of mean was reported by number of primary branches plant⁻¹ (37.20%) followed by number of secondary branches plant⁻¹ (30.58%) whereas the lowest genetic advance as per cent of mean was recorded by oil content (4.07%).

4.6. Gene action studies

The environment wise nature of gene action of pooled data was exhibited by various traits which was given in Table no. 13.

The pooled data at ARS, Phondaghat (Table 13), most of the characters showed additive gene effects (days to 50 per cent flowering, plant height, number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of capitula plant⁻¹, number of seeds capitulum⁻¹, 1000 seed weight, seed yield plant⁻¹, seed yield plot⁻¹ and days to maturity) except capitulum diameter, oil content and protein content which is under the control of non-additive gene action.

In the pooled investigation at ARS, Shirgaon (Table 13), most of the characters showed additive gene effects (days to 50 per cent flowering, plant height, number of primary branches plant⁻¹, total number of secondary branches plant⁻¹, number of capitula plant⁻¹, number of seeds capitulum⁻¹, 1000 seed weight, seed yield plant⁻¹, seed yield plot⁻¹ and days to maturity) except capitulum diameter, oil content and protein content which is under the control of non-additive gene action.

In pooled data of Department of Agril. Botany, Dapoli (Table 13), most of the traits showed additive gene effects (days to 50 per cent flowering, plant height, number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of capitula plant⁻¹, number of seeds capitulum⁻¹, 1000 seed weight, seed

yield plant⁻¹, seed yield plot⁻¹ and days to maturity) except capitulum diameter, oil content and protein content which is under the control of non-additive gene action.

The pooled results at RARS, Karjat (Table 13), most of the characters showed additive gene effects (days to 50 per cent flowering, plant height, number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of capitula plant⁻¹, number of seeds capitulum⁻¹, 1000 seed weight, seed yield plant⁻¹, seed yield plot⁻¹ and days to maturity) except capitulum diameter, oil content and protein content which is under the control of non-additive gene action.

The pooled data of ARS, Palghar (Table 13), most of the characters showed additive gene effects (days to 50 per cent flowering, plant height, number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of capitula plant⁻¹, number of seeds capitulum⁻¹, 1000 seed weight, seed yield plant⁻¹, seed yield plot⁻¹ and days to maturity) except capitulum diameter, oil content and protein content which is under the control of non-additive gene action.

4.7. Genetic diversity (D² analysis)

4.7.1. Clustering pattern of genotypes

The cluster formation was done by Tochers' method suggested by Rao (1952). The environment wise distribution of 40 genotypes over two seasons in different clusters were presented in table 14 and depicted in Fig. 2.1 and 2.2.

The magnitude of D² values of pooled data, environment wise clusters of the forty genotypes were grouped in 5 (E1), 4 (E2), 4 (E3), 8 (E4) and 4 (E5), respectively.

The pooled results of ARS, Phondaghat (Table 14), the forty genotypes were grouped in 5 clusters on the basis of magnitude of D² values. Cluster I with 24 genotypes emerged as the largest cluster followed by cluster IV with 10 genotypes, cluster II with 4 genotypes whereas the cluster III and V consisted only single genotype each, thus these clusters remained solitary.

On the basis of magnitude of pooled D² values, the forty genotypes were grouped into 4 clusters of the experiment at ARS, Shirgaon (Table 14). Cluster I with 30 genotypes emerged as the largest cluster followed by cluster III with 5

Table 14: Environment wise grouping of 40 Niger genotypes of pooled data into different clusters by Tochers' method.

Cluster No.	ARS, Phondaghat (E1)		ARS, Shirgaon (E2)			Dept. of Agril. Botany, Dapoli (E3)		
	Number of Genotypes	Name of the Genotypes	Cluster No.	Number of Genotypes	Name of the Genotypes	Cluster No.	Number of Genotypes	Name of the Genotypes
I	24	G3, G4, G5, G6, G7, G8, G9, G11, G12, G13, G14, G15, G17, G19, G21, G22, G23, G29, G30, G31, G33, G34, G35, G37	I	30	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G30, G31, G33, G34, G35, G37, G39	I	32	G1, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G27, G28, G29, G30, G31, G33, G34, G35, G37, G39
II	4	G25, G26, G27, G28	II	4	G32, G36, G38, G40	II	5	G24, G32, G36, G38, G40
III	1	G39	III	5	G25, G26, G27, G28, G29	III	2	G25, G26
IV	10	G1, G2, G10, G16, G18, G20, G24, G32, G38, G40	IV	1	G24	IV	1	G2
V	1	G36						

(Table Contd...)

RARS, Karjat (E4)			ARS, Palghar (E5)		
Cluster No.	Number of Genotypes	Name of the Genotypes	Cluster No.	Number of Genotypes	Name of the Genotypes
I	20	G3, G7, G8, G9, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G29, G30, G31	I	27	G1, G2, G3, G5, G6, G7, G8, G9, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G30, G31, G33, G34, G35, G37
II	5	G1, G2, G4, G6, G10	II	5	G25, G26, G27, G28, G29
III	7	G33, G34, G35, G37, G38, G39, G40	III	7	G4, G10, G32, G36, G38, G39, G40
IV	1	G28	IV	1	G24
V	1	G5			
VI	1	G36			
VII	3	G25, G26, G27			
VIII	2	G24, G32			

genotypes, cluster II with 4 genotypes while the cluster IV was solitary.

The pooled data at Department of Agril. Botany, Dapoli (Table 14), the forty genotypes were grouped in 4 clusters on the basis of magnitude of D^2 values. Cluster I with 32 genotypes emerged as the largest cluster followed by cluster II with 5 genotypes, cluster III with 2 genotypes whereas the cluster IV was solitary.

The pooled D^2 values, the forty genotypes were grouped in 8 clusters of the experiment conducted at RARS, Karjat (Table 14). Cluster I with 20 genotypes emerged as the largest cluster followed by cluster III with 7 genotypes, cluster II with 5 genotypes cluster VII with 3 genotypes and cluster VIII with 2 genotypes whereas the cluster IV, V and VI were solitary in regard to the multi-varietal composition.

The results of ARS, Palghar (Table 14), the forty genotypes were grouped in 4 clusters on the basis of magnitude of D^2 values. Cluster I with 27 genotypes emerged as the largest cluster followed by cluster III with 7 genotypes, cluster II with 5 genotypes while the cluster IV was solitary.

4.7.2. Intra and Inter cluster divergence

The environment wise average intra and inter cluster D^2 and D values over two seasons was presented in Table no. 15 and their mutual relationship was depicted in Fig. 3.

On the basis of pooled data, the location wise highest intra cluster distance was observed for cluster IV ($D=4.69$), I ($D=3.04$), II ($D=4.12$), VIII ($D=3.10$) and III ($D=3.61$) for E1, E2, E3, E4 and E5, respectively.

The environment wise highest inter cluster distance for pooled data was observed between cluster II and V ($D=13.26$), II and III ($D=7.28$), III and IV ($D=7.89$), IV and VIII ($D=8.45$), and I and IV ($D=7.54$) for E1, E2, E3, E4 and E5, respectively whereas the environment wise lowest inter cluster distance was observed between cluster III and IV ($D=4.52$), I and II ($D=4.88$), I and IV ($D=4.75$), I and IV ($D=3.20$), and I and II ($D=4.59$) for E1, E2, E3, E4 and E5, respectively.

The pooled results of ARS, Phondaghat (Table 15) showed the highest intra cluster distance was observed for cluster IV ($D=4.69$) followed by cluster I ($D=3.90$) and cluster II ($D=2.62$). The cluster III and V showed no intra cluster

distance being solitary. The maximum inter cluster distance was observed between cluster II and V ($D=13.26$) followed by cluster I and V ($D=9.78$), cluster II and IV ($D=9.17$), cluster II and III ($D=8.41$) while cluster III and VI ($D=4.52$) and cluster I and III ($D=5.36$) noticed low inter cluster distance among themselves and others.

The pooled data at ARS, Shirgaon (Table 15) observed the highest intra cluster distance was observed for cluster I ($D=3.04$) followed by cluster III ($D=3.01$) and cluster II ($D=2.98$). The cluster IV showed no intra cluster distance being solitary. The maximum inter cluster distance was observed between cluster II and III ($D=7.28$) followed by cluster I and IV ($D=6.29$) and cluster III and IV ($D=5.99$) while inter cluster distance between cluster I and II ($D=4.88$), recorded the lowest inter cluster distance.

During the pooled investigation at Department of Agril. Botany, Dapoli (Table 15), the highest intra cluster distance was observed for cluster II ($D=4.12$) followed by cluster I ($D=3.70$) and cluster III ($D=1.73$). The cluster IV showed no intra cluster distance being solitary. The maximum inter cluster distance was observed between cluster III and IV ($D=7.89$) followed by cluster II and III ($D=7.59$) while inter cluster distance between cluster I and IV ($D=4.75$) noticed the lowest inter cluster distance among themselves and others.

In case pooled data of RARS, Karjat (Table 15), the highest intra cluster distance was observed for cluster VIII ($D=3.10$) followed by cluster III ($D=3.09$), cluster II ($D=2.69$), cluster VII ($D=2.53$) and cluster I ($D=2.46$). The cluster IV, V and VI showed no intra cluster distance being solitary. The maximum inter cluster distance was observed between cluster IV and VIII ($D=8.45$) followed by cluster I and VIII ($D=8.24$), cluster IV and VI ($D=7.79$) and cluster VI and VII ($D=7.78$) whereas cluster I and IV ($D=3.20$), cluster I and V ($D=3.26$), cluster V and VII ($D=3.31$), cluster IV and V ($D=3.41$) and cluster II and V ($D=3.72$) noticed low inter cluster distance among themselves and others.

The pooled results of ARS, Palghar (Table 15) exhibited the highest intra cluster distance was observed for cluster III ($D=3.61$) followed by cluster I ($D=2.65$) and cluster II ($D=2.64$). The cluster IV showed no intra cluster distance

Table 15: Environment wise average intra and inter cluster divergence (D & D²) of pooled data in 40 genotypes of Niger.

ARS, Phondaghat						ARS, Shirgaon					Dept. of Agril. Botany, Dapoli				
Cluster	I	II	III	IV	V	Cluster	I	II	III	IV	Cluster	I	II	III	IV
I	3.90 (15.21)	5.87 (34.46)	5.36 (28.73)	5.98 (35.76)	9.78 (95.65)	I	3.04 (9.24)	4.88 (23.81)	5.05 (25.50)	6.29 (39.56)	I	3.70 (13.69)	5.93 (35.16)	5.66 (32.40)	4.75 (22.56)
II		2.62 (6.86)	8.41 (70.73)	9.17 (84.09)	13.26 (175.83)	II		2.98 (8.88)	7.28 (53.00)	5.14 (26.42)	II		4.12 (16.97)	7.59 (57.61)	5.67 (32.15)
III			0.00 (0.00)	4.52 (20.43)	5.64 (31.81)	III			3.01 (9.06)	5.99 (35.88)	III			1.73 (2.99)	7.89 (62.25)
IV				4.69 (22.00)	6.68 (44.62)	IV				0.00 (0.00)	IV				0.00 (0.00)
V					0.00 (0.00)										

RARS, Karjat									ARS, Palghar				
Cluster	I	II	III	IV	V	VI	VII	VIII	Cluster	I	II	III	IV
I	2.46 (6.05)	4.76 (22.66)	4.52 (20.43)	3.20 (10.24)	3.26 (10.63)	6.70 (44.89)	4.49 (20.16)	8.24 (67.90)	I	2.65 (7.02)	4.59 (21.07)	5.30 (28.09)	7.54 (56.85)
II		2.69 (7.24)	4.46 (19.89)	5.06 (25.60)	3.72 (13.84)	4.86 (23.62)	4.57 (20.88)	4.74 (22.47)	II		2.64 (6.97)	6.17 (38.07)	6.45 (41.60)
III			3.09 (9.55)	5.50 (30.25)	5.16 (26.63)	4.24 (17.98)	6.00 (36.00)	6.36 (40.45)	III			3.61 (13.03)	4.94 (24.40)
IV				0.00 (0.00)	3.41 (11.63)	7.79 (60.68)	3.57 (12.74)	8.45 (71.40)	IV				0.00 (0.00)
V					0.00 (0.00)	6.79 (46.10)	3.31 (10.96)	7.31 (53.44)					
VI						0.00 (0.00)	7.78 (60.53)	4.69 (22.00)					
VII							2.53 (6.40)	7.40 (54.77)					
VIII								3.10 (9.61)					

(Figures in parenthesis indicate D² values)

being solitary. With regards to inter cluster distance, it was maximum between cluster I and IV ($D=7.54$) followed by cluster II and IV ($D=6.45$) and cluster II and III ($D=6.17$) while inter cluster distance between cluster I and II ($D=4.59$) recorded the lowest inter cluster distance.

4.7.3. Cluster means

The cluster means for thirteen characters among forty genotypes tested for two seasons and five environments were presented in Table 16.

4.7.3.1. Days to 50 per cent flowering

In the experiment at ARS, Phondaghat (Table 16), cluster wise mean for this character varied between 46.75 days (cluster II) to 50.62 days (cluster IV) with population mean of 49.05 days. The genotypes from cluster IV were late for this character.

In investigation at ARS, Shirgaon (Table 16), cluster mean for this character ranged from 41.50 days (cluster IV) to 50.36 days (cluster I) with population mean of 46.31 days. The genotypes from cluster I were late for this character.

During the experiment of Department of Agril. Botany, Dapoli (Table 16), cluster mean for this character varied between 40.58 days (cluster III) to 50.67 days (cluster IV) with population mean of 46.74 days. The genotypes from cluster IV were late for this character.

The results of RARS, Karjat (Table 16), cluster mean for this character ranged from 45.17 days (cluster VII) to 55.50 days (cluster VI) with population mean of 50.10 days. The genotypes from cluster VI were late for this character.

In the investigation at ARS, Palghar (Table 16), cluster mean for this character varied between 41.17 days (cluster IV) to 49.54 days (cluster I) with population mean of 45.42 days. The genotypes from cluster I were late for this character.

4.7.3.2. Plant height (cm)

The results of ARS, Phondaghat (Table 16), cluster mean for this character varied between 119.00 cm (cluster III) to 138.52 cm (cluster IV) with population mean of 126.32 cm. The genotypes from cluster III were showed minimum plant height.

The data of ARS, Shirgaon (Table 16), cluster mean for this character ranged from 118.50 cm (cluster II) to 130.13 cm (cluster II) with population mean of 123.95 cm. The genotypes from cluster III were noted for dwarf stature of plant.

The results of Department of Agril. Botany, Dapoli (Table 16), cluster mean for this character varied between 124.50 cm (cluster III) to 143.50 cm (cluster II) with population mean of 135.96 cm. The genotypes from cluster III were minimum height of the plant.

The data of RARS, Karjat (Table 16), cluster mean for this character ranged from 128.11 cm (cluster VII) to 144.60 cm (cluster III) with population mean of 137.17 cm. The genotypes from cluster VII were noticed for low heighted plant.

The cluster mean performance of ARS, Palghar (Table 16) for this character varied between 131.83 cm (cluster IV) to 143.10 cm (cluster III) with population mean of 136.81 cm. The genotypes from cluster IV were observed dwarf stature of the plant.

4.7.3.3. Number of primary branches plant⁻¹

In the inquisition at ARS, Phondaghat (Table 16), cluster mean for this character ranged from 5.83 (cluster II) to 13.00 (cluster V) with population mean of 9.49. The genotypes from cluster V were maximum number of primary branches plant⁻¹.

The data of ARS, Shirgaon (Table 16) cluster mean for this character varied between 8.60 (cluster III) to 13.33 (cluster IV) with population mean of 10.91. The genotypes from cluster IV were a greater number of primary branches plant⁻¹.

The cluster mean performance of Department of Agril. Botany, Dapoli (Table 16) for this character ranged from 6.92 (cluster III) to 11.83 (cluster IV) with population mean of 9.39. The genotypes from cluster IV were maximum number of primary branches plant⁻¹.

In the investigation of RARS, Karjat (Table 16), cluster mean for this character varied between 6.00 (cluster V) to 12.42 (cluster VIII) with population mean of 8.54. The genotypes from cluster VIII were a greater number of primary branches plant⁻¹.

The results of ARS, Palghar (Table 16), cluster mean for this character ranged from 8.27 (cluster I) to 13.83 (cluster IV) with population mean of 10.54. The genotypes from cluster IV were maximum number of primary branches plant⁻¹.

4.7.3.4. Number of secondary branches plant⁻¹

The cluster mean performance in experimet of ARS, Phondaghat (Table 16) for this character varied between 10.38 (cluster II) to 24.67 (cluster V) with population mean of 17.97. The genotypes from cluster V were a greater number of secondary branches plant⁻¹.

In the inquisition at ARS, Shirgaon (Table 16), cluster mean for this character ranged from 17.40 (cluster III) to 25.83 (cluster IV) with population mean of 22.09. The genotypes from cluster IV were maximum number of secondary branches plant⁻¹.

The pooled data of Department of Agril. Botany, Dapoli (Table 16), cluster mean for this character ranged from 13.17 (cluster III) to 19.73 (cluster II) with population mean of 16.94. The genotypes from cluster II were higher number of secondary branches plant⁻¹.

The cluster mean performance of RARS, Karjat (Table 16) for this character varied between 11.33 (cluster V) to 22.33 (cluster VIII) with population mean of 15.64. The genotypes from cluster VIII were maximum number of secondary branches plant⁻¹.

In the investigation of ARS, Palghar (Table 16), cluster mean for this character ranged from 15.00 (cluster II) to 25.33 (cluster IV) with population mean of 19.28. The genotypes from cluster IV were large number of secondary branches plant⁻¹.

4.7.3.5. Number of capitula plant⁻¹

The cluster mean performance of ARS, Phondaghat (Table 16) for this character ranged from 26.96 (cluster II) to 67.33 (cluster V) with population mean of 46.33. The genotypes from cluster V were higher number of capitula plant⁻¹.

The results of ARS, Shirgaon (Table 16), cluster mean for this character varied between 29.83 (cluster III) to 44.58 (cluster II) with population mean of 38.95. The genotypes from cluster II were maximum number of capitula plant⁻¹.

In the inquisition of Department of Agril. Botany, Dapoli (Table 16), cluster mean for this character ranged from 29.33 (cluster III) to 59.00 (cluster IV) with population mean of 44.37. The genotypes from cluster IV were greater number of capitula plant⁻¹.

In case of RARS, Karjat (Table 16), cluster mean for this character ranged from 30.17 (cluster IV) to 51.67 (cluster VIII) with population mean of 38.89. The genotypes from cluster VIII were maximum number of capitula plant⁻¹.

In the experiment at ARS, Palghar (Table 16), cluster mean for this character varied between 33.29 (cluster I) to 49.33 (cluster IV) with population mean of 40.46. The genotypes from cluster IV were higher number of capitula plant⁻¹.

4.7.3.6. Capitulum diameter (cm)

The cluster mean performance of ARS, Phondaghat (Table 16) for this character ranged from 0.92 cm (cluster II) to 1.27 cm (cluster V) with population mean of 1.11 cm. The genotypes from cluster V were more far-flung diameter of capitulum.

In the investigation at ARS, Shirgaon (Table 16), cluster mean for this character varied between 0.94 cm (cluster III) to 1.15 cm (cluster II) with population mean of 1.05 cm. The genotypes from cluster II were bigger capitulum diameter.

The results of Department of Agril. Botany, Dapoli (Table 16), seasonal cluster mean for this character was ranged from 0.96 cm (cluster III) to 1.22 cm (cluster II) with population mean of 1.09 cm. The genotypes from cluster II were broader capitulum diameter.

During the experiment at RARS, Karjat (Table 16), cluster mean performance for this character varied between 0.87 cm (cluster VII) to 1.18 cm (cluster VI) with population mean of 1.00 cm. The genotypes from cluster VI were bigger capitulum diameter.

In the investigation of ARS, Palghar (Table 16), season wise cluster mean for this character was ranged from 0.97 cm (cluster II) to 1.12 cm (cluster III) with population mean of 1.03 cm. The genotypes from cluster III were more far-flung capitulum diameter.

4.7.3.7. Number of seeds capitulum⁻¹

The results of ARS, Phondaghat (Table 16), cluster mean for this character ranged from 31.13 (cluster II) to 42.17 (cluster V) with population mean of 36.13. The genotypes from cluster V were higher number of seeds capitulum⁻¹.

The cluster mean performance of ARS, Shirgaon (Table 16) for this character varied between 26.90 (cluster III) to 35.92 (cluster II) with population mean of 30.91. The genotypes from cluster II were a greater number of seeds capitulum⁻¹.

In the inquisition at the Department of Agril. Botany, Dapoli (Table 16), cluster mean performance for this character ranged from 29.67 (cluster IV) to 39.37 (cluster II) with population mean of 32.63. The genotypes from cluster II were higher number of seeds capitulum⁻¹.

In case of RARS, Karjat (Table 16), cluster mean for this character varied between 18.00 (cluster IV) to 25.67 (cluster VI) with population mean of 21.52. The genotypes from cluster VI were maximum number of seeds capitulum⁻¹.

In the experiment of ARS, Palghar (Table 16), cluster mean performance for this character ranged from 22.90 (cluster II) to 29.79 (cluster III) with population mean of 26.34. The genotypes from cluster III were a greater number of seeds capitulum⁻¹.

4.7.3.8. 1000 seed weight (g)

The results of ARS, Phondaghat (Table 16), cluster mean for this character ranged from 2.37g (cluster II) to 2.88g (cluster V) with population mean of 2.67g. The genotypes from cluster V were more weight of 1000 seeds.

In case of experiment at ARS, Shirgaon (Table 16), cluster mean performance for this character varied between 2.33g (cluster III) to 2.73g (cluster IV) with population mean of 2.59g. The genotypes from cluster IV were maximum weight of 1000 seeds.

In the investigation at Department of Agril. Botany, Dapoli (Table 16), cluster mean for this character varied between 2.20g (cluster III) to 2.78g (cluster II) with population mean of 2.57g. The genotypes from cluster II were more weight of 1000 seeds.

In the experiment at RARS, Karjat (Table 16), cluster mean for this character varied between 1.68g (cluster IV) to 2.68g (cluster VI) with population mean of 2.40g. The genotypes from cluster VI were maximum weight of 1000 seeds.

In the inquisition at ARS, Palghar (Table 23E), cluster mean for this character varied from 2.15g (cluster II) to 2.67g (cluster IV) with population mean of 2.50g. The genotypes from cluster IV were more weight of 1000 seeds.

4.7.3.9. Seed yield plant⁻¹ (g)

During the experiment at ARS, Phondaghat (Table 16), cluster mean for this character varied from 2.55g (cluster III) to 3.57g (cluster V) with population mean of 2.84g. The genotypes from cluster V were maximum seed yield plant⁻¹.

In the investigation at ARS, Shirgaon (Table 16), cluster mean for this trait varied between 2.73g (cluster I) to 3.43g (cluster II) with population mean of 3.07g. The genotypes from cluster II were greater seed yield plant⁻¹.

In the experiment of Department of Agril. Botany, Dapoli (Table 16), cluster mean performance for this character varied from 3.38g (cluster I) to 4.10g (cluster II) with population mean of 3.62g. The genotypes from cluster II were greater seed yield plant⁻¹.

In case of RARS, Karjat (Table 16), cluster mean for this character varied from 2.28g (cluster VII) to 2.85g (cluster VI) with population mean of 2.52g. The genotypes from cluster VI were maximum seed yield plant⁻¹.

During the experiment at ARS, Palghar (Table 16), cluster mean for this character ranged from 2.50g (cluster I) to 3.08g (cluster IV) with population mean of 2.74g. The genotypes from cluster IV were greater seed yield plant⁻¹.

4.7.3.10. Seed yield plot⁻¹ (g)

In the investigation at ARS, Phondaghat (Table 16), cluster mean for this character varied from 221.75g (cluster I) to 269.50g (cluster V) with population mean of 236.47g. The genotypes from cluster V were more seed yield plot⁻¹.

In case of ARS, Shirgaon (Table 16), cluster mean for this character varied from 223.80g (cluster I) to 271.67g (cluster IV) with population mean of 244.67g. The genotypes from cluster IV were maximum seed yield plot⁻¹.

During the experiment at Department of Agril. Botany, Dapoli (Table 16), cluster mean for this character ranged from 226.52g (cluster I) to 264.00g (cluster IV) with population mean of 249.72g. The genotypes from cluster IV were higher seed yield plot⁻¹.

The results of experiment at RARS, Karjat (Table 16), cluster mean for this character varied between 188.14g (cluster III) to 231.17g (cluster VI) with population mean of 203.00g. The genotypes from cluster VI were more seed yield plot⁻¹.

In the inquisition at ARS, Palghar (Table 16), cluster mean for this character varied from 202.27g (cluster II) to 260.50g (cluster IV) with population mean of 229.53g. The genotypes from cluster IV were higher seed yield plot⁻¹.

4.7.3.11. Days to maturity

In case of ARS, Phondaghat (Table 16), cluster mean for this character ranged from 77.21 days (cluster II) to 85.41 days (cluster I) with population mean of 83.16 days. The genotypes from cluster II were early matured whereas genotypes from cluster I required more days for maturity.

In the experiment at ARS, Shirgaon (Table 16), cluster mean for this character varied from 74.17 days (cluster IV) to 83.52 days (cluster I) with population mean of 79.95 days. The genotypes from cluster IV were early matured whereas genotypes from cluster I required more days for maturity.

In the inquisition at Department of Agril. Botany, Dapoli (Table 16), cluster mean for this character ranged from 73.08 days (cluster IV) to 82.67 days (cluster III) with population mean of 79.16 days. The genotypes from cluster III were early matured whereas genotypes from cluster IV required more days for maturity.

During the experiment of RARS, Karjat (Table 16), cluster mean for this character varied from 81.39 days (cluster I) to 88.71 days (cluster VII) with population mean of 85.68 days. The genotypes from cluster VII were early matured whereas genotypes from cluster I required more days for maturity.

In the investigation at ARS, Palghar (Table 16), cluster mean for this character varied between 74.83 days (cluster I) to 84.59 days (cluster II) with

population mean of 80.28 days. The genotypes from cluster II were early matured whereas genotypes from cluster I required more days for maturity.

4.7.3.12. Oil content (%)

During the experiment at ARS, Phondaghat (Table 16), cluster mean for this character ranged from 35.33% (cluster II) to 40.67% (cluster V) with population mean of 37.82%. The genotypes from cluster V were maximum oil content.

In case of ARS, Shirgaon (Table 16), cluster mean for this character varied from 36.53% (cluster III) to 40.17% (cluster II & IV) with population mean of 38.68%. The genotypes from cluster II & IV were higher oil content.

In the investigation at Department of Agril. Botany, Dapoli (Table 16), cluster mean for this character varied between 38.99% (cluster I) to 41.73% (cluster II) with population mean of 39.99%. The genotypes from cluster II were more amount of oil content.

The results of RARS, Karjat (Table 16), cluster mean for this character varied between 35.28% (cluster VII) to 40.83% (cluster VI) with population mean of 37.71%. The genotypes from cluster VI were maximum oil content.

In the inquisition at ARS, Palghar (Table 16), cluster mean for this character ranged from 36.17% (cluster II) to 40.33% (cluster IV) with population mean of 38.22%. The genotypes from cluster IV were higher oil content.

4.7.3.13. Protein content (%)

The results of ARS, Phondaghat (Table 16), cluster mean for this character varied between 17.58% (cluster II) to 21.17% (cluster V) with population mean of 19.09%. The genotypes from cluster V were greater protein content.

In the investigation at ARS, Shirgaon (Table 16), cluster mean for this character varied between 18.91% (cluster I) to 21.67% (cluster II) with population mean of 20.12%. The genotypes from cluster II were higher amount of protein content.

In case of Department of Agril. Botany, Dapoli (Table 16), cluster mean for this character varied between 19.17% (cluster IV) to 21.97% (cluster II) with population mean of 20.09%. The genotypes from cluster II were maximum protein content.

Table 16: Environment wise cluster mean performance of pooled data for 13 characters in 40 genotypes of Niger.

Sr. No.	Characters	ARS, Phondaghat (E1)						ARS, Shirgaon (E2)					Dept. of Agril. Botany, Dapoli (E3)				
		Clusters						Clusters					Clusters				
		I	II	III	IV	V	PM	I	II	III	IV	PM	I	II	III	IV	PM
1.	DFPF	50.05	46.75	48.67	50.62	49.17	49.05	50.36	49.42	43.97	41.50	46.31	49.41	46.30	40.58	50.67	46.74
2.	PH (cm)	131.73	123.04	119.00	138.52	119.33	126.32	125.33	130.13	118.50	121.83	123.95	141.83	143.50	124.50	134.00	135.96
3.	NPBPP	8.22	5.83	9.17	11.22	13.00	9.49	9.41	12.29	8.60	13.33	10.91	8.40	10.40	6.92	11.83	9.39
4.	NSBPP	14.24	10.38	19.50	21.05	24.67	17.97	19.60	25.54	17.40	25.83	22.09	15.68	19.73	13.17	19.17	16.94
5.	NCPP	35.28	26.96	50.50	51.58	67.33	46.33	37.57	44.58	29.83	43.83	38.95	39.81	49.33	29.33	59.00	44.37
6.	CD (cm)	1.08	0.92	1.18	1.09	1.27	1.11	1.05	1.15	0.94	1.07	1.05	1.07	1.22	0.96	1.12	1.09
7.	NSPC	32.28	31.13	39.67	35.40	42.17	36.13	30.16	35.92	26.90	30.67	30.91	31.47	39.37	30.00	29.67	32.63
8.	1000 SW (g)	2.63	2.37	2.75	2.70	2.88	2.67	2.57	2.72	2.33	2.73	2.59	2.57	2.78	2.20	2.72	2.57
9.	SYPP (g)	2.61	2.58	2.55	2.89	3.57	2.84	2.73	3.43	2.74	3.39	3.07	3.38	4.10	3.42	3.59	3.62
10.	SYPP (g)	221.75	226.50	226.17	238.43	269.50	236.47	223.80	253.67	229.53	271.67	244.67	226.52	261.20	247.17	264.00	249.72
11.	DM	85.41	77.21	83.17	85.20	84.83	83.16	83.52	83.42	78.70	74.17	79.95	81.07	79.80	73.08	82.67	79.16
12.	OC (%)	36.22	35.33	39.00	37.87	40.67	37.82	37.86	40.17	36.53	40.17	38.68	38.99	41.73	39.25	40.00	39.99
13.	PC (%)	18.29	17.58	19.33	19.08	21.17	19.09	18.91	21.67	19.07	20.83	20.12	19.80	21.97	19.42	19.17	20.09

DFPF: Days to 50 per cent flowering, PH: Plant height, NPBPP: No. of primary branches plant⁻¹, NSBPP: No. of secondary branches plant⁻¹, NCPP: No. of capitula plant⁻¹, CD: Capitulum diameter
NSPC: No. of seeds capitulum⁻¹, SW: Seed weight, SYPP: Seed yield plant⁻¹, SYPP: Seed yield plot⁻¹, DM: Days to maturity, OC: Oil content, PC: Protein content, PM: Population Mean

Sr. No.	Characters	RARS, Karjat (E4)									ARS, Palghar (E5)				
		Clusters									Clusters				
		I	II	III	IV	V	VI	VII	VIII	PM	I	II	III	IV	PM
1.	DFPF	52.83	48.47	55.05	48.33	48.00	55.50	45.17	47.42	50.10	49.54	41.73	49.24	41.17	45.42
2.	PH (cm)	136.23	138.23	144.60	136.83	135.50	141.83	128.11	136.00	137.17	136.99	135.33	143.10	131.83	136.81
3.	NPBPP	6.26	8.83	9.79	6.50	6.00	11.17	7.33	12.42	8.54	8.33	8.27	11.74	13.83	10.54
4.	NSBPP	12.39	16.27	16.45	12.00	11.33	20.83	13.50	22.33	15.64	15.61	15.00	21.19	25.33	19.28
5.	NCPP	33.24	44.33	38.00	30.17	37.83	43.17	32.72	51.67	38.89	33.29	33.37	45.83	49.33	40.46
6.	CD (cm)	0.98	1.01	1.05	0.87	0.97	1.18	0.92	0.98	1.00	0.99	0.97	1.12	1.05	1.03
7.	NSPC	20.35	22.43	21.38	18.00	22.83	25.67	19.17	22.33	21.52	23.83	22.90	29.79	28.83	26.34
8.	1000 SW (g)	2.39	2.57	2.53	1.68	2.51	2.68	2.22	2.59	2.40	2.52	2.15	2.64	2.67	2.50
9.	SYPP (g)	2.29	2.49	2.52	2.34	2.62	2.85	2.28	2.76	2.52	2.50	2.59	2.78	3.08	2.74
10.	SYPP (g)	191.72	211.63	188.14	191.33	191.83	231.17	195.22	222.92	203.00	214.14	202.27	241.19	260.50	229.53
11.	DM	88.71	86.67	86.83	86.33	85.83	86.83	81.39	82.83	85.68	84.59	74.83	83.52	78.17	80.28
12.	OC (%)	36.32	37.80	37.36	36.33	37.67	40.83	35.28	40.08	37.71	36.75	36.17	39.62	40.33	38.22
13.	PC (%)	18.70	19.50	19.79	18.50	18.83	22.17	18.17	21.58	19.66	18.62	18.83	20.33	20.17	19.49

DFPF: Days to 50 per cent flowering, PH: Plant height, NPBPP: No. of primary branches plant⁻¹, NSBPP: No. of secondary branches plant⁻¹, NCPP: No. of capitula plant⁻¹, CD: Capitulum diameter
NSPC: No. of seeds capitulum⁻¹, SW: Seed weight, SYPP: Seed yield plant⁻¹, SYPP: Seed yield plot⁻¹, DM: Days to maturity, OC: Oil content, PC: Protein content, PM: Population Mean

During the experiment at RARS, Karjat (Table 16), cluster mean for this character varied between 18.50% (cluster VII) to 22.17% (cluster VI) with population mean of 19.66%. The genotypes from cluster VI were higher protein content.

In the inquisition at ARS, Palghar (Table 16), cluster mean for this character varied between 18.62% (cluster I) to 20.33% (cluster III) with population mean of 19.49%. The genotypes from cluster III were maximum protein content

4.7.4. Per cent contribution of various characters for divergence

The 40 genotypes of niger were studied for 13 characters and the environment wise contribution of various characters towards divergence was presented in Table 17 and depicted in Fig. 4.

On the basis of pooled data, the environment wise contribution of various traits towards divergence was varied from 0.00% (oil content) to 32.44% (number of capitula plant⁻¹), 1.28% (number of secondary branches plant⁻¹) to 26.28% (capitulum diameter), 0.26% (1000 seed weight) to 30.13% (days to 50 per cent flowering), 0.13% (protein content) to 33.59% (days to 50 per cent flowering) and 0.77% (1000 seed weight) to 32.56% (days to 50 per cent flowering) for E1, E2, E3, E4 and E5, respectively.

On the basis of pooled data of ARS, Phondaghat (Table 17), out of 13 characters studied the character number of capitulum plant⁻¹ (32.44%) contributed the highest for divergence followed by capitulum diameter (20.38%), days to 50 per cent flowering (12.82%), number of primary branches plant⁻¹ (7.95%), plant height (6.41%), seed yield plant⁻¹ (4.62%), days to maturity (4.36%) and protein content (4.10%). However, the contribution of number of secondary branches plant⁻¹ (3.08%), number of seeds capitulum⁻¹ (2.95%), 1000 seed weight (0.51) and seed yield plot⁻¹ (0.38%) exhibited lowest contribution for divergence. The oil content wasn't contributed for the divergence.

The pooled data of ARS, Shirgaon (Table 17), out of 13 characters studied the character contributed the highest for capitulum diameter (26.28%) divergence followed by days to 50 per cent flowering (18.08%), number of primary branches plant⁻¹ (13.21%), seed yield plot⁻¹ (8.08%), number of seeds capitulum⁻¹ (7.69%),

and protein content (6.28%). However, the contribution of days to maturity (3.46%), 1000 seed weight (3.85%), number of capitulum plant⁻¹ (3.08%), seed yield plant⁻¹ (3.08%), oil content (2.95%), plant height (2.69%) and number of secondary branches plant⁻¹ (1.28%) recorded lowest contribution for divergence.

The pooled results at the Department of Agril. Botany, Dapoli (Table 17), out of 13 characters studied the character contributed the highest for days to 50 per cent flowering (30.13%) divergence followed by number of seeds capitulum⁻¹ (17.82%), number of primary branches plant⁻¹ (10.51%), capitulum diameter (10.26%), protein content (8.72%), number of secondary branches plant⁻¹ (6.54%), plant height (5.00%) and days to maturity (4.62%). However, the contribution of seed yield plant⁻¹ (2.05%), seed yield plot⁻¹ (1.67%), number of capitulum plant⁻¹ (3.08%), seed yield plant⁻¹ (3.08%), oil content (1.41%), total number of seeds capitulum⁻¹ (1.03%) and 1000 seed weight (0.26%) recorded lowest contribution for divergence.

The pooled data of RARS, Karjat (Table 17), out of 13 characters studied the character contributed the highest for days to 50 per cent flowering (33.59%) divergence followed by number of primary branches plant⁻¹ (31.03%) and number of capitulum plant⁻¹ (18.33%). However, the contribution of capitulum diameter (3.46%), number of seeds capitulum⁻¹ (2.82%), oil content (2.31%), 1000 seed weight (2.05%), days to maturity (2.05%), seed yield plant⁻¹ (1.41%), seed yield plot⁻¹ (1.15%), plant height (1.15%) number of secondary branches plant⁻¹ (0.51%) and protein content (0.13) recorded least contribution for divergence.

On the basis of pooled data of ARS, Palghar (Table 17), out of 13 characters studied the character contributed the highest for days to 50 per cent flowering (32.56%) divergence followed by number of primary branches plant⁻¹ (16.28%), capitulum diameter (14.87%), number of capitulum plant⁻¹ (13.21%), plant height (5.90%), protein content (4.49%). However, the contribution of seed yield plot⁻¹ (3.08%), seed yield plant⁻¹ (2.31%), oil content (2.31%), number of secondary branches plant⁻¹ (1.92%), days to maturity (1.28%), number of seeds capitulum⁻¹ (1.03%) and 1000 seed weight (0.77%) recorded lowest contribution for divergence.

Table 17: Environment wise contribution of various characters towards divergence of pooled data in 40 genotypes of Niger.

Sr. No.	Environments	ARS, Phondaghat (E1)		ARS, Shirgaon (E2)		Dept. of Agril. Botany, Dapoli (E3)		RARS, Karjat (E4)		ARS, Palghar (E5)	
	Characters	Times ranked 1 st	Per cent contribution	Times ranked 1 st	Per cent contribution	Times ranked 1 st	Per cent contribution	Times ranked 1 st	Per cent contribution	Times ranked 1 st	Per cent contribution
1.	DFFP	100	12.82%	141	18.08%	235	30.13%	262	33.59%	254	32.56%
2.	PH (cm)	50	6.41%	21	2.69%	39	5.00%	9	1.15%	46	5.90%
3.	NPBPP	62	7.95%	103	13.21%	82	10.51%	242	31.03%	127	16.28%
4.	NSBPP	24	3.08%	10	1.28%	51	6.54%	4	0.51%	15	1.92%
5.	NCPP	253	32.44%	24	3.08%	139	17.82%	143	18.33%	103	13.21%
6.	CD (cm)	159	20.38%	205	26.28%	80	10.26%	27	3.46%	116	14.87%
7.	NSPC	23	2.95%	60	7.69%	8	1.03%	22	2.82%	8	1.03%
8.	1000 SW (g)	4	0.51%	30	3.85%	2	0.26%	16	2.05%	6	0.77%
9.	SYPP (g)	36	4.62%	24	3.08%	16	2.05%	11	1.41%	18	2.31%
10.	SYPP (g)	3	0.38%	63	8.08%	13	1.67%	9	1.15%	24	3.08%
11.	DM	34	4.36%	27	3.46%	36	4.62%	16	2.05%	10	1.28%
12.	OC (%)	0	0.00%	23	2.95%	11	1.41%	18	2.31%	18	2.31%
13.	PC (%)	32	4.10%	49	6.28%	68	8.72%	1	0.13%	35	4.49%

E1: ARS, Phondaghat; E2 : ARS, Shirgaon; E3 : Department of Agril. Botany, Dapoli; E4 : RARS, Karjat; E5 : ARS, Palghar

DFFP: Days to 50 per cent flowering

NCPP: No. of capitula plant⁻¹

SYPP: Seed yield plant⁻¹

PC: Protein content

PH: Plant height

CD: Capitulum diameter

SYPP: Seed yield plot⁻¹

NPBPP: No. of primary branches plant⁻¹

NSPC: No. of seeds capitulum⁻¹

DM: Days to maturity

NSBPP: No. of secondary branches plant⁻¹

SW: Seed weight

OC: Oil content

4.8. Stability Analysis and Genotype x Environment Interaction (GEI)

4.8.1. Combined Analysis of Variance

Combined analysis of variance showed that mean squares due to genotype, environment and genotype x environment interaction (GEI) highly significant ($p < 0.01$) for all the traits under study (Table 18). The sum of square per cent explained of genotype, environment and GEI for days to 50 per cent flowering (5.12%, 44.21% and 50.64%), plant height (26.46%, 14.08% and 59.45%), number of primary branches plant⁻¹ (23.55%, 18.66% and 57.67%), number of secondary branches plant⁻¹ (31.30%, 16.14% and 52.32%), number of capitula plant⁻¹ (20.67%, 14.59% and 64.70%), capitulum diameter (18.85%, 31.96% and 49.18%), number of seeds plant⁻¹ (45.18%, 16.87% and 37.86%), 1000 seed weight (29.99%, 67.40% and 0.83%), seed yield plant⁻¹ (40.04%, 10.52% and 49.01%), seed yield plot⁻¹ (24.31%, 3.55% and 71.57%), days to maturity (11.54%, 42.71% and 45.68%), oil content (23.45%, 7.41% and 68.45%) and protein content (23.09%, 26.36% and 50.00%), respectively. This showed that environments were diverse and affects the performance potential of genotypes. In the present investigation, the maximum contribution of per cent genotype x environment sum of squares was observed for all the traits except number of seeds capitulum⁻¹ and 1000 seed weight under study.

4.8.2. ANOVA for AMMI model

The AMMI model combines the analysis of variance for the genotype and environment main effects with principal components analysis of the G × E interaction (Gauch and Zobel 1988 & 1996). The statistical data of all the traits were subjected to combined analysis of variance and AMMI analysis which is a combination of analysis of variance and multiplication effect analysis. Briefly, analysis of variance is used to partition variance into three components: genotype deviations from the grand mean, environment deviations from the grand mean and GE deviations from the grand mean. Subsequently, multiplication effect analysis is used to partition GE deviations into different interaction principal component axes (IPCA), which can be tested for statistical significance through ANOVA. In this study, the analysis of variance for AMMI model revealed significant difference for

Table 18: Combined ANOVA for different traits of 40 Niger genotypes tested at five environments.

Characters	Days to 50 per cent flowering					Plant height (cm)					Number of primary branches plant ⁻¹				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	82.32	2.11**	0.40	5.12	39	2275.47	58.34**	1.78	26.46	39	143.53	3.68**	1.63	23.55
Replication (R)	2	0.52	0.26	0.69		2	1.11	0.56	0.08		2	0.73	0.37	1.59	
Environment (E)	4	710.70	177.67**	34.04	44.21	4	1211.04	302.76**	9.23	14.08	4	113.71	28.42**	12.61	18.66
G x E	156	814.10	5.21**	0.70	50.64	156	5113.24	32.77**	0.30	59.45	156	351.50	2.25**	0.92	57.67
Residual	36	44.55	1.23	0.31		36	284.15	7.89	0.19		36	23.92	0.66	0.54	
Pooled Error	390	2882.47	7.91			390	41595.42	106.65			390	947.85	2.43		
Characters	Number of secondary branches plant ⁻¹					Number of capitula plant ⁻¹					Capitulum diameter (cm)				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	558.46	14.32**	2.39	31.30	39	1694.00	43.43**	1.27	20.67	39	0.23	0.006	1.57	18.85
Replication (R)	2	4.36	2.18	1.66		2	2.60	1.30	0.44		2	0.0001	0.0001	0.65	
Environment (E)	4	288.08	72.02**	12.03	16.14	4	1195.69	298.92**	8.79	14.59	4	0.39	0.098**	25.35	31.96
G x E	156	933.57	5.98**	0.48	52.32	156	5301.25	33.98**	0.76	64.70	156	0.60	0.004	0.50	49.18
Residual	36	70.73	1.96	0.54		36	248.58	6.90	1.00		36	0.039	0.001	0.67	
Pooled Error	390	4790.85	12.28			390	17424.39	44.67			390	2.97	0.008		

*Significant at 5% level of significance

**Significant at 1% level of significance

(Table Contd...)

Characters	Number of seeds capitulum ⁻¹					1000 Seed weight (g)					Seed yield plant ⁻¹ (g)				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	1246.59	31.96**	4.77	45.18	39	1.01	0.02	0.93	29.99	39	7.46	0.19*	3.26	40.04
Replication (R)	2	2.25	1.13	0.43		2	0.06	0.03	1.31		2	0.08	0.04	1.91	
Environment (E)	4	465.50	116.37**	17.37	16.87	4	2.27	0.56*	20.37	67.40	4	1.96	0.49**	8.38	10.52
G x E	156	1044.64	6.69**	0.17	37.86	156	0.028	0.02	1.11	0.83	156	9.13	0.05	0.25	49.01
Residual	36	53.28	1.48	0.37		36	0.06	0.001	0.47		36	0.17	0.004	0.43	
Pooled Error	390	14600.11	37.43			390	9.77	0.02			390	90.92	0.23		
Characters	Seed yield plot ⁻¹ (g)					Days to maturity					Oil content (%)				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	22224.69	569.86**	1.35	24.31	39	236.67	6.06**	1.01	11.54	39	156.05	4.00**	1.37	23.45
Replication (R)	2	710.06	355.03	1.79		2	1.57	0.78	0.61		2	4.55	2.28	1.27	
Environment (E)	4	3063.10	765.77**	1.82	3.35	4	875.87	218.97**	36.46	42.71	4	49.35	12.33**	4.22	7.41
G x E	156	65441.41	419.49**	0.80	71.57	156	936.81	6.00**	0.42	45.68	156	455.60	2.92**	0.84	68.45
Residual	36	250.88	6.96	0.08		36	41.51	1.15	0.28		36	3.80	0.10	0.74	
Pooled Error	390	203262.91	521.18			390	5504.64	14.11			390	1347.61	3.45		

*Significant at 5% level of significance

**Significant at 1% level of significance

(Table Contd...)

Character	Protein content (%)				
Source	DF	SS	MS	F	SS% Explained
Genotype (G)	39	50.20	1.28**	1.84	23.09
Replication (R)	2	1.20	0.60	2.82	
Environment (E)	4	57.30	14.32**	20.56	26.36
G x E	156	108.68	0.69*	0.50	50.00
Residual	36	6.53	0.18	0.53	
Pooled Error	390	543.57	1.39		

*Significant at 5% level of significance **Significant at 1% level of significance

genotypes, environment, GEI interaction and its interaction principal component (IPCA) for all the traits which was presented in Table no. 19.

With regards to the days to 50 per cent flowering (Table 19), the maximum per cent sum of squares due to genotype (61.19%) followed by genotype x environment (26.54%), IPCA1 (14.30%), environment (12.27%), IPCA2 (7.80%) and IPCA3 (2.50%), respectively.

Data regarding to the plant height (Table 19), the highest per cent sum of squares due to environment (36.59%) followed by genotype x environment (35.88%), genotype (27.52%), IPCA1 (22.49%), IPCA2 (9.58%) and IPCA3 (2.20%), respectively.

As per the number of primary branches plant⁻¹ (Table 19), the maximum per cent sum of squares due to genotype (65.76%) followed by genotype x environment (23.78%), environment (10.46%), IPCA1 (9.45%), IPCA2 (6.60%) and IPCA3 (4.71%). The results of number of secondary branches plant⁻¹ (Table 19), the highest per cent sum of squares due to genotype (57.73%) followed by genotype x environment (25.49%), environment (16.78%), IPCA1 (9.35%), IPCA2 (7.63%) and IPCA3 (5.74%).

With regards to the number of capitula plant⁻¹ (Table 19), the maximum per cent sum of squares due to genotype (55.19%) followed by genotype x environment (38.90%), IPCA1 (21.85%), IPCA2 (10.92%), environment (5.91%) and IPCA3 (4.10%). As per the capitulum diameter (Table 19), the highest per cent sum of squares due to genotype (54.02%) followed by genotype x environment (31.03%), IPCA1 (18.97%), environment (14.37%), IPCA2 (5.17%) and IPCA3 (4.60%), respectively.

The data regards with the number of seeds capitulum⁻¹ (Table 19), the maximum per cent sum of squares due to environment (67.20%) followed by

genotype (20.52%), genotype $\times$ environment (10.78%), IPCA1 (4.07%), IPCA2 (3.37%) and IPCA3 (2.54%), respectively. With regards to the 1000 seed weight (Table 19), the highest per cent sum of squares due to genotype (69.68%) followed by environment (15.71%), genotype $\times$ environment (14.44%), IPCA1 (7.62%), IPCA2 (3.33%) and IPCA3 (2.38%), respectively.

The results of seed yield plant⁻¹ (Table 19), the maximum per cent sum of squares due to environment (67.53%) followed by genotype (24.71%), genotype $\times$ environment (7.77%), IPCA1 (3.13%), IPCA2 (2.53%) and IPCA3 (1.65%), respectively. As per the seed yield plot⁻¹ (Table 26J), the highest per cent sum of squares due to genotype (53.91%) followed by environment (33.10%), genotype $\times$ environment (12.99%), IPCA1 (8.12%), IPCA2 (4.21%) and IPCA3 (0.42%), respectively.

The data regards with the days to maturity (Table 19), the maximum per cent sum of squares due to genotype (50.35%) followed by environment (29.79%), genotype $\times$ environment (19.86%), IPCA1 (7.86%), IPCA2 (5.70%) and IPCA3 (4.99%).

As per the oil content (Table 19), the highest per cent sum of squares due to genotype (58.74%) followed by environment (26.33%), genotype $\times$ environment (14.92%), IPCA1 (11.28%), IPCA2 (1.83%) and IPCA3 (1.26%), respectively. With regards to the protein content (Table 19), the maximum per cent sum of squares due to genotype (61.20%) followed by genotype $\times$ environment (20.21%), environment (18.59%), IPCA1 (9.42%), IPCA2 (4.66%) and IPCA3 (3.62%), respectively.

4.8.4. Estimation of Stability, GEI and Interpretation of AMMI GGE biplots

Table 20 to 32 describes the general mean, stability parameters like regression coefficient (b_i), deviation from regression (S^2_{di}), the IPCA scores, ASV and GSI of 40 niger genotypes. Purchase *et. al.* (2000) developed the AMMI stability value (ASV) based on the AMMI model's IPCA1 and IPCA2 (Interaction Principal Components Axes 1 and 2, respectively) scores for each genotype. Since ASV only

Table 19: ANOVA for AMMI model of pooled data for different characters of 40 Niger genotypes tested at five environments.

Characters	Days to 50 per cent flowering					Plant height (cm)					Number of primary branches plant ⁻¹				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	1404.59	36.01**	9.22	61.19	39	4829.87	123.84**	3.06	27.52	39	521.82	13.38**	11.06	65.76
Environment (E)	4	281.61	70.40**	18.02	12.27	4	6420.96	1605.24**	39.77	36.59	4	83.03	20.75**	17.15	10.46
Genotype x Environment	156	609.31	3.90**	-	26.54	156	6296.58	40.36**	-	35.88	156	188.72	1.20**	-	23.78
IPCA1	42	328.20	7.81**	2.00	14.30	42	3946.38	93.96**	2.32	22.49	42	75.00	1.78**	1.47	9.45
IPCA2	40	179.16	4.47**	1.14	7.80	40	1680.27	42.00**	1.04	9.58	40	52.41	1.31**	1.08	6.60
IPCA3	38	57.38	1.51**	0.38	2.50	38	385.76	10.15**	0.25	2.20	38	37.39	0.98*	0.81	4.71
Residual	36	44.55	1.23	0.31		36	284.15	7.89	0.19		36	23.92	0.66	0.54	
Pooled Residual	156	609.31	3.90	-		156	6296.58	40.36	-		156	188.72	1.20	-	
Total	199	2295.52	11.53	2.95		199	17547.42	88.17	2.18		199	793.58	3.98	3.29	
Characters	Number of secondary branches plant ⁻¹					Number of capitula plant ⁻¹					Capitulum diameter (cm)				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	1475.18	37.82**	9.06	57.73	39	6776.55	173.75**	5.67	55.19	39	0.94	0.024**	6.87	54.02
Environment (E)	4	428.92	107.23**	25.68	16.78	4	726.26	181.56**	5.93	5.91	4	0.25	0.063**	17.92	14.37
Genotype x Environment	156	651.30	4.17**	-	25.49	156	4776.63	30.61**	-	38.90	156	0.54	0.003**	-	31.03
IPCA1	42	239.04	5.69**	1.57	9.35	42	2683.64	63.89**	9.25	21.85	42	0.33	0.008**	4.93	18.97
IPCA2	40	194.91	4.87**	1.34	7.63	40	1340.73	33.51**	4.85	10.92	40	0.09	0.002*	1.39	5.17
IPCA3	38	146.61	3.85**	1.06	5.74	38	503.66	13.25**	1.91	4.10	38	0.08	0.002*	1.30	4.60
Residual	36	70.73	1.96	0.54		36	248.58	6.90	1.00		36	0.039	0.001	0.67	
Pooled Residual	114	412.25	3.61	-		36	248.58	6.90	-		74	0.12	0.001	-	
Total	199	2555.40	12.84	3.07		199	12279.45	61.70	2.01		199	1.74	0.008	2.49	

*Significant at 5% level of significance

**Significant at 1% level of significance

(Table Contd...)

Characters	Number of seeds capitulum ⁻¹					1000 seed weight (g)					Seed yield plant ⁻¹ (g)				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	1370.04	35.12**	7.61	20.52	39	4.39	0.112**	19.12	69.68	39	9.86	0.252**	12.70	24.71
Environment (E)	4	4486.04	1121.52**	243.18	67.20	4	0.99	0.248**	42.12	15.71	4	26.95	0.737**	338.52	67.53
Genotype x Environment	156	719.43	4.61**	-	10.78	156	0.91	0.005*	-	14.44	156	3.10	0.019*	-	7.77
IPCA1	42	271.91	6.47**	1.64	4.07	42	0.48	0.011**	2.98	7.62	42	1.25	0.029**	2.61	3.13
IPCA2	40	224.65	5.61**	1.43	3.37	40	0.21	0.005*	1.42	3.33	40	1.01	0.025**	2.22	2.53
IPCA3	38	169.58	4.46**	1.13	2.54	38	0.15	0.004*	1.05	2.38	38	0.66	0.017*	1.53	1.65
Residual	36	53.28	1.48	0.37		36	0.06	0.001	0.47		36	0.17	0.004	0.43	
Pooled Residual	114	447.52	3.92	-		114	0.43	0.003	-		74	0.84	0.011	-	
Total	199	6675.56	33.04	7.16		199	6.30	0.031	5.37		199	39.91	0.200	10.07	
Character	Seed yield plot ⁻¹ (g)					Days to maturity					Oil content (%)				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	55760.13	1429.74**	16.60	53.91	39	1590.36	40.77**	10.14	50.35	39	409.76	10.50**	15.74	58.74
Environment (E)	4	34234.06	8558.51**	99.37	33.10	4	940.80	235.20**	58.49	29.79	4	183.70	45.92**	68.82	26.33
Genotype x Environment	156	13435.23	86.12**	-	12.99	156	627.30	4.02**	-	19.86	156	104.09	0.66*	-	14.92
IPCA1	42	8400.21	200.00**	2.32	8.12	42	248.13	5.90**	1.46	7.86	42	78.67	1.87**	8.39	11.28
IPCA2	40	4353.53	108.83**	1.26	4.21	40	180.09	4.50**	1.12	5.70	40	12.80	0.32*	1.43	1.83
IPCA3	38	430.60	11.33**	0.13	0.42	38	157.56	4.14**	1.03	4.99	38	8.81	0.23*	1.04	1.26
Residual	36	250.88	6.96	0.08		36	41.51	1.15	0.28		36	3.80	0.10	0.74	
Pooled Residual	156	13435.23	86.12	-		156	627.30	4.02	-		114	25.42	0.22	-	
Total	199	103429.42	519.34	6.03		199	3158.47	15.87	3.94		199	697.56	3.50	5.25	

*Significant at 5% level of significance

**Significant at 1% level of significance

(Table Contd...)

Characters	Protein content (%)				
Source	DF	SS	MS	F	SS% Explained
Genotype (G)	39	159.54	4.09**	12.11	61.20
Environment (E)	4	48.45	12.11**	35.87	18.59
Genotype x Environment	156	52.68	0.33*	-	20.21
IPCA1	42	24.56	0.58*	1.73	9.42
IPCA2	40	12.14	0.30*	0.89	4.66
IPCA3	38	9.44	0.24*	0.73	3.62
Residual	36	6.53	0.18	0.53	
Pooled Residual	156	52.68	0.33	-	
Total	199	260.69	1.31	3.87	

*Significant at 5% level of significance

**Significant at 1% level of significance

consider the IPCA score without considering the mean performance of the genotypes, stable genotypes identified using ASV may gave inferior performance. A new approach known as genotype selection index (GSI) was recommended by Farshadfar (2008). Using AMMI stability value and mean performance, GSI incorporates both mean and stability in a single criterion. Low value of this parameter shows desirable genotypes with high mean and stability. The selection of stable genotypes decided by those genotypes give higher mean performance, bi value equal to one, S^2_{di} value close to zero, low ASV with less GSI (Farshadfar *et al.*, 2011).

AMMI and GGE models were considered as an emerging novel and prestigious models for data analysis of multi-location trials (Yan and Kang, 2003). AMMI biplots were recently preferred biplots to visualize adaptability and stability of genotypes across tested environments (Gauch and Zobel, 1997; Gauch, 2006). Moreover, the model also useful on grouping similar performance genotypes and/or environments and also provide some information about GEI in order to identify the genotypes adapted to specific environment.

In AMMI1 biplot, the genotypes with IPCA1 scores close to zero likely adapted to wide environment or less influenced by the environments. The larger scores depict more specific adaptation in combination with environments of the same sign IPCA1 scores (Ebdon and Gauch, 2002). Furthermore, the relative magnitude and direction of genotypes along the abscissa and ordinate axis in biplot is also important to understand the response pattern of genotypes across environments and to differentiate high yielding and adaptable genotypes (Samonte *et al.*, 2005).

The AMMI2 biplot explained 100% of the GE interaction, making it a useful test for interaction. In order to estimate specific adaptation and study their stability, biplot diagram was used (Mohammadi and Amri, 2008). From the polygon view of the GGE biplot, the vertex genotype showed the one that give the best performance for each environment in which genotypes lie. Genotypes positioned on the polygon vertex might be have the longest distance from biplot origin, supposed to the most responsive. Those genotypes that are located close to any environment show specific adaptation to that environment. Those genotypes which are away from the center of biplot, have high $G \times E$ interaction and those genotypes that nearest to center of biplot, have high stability. In addition, no location fell into sector with any genotype vertex, it implies that, these are the poorest genotypes in some or all of the locations.

The GGE biplot also view the discriminating and representativeness ability of environments to identify an environment that efficiently discernment the superior genotype in the tested environments. A long environmental vector from origin showed a high capacity to discriminate genotype (Yan and Tinker, 2006).

1. Days to 50 per cent flowering

Considering all the stability parameters (Table 20), genotype, G24 (GM=43 days, $b_i=0.871$, $S^2d_i=-0.231$, $IPCA1=-0.80$, $IPCA2=0.019$, $ASV=1.47$, $GSI=30$) observed more stable for earliness (Table 29A) followed by the genotype, G25 (GM=43 days, $b_i=1.390$, $S^2d_i=0.850$, $IPCA1=-0.70$, $IPCA2=0.016$, $ASV=1.28$, $GSI=28$) while genotypes G10 (GM=49 days, $b_i=1.061$, $S^2d_i=0.798$, $IPCA1=0.10$, $IPCA2=-0.029$, $ASV=0.19$, $GSI=8$) registered more stable for mid-late flowering followed by G23 (GM=49 days, $b_i=1.256$, $S^2d_i=0.824$, $IPCA1=-0.12$, $IPCA2=0.017$, $ASV=0.22$, $GSI=10$) and G20 (GM=50 days, $b_i=1.124$, $S^2d_i=-0.870$, $IPCA1=-0.10$, $IPCA2=-0.009$, $ASV=0.18$, $GSI=6$). The genotype, G35 (GM=53 days, $b_i=0.923$, $S^2d_i=-1.834$, $IPCA1=0.69$, $IPCA2=0.004$, $ASV=1.26$, $GSI=19$) recorded highly stable for late flowering followed by G16 (GM=52 days, $b_i=1.306$, $S^2d_i=1.879$, $IPCA1=-0.31$, $IPCA2=0.009$, $ASV=0.57$, $GSI=11$).

Table 20: Estimation of stability parameters of 40 Niger genotypes for days to 50 per cent flowering.

Sr. No.	Genotype Code	Days to 50 per cent flowering (Days)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	50	4	1.355	-0.724	-0.50	-0.025	0.92	14	18
2.	G 2	52	2	1.535	0.178	-0.80	-0.032	1.47	21	23
3.	G 3	50	4	1.831**	6.095**	1.40	-0.029	2.56	27	31
4.	G 4	51	3	1.401	-1.971	-0.70	-0.037	1.28	19	22
5.	G 5	50	4	1.959**	0.604	-1.10	-0.019	2.02	24	28
6.	G 6	48	6	1.509	3.741**	-0.20	-0.020	0.37	7	13
7.	G 7	49	5	1.388	6.180**	-0.19	-0.028	0.35	6	11
8.	G 8	51	3	1.639	2.439**	-0.41	-0.028	0.75	12	15
9.	G 9	52	2	1.678**	7.377**	1.25	-0.015	2.29	25	27
10.	G 10	49	5	1.061	0.798	0.10	-0.029	0.19	3	8
11.	G 11	50	4	1.096	0.547	1.30	-0.007	2.38	26	30
12.	G 12	50	4	1.110	-0.941	-0.61	-0.016	1.12	17	21
13.	G 13	51	3	0.661*	-1.840	-0.40	0.014	0.73	10	13
14.	G 14	52	2	1.031	-0.794*	-0.30	0.010	0.55	8	10
15.	G 15	52	2	1.577**	-1.336	-0.51	0.014	0.93	15	17
16.	G 16	52	2	1.306	1.879	-0.31	0.009	0.57	9	11
17.	G 17	50	4	0.686	-2.088**	1.00	0.007	1.83	23	27
18.	G 18	51	3	0.917	-0.825	0.00	0.019	0.02	1	4
19.	G 19	49	5	1.104	-0.665*	0.20	0.010	0.37	7	12
20.	G 20	50	4	1.124	-0.870	-0.10	-0.009	0.18	2	6
21.	G 21	52	2	0.887*	1.485	-0.49	0.009	0.90	13	15
22.	G 22	50	4	1.043	1.933**	1.30	0.007	2.38	26	30
23.	G 23	49	5	1.256	0.824	-0.12	0.017	0.22	5	10
24.	G 24	43	9	0.871	-0.231	-0.80	0.019	1.47	21	30
25.	G 25	43	9	1.390	0.850	-0.70	0.016	1.28	19	28
26.	G 26	42	10	0.438	2.909**	-0.50	0.006	0.92	14	24
27.	G 27	45	8	0.516	-0.934	-0.52	0.014	0.95	16	24
28.	G 28	46	7	0.058	0.746	-0.40	0.070	0.74	11	18
29.	G 29	46	7	0.443*	-1.784	-0.30	0.038	0.55	8	15
30.	G 30	49	5	0.328	4.504**	0.19	0.000	0.35	6	11
31.	G 31	49	5	0.388	0.328	-0.10	0.001	0.18	2	7
32.	G 32	49	5	0.789	-0.815	-0.80	0.012	1.47	21	26
33.	G 33	51	3	0.480	0.189*	0.70	0.014	1.28	19	22
34.	G 34	52	2	0.288	2.655**	0.80	-0.004	1.47	21	23
35.	G 35	53	1	0.923	-1.834	0.69	0.004	1.26	18	19
36.	G 36	51	3	1.320	0.067	0.70	0.007	1.28	19	22
37.	G 37	53	1	0.538	12.979**	0.81	0.002	1.48	22	23
38.	G 38	50	4	0.400	15.356**	0.52	0.005	0.95	16	20
39.	G 39	50	4	0.613*	5.376**	0.71	0.003	1.30	20	24
40.	G 40	49	5	0.562	19.360**	0.11	0.014	0.20	4	9

*Significant at 5% level of significance

**Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression Coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI Stability Value, RASVi: Rank of ASV, GSI: Genotype Selection Index

In Fig. 5.1 where IPCA1 was plotted against mean, the vertical line passing through the origin is the grand mean. Accordingly, G24, G26, G25, G27, G28, G30, G5, G10, G31, G3, G1 and G6 were gave mean performance below the grand mean which were located to left side of the vertical line. Among all, genotypes G26, G24 and G25 have negative IPCA1 score which indicates, these genotypes were very early for 50 per cent flowering. The environments E5, E3, E2, E1 and E4 noted for the lowest mean days to 50 per cent flowering compared to the other sites since it is found in the left side of the Figure 5.1. On the other hand, those genotypes which was found in the right side of the vertical line gave mean days to 50 per cent flowering above the grand mean. Among all, genotypes, G37, G35 and G34 have positive IPCA1 score which indicates, these genotypes were very late for 50 per cent flowering. Genotype, G3 was more specifically adapted to E3 and E5 sites whereas G22 was more favorable to site E2. Also, no any genotypes specifically adapted to E1 and E4 sites. Genotypes G18, G20, G40, G10, G31, G23, G30 and G6 were located near to central line of IPCA1 scores which indicates, these genotypes have highest additive main effect. Among all, G5, G2, G32, G24, G25, G4, G2, G11, G9, G22 and G17 were located far from central line of IPCA1 score which were indicating the maximum interaction between genotype and environment.

The AMMI2 biplot (Figure 5.2) explained GE interaction, making it a useful test for interaction. It was observed that most of the genotypes and environments were dispersed around the biplot. Genotypes farther from the center of biplot show specific adaptation. Here in this study G30, G31, G16, G26 and G14 were more stable than the other genotypes since they were found near to the origin and have general adaptability. However, G16 was stable and required more days for 50 per cent flowering than grand mean. The other genotypes showed specific to the certain environments. for instance, G29, G24 and G32 were more adapted to E4 whereas G22 and G17 were specifically adapted to site E1. The G3, G9, G11 and G34 were more favorable to site E2 while G5, G2 and G4 more consentient in E3 and E5 sites. In the present investigation, G22 was the best at E1, G3 was good at E2, G24 and G29 were the best at E4 and G4, G5 and G2 was the better in E5 and E3 (Fig. 5.2), suggesting that these genotype won to which environment lie. These

genotypes positioned on the polygon vertex might be have the longest distance from biplot origin, supposed to the most responsive and have highest interaction between genotype and environment.

Among tested environments, E1, E4 and E3 were the most discriminating environments that provided adequate information on the performance of the genotypes. Further explanation, E1, E4 and E3 environments were powerful for genotype evaluation and interesting sites to identify superior genotypes. On other hand, E2 and E5 environments falls close to the bi-plot origin and the least discriminating environment (Fig. 5.2) and it provided little information about the performance difference of genotypes.

2. Plant height (cm)

With regards to plant height (Table 21), genotype, G8 (GM=124 cm, bi=1.822, $S^2di=-0.702$, IPCA1=-0.69, IPCA2=0.020, ASV=3.16, GSI=25) observed more stable for dwarf stature of the plant. The genotype, G24 (GM=129 cm, bi=-0.970, $S^2di=-4.551$, IPCA1=0.41, IPCA2=0.013, ASV=1.88, GSI=19) registered more stable for medium height followed by G32 (GM=130 cm, bi=0.984, $S^2di=0.480$, IPCA1=-1.20, IPCA2=0.014, ASV=5.50, GSI=27) while considering all the stability parameters. The genotype, G28 (GM=134 cm, bi=0.932, $S^2di=-6.710$, IPCA1=-0.10, IPCA2=-0.006, ASV=0.46, GSI=12) recorded highly stable for tallness.

In AMMI1 biplot (Fig. 6.1), IPCA1 was plotted against mean, the vertical line passing through the origin is the grand mean. Accordingly, the mean performance of genotypes was observed less than grand mean and which were located to left side of the vertical line. Among all, genotypes G25, G8 and G3 have negative IPCA1 score which indicates, these genotypes were dwarf plant stature while genotypes, G26 and G24 have positive IPCA1 score with dwarf stature of the plant. The environments E2 and E1 noted for the lowest mean plant height compared to the other sites since it is found in the left side of the Figure 6.1. On the other hand, those genotypes and environments (E4, E5 and E3) which was found in the right side of the vertical line gave mean height of the plant at maturity above the grand mean. Among all, genotypes, G40, G38, G39 and G14 have positive IPCA1 score which indicates, these genotypes were tall plant heighted. Genotypes, G1, G18, G13

Table 21: Estimation of stability parameters of 40 Niger genotypes for plant height (cm).

Sr. No.	Genotype Code	Plant height (cm)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	137	7	1.637**	30.651**	-1.20	0.001	5.50	14	21
2.	G 2	136	8	0.796	36.968**	-2.10	0.013	9.63	25	33
3.	G 3	128	15	2.480**	-16.859**	-2.00	-0.018	9.17	24	39
4.	G 4	137	7	1.340	-7.321	-0.41	-0.005	1.88	5	12
5.	G 5	134	10	2.578**	9.501	-0.80	-0.018	3.67	10	20
6.	G 6	135	9	2.634**	6.356	-1.00	-0.010	4.59	12	21
7.	G 7	133	11	-1.546*	9.591	0.41	-0.006	1.88	5	16
8.	G 8	124	16	1.822**	-0.702	-0.69	0.020	3.16	9	25
9.	G 9	131	12	0.916	14.817**	-1.00	-0.010	4.59	12	24
10.	G 10	136	8	1.889**	9.790	-1.50	-0.018	6.88	18	26
11.	G 11	134	10	1.105	-15.139**	-0.61	0.006	2.80	7	17
12.	G 12	133	11	0.819	4.499	-1.60	-0.012	7.34	19	30
13.	G 13	138	6	1.368	-17.251**	-1.30	0.001	5.96	16	22
14.	G 14	140	4	0.034	-19.463**	0.80	0.024	3.67	10	14
15.	G 15	131	12	1.180	62.551**	-0.40	0.001	1.83	4	16
16.	G 16	135	9	1.020	-8.932	-1.10	-0.008	5.04	13	22
17.	G 17	138	6	-0.075	-7.449	0.60	-0.019	2.75	6	12
18.	G 18	138	6	0.882*	-6.681	-1.20	0.010	5.50	14	20
19.	G 19	136	8	-0.251	15.837**	-0.67	0.001	3.07	8	16
20.	G 20	143	2	0.543	-27.982**	-1.90	-0.019	8.71	23	25
21.	G 21	137	7	0.947	5.594*	-0.39	-0.009	1.79	3	10
22.	G 22	135	9	-0.290	-15.910**	-1.20	0.002	5.50	14	23
23.	G 23	133	11	0.195	-15.464**	0.39	-0.021	1.79	3	14
24.	G 24	129	14	-0.970	-4.551	0.41	0.013	1.88	5	19
25.	G 25	121	18	1.039	-24.114**	-0.03	0.008	0.12	1	19
26.	G 26	122	17	-0.336	-31.277**	1.21	0.009	5.55	15	32
27.	G 27	134	10	0.608*	-25.306**	0.61	-0.020	2.80	7	17
28.	G 28	134	10	0.932	-6.710	-0.10	-0.006	0.46	2	12
29.	G 29	133	11	0.359	-32.785**	1.41	-0.007	6.47	17	28
30.	G 30	138	6	-0.004	35.219**	0.91	-0.013	4.17	11	17
31.	G 31	135	9	0.512	-5.105*	1.60	-0.008	7.34	19	28
32.	G 32	130	13	0.984	0.480	-1.20	0.014	5.50	14	27
33.	G 33	136	8	-0.078*	-9.731	0.80	0.028	3.67	10	18
34.	G 34	135	9	0.596	-33.499**	1.00	0.011	4.59	12	21
35.	G 35	139	5	1.368	19.496**	2.20	0.009	10.09	26	31
36.	G 36	135	9	1.008	1.119	1.79	0.002	8.21	21	30
37.	G 37	134	10	0.740	36.566**	1.80	0.008	8.25	22	32
38.	G 38	141	3	2.378**	-11.547	2.30	-0.040	10.55	27	30
39.	G 39	140	4	2.536**	39.537**	2.60	0.009	11.92	28	32
40.	G 40	145	1	1.711**	-19.859**	1.70	-0.014	7.80	20	21

*Significant at 5% level of significance

**Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression Coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI Stability Value, RASVi: Rank of ASV, GSI: Genotype Selection Index

and G10 were more specifically adapted to E4 site whereas genotypes G20 was more specifically adapted to site E3. The G2 was more favorable to E5 site while G8 was most suited for site E2. No any genotypes specifically adapted to site E1. Genotypes, G24, G23, G4, G7, G28, G4 and G21 were located near to central line of IPCA1 scores which indicates, these genotypes have highest additive main effect. Among all, G2, G3, G20, G12, G10, G39, G38 and G35 were located away from central line of IPCA1 score which were indicating the maximum interaction between genotype and environment.

In figure 6.2 where IPCA2 was plotted against IPCA1 which explained GE interaction, making it a useful test for interaction. It was observed that most of the genotypes and environments were sparged around the biplot. Genotypes farther from the center of biplot show specific adaptation. In the present study, G23, G7, G28, G4, G15 and G19 were more stable than the other genotypes since they were found near to the origin and have general adaptability. However, G4 was stable and dwarfish genotype than grand mean. The other genotypes showed specific to the certain environments. for example, G39, G38, G35 and G36 were more adapted to E1 whereas G33, G14 and G8 were specifically adapted to site E3. The G2, G3 and G32 were more favorable to site E5 while G20, G10, G5, G6 and G16 were more specifically adapted to E2 and E4 sites. Also, no any environment fell into sector with G40 and G27 vertex, it implies that, these are the poorest genotypes in some or all of the locations. In the present investigation, G2 and G3 were the best at E5, G39 was the best at E1, G33 was the better in E3 and G20 was good at E2 and E4 (Fig. 6.2), suggesting that these genotype won to which environment lie. These genotypes positioned on the polygon vertex might be have the longest distance from biplot origin, supposed to the most responsive and have highest interaction between genotype and environment.

Among tested environments, E1, E4, E3 and E2 were the most discriminating environments that provided adequate information on the performance of the genotypes. Further explanation, E1, E4, E3 and E2 environments were powerful for genotype evaluation and interesting sites to identify superior genotypes. On other hand, E5 environment falls close to the bi-plot origin and the least discriminating

environment (Fig. 6.2) and it provided little information about the performance difference of genotypes.

3. Number of primary branches plant⁻¹

Considering all the stability parameters (Table 22), genotype, G24 (GM=13, bi=1.193, S²di=-0.501, IPCA1=0.25, IPCA2=0.032, ASV=0.46, GSI=10) observed more stable for higher number of primary branches plant⁻¹ followed by the genotype, G36 (GM=12, bi=1.160, S²di=-0.247, IPCA1=-0.20, IPCA2=0.021, ASV=0.36, GSI=8), G32 (GM=12, bi=0.993, S²di=-0.586, IPCA1=0.00, IPCA2=0.040, ASV=0.04, GSI=3), G35 (GM=11, bi=1.899, S²di=-0.099, IPCA1=0.49, IPCA2=-0.008, ASV=0.89, GSI=21) and G10 (GM=11, bi=1.031, S²di=3.379, IPCA1=-0.60, IPCA2=-0.001, ASV=1.09, GSI=24) while genotype, G31 (GM=7, bi=1.231, S²di=0.670, IPCA1=0.51, IPCA2=-0.025, ASV=0.93, GSI=27) registered more stable for lesser number of primary branches plant⁻¹ followed by the genotype, G15 (GM=7, bi=1.302, S²di=-0.351, IPCA1=-0.10, IPCA2=0.031, ASV=0.18, GSI=10) and G28 (GM=7, bi=1.336, S²di=0.301, IPCA1=0.31, IPCA2=-0.009, ASV=0.56, GSI=20).

In figure 7.1, IPCA1 was plotted against mean, the vertical line passing through the origin is the grand mean. Accordingly, those genotypes and environment (E2) which was found in the right side of the vertical line were observed more average number of primary branches plant⁻¹ than grand mean. Among all, genotypes, G24, G32, G4 and G40 have positive IPCA1 score which indicates, these genotypes were noted for more average number of primary branches plant⁻¹. On the other hand, the mean performance for most of the genotypes were recorded below the grand mean and which were located to left side of the vertical line. Among all, genotypes, G26, G3, G31, G15 and G19 have located extreme left side which indicates, these genotypes had lower average number of primary branches plant⁻¹. The lowest number of primary branches plant⁻¹ was observed for E4, E3, E1 and E5 than grand mean hence they were found in the left side of the Figure 7.1. Genotypes, G11, G33 and G37 were more specifically adapted to E3 site whereas genotypes G13 and G18 were more specifically adapted to site E4. The G9, G16, G6 and G20 were more favorable to E5 site. No any genotypes specifically adapted to E1 and E2 sites. Genotypes, G24, G36, G32, G40,

Table 22: Estimation of stability parameters of 40 Niger genotypes for number of primary branches plant⁻¹.

Sr. No.	Genotype code	Number of primary branches plant ⁻¹								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	11	3	0.335	1.465	-0.80	-0.009	1.46	24	27
2.	G 2	11	3	0.429	0.756	-0.10	-0.020	0.18	3	6
3.	G 3	7	7	0.865	0.419	0.29	0.000	0.53	11	18
4.	G 4	11	3	0.343	1.788**	0.50	-0.024	0.91	19	22
5.	G 5	7	7	0.677	0.877	-0.20	-0.020	0.36	6	13
6.	G 6	9	5	-0.062*	3.657**	-0.22	-0.012	0.40	8	13
7.	G 7	8	6	1.506	5.955**	-0.11	-0.014	0.20	4	10
8.	G 8	7	7	0.927	1.901**	-0.40	-0.006	0.73	16	23
9.	G 9	9	5	0.585	2.532**	-0.91	0.002	1.66	26	31
10.	G 10	11	3	1.031	3.979	-0.60	-0.001	1.09	21	24
11.	G 11	8	6	1.069	0.245*	0.15	-0.010	0.27	5	11
12.	G 12	8	6	1.641	1.241	0.09	-0.029	0.17	2	8
13.	G 13	8	6	1.849**	2.349**	-1.00	-0.026	1.82	28	34
14.	G 14	8	6	1.173	-0.510	-0.21	0.001	0.38	7	13
15.	G 15	7	7	1.302	-0.351	-0.10	0.031	0.18	3	10
16.	G 16	9	5	2.528**	0.262	-0.81	0.001	1.47	25	30
17.	G 17	8	6	2.567**	-0.487	-0.32	-0.030	0.58	14	20
18.	G 18	8	6	1.908**	0.709	-0.92	0.012	1.67	27	33
19.	G 19	7	7	2.625**	2.828**	-0.11	0.011	0.20	4	11
20.	G 20	9	5	2.363**	0.834	-0.50	0.022	0.91	19	24
21.	G 21	7	7	0.135	-0.131	-0.30	-0.025	0.55	12	19
22.	G 22	8	6	0.448	-0.456	-0.39	0.011	0.71	15	21
23.	G 23	8	6	0.592	-0.506	0.29	0.010	0.53	11	17
24.	G 24	13	1	1.193	-0.501	0.25	0.032	0.46	9	10
25.	G 25	8	6	0.718*	-0.291	0.71	0.004	1.29	23	29
26.	G 26	7	7	1.205	-0.642	1.10	-0.008	2.00	29	36
27.	G 27	8	6	0.929	-0.399	0.62	-0.001	1.13	22	28
28.	G 28	7	7	1.336	0.301	0.31	-0.009	0.56	13	20
29.	G 29	7	7	1.685	-0.694*	0.41	-0.011	0.75	17	24
30.	G 30	8	6	1.009	-0.341	0.11	-0.021	0.20	4	10
31.	G 31	7	7	1.231	0.670	0.51	-0.025	0.93	20	27
32.	G 32	12	2	0.993	-0.586	0.00	0.040	0.04	1	3
33.	G 33	9	5	2.024**	-0.556	0.39	0.052	0.71	15	20
34.	G 34	9	5	1.501	-0.587	-0.11	0.023	0.20	4	9
35.	G 35	11	3	1.899**	-0.099	0.49	-0.008	0.89	18	21
36.	G 36	12	2	1.160	-0.247	-0.20	0.021	0.36	6	8
37.	G 37	8	6	-1.070	5.932**	-0.15	0.023	0.27	5	11
38.	G 38	10	4	-0.504*	6.034**	-0.28	0.004	0.51	10	14
39.	G 39	10	4	-0.610	7.401**	0.60	0.003	1.09	21	25
40.	G 40	11	3	-0.219	6.470**	0.21	0.009	0.38	7	10

*Significant at 5% level of significance

**Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression Coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI Stability Value, RASVi: Rank of ASV, GSI: Genotype Selection Index

G2, G34, G7, G12, G30, G19 and G15 were located near to central line of IPCA1 scores which indicates, these genotypes have highest additive main effect. In the present investigation, G24, G36, G32 and G2 were stable with highest average number of primary branches plant⁻¹ whereas G19, G15 and G7 were stable with lowest number of primary branches plant⁻¹. Among all, G13, G18, G9, G16, G1, G26, G25, G27 and G39 were located far from central line of IPCA1 score which were indicating the maximum interaction between genotype and environment.

In AMMI2 (Figure 7.2), IPCA2 was plotted against IPCA1 which clear up the GE interaction, making it a useful test for interaction. It was observed that most of the genotypes and environments were spread around the biplot. Genotypes farther from the center of biplot show specific adaptation. In the present study, G14, G22, G19, G3, G40 and G4 were more stable than the other genotypes since they were found near to the origin and have general adaptability. However, G14 was stable with highest number of primary branches plant⁻¹ than grand mean. The other genotypes showed specific to the certain environments. for instance, G26, G25, G29 and G27 were more adapted to E1 whereas G33, G32, G24 and G15 were specifically adapted to site E3. The G9, G18 and G20 were more favorable to site E5 while G13, G17, G1 and G21 were more specifically adapted to E2 and E4 sites. In the present investigation, G26 was the best at E1, G13 and G17 were good at E2 and E4; G9 and G18 were the better in E5 and at E3, G33 and G32 were the best (Fig. 7.2), suggesting that these genotype won to which environment lie. These genotypes positioned on the polygon vertex might be have the longest distance from biplot origin, supposed to the most responsive and have highest interaction between genotype and environment.

Among tested environments, E1, E4 and E3 were the most discriminating environments that provided adequate information on the performance of the genotypes. Further explanation, E1, E4 and E3 environments were powerful for genotype evaluation and interesting sites to identify superior genotypes. On other hand, E2 and E5 environments falls close to the bi-plot origin and the least discriminating environment (Fig. 7.2) and it provided little information about the performance difference of genotypes.

4. Number of secondary branches plant⁻¹

As regards to number of secondary branches plant⁻¹ (Table 23), genotype, G36 (GM=23, bi=0.956, S²di=-0.831, IPCA1=0.79, IPCA2=-0.022, ASV=0.97, GSI=26) observed more stable for higher number of secondary branches plant⁻¹ followed by the genotype, G24 (GM=22, bi=1.005, S²di=-2.732, IPCA1=-0.55, IPCA2=-0.002, ASV=0.67, GSI=22), G32 (GM=22, bi=1.055, S²di=-3.351, IPCA1=-0.77, IPCA2=0.000, ASV=0.94, GSI=26) and G10 (GM=21, bi=0.878, S²di=-4.426, IPCA1=-0.71, IPCA2=-0.014, ASV=0.87, GSI=26) while genotype, G26 (GM=13, bi=1.107, S²di=-1.007, IPCA1=0.49, IPCA2=0.004, ASV=0.60, GSI=28) registered more stable for lesser number of secondary branches plant⁻¹ followed by G11 (GM=14, bi=1.723, S²di=0.034, IPCA1=-0.15, IPCA2=0.006, ASV=0.18, GSI=18) while considering all the stability parameters.

In AMMI1 biplot (Fig. 8.1), IPCA1 was plotted against mean, the vertical line passing through the origin is the grand mean. Accordingly, those genotypes and environments (E1) which were found in the right side of the vertical line were observed more average number of secondary branches plant⁻¹ than grand mean. Among all, genotypes G36, G40 and G38 have positive IPCA1 score which indicates, these genotypes were registered for more average number of secondary branches plant⁻¹ while G32, G24 and G10 have negative IPCA1 score with more average number of secondary branches plant⁻¹. On the other hand, the mean performance for most of the genotypes were recorded below the grand mean and which were located to left side of the vertical line. Among all, genotype, G26, G29, and G28 have positive IPCA1 score which indicates, these genotypes had lower average number of secondary branches plant⁻¹. The lowest number of secondary branches plant⁻¹ was observed in E5, E3, E4 and E2 than grand mean hence they were found in the left side of the Figure 8.1. Genotypes G33, G9 and G20 were more specifically adapted to E4 and E2 sites whereas genotypes, G25 and G7 were more specifically adapted to site E3. No any genotypes specifically adapted to site E5 and E1. Genotypes, G39, G33, G9, G8, G37, G22, G27, G28 and G17 were located near to central line of IPCA1 scores which indicates, these genotypes have highest additive main effect.

Table 23: Estimation of stability parameters of 40 Niger genotypes for number of secondary branches plant⁻¹.

Sr. No.	Genotype code	Number of secondary branches plant ⁻¹								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	18	6	0.407	9.637**	-0.80	0.020	0.98	26	32
2.	G 2	20	4	-0.478*	-2.551	-0.97	-0.001	1.19	29	33
3.	G 3	14	10	0.747	-3.280	-0.79	-0.019	0.97	25	35
4.	G 4	20	4	0.515	-0.980	-1.33	-0.010	1.63	30	34
5.	G 5	15	9	0.416	-3.281	0.49	0.026	0.60	17	26
6.	G 6	16	8	-0.020	13.034**	1.35	-0.005	1.66	31	39
7.	G 7	15	9	0.471	15.326**	0.09	-0.010	0.11	3	12
8.	G 8	15	9	-0.349	11.232**	0.03	0.031	0.05	2	11
9.	G 9	17	7	-0.499*	4.001	0.11	-0.007	0.14	6	13
10.	G 10	21	3	0.878	-4.426	-0.71	-0.014	0.87	23	26
11.	G 11	14	10	1.723	0.034	-0.15	0.006	0.18	8	18
12.	G 12	16	8	2.041**	-3.269	0.24	-0.011	0.29	11	19
13.	G 13	15	9	1.113	-1.542	-0.54	-0.001	0.66	19	28
14.	G 14	15	9	1.484	-1.707	-0.10	0.024	0.12	4	13
15.	G 15	14	10	1.053	-2.967	-0.19	0.022	0.23	10	20
16.	G 16	17	7	2.351**	0.815	1.58	0.004	1.94	32	39
17.	G 17	15	9	2.968**	-3.105	-0.95	0.021	1.17	28	37
18.	G 18	15	9	1.893**	-2.819*	0.36	-0.012	0.44	14	23
19.	G 19	15	9	3.274**	1.658	0.27	0.011	0.33	12	21
20.	G 20	17	7	2.409**	-1.243	0.65	-0.021	0.80	22	29
21.	G 21	15	9	0.239	-0.406	0.53	0.012	0.65	18	27
22.	G 22	14	10	0.552*	-3.038	0.01	-0.001	0.01	1	11
23.	G 23	15	9	0.083	-3.678	0.49	0.001	0.60	17	26
24.	G 24	22	2	1.005	-2.732	-0.55	-0.002	0.67	20	22
25.	G 25	15	9	0.486	-3.600	-0.91	-0.008	1.12	27	36
26.	G 26	13	11	1.107	-1.007	0.49	0.004	0.60	17	28
27.	G 27	15	9	2.027**	-2.398	0.09	0.029	0.11	3	12
28.	G 28	14	10	0.764	-1.379	0.15	0.031	0.19	9	19
29.	G 29	14	10	1.828**	-3.848	0.40	0.022	0.49	15	25
30.	G 30	16	8	1.092	-2.207	-0.12	0.050	0.16	7	15
31.	G 31	15	9	1.413	-2.636*	0.30	0.016	0.37	13	22
32.	G 32	22	2	1.055*	-3.351	-0.77	0.000	0.94	24	26
33.	G 33	17	7	1.491	-2.183	0.11	-0.004	0.13	5	12
34.	G 34	16	8	1.842**	-2.675	-0.09	-0.003	0.11	3	11
35.	G 35	19	5	1.756	-2.581	-0.64	-0.006	0.78	21	26
36.	G 36	23	1	0.956	-0.831	0.79	-0.022	0.97	25	26
37.	G 37	15	9	0.798	14.729**	0.09	0.001	0.11	3	12
38.	G 38	20	4	-0.230*	7.012**	0.65	-0.009	0.80	22	26
39.	G 39	20	4	0.136	12.435**	-0.10	-0.017	0.12	4	8
40.	G 40	22	2	0.001	29.079**	0.41	-0.016	0.50	16	18

*Significant at 5% level of significance

**Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression Coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI Stability Value, RASVi: Rank of ASV, GSI: Genotype Selection Index

In the present investigation, G39 was stable with highest average number of secondary branches plant⁻¹ whereas G22, G27, G28, G7 and G33 were stable with lowest number of secondary branches plant⁻¹. Among all, G4, G2, G17, G25, G1, G32, G10, G3, G16 and G6 were located far from central line of IPCA1 score which were indicating the maximum interaction between genotype and environment.

In Figure 8.2 where IPCA2 was plotted against IPCA1 which evinced the GE interaction, making it a useful test for interaction. It was noticed that most of the genotypes and environments were scattered around the biplot. Genotypes farther from the center of biplot show specific adaptation. In the present study, G11, G37, G22, G24, G36, G13 and G9 were more stable than the other genotypes since they were found near to the origin and have general adaptability. However, G11, G22 and G36 were stable with highest number of secondary branches plant⁻¹ than grand mean. The other genotypes showed specific to the certain environments. for example, G30, G17 and G1 were more adapted to E3 whereas G16 and G6 were specifically adapted to site E5. The genotypes, G4, G3, G2, G10 and G25 were more favorable to site E1 while G20, G26 and G40 were more specifically adapted to E4 while G16, G6 and G38 were more suited to E4 site. In the present investigation, G3 and G4 were the best at E1, G30 and G17 were good at E2 and E3, G26 was the better in E4 and G16 was the best at E5 (Fig. 8.2), suggesting that these genotype won to which environment lie. These genotypes positioned on the polygon vertex might be have the longest distance from biplot origin, supposed to the most responsive and have highest interaction between genotype and environment.

Among tested environments, E1, E3 and E5 were the most discriminating environments that provided adequate information on the performance of the genotypes. Further explanation, E1, E3 and E5 environments were powerful for genotype evaluation and interesting sites to identify superior genotypes. On other hand, E2 and E4 environments falls close to the bi-plot origin and the least discriminating environment (Fig. 8.2) and it provided little information about the performance difference of genotypes.

5. Number of capitula plant⁻¹

With regards to number of capitula plant⁻¹ (Table 24), genotype, G36 (GM=52, bi=0.923, S²di=0.876, IPCA1=2.42, IPCA2=-0.04, ASV=4.84, GSI=39) observed more stable for maximum number of capitula plant⁻¹ followed by the genotype, G24 (GM=50, bi=0.921, S²di=0.699, IPCA1=1.08, IPCA2=-0.85, ASV=2.32, GSI=27), G32 (GM=48, bi=1.392, S²di=-4.387, IPCA1=1.14, IPCA2=-1.12, ASV=2.54, GSI=31), G35 (GM=43, bi=1.228, S²di=-1.898, IPCA1=0.29, IPCA2=0.40, ASV=0.70, GSI=14) and G14 (GM=38, bi=1.027, S²di=-6.502, IPCA1=0.00, IPCA2=0.97, ASV=0.97, GSI=22) while genotype, G29 (GM=30, bi=1.067, S²di=-2.716, IPCA1=-0.32, IPCA2=-0.23, ASV=0.68, GSI=25) registered more stable for minimum number of capitula plant⁻¹ followed by G28 (GM=31, bi=1.155, S²di=-2.573, IPCA1=-0.72, IPCA2=1.10, ASV=1.81, GSI=39) while considering all the stability parameters.

In figure 9.1 where IPCA1 was plotted against mean, the vertical line passing through the origin is the grand mean. Accordingly, those genotypes and environment (E3) which were reported in the right side of the vertical line were observed more average number of capitula plant⁻¹ than grand mean. Among all, genotypes, G36, G24, G40, G32 and G10 have positive IPCA1 score which indicates, these genotypes were registered for more average number of capitula plant⁻¹. On the other hand, the mean performance for most of the genotypes were recorded below the grand mean and which were located to left side of the vertical line. Among all, genotypes, G29, G28 and G26 have negative IPCA1 score which indicates, these genotypes had lowest average number of capitula plant⁻¹. main effect. In the present investigation, G40, G1 and G35 were stable with highest average number of capitula plant⁻¹ whereas G22, G3, G34 and G14 were most stable with lowest number of capitula plant⁻¹. Among all, G31, G4, G5, G2, G8, G18, G36, G10, G20, G9 and G13 were located far from central line of IPCA1 score which were indicating the maximum interaction between genotype and environment.

In AMMI2 biplot (Figure 9.2), IPCA2 was plotted against IPCA1 which expound the GE interaction, making it a useful test for interaction. It was noticed that most of the genotypes and environments were spread around the biplot. Genotypes farther from the center of biplot show specific adaptation. In the present

Table 24: Estimation of stability parameters of 40 Niger genotypes for number of capitula plant⁻¹.

Sr. No.	Genotype code	Number of capitula plant ⁻¹								
		Mean	RMi	Bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	46	6	0.879	-23.14**	0.25	-0.06	0.50	3	9
2.	G 2	44	8	0.391	57.907**	-1.33	1.98	3.32	32	40
3.	G 3	35	16	0.067	18.610**	-0.42	-0.24	0.87	8	24
4.	G 4	43	9	0.149	6.467	-1.36	-0.77	2.83	30	39
5.	G 5	35	16	-0.222	22.830**	-1.30	-0.60	2.67	29	45
6.	G 6	34	17	0.916	73.111**	-0.96	-0.01	1.92	21	38
7.	G 7	35	16	0.535	49.945**	-0.87	0.38	1.78	18	34
8.	G 8	33	18	0.221*	67.831**	-1.20	-0.67	2.49	26	44
9.	G 9	40	11	0.667	52.570**	1.86	0.52	3.76	34	45
10.	G 10	47	5	0.188	53.024**	2.09	-0.63	4.23	37	42
11.	G 11	33	18	1.328	2.697*	-0.86	-0.26	1.74	17	35
12.	G 12	35	16	1.767	-7.993	-0.30	-0.43	0.74	6	22
13.	G 13	38	13	1.850**	-14.50**	1.69	2.02	3.94	35	48
14.	G 14	38	13	1.027	-6.502	0.00	0.97	0.97	9	22
15.	G 15	35	16	-0.831*	-13.61**	-0.39	-1.90	2.05	22	38
16.	G 16	37	14	3.116**	11.297	0.70	0.76	1.59	15	29
17.	G 17	35	16	3.344**	-3.877	-0.72	1.77	2.28	24	40
18.	G 18	39	12	1.269	10.789	2.81	-0.25	5.63	39	51
19.	G 19	36	15	3.616**	-1.703	0.88	-0.22	1.78	18	33
20.	G 20	42	10	2.316**	5.326	2.05	0.37	4.12	36	46
21.	G 21	36	15	0.215	6.295	-0.17	-0.16	0.38	2	17
22.	G 22	32	19	0.026	-2.040	-0.09	-0.26	0.32	1	20
23.	G 23	34	17	-1.274*	-6.716	-0.73	-1.21	1.90	20	37
24.	G 24	50	2	0.921	0.699	1.08	-0.85	2.32	25	27
25.	G 25	32	19	0.538	-6.749	-0.86	-1.46	2.26	23	42
26.	G 26	31	20	0.058	21.315**	-1.15	-1.19	2.59	28	48
27.	G 27	32	19	0.995	-5.755	-0.61	-0.42	1.29	12	31
28.	G 28	31	20	1.155	-2.573	-0.72	1.10	1.81	19	39
29.	G 29	30	21	1.067	-2.716	-0.32	-0.23	0.68	4	25
30.	G 30	36	15	1.125	2.705	-1.03	2.29	3.08	31	46
31.	G 31	36	15	0.981	3.772	-1.71	0.43	3.45	33	48
32.	G 32	48	4	1.392	-4.387	1.14	-1.12	2.54	27	31
33.	G 33	35	16	0.388	21.823**	0.07	-1.01	1.02	10	26
34.	G 34	36	15	1.421	-4.388	0.09	-1.08	1.09	11	26
35.	G 35	43	9	1.228	-1.898	0.29	0.40	0.70	5	14
36.	G 36	52	1	0.923	0.876	2.42	-0.04	4.84	38	39
37.	G 37	35	16	-0.625	90.045**	-0.76	0.66	1.66	16	32
38.	G 38	44	8	0.761	-45.18**	-0.62	0.82	1.49	14	22
39.	G 39	45	7	-0.191*	69.057**	0.70	0.18	1.41	13	20
40.	G 40	49	3	0.252	64.358**	0.38	0.41	0.86	7	10

*Significant at 5% level of significance

**Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression Coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI Stability Value, RASVi: Rank of ASV, GSI: Genotype Selection Index

study, G21, G1, G29, G22, G35 and G3 were more stable than the other genotypes since they were found near to the origin and have general adaptability. The lowest number of capitula plant⁻¹ was observed in E5, E4, E2 and E1 than grand mean hence they were found in the left side of the Figure 9.1. Genotypes G4 and G2 were more specifically adapted to E3 site whereas genotypes G30, G31 and G5 were more specifically adapted to site E4. The G21, G12, G15, G37, G7 and G17 were more favorable to site E5. No any genotypes specifically adapted to sites E1 and E2. Genotypes, G40, G1, G35, G14, G34, G3, G22 and G21 were located near to central line of IPCA1 scores which indicates, these genotypes have highest additive

However, G21 and G1 were stable with highest number of capitula plant⁻¹ than grand mean. The other genotypes showed specific to the certain environments. for instance, G18, G10, G32, G36, G24 and G20 were more adapted to E1 whereas G2, G30 and G17 were specifically adapted to site E3. The G15, G20, G26, G23, G33 and G34 were more favorable to E4 and E5 sites while G4, G5 and G8 were more favorable at site E2. Genotypes G9, G37 and G29 were more specifically adapted to E5 site. Also, no any environment felt into sector with G31 and G13 vertex, it implies that, these are the poorest genotypes in some or all of the locations. In the present investigation, G18 and G32 were the best at E1, G2 and G30 were good at E3, G4 was the better in E2 and G15, G25 and G26 were the best at E4 and E5 (Fig. 9.2), suggesting that these genotype won to which environment lie. These genotypes positioned on the polygon vertex might be have the longest distance from biplot origin, supposed to the most responsive and have highest interaction between genotype and environment.

Among tested environments, E1, E3, E4 and E2 were the most discriminating environments that provided adequate information on the performance of the genotypes. Further explanation, E1, E3, E4 and E2 environments were powerful for genotype evaluation and interesting sites to identify superior genotypes. On other hand, E5 environment falls close to the bi-plot origin and the least discriminating environment (Fig. 9.2) and it provided little information about the performance difference of genotypes.

6. Capitulum diameter (cm)

As per capitulum diameter (Table 25), genotype, G36 (GM=1.25 cm, bi=1.142, $S^2di=-0.002$, IPCA1=-0.061, IPCA2=-0.038, ASV=0.44, GSI=19) observed more stable for broader capitulum diameter followed by the genotype, G39 (GM=1.14 cm, bi=1.584, $S^2di=-0.002$, IPCA1=-0.087, IPCA2=-0.029, ASV=0.23, GSI=13), G15 (GM=1.11 cm, bi=1.656, $S^2di=0.001$, IPCA1=0.067, IPCA2=0.103, ASV=0.27, GSI=18), G2 (GM=1.06 cm, bi=1.041, $S^2di=-0.001$, IPCA1=-0.049, IPCA2=0.134, ASV=0.23, GSI=19), G30 (GM=1.05 cm, bi=0.891, $S^2di=0.002$, IPCA1=-0.018, IPCA2=-0.102, ASV=0.12, GSI=15), G32 (GM=1.03 cm, bi=0.852, $S^2di=0.002$, IPCA1=0.020, IPCA2=-0.078, ASV=0.11, GSI=16) and G10 (GM=1.03 cm, bi=1.049, $S^2di=0.003$, IPCA1=0.023, IPCA2=0.043, ASV=0.10, GSI=15) while genotype, G26 (GM=0.90 cm, bi=1.083, $S^2di=-0.001$, IPCA1=-0.016, IPCA2=0.204, ASV=0.21, GSI=28) registered more stable for smaller diameter of capitulum followed by G20 (GM=0.96 cm, bi=1.492, $S^2di=0.001$, IPCA1=0.093, IPCA2=-0.178, ASV=0.39, GSI=33) while considering all the stability parameters.

In AMMI1 (Figure 10.1) IPCA1 was plotted against mean, the vertical line passing through the origin is the grand mean. Accordingly, those genotypes and environments (E1 and E3) which were reported in the right side of the vertical line were observed bigger capitulum diameter than grand mean. Among all, genotype G15 have positive IPCA1 score which indicates, these genotypes were noted for larger mean diameter of capitulum whereas genotypes G36, G40, G38, G39, G35 and G24 have negative IPCA1 score with more far-flung capitulum diameter. On the other hand, the mean performance for most of the genotypes were recorded below the grand mean and which were located to left side of the vertical line. Among all, genotypes, G26, G25 and G7 have positive IPCA1 score which indicates, these genotypes had smallest average capitulum diameter. The lowest capitulum diameter was observed in E4, E5 and E2 than grand mean hence they were found in the left side of the Figure 10.1. Genotypes, G25, G23, G7, G37, G17 and G19 were more specifically adapted to E4 site. No any genotypes specifically adapted to sites E1, E2, E3 and E5. Genotypes, G30, G10, G32, G23, G25, G26 and G31 were located near to central line of IPCA1 scores which indicates, these

Table 25: Estimation of stability parameters of 40 Niger genotypes for capitulum diameter (cm).

Sr. No.	Genotype code	Capitulum diameter (cm)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	1.08	8	0.973	0.003**	0.156	-0.139	0.60	25	33
2.	G 2	1.06	10	1.041	-0.001	-0.049	0.134	0.23	9	19
3.	G 3	1.07	9	0.015	0.003**	0.067	0.112	0.27	12	21
4.	G 4	1.08	8	0.666	0.000	0.092	-0.008	0.34	14	22
5.	G 5	1.01	15	-0.775*	-0.002	-0.176	-0.009	0.65	28	43
6.	G 6	1.04	12	0.991	0.003**	0.111	-0.066	0.42	17	29
7.	G 7	0.95	19	0.216	0.000	-0.057	0.115	0.24	10	29
8.	G 8	1.03	13	0.558	0.001	0.267	-0.041	0.99	32	45
9.	G 9	1.01	15	1.292	0.001	0.072	0.055	0.27	12	27
10.	G 10	1.03	13	1.049	0.003	0.023	0.043	0.10	2	15
11.	G 11	1.02	14	1.282	-0.001	0.120	0.043	0.45	19	33
12.	G 12	1.03	13	*0.983	-0.001	0.233	-0.028	0.87	31	44
13.	G 13	1.01	15	1.350	-0.001	0.083	0.012	0.31	13	28
14.	G 14	1.02	14	0.676	-0.002	0.170	-0.061	0.63	26	40
15.	G 15	1.11	6	1.656	0.001	0.067	0.103	0.27	12	18
16.	G 16	1.04	12	2.009**	0.000	0.167	-0.121	0.63	26	38
17.	G 17	1.02	14	2.533**	0.001	-0.081	-0.056	0.31	13	27
18.	G 18	1.02	14	2.925**	-0.002	0.128	0.105	0.49	20	34
19.	G 19	1.03	13	2.210**	0.000	-0.102	0.138	0.40	16	29
20.	G 20	0.96	18	1.492	0.001	0.093	0.178	0.39	15	33
21.	G 21	1.01	15	-0.166	-0.002	-0.139	-0.052	0.52	23	38
22.	G 22	1.09	7	-0.200	-0.002	0.143	-0.035	0.53	24	31
23.	G 23	0.99	16	-0.325	-0.002	0.029	-0.001	0.11	3	19
24.	G 24	1.06	10	-0.174	-0.001	-0.179	0.024	0.66	29	39
25.	G 25	0.95	19	-0.226*	-0.001	-0.004	0.014	0.02	1	20
26.	G 26	0.90	20	1.083	-0.001	-0.016	0.204	0.21	8	28
27.	G 27	0.95	19	1.033	-0.002	-0.172	-0.018	0.64	27	46
28.	G 28	0.98	17	1.216	0.000	-0.207	-0.133	0.78	30	47
29.	G 29	1.01	15	-0.726*	0.000	-0.137	-0.010	0.51	22	37
30.	G 30	1.05	11	0.891	0.002	-0.018	-0.102	0.12	4	15
31.	G 31	1.08	8	0.571	0.012	0.034	-0.121	0.17	7	15
32.	G 32	1.03	13	0.852	0.002	0.020	-0.078	0.11	3	16
33.	G 33	1.06	10	0.211	0.004**	-0.118	-0.139	0.15	6	16
34.	G 34	1.06	10	1.080*	0.010**	-0.131	-0.029	0.13	5	15
35.	G 35	1.13	5	1.093	0.005**	-0.066	-0.060	0.10	2	7
36.	G 36	1.25	1	1.142	-0.002	-0.061	-0.038	0.44	18	19
37.	G 37	0.98	17	1.433	-0.001	-0.092	0.096	0.50	21	38
38.	G 38	1.17	3	1.709**	-0.002	-0.110	-0.006	0.25	11	14
39.	G 39	1.14	4	1.584	-0.002	-0.087	-0.029	0.23	9	13
40.	G 40	1.21	2	1.275	0.008**	-0.071	0.003	0.34	14	16

*Significant at 5% level of significance

**Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression Coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI Stability Value, RASVi: Rank of ASV, GSI: Genotype Selection Index

genotypes have highest additive main effect. In the present investigation, G31 was stable with highest average diameter of capitulum whereas G25, G30, G26, G10 and G32 were most stable with smaller capitulum diameter. Among all, G28, G24, G5, G27, G21, G29, G8, G12, G11, G16, G1 and G22 were located far from central line of IPCA1 score which were indicating the maximum interaction between genotype and environment.

In Figure 10.2 where IPCA2 was plotted against IPCA1 which explained the GE interaction, making it a useful test for interaction. It was reported that most of the genotypes and environments were scattered around the biplot. Genotypes farther from the center of biplot show specific adaptation. In the present study, G36, G23, G25, G10 and G40 were more stable than the other genotypes since they were found near to the origin and have general adaptability. However, G36 and G10 were stable with broader diameter of capitulum than grand mean. The other genotypes showed specific to the certain environments. for instance, G26, G20, G19, G2, G7 and G37 were more adapted to E4 whereas G8, G12 and G22 were specifically adapted to site E2. The G1, G16, G31 and G32 were more favorable to site E1 while G28, G33, G5, G27 and G21 were favorable at sites E3 and E5. Also, no any environment fell into sector with G24 vertex, it implies that, these are the poorest genotypes in some or all of the locations. In the present investigation, G1 was the best at E1, G8 was good at E2; G20, G26 and G19 were the better in E4 and G28 and G33 were the best at E3 and E5 (Fig. 10.2), suggesting that these genotype won to which environment lie. These genotypes positioned on the polygon vertex might be have the longest distance from biplot origin, supposed to the most responsive and have highest interaction between genotype and environment.

Among tested environments, E4, E3, E1 and E5 were the most discriminating environments that provided adequate information on the performance of the genotypes. Further explanation, E4, E3, E1 and E5 environments were powerful for genotype evaluation and interesting sites to identify superior genotypes. On other hand, E2 environment falls close to the bi-plot origin and the least discriminating environment (Fig. 10.2) and it provided little information about the performance difference of genotypes.

7. Number seeds capitulum⁻¹

Considering all the stability parameters (Table 26), genotype, G36 (GM=36, bi=1.427, S²di=-4.262, IPCA1=0.07, IPCA2=0.021, ASV=0.09, GSI=4) observed more stable for higher number of seeds capitulum⁻¹ followed by the genotype, G40 (GM=35, bi=1.155, S²di=-7.178, IPCA1=-0.16, IPCA2=0.024, ASV=0.20, GSI=9), G38 (GM=34, bi=1.497, S²di=-3.960, IPCA1=-0.10, IPCA2=0.026, ASV=0.12, GSI=7), G32 (GM=32, bi=1.280, S²di=-7.894, IPCA1=0.57, IPCA2=-0.001, ASV=0.69, GSI=22), G24 (GM=31, bi=0.997, S²di=-1.612, IPCA1=1.18, IPCA2=0.012, ASV=1.43, GSI=37), G39 (GM=31, bi=1.047, S²di=-5.387, IPCA1=-0.19, IPCA2=0.016, ASV=0.23, GSI=13) and G31 (GM=30, bi=1.037, S²di=-0.830, IPCA1=-0.31, IPCA2=0.005, ASV=0.38, GSI=19) while genotype, G27 (GM=25, bi=1.167, S²di=-9.717, IPCA1=0.89, IPCA2=-0.024, ASV=1.08, GSI=40) registered more stable for lesser number of seeds capitulum⁻¹ followed by G17 (GM=25, bi=1.569, S²di=-8.788, IPCA1=0.84, IPCA2=0.008, ASV=1.02, GSI=38).

In Figure 11.1, IPCA1 was plotted against mean, the vertical line passing through the origin is the grand mean. Accordingly, most of the genotypes and environments (E1, E3 and E2) which were found in the right side of the vertical line were observed more average number of seeds capitulum⁻¹ than grand mean. Among all, genotypes, G36, G32 and G24 have positive IPCA1 score which indicates, these genotypes were registered for more average number of seeds capitulum⁻¹ while genotypes G40, G38, G39 and G35 have negative IPCA1 score with more average number of seeds capitulum⁻¹. On the other hand, the mean performance for some genotypes were noticed below the grand mean and which were located to left side of the vertical line. Among all, genotypes, G27, G29 and G17 have positive IPCA1 score which indicates, these genotypes had lowest average number of seeds capitulum⁻¹ while G7 have negative IPCA score with lowest average number of seeds capitulum⁻¹. The lowest number of seeds capitulum⁻¹ was observed in E4 and E5 than grand mean hence they were found in the left side of the Figure 11.1. Genotypes, G7, G17 and G11 were more specifically adapted to E5 site. No any genotypes specifically adapted to sites E1, E2, E3 and E4. Genotypes, G36, G40, G38, G35, G4, G5, G13, G26, G25 and G28 were located near

Table 26: Estimation of stability parameters of 40 Niger genotypes for number of seeds capitulum⁻¹.

Sr. No.	Genotype code	Number of seeds capitulum ⁻¹								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	27	9	0.529	-11.09**	1.17	-0.005	1.42	31	40
2.	G 2	29	7	0.085	-8.125**	-0.59	-0.240	0.75	20	27
3.	G 3	28	8	-0.463*	-9.505**	0.87	0.002	1.05	28	36
4.	G 4	29	7	0.469	-1.537	0.14	-0.018	0.17	6	13
5.	G 5	29	7	0.251	-10.03**	-0.03	0.001	0.04	2	9
6.	G 6	28	8	0.199	-1.466	0.27	-0.006	0.33	11	19
7.	G 7	25	11	-0.151*	-3.634	-0.70	-0.015	0.85	22	33
8.	G 8	28	8	-0.118	-1.929	-0.74	0.004	0.90	24	32
9.	G 9	28	8	0.339	-12.30**	-1.24	-0.016	1.50	33	41
10.	G 10	29	7	0.860	-9.928**	-0.67	-0.032	0.81	21	28
11.	G 11	26	10	2.264**	-8.750**	0.72	-0.022	0.87	23	33
12.	G 12	26	10	1.926	-10.90**	-1.26	-0.013	1.53	34	44
13.	G 13	27	9	1.611	-11.04**	0.02	-0.026	0.04	2	11
14.	G 14	27	9	0.633	-10.79**	-0.61	-0.0009	0.74	19	28
15.	G 15	30	6	-0.245	-6.842	0.53	-0.015	0.64	17	23
16.	G 16	28	8	2.600**	-4.679	-0.91	0.014	1.10	30	38
17.	G 17	25	11	1.569	-8.788	0.84	0.008	1.02	27	38
18.	G 18	30	6	2.975**	-8.647**	0.25	0.022	0.30	10	16
19.	G 19	28	8	1.642	-10.35**	1.29	0.002	1.56	35	43
20.	G 20	26	10	2.330**	-11.38**	-0.30	0.012	0.36	12	22
21.	G 21	27	9	-0.077*	-7.632	0.53	0.002	0.64	17	26
22.	G 22	29	7	0.604	-6.035	-0.80	0.048	0.97	26	33
23.	G 23	27	9	-0.688	-5.491	-0.25	-0.006	0.30	10	19
24.	G 24	31	5	0.997	-1.612	1.18	0.012	1.43	32	37
25.	G 25	27	9	-0.077	-8.335**	-0.07	-0.016	0.09	3	12
26.	G 26	26	10	1.699*	-9.503**	-0.01	0.007	0.01	1	11
27.	G 27	25	11	1.167	-9.717	0.89	-0.024	1.08	29	40
28.	G 28	26	10	1.594	-6.860	-0.10	0.003	0.12	4	14
29.	G 29	25	11	2.618**	-9.175**	0.44	0.002	0.53	16	27
30.	G 30	28	8	1.629	-11.03**	-0.79	-0.012	0.96	25	33
31.	G 31	30	6	1.037	-0.830	-0.31	0.005	0.38	13	19
32.	G 32	32	4	1.280	-7.894	0.57	-0.001	0.69	18	22
33.	G 33	28	8	0.233	-7.078	-0.36	0.000	0.44	15	23
34.	G 34	29	7	0.358	-3.505*	0.20	-0.001	0.24	9	16
35.	G 35	31	5	-0.023	-2.451	-0.11	0.025	0.14	5	10
36.	G 36	36	1	1.427	-4.262	0.07	0.021	0.09	3	4
37.	G 37	27	9	0.920*	-2.659	0.35	0.004	0.42	14	23
38.	G 38	34	3	1.497	-3.960	-0.10	0.026	0.12	4	7
39.	G 39	31	5	1.047	-5.387	-0.19	0.016	0.23	8	13
40.	G 40	35	2	1.155	-7.178	-0.16	0.024	0.20	7	9

*Significant at 5% level of significance

**Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression Coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI Stability Value, RASVi: Rank of ASV, GSI: Genotype Selection Index

to central line of IPCA1 scores which indicates, these genotypes have highest additive main effect. In the present investigation, G36 and G38 were stable with highest average number of seeds capitulum⁻¹ whereas G5, G13 and G26 were most stable with lower number of seeds capitulum⁻¹. Among all, G12, G9, G16, G30, G22, G8, G19, G24, G1, G7, G3 and G17 were located far from central line of IPCA1 score which were indicating the maximum interaction between genotype and environment.

In AMMI2 biplot (Figure 11.2), IPCA2 was plotted against IPCA1 which expound the GE interaction, making it a useful test for interaction. It was reported that most of the genotypes and environments were dispersed around the biplot. Genotypes farther from the center of biplot show specific adaptation. In the present study, G5, G33, G26, G31, G34, G6, G23 and G14 were more stable than the other genotypes since they were found near to the origin and have general adaptability. However, G5 was stable with highest number of seeds capitulum⁻¹ than grand mean. The other genotypes showed specific to the certain environments. for example, G22, G38, G35, G18, G36 and G16 were more adapted to E4 and E5 sites whereas G27, G11 and G15 were specifically adapted to site E3. The G12, G9 and G30 were more favorable to sites E1 and E2. Also, no any environment fell into sector with G10, G19 and G24 vertex, it implies that, these are the poorest genotypes in some or all of the locations. In the present investigation, G9 and G12 were the best at E1 and E2, G27 was good at E3, G22 was the better in E4 and E5 (Fig. 11.2), suggesting that these genotype won to which environment lie. These genotypes positioned on the polygon vertex might be have the longest distance from biplot origin, supposed to the most responsive and have highest interaction between genotype and environment.

Among tested environments, E3, E4, E1 and E2 were the most discriminating environments that provided adequate information on the performance of the genotypes. Further explanation, E3, E4, E1 and E2 environments were powerful for genotype evaluation and interesting sites to identify superior genotypes. On other hand, E5 environment falls close to the bi-plot origin and the least discriminating

environment (Fig. 11.2) and it provided little information about the performance difference of genotypes.

8. 1000 seed weight (cm)

As regard to 1000 seed weight (Table 27), genotype, G36 (GM=2.77g, bi=0.920, S^2di =0.012, IPCA1=0.013, IPCA2=0.020, ASV=0.03, GSI=3) observed highly stable for more weight of 1000 seed followed by the genotype, G24 (GM=2.71g, bi=1.053, S^2di =-0.008, IPCA1=0.108, IPCA2=0.090, ASV=0.25, GSI=19), G10 (GM=2.68g, bi=1.150, S^2di =-0.001, IPCA1=0.152, IPCA2=0.003, ASV=0.34, GSI=23), G12 (GM=2.68g, bi=0.893, S^2di =-0.003, IPCA1=0.028, IPCA2=0.023, ASV=0.07, GSI=10), G3 (GM=2.65g, bi=0.919, S^2di =0.010, IPCA1=0.059, IPCA2=-0.005, ASV=0.13, GSI=16), G4 (GM=2.65g, bi=0.987, S^2di =-0.008, IPCA1=0.206, IPCA2=0.049, ASV=0.46, GSI=27), G7 (GM=2.59g, bi=1.015, S^2di =0.039, IPCA1=0.016, IPCA2=0.002, ASV=0.04, GSI=13) and G37 (GM=2.59g, bi=0.898, S^2di =0.030, IPCA1=-0.032, IPCA2=0.030, ASV=0.08, GSI=17) while genotype, G29 (GM=2.22g, bi=0.855, S^2di =0.000, IPCA1=-0.164, IPCA2=-0.080, ASV=0.37, GSI=44) registered highly stable for lesser weight of 1000 seed followed by G25 (GM=2.29g, bi=1.098, S^2di =-0.002, IPCA1=-0.082, IPCA2=0.040, ASV=0.19, GSI=37) while considering all the stability parameters.

In AMMI1 biplot (Fig. 12.1), IPCA1 was plotted against mean, the vertical line passing through the origin is the grand mean. Accordingly, most of the genotypes and environments (E5, E2, E3 and E1) which were found in the right side of the vertical line were observed more average weight of 1000 seeds than grand mean. Among all, genotypes, G36, G38, G40, G24, G10 and G12 have positive IPCA1 score which indicates, these genotypes were registered for more average weight of 1000 seeds. On the other hand, the mean performance for few genotypes were noticed below the grand mean and which were located to left side of the vertical line. Among all, genotypes, G28, G29, G25, G26, G25 and G8 have negative IPCA1 score which indicates, these genotypes had lowest average weight of 1000 seeds hence they were found in the left side of the Figure 12.1. Genotype G15 was more specifically adapted to site E5 while G24, G5, G32 and G31 were more favorable to

Table 27: Estimation of stability parameters of 40 Niger genotypes for 1000 seed weight (g).

Sr. No.	Genotype code	1000 seed weight (g)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	2.53	14	1.102	0.028	0.033	0.000	0.07	6	20
2.	G 2	2.65	5	1.651	0.033*	0.123	0.001	0.27	17	22
3.	G 3	2.65	5	0.919	0.010	0.059	-0.005	0.13	11	16
4.	G 4	2.65	5	0.987	-0.008	0.206	0.049	0.46	22	27
5.	G 5	2.58	11	-0.762*	0.010	0.067	0.001	0.15	12	23
6.	G 6	2.52	15	1.252	0.001	0.038	-0.001	0.08	7	22
7.	G 7	2.59	10	1.015	0.039	0.016	0.002	0.04	3	13
8.	G 8	2.36	21	1.147	0.043*	-0.034	0.090	0.12	10	31
9.	G 9	2.52	15	-0.080	-0.005	0.020	-0.010	0.05	4	19
10.	G 10	2.68	4	1.150	-0.001	0.152	0.003	0.34	19	23
11.	G 11	2.51	16	1.038	0.005	0.014	0.051	0.06	5	21
12.	G 12	2.68	4	0.893	-0.003	0.028	0.023	0.07	6	10
13.	G 13	2.48	19	0.912	0.006	-0.036	-0.090	0.12	10	29
14.	G 14	2.52	15	2.593**	0.001	-0.094	0.004	0.21	15	30
15.	G 15	2.49	18	2.045**	0.024	-0.200	0.070	0.45	21	39
16.	G 16	2.53	14	1.843	0.029	-0.060	0.090	0.16	13	27
17.	G 17	2.64	6	2.100**	0.020	-0.005	-0.003	0.01	1	7
18.	G 18	2.51	16	2.314**	0.018	-0.037	0.035	0.09	8	24
19.	G 19	2.52	15	1.272	-0.003	-0.069	0.001	0.15	12	27
20.	G 20	2.51	16	2.680**	0.022	-0.031	-0.001	0.07	6	22
21.	G 21	2.56	12	0.426	0.012*	0.133	-0.050	0.30	18	30
22.	G 22	2.60	8	2.126**	0.030	0.023	-0.003	0.05	4	12
23.	G 23	2.50	17	0.802	0.000	0.005	-0.060	0.06	5	22
24.	G 24	2.71	3	1.053	-0.008	0.108	0.090	0.25	16	19
25.	G 25	2.29	23	1.098	-0.002	-0.082	0.040	0.19	14	37
26.	G 26	2.30	22	1.450	0.007	-0.303	0.140	0.68	23	45
27.	G 27	2.21	25	1.257	0.026	0.441	0.030	0.97	25	50
28.	G 28	2.12	26	0.293*	0.010	-0.416	-0.100	0.92	24	50
29.	G 29	2.22	24	0.855	0.000	-0.164	-0.080	0.37	20	44
30.	G 30	2.40	20	1.074	0.094**	0.047	-0.050	0.12	10	30
31.	G 31	2.60	9	-0.339*	0.005	0.044	-0.060	0.11	9	18
32.	G 32	2.59	10	-0.317	0.002	0.068	-0.040	0.16	13	23
33.	G 33	2.59	10	0.325	0.000	-0.012	-0.001	0.03	2	12
34.	G 34	2.54	13	0.273	0.003*	-0.072	-0.001	0.16	13	26
35.	G 35	2.68	4	-0.070	0.023	-0.023	-0.002	0.05	4	8
36.	G 36	2.77	1	0.920	0.012	0.013	0.020	0.03	2	3
37.	G 37	2.59	10	0.898	0.030	-0.032	0.030	0.08	7	17
38.	G 38	2.76	2	-0.147	0.054*	0.018	-0.010	0.04	3	5
39.	G 39	2.62	7	0.087	0.015	-0.009	-0.030	0.04	3	10
40.	G 40	2.77	1	0.039	0.049*	0.023	-0.020	0.05	4	5

*Significant at 5% level of significance

**Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression Coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI Stability Value, RASVi: Rank of ASV, GSI: Genotype Selection Index

E3 site. No any genotypes specifically adapted to sites E1, E2 and E4. Most of the genotypes except few were located near to central line of IPCA1 scores which indicates, these genotypes have highest additive main effect. In the present investigation, G36, G38, G40 and G12 were stable with highest average weight of 1000 seeds whereas G8 was most stable with minimum weight of 1000 seeds. Among all, G28, G26, G15, G29, G27, G4, G10 and G21 were located away from central line of IPCA1 score which were indicating the maximum interaction between genotype and environment.

In Figure 12.2 where IPCA2 was plotted against IPCA1 which evinced the GE interaction, making it a useful test for interaction. It was reported that most of the genotypes and environments were spread around the biplot. Genotypes farther from the center of biplot show specific adaptation. In the present study, most of the genotypes except few were more stable than the other genotypes since they were found near to the origin and have general adaptability. However, G36, G24 and G40 were stable with highest weight of 1000 seeds than grand mean. The other genotypes showed specific to the certain environments. for instance, G26, G8, G16 and G15 were more adapted to E1 and E3 sites whereas G21, G27 and G4 were specifically adapted to site E4. The G28, G29, G31, G23 and G13 were more favorable to sites E2 and E5. In the present investigation, G26 and G16 were the best at E1 and E3; G27 and G21 were good at E4, G28 and G29 were the better in E2 and E5 (Fig. 12.2), suggesting that these genotype won to which environment lie. These genotypes positioned on the polygon vertex might be have the longest distance from biplot origin, supposed to the most responsive and have highest interaction between genotype and environment.

Among tested environments, E3, E4, E2 and E5 were the most discriminating environments that provided adequate information on the performance of the genotypes. Further explanation, E3, E4, E2 and E5 environments were powerful for genotype evaluation and interesting sites to identify superior genotypes. On other hand, E1 environment falls close to the bi-plot origin and the least discriminating environment (Fig. 12.2) and it provided little information about the performance difference of genotypes.

9. Seed yield plant⁻¹ (g)

Considering all the stability parameters (Table 28), genotype, G36 (GM=3.5g, bi=1.102, S²di=0.006, IPCA1=-0.129, IPCA2=-0.272, ASV=0.16, GSI=8) observed more stable for higher seed yield plant⁻¹ followed by the genotype, G24 (GM=3.3g, bi=0.966, S²di=-0.057, IPCA1=-0.075, IPCA2=-0.101, ASV=0.26, GSI=17), G38 (GM=3.3g, bi=0.814, S²di=0.056, IPCA1=-0.171, IPCA2=-0.144, ASV=0.22, GSI=14), G40 (GM=3.3g, bi=1.362, S²di=-0.042, IPCA1=-0.122, IPCA2=-0.175, ASV=0.15, GSI=8), G32 (GM=3.2g, bi=0.922, S²di=-0.063, IPCA1=-0.296, IPCA2=-0.140, ASV=0.38, GSI=23), G10 (GM=2.9g, bi=-0.947, S²di=-0.075, IPCA1=0.015, IPCA2=0.157, ASV=0.16, GSI=11), G35 (GM=2.9g, bi=0.936, S²di=-0.055, IPCA1=-0.143, IPCA2=-0.115, ASV=0.32, GSI=21), G26 (GM=2.9g, bi=1.236, S²di=0.015, IPCA1=-0.008, IPCA2=-0.188, ASV=0.05, GSI=6), G33 (GM=2.8g, bi=0.884, S²di=-0.042, IPCA1=-0.021, IPCA2=-0.114, ASV=0.18, GSI=14), G1 (GM=2.8g, bi=1.384, S²di=-0.046, IPCA1=-0.004, IPCA2=0.095, ASV=0.10, GSI=9) and G6 (GM=2.8g, bi=-0.889, S²di=-0.049, IPCA1=0.113, IPCA2=-0.161, ASV=0.21, GSI=16), while genotype, G7 (GM=2.5g, bi=-1.143, S²di=-0.072, IPCA1=-0.101, IPCA2=0.122, ASV=0.17, GSI=16) registered highly stable for lesser seed yield plant⁻¹ followed by G20 (GM=2.5g, bi=1.062, S²di=-0.047, IPCA1=-0.081, IPCA2=0.216, ASV=0.17, GSI=16).

In AMMI1 biplot (Figure 13.1), IPCA1 was plotted against mean seed yield plant⁻¹, the vertical line passing through the origin is the grand mean. Accordingly, those genotypes and environment (E3) which were found in the right side of the vertical line were observed more average seed yield plant⁻¹ than grand mean. Among all, genotypes, G36, G24, G40, G38 and G32 have negative IPCA1 score with more average seed yield plant⁻¹. On the other hand, the mean performance for most of the genotypes were noticed below the grand mean and which were located to left side of the vertical line. Among all, genotypes, G7, G20, G9, G12 and G19 have negative IPCA1 score which indicates, these genotypes had lowest average seed yield plant⁻¹ while genotype G28 have positive IPCA1 score with lowest average seed yield plant⁻¹. The lowest seed yield plant⁻¹ was observed in E4, E5, E1 and E4 than grand mean hence they were found in the left side of the Figure 13.1.

Table 28: Estimation of stability parameters of 40 Niger genotypes for seed yield plant⁻¹ (g).

Sr. No.	Genotype code	Seed yield plant ⁻¹ (g)								
		Mean	RYi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	2.8	5	1.384	-0.046	0.004	0.095	0.10	4	9
2.	G 2	2.9	4	0.706	-0.035	-0.870	-0.084	1.08	24	28
3.	G 3	2.7	6	0.970	-0.054	-0.180	0.024	0.22	12	18
4.	G 4	2.9	4	0.114	-0.006	-0.297	0.077	0.37	19	23
5.	G 5	2.7	6	-0.261	-0.058	-0.151	0.370	0.41	22	28
6.	G 6	2.8	5	-0.889	0.049	0.113	-0.161	0.21	11	16
7.	G 7	2.5	8	-1.143	-0.072	-0.101	0.122	0.17	8	16
8.	G 8	2.7	6	-0.803	-0.061*	-0.212	0.232	0.35	18	24
9.	G 9	2.6	7	-1.533	-0.078*	-0.076	0.227	0.25	14	21
10.	G 10	2.9	4	-0.947	-0.075	0.015	0.157	0.16	7	11
11.	G 11	2.8	5	-0.011	-0.051	0.201	-0.164	0.30	16	21
12.	G 12	2.6	7	0.813	-0.076*	-0.057	-0.123	0.14	5	12
13.	G 13	2.7	6	1.080	-0.031	0.122	-0.037	0.16	7	13
14.	G 14	2.7	6	0.405	-0.005	0.060	0.066	0.10	4	10
15.	G 15	2.7	6	0.427	-0.061	-0.015	-0.025	0.03	1	7
16.	G 16	2.7	6	4.064**	0.059*	-0.140	-0.080	0.19	10	16
17.	G 17	2.7	6	3.795**	-0.034	0.179	-0.137	0.26	15	21
18.	G 18	2.7	6	2.096**	0.029	0.320	-0.083	0.40	21	27
19.	G 19	2.6	7	2.874**	-0.037	-0.164	0.068	0.21	11	18
20.	G 20	2.5	8	1.062	-0.047	-0.081	0.216	0.17	8	16
21.	G 21	2.8	5	0.452	-0.052*	-0.052	-0.132	0.08	3	8
22.	G 22	2.7	6	0.492	-0.015	0.287	0.049	0.41	22	28
23.	G 23	2.8	5	0.295	-0.045	-0.007	-0.216	0.10	4	9
24.	G 24	3.3	2	0.966	-0.057	-0.075	-0.101	0.26	15	17
25.	G 25	2.7	6	-1.150*	-0.064*	0.102	-0.242	0.23	13	19
26.	G 26	2.9	4	1.236	0.015	-0.008	-0.188	0.05	2	6
27.	G 27	2.7	6	3.185**	-0.029	0.047	0.054	0.30	16	22
28.	G 28	2.5	8	1.819	-0.041	0.433	0.296	0.55	23	31
29.	G 29	2.7	6	-0.680*	-0.057	0.155	-0.147	0.23	13	19
30.	G 30	2.7	6	1.389	-0.064*	0.136	0.130	0.26	15	21
31.	G 31	2.7	6	0.637	-0.037	-0.103	0.195	0.19	10	16
32.	G 32	3.2	3	0.922	-0.063	-0.296	-0.140	0.38	20	23
33.	G 33	2.8	5	0.884	-0.042	-0.021	-0.114	0.18	9	14
34.	G 34	2.7	6	1.464	-0.024	0.182	0.175	0.25	14	20
35.	G 35	2.9	4	0.936	-0.055	-0.143	0.115	0.32	17	21
36.	G 36	3.5	1	1.102	0.006	-0.129	-0.272	0.16	7	8
37.	G 37	2.7	6	1.376	0.000	0.311	0.033	0.41	22	28
38.	G 38	3.3	2	0.814	0.056	-0.171	-0.144	0.22	12	14
39.	G 39	2.9	4	2.968**	0.013	0.017	0.062	0.18	9	13
40.	G 40	3.3	2	1.362	-0.042	-0.122	-0.175	0.15	6	8

*Significant at 5% level of significance

**Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression Coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI Stability Value, RASVi: Rank of ASV, GSI: Genotype Selection Index

Genotypes, G21, G23, G33 and G1 were more specifically adapted to E2 site while G19, G8, G3, G31, G5 and G16 were more favorable to site E1. Genotypes, G25, G26, G10, G39, G23, G1 and G15 were located near to central line of IPCA1 scores which indicates, these genotypes have highest additive main effect. In the present investigation, G24 and G10 were stable with highest average seed yield plant⁻¹ whereas G15 and G1 were most stable with low seed yield plant⁻¹. Among all, G4, G32, G8, G3, G38, G19, G28, G18, G37 and G22 were located far from central line of IPCA1 score which were indicating the maximum interaction between genotype and environment.

In Figure 13.2 where IPCA2 was plotted against IPCA1 which elucidated the GE interaction, making it a useful test for interaction. It was found that most of the genotypes and environments were scattered around the biplot. Genotypes farther from the center of biplot show specific adaptation. In the present study, G36, G15, G13, G14, G3 and G13 were more stable than the other genotypes since they were found near to the origin and have general adaptability. However, G36 was stable with highest seed yield plant⁻¹ than grand mean. The other genotypes showed specific to the certain environments. for instance, G5, G8, G9 and G20 were more adapted to E4 site whereas G28, G22, G37 and G34 were specifically adapted to site E5. The G38, G23 and G26 were more favorable to sites E1 and E2 while G32 and G38 were most favorable at site E3. Also, no any environment fell into sector with G25, G11 and G18 vertex, it implies that, these are the poorest genotypes in some or all of the locations. In the present investigation, G38 was the best at E1 and E2, G28 and G18 were good at E5, G5 and G8 were the best at E4 and G32 was the better in E3 (Fig. 13.2), indicating that these genotype won to which environment lie. These genotypes positioned on the polygon vertex might be have the longest distance from biplot origin, supposed to the most responsive and have highest interaction between genotype and environment.

Among tested environments, E1, E3 and E4 were the most discriminating environments that provided adequate information on the performance of the genotypes. Further explanation, E1, E3 and E4 environments were powerful for genotype evaluation and interesting sites to identify superior genotypes. On other

hand, E2 and E5 environments falls close to the bi-plot origin and the least discriminating environment (Fig. 13.2) and it provided little information about the performance difference of genotypes.

10. Seed yield plot⁻¹ (g)

With regards to seed yield plot⁻¹ (Table 29), genotype, G36 (GM=265g, bi=1.840, S²di=0.10, IPCA1=-0.82, IPCA2=-0.009, ASV=1.58, GSI=15) observed more stable for higher seed yield plot⁻¹ followed by the genotype, G24 (GM=260g, bi=1.032, S²di=0.01, IPCA1=0.40, IPCA2=-0.010, ASV=0.77, GSI=9), G32 (GM=257g, bi=1.557, S²di=0.59, IPCA1=-0.10, IPCA2=-0.013, ASV=0.19, GSI=6), G10 (GM=257g, bi=1.316, S²di=0.10, IPCA1=-0.61, IPCA2=-0.011, ASV=1.18, GSI=13) and G4 (GM=253g, bi=1.522, S²di=0.05, IPCA1=-0.20, IPCA2=-0.004, ASV=0.39, GSI=8) while genotype, G23 (GM=200g, bi=-0.960, S²di=1.40, IPCA1=-0.81, IPCA2=0.023, ASV=1.56, GSI=38) registered highly stable for lesser seed yield plot⁻¹ followed by G28 (GM=205g, bi=0.942, S²di=1.15, IPCA1=0.43, IPCA2=0.014, ASV=0.83, GSI=31) while considering all these stability parameters.

In Figure 14.1 where IPCA1 was plotted against mean seed yield plot⁻¹, the vertical line passing through the origin is the grand mean. Accordingly, those genotypes and environment (E3) which were noticed in the right side of the vertical line were observed more average seed yield plot⁻¹ than grand mean. Among all, genotypes G24 have positive IPCA1 score with highest average seed yield plot⁻¹ while G36, G10, G32, G4, G2 and G25 have negative IPCA1 score with more average seed yield plot⁻¹. On the other hand, the mean performance for most of the genotypes were noticed below the grand mean and which were located to left side of the vertical line. Among all, genotypes, G23, G17, G6, G28 and G16 were located extreme left side of the biplot which indicates, these genotypes had lowest average seed yield plot⁻¹. The lowest seed yield plot⁻¹ was observed in E4, E5, E1 and E2 than grand mean hence they were found in the left side of the Figure 14.1. Genotype G23 was more specifically adapted to E4 site while G38 and G40 were more favorable to site E1. The G7, G35 and G12 were more suited to site E2. No any genotypes specifically adapted to sites E3 and E5. Genotypes, G24, G4, G38, G31, G18, G5, G28 G10 and G36 were located near to central line of IPCA1 scores which

Table 29: Estimation of stability parameters of 40 Niger genotypes for seed yield plot⁻¹ (g).

Sr. No.	Genotype code	Seed yield plot ⁻¹ (g)								
		Mean	RYi	Bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	229	7	3.361**	1.04	-2.20	-0.008	4.24	27	34
2.	G 2	246	5	0.291	0.04	-0.70	0.005	1.35	11	16
3.	G 3	214	15	0.642	11.00*	2.20	-0.003	4.24	27	42
4.	G 4	253	4	1.522	0.05	-0.20	-0.004	0.39	4	8
5.	G 5	209	19	2.399*	0.70	0.20	0.005	0.39	4	23
6.	G 6	203	23	4.282**	3.05**	3.90	0.009	7.52	31	54
7.	G 7	222	9	2.711**	4.07**	1.50	-0.014	2.89	23	32
8.	G 8	214	14	0.897	1.00	2.60	-0.017	5.02	29	43
9.	G 9	221	10	4.041**	16.80**	-0.41	0.012	0.79	8	18
10.	G 10	257	3	1.316	0.10	-0.61	-0.011	1.18	10	13
11.	G 11	216	13	-0.771*	0.30	0.81	0.008	1.56	13	26
12.	G 12	222	9	-0.127	1.01	1.11	-0.002	2.14	18	27
13.	G 13	217	12	-0.101	0.90	1.92	-0.004	3.70	25	37
14.	G 14	221	10	0.766	0.17	-0.81	-0.015	1.56	13	23
15.	G 15	221	10	2.173*	14.39**	-0.22	-0.003	0.42	6	16
16.	G 16	206	21	2.133*	0.03	-1.00	0.018	1.93	17	38
17.	G 17	201	24	5.271**	23.67**	2.20	0.025	4.24	27	51
18.	G 18	207	20	2.381*	1.09	0.01	0.007	0.02	1	21
19.	G 19	210	18	5.746**	18.02**	-0.71	-0.002	1.37	12	30
20.	G 20	208	20	4.478**	5.09**	-2.45	0.013	4.73	28	48
21.	G 21	210	19	1.810	0.76	-1.40	0.001	2.70	20	39
22.	G 22	211	18	-0.420	0.24	-0.61	0.008	1.18	10	28
23.	G 23	200	25	-0.960	-1.40	-0.81	0.023	1.56	13	38
24.	G 24	260	2	1.032	0.01	0.40	-0.010	0.77	7	9
25.	G 25	232	6	0.400	0.99	-2.10	-0.009	4.05	26	32
26.	G 26	221	10	-0.490	1.00	-1.42	0.018	2.74	22	32
27.	G 27	214	14	0.323	0.67	-2.61	-0.006	5.03	30	44
28.	G 28	205	22	0.942	1.15	0.43	0.014	0.83	9	31
29.	G 29	218	11	-0.916*	0.40	-1.20	0.006	2.31	19	30
30.	G 30	212	17	0.289	0.09	1.70	0.002	3.28	24	41
31.	G 31	209	19	4.758**	7.50**	-0.21	0.004	0.41	5	24
32.	G 32	257	3	1.557	0.59	-0.10	-0.013	0.19	3	6
33.	G 33	207	20	0.276	0.80	2.60	0.004	5.02	29	49
34.	G 34	213	16	2.698*	1.02	0.90	-0.008	1.74	15	31
35.	G 35	221	10	0.633	10.99*	1.41	0.006	2.72	21	31
36.	G 36	265	1	1.840	0.10	-0.82	-0.009	1.58	14	15
37.	G 37	217	12	-4.660**	5.60**	-2.20	-0.005	4.24	27	39
38.	G 38	222	9	-3.610**	1.01	-0.05	-0.140	0.17	2	11
39.	G 39	218	12	-3.950**	1.05	-0.91	-0.004	1.76	16	28
40.	G 40	224	8	-5.620**	27.70**	-0.41	-0.019	0.79	8	16

*Significant at 5% level of significance

**Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression Coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI Stability Value, RASVi: Rank of ASV, GSI: Genotype Selection Index

indicates, these genotypes have highest additive main effect. In the present investigation, G24 and G4 were stable with highest average seed yield plot⁻¹ whereas G18, G31 and G5 were most stable with minimum seed yield plot⁻¹. Among all, G27, G20, G37, G1, G25, G6, G33, G8, G17, G3 and G13 were located far from central line of IPCA1 score which were indicating the greatest interaction between genotype and environment.

In AMMI2 biplot (Figure 14.2), IPCA2 was plotted against IPCA1 which elucidated the GE interaction, making it a useful test for interaction. It was found that most of the genotypes and environments were sparged around the biplot. Genotypes farther from the center of biplot show specific adaptation. In the present study, G36, G15, G4, G39 and G2 were more stable than the other genotypes since they were found near to the origin and have general adaptability. However, G31 and G4 were stable with highest seed yield plot⁻¹ than grand mean. The other genotypes showed specific to the certain environments. for instance, G8, G7, G34, G24 and G40 were more adapted to E2 site whereas G17, G23 and G28 were specifically adapted to site E4. The G6 and G33 were more favorable to site E3 while G25, G1 and G37 were favorable to E5 site. The G14, G32, G10 and G38 were most suited to site E1. Also, no any environment fell into sector with G20, G27 and G8 vertex, it implies that, these are the poorest genotypes in some or all of the locations. In the present investigation, G14 was the best at E5, G8 was good at E2, G17 and G23 were the better in E4, G25 and G1 were the best at E1 and G6 was good in E3 (Fig. 14.2), suggesting that these genotype won to which environment lie. These genotypes positioned on the polygon vertex might be have the longest distance from biplot origin, supposed to the most responsive and have highest interaction between genotype and environment.

Among tested environments, E1, E3 and E4 were the most discriminating environments that provided adequate information on the performance of the genotypes. Further explanation, E1, E3 and E4 environments were powerful for genotype evaluation and interesting sites to identify superior genotypes. On other hand, E2 and E5 environments falls close to the bi-plot origin and the least

discriminating environment (Fig. 14.2) and it provided little information about the performance difference of genotypes.

11. Days to maturity

Considering all the stability parameters (Table 30), genotype, G24 (GM=76 days, $b_i=0.836$, $S^2d_i=0.519$, $IPCA1=-0.12$, $IPCA2=0.014$, $ASV=0.17$, $GSI=15$) observed more stable for earliness followed by the genotype, G26 (GM=76 days, $b_i=1.073$, $S^2d_i=-0.436$, $IPCA1=-0.15$, $IPCA2=0.009$, $ASV=0.21$, $GSI=17$) while genotype, G28 (GM=80 days, $b_i=1.068$, $S^2d_i=-2.579$, $IPCA1=0.13$, $IPCA2=0.029$, $ASV=0.18$, $GSI=14$) registered more stable for mid-late maturity. The genotype, G36 (GM=85 days, $b_i=0.956$, $S^2d_i=0.137$, $IPCA1=-0.51$, $IPCA2=-0.009$, $ASV=0.70$, $GSI=19$) recorded highly stable for late maturity followed by G10 (GM=85 days, $b_i=1.141$, $S^2d_i=-1.867$, $IPCA1=-0.21$, $IPCA2=-0.001$, $ASV=0.29$, $GSI=12$), G9 (GM=87days, $b_i=1.035$, $S^2d_i=-2.820$, $IPCA1=-1.10$, $IPCA2=0.010$, $ASV=1.52$, $GSI=25$) and G8 (GM=87days, $b_i=1.014$, $S^2d_i=-0.160$, $IPCA1=-0.31$, $IPCA2=-0.014$, $ASV=0.43$, $GSI=13$).

In AMMI1 (Figure 15.1), $IPCA1$ was plotted against mean, the vertical line passing through the origin is the grand mean. Accordingly, G25, G24, G26, G27 and G38 were gave mean performance below the grand mean which were located to left side of the vertical line. Among all, genotypes, G24 and G26 have negative $IPCA1$ score which was required lowest days for maturity. The environment E3 was noted for the lowest mean days to maturity compared to the other sites since it is found in the left side of the Figure 15.1. On the other hand, those genotypes and environments (E4, E1, E5 and E2) which was found in the right side of the vertical line gave mean days to maturity above the grand mean. Among all, genotypes, G69 G8 and G4 have negative $IPCA1$ score which indicates, these genotypes were very late for maturity. Genotype, G9 was more specifically adapted to E4 site whereas G31 was more favorable to site E3. Also, no any genotypes specifically adapted to E2, E5 and E1 sites. Genotypes G14, G1, G13, G10, G19, G28, G27, G26 and G24 were located near to central line of $IPCA1$ scores which indicates, these genotypes have highest additive main effect. Among all, G9, G34, G22, G3, G29, G33, G30, G5 and G32 were located far from central line of $IPCA1$ score which were indicating

Table 30: Estimation of stability parameters of 40 Niger genotypes for days to maturity.

Sr. No.	Genotype code	Days to maturity (Days)								
		Mean	RMi	Bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	84	4	1.743	-4.074**	0.00	-0.004	0.00	1	5
2.	G 2	86	2	1.827*	3.298**	0.32	-0.032	0.44	13	15
3.	G 3	85	3	1.521	1.803	-0.71	-0.010	0.98	20	23
4.	G 4	86	2	2.072	-0.856	0.42	-0.028	0.58	15	17
5.	G 5	85	3	1.988*	3.546**	0.59	-0.036	0.81	18	21
6.	G 6	84	4	1.573	-0.386	-0.41	0.014	0.57	14	18
7.	G 7	85	3	1.981*	-3.199**	-0.52	-0.003	0.72	17	20
8.	G 8	87	1	1.014	-0.160	-0.31	-0.014	0.43	12	13
9.	G 9	87	1	1.035	-2.820	-1.10	0.010	1.52	24	25
10.	G 10	85	3	1.141	-1.867	-0.21	-0.001	0.29	9	12
11.	G 11	85	3	1.286	-1.241	-0.32	0.000	0.44	13	16
12.	G 12	85	3	1.016	-3.608**	-0.25	0.009	0.34	10	13
13.	G 13	85	3	0.689*	-2.816	-0.11	-0.004	0.15	4	7
14.	G 14	86	2	1.364	-4.498**	0.09	0.000	0.12	3	5
15.	G 15	86	2	1.172	-4.231**	0.31	-0.021	0.43	12	14
16.	G 16	86	2	1.006	-3.063*	0.41	-0.014	0.57	14	16
17.	G 17	84	4	0.990*	-3.482**	-0.51	-0.024	0.70	16	20
18.	G 18	84	4	0.698	-3.514**	0.30	-0.004	0.41	11	15
19.	G 19	82	6	1.243	-2.792	0.21	0.021	0.29	9	15
20.	G 20	84	4	0.645	-4.044**	-0.03	0.009	0.04	2	6
21.	G 21	86	2	0.762	-0.393*	0.41	-0.016	0.57	14	16
22.	G 22	84	4	0.830	-2.657	-0.81	0.046	1.12	21	25
23.	G 23	83	5	0.779	-3.502*	0.31	0.021	0.43	12	17
24.	G 24	76	10	0.836	0.519	-0.12	0.014	0.17	5	15
25.	G 25	75	11	-0.545*	5.327**	0.32	0.020	0.44	13	24
26.	G 26	76	10	1.073	-0.436	-0.15	0.009	0.21	7	17
27.	G 27	79	9	0.315	-1.309	0.19	0.010	0.26	8	17
28.	G 28	80	8	1.068	-2.579	0.13	0.029	0.18	6	14
29.	G 29	81	7	1.265	-3.489**	1.00	0.024	1.38	23	30
30.	G 30	84	4	0.270	-3.027*	0.61	0.022	0.84	19	23
31.	G 31	81	7	2.176**	1.197	2.30	0.012	3.17	25	32
32.	G 32	83	5	1.065	-1.032	0.51	-0.021	0.70	16	21
33.	G 33	84	4	0.355	-2.393	0.81	0.006	1.12	21	25
34.	G 34	85	3	0.459	-1.865	-0.92	-0.040	1.27	22	25
35.	G 35	85	3	0.919	-2.849*	-0.25	-0.001	0.34	10	13
36.	G 36	85	3	0.956	0.137	-0.51	-0.009	0.70	16	19
37.	G 37	85	3	0.494	18.337**	-0.41	0.012	0.57	14	17
38.	G 38	83	5	1.024	12.664**	-0.51	-0.003	0.70	16	21
39.	G 39	83	5	1.183	10.027**	-0.42	-0.005	0.58	15	20
40.	G 40	84	4	0.919	6.997**	-0.52	-0.022	0.72	17	21

*Significant at 5% level of significance

**Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression Coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI Stability Value, RASVi: Rank of ASV, GSI: Genotype Selection Index

the maximum interaction between genotype and environment.

The Figure 15.2, evinced GE interaction, making it a useful test for interaction. It was observed that most of the genotypes and environments were dispersed around the biplot. Genotypes farther from the center of biplot show specific adaptation. Here in this study G14, G13, G10, G26, G11 and G35 were more stable than the other genotypes since they were found near to the origin and have general adaptability. However, G14 were stable and required less days to maturity than grand mean. The other genotypes showed specific to the certain environments. for instance, G22, G9, G17 and G28 were more adapted to E4 whereas G4, G34, G40 and G8 were specifically adapted to sites E1 and E2. The G31, G29 and G33 were more favorable to E3 and E5 sites. Also, no any environment fell into sector with G2 and G5 vertex, it implies that, these are the poorest genotypes in some or all of the locations. In the present investigation, G4 and G34 were the best at E1 and E2, G22 and G9 were good at E4 and G31 was the better in E3 and E5 (Fig. 15.2), suggesting that these genotype won to which environment lie. These genotypes positioned on the polygon vertex might be have the longest distance from biplot origin, supposed to the most responsive and have highest interaction between genotype and environment.

Among tested environments, E1, E3 and E4 were the most discriminating environments that provided adequate information on the performance of the genotypes. Further explanation, E1, E3 and E4 environments were powerful for genotype evaluation and interesting sites to identify superior genotypes. On other hand, E2 and E5 environments falls close to the bi-plot origin and the least discriminating environment (Fig. 15.2) and it provided little information about the performance difference of genotypes.

12. Oil Content (%)

As regards to oil content (Table 31), genotype, G36 (GM=41.30%, bi=1.060, $S^2di=0.772$, IPCA1=-0.11, IPCA2=-0.016, ASV=0.68, GSI=8) observed more stable for higher oil content followed by the genotype, G24 (GM=40.47%, bi=1.065, $S^2di=-2.315$, IPCA1=-0.01, IPCA2=-0.031, ASV=0.07, GSI=4), G40 (GM=40.47%, bi=1.212, $S^2di=-1.552$, IPCA1=-0.12, IPCA2=-0.025, ASV=0.74, GSI=10), G32 (GM=40.10%,

Table 31: Estimation of stability parameters of 40 Niger genotypes for oil content (%).

Sr. No.	Genotype code	Oil content (%)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	38.17	10	0.988	6.361**	-0.66	-0.016	4.05	25	35
2.	G 2	38.13	11	0.115	4.335**	0.04	-0.019	0.25	3	14
3.	G 3	36.97	22	-0.511	-0.489	-0.29	0.009	1.78	17	39
4.	G 4	38.33	8	0.513	-0.712	-0.04	0.039	0.25	3	11
5.	G 5	38.07	12	0.051	-0.283*	-0.26	-0.019	1.60	15	27
6.	G 6	38.33	8	-1.370*	0.428	-0.22	0.000	1.35	13	21
7.	G 7	37.97	13	-0.701	2.838*	-0.73	-0.016	4.48	27	40
8.	G 8	37.67	17	-1.117	7.143**	-0.71	0.015	4.36	26	43
9.	G 9	38.43	7	0.676	4.630**	-0.50	-0.044	3.07	20	27
10.	G 10	39.90	5	0.991	-1.237	-0.08	-0.015	0.49	5	10
11.	G 11	38.30	9	-0.332	0.110	0.01	0.007	0.06	1	10
12.	G 12	35.73	34	0.957	0.443	0.10	-0.046	0.61	6	40
13.	G 13	37.90	14	0.889	0.460	-0.82	-0.009	5.04	29	43
14.	G 14	35.33	35	1.069	0.354	1.01	0.024	6.20	33	68
15.	G 15	36.57	27	0.044	0.877	0.25	-0.032	1.54	14	41
16.	G 16	37.70	16	4.066**	1.633	-0.85	-0.100	5.22	30	46
17.	G 17	37.83	15	3.833**	0.832	0.18	0.015	1.11	12	27
18.	G 18	36.87	23	1.967	0.768	0.56	0.0181	3.44	21	44
19.	G 19	37.33	19	4.634**	-0.681	-0.34	0.027	2.09	19	38
20.	G 20	36.30	31	4.147**	-0.827	-0.01	0.016	0.06	1	32
21.	G 21	37.00	21	0.559	-0.121*	-0.17	-0.012	1.04	11	32
22.	G 22	36.30	31	0.566	2.735*	-0.58	0.041	3.56	22	53
23.	G 23	36.13	32	-0.070	2.428*	0.99	-0.010	6.08	32	64
24.	G 24	40.47	2	1.065	-2.315	-0.01	-0.031	0.07	2	4
25.	G 25	36.53	28	-0.188*	-0.433	0.50	0.045	3.07	20	48
26.	G 26	36.77	24	0.122	-0.684	0.13	0.035	0.80	9	33
27.	G 27	36.63	25	2.040*	-0.315	0.65	0.019	3.99	24	49
28.	G 28	36.60	26	3.853**	0.825	-0.07	-0.034	0.43	4	30
29.	G 29	35.93	32	3.437**	3.127**	0.64	-0.012	3.93	23	55
30.	G 30	36.40	30	2.678**	-0.480	-0.31	0.031	1.90	18	48
31.	G 31	37.83	15	1.804	-1.035	0.26	0.021	1.60	15	30
32.	G 32	40.10	3	1.089	-0.139	0.04	-0.031	0.25	3	6
33.	G 33	37.30	20	1.084	2.835*	0.16	0.039	0.98	10	30
34.	G 34	36.43	29	3.611**	1.034	0.64	-0.044	3.93	23	52
35.	G 35	37.43	18	2.094*	0.552	0.18	0.058	1.11	12	30
36.	G 36	41.30	1	1.060	0.772	-0.11	-0.016	0.68	7	8
37.	G 37	35.80	33	-0.965*	4.847**	0.88	-0.038	5.41	31	64
38.	G 38	39.10	6	-0.628	4.845**	-0.12	0.000	0.74	8	14
39.	G 39	39.93	4	0.057	-1.090	-0.28	-0.009	1.72	16	20
40.	G 40	40.47	2	1.212	-1.552	-0.12	-0.025	0.74	8	10

*Significant at 5% level of significance

**Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression Coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI Stability Value, RASVi: Rank of ASV, GSI: Genotype Selection Index

bi=1.089, S^2di =-0.139, IPCA1=0.04, IPCA2=-0.031, ASV=0.25, GSI=6) and G10 (GM=39.90%, bi=0.991, S^2di =-1.237, IPCA1=-0.08, IPCA2=-0.015, ASV=0.49, GSI=10) while genotype, G12 (GM=35.73%, bi=0.957, S^2di =0.443, IPCA1=0.10, IPCA2=-0.046, ASV=0.61, GSI=40) registered highly stable for lesser oil content while considering all the stability parameters.

In Figure 16.1 where IPCA1 was plotted against mean oil content, the vertical line passing through the origin is the grand mean. Accordingly, those genotypes and environment (E3) which were noticed in the right side of the vertical line were observed more average oil content than grand mean. Among all, genotypes G24 and G32 have positive IPCA1 score with highest average seed yield plot⁻¹ while G36, G40, G10, G39 and G38 have negative IPCA1 score with more average oil content. On the other hand, the mean performance for most of the genotypes were noticed below the grand mean and which were located to left side of the vertical line. Among all, genotypes, G14, G37, G12, G29 and G23 were located extreme left side of the biplot which indicates, these genotypes had lowest average oil content. The lowest oil content was observed in E1, E4, E5 and E2 than grand mean hence they were found in the left side of the Figure 16.1. Genotypes, G1, G7, G13 and G16 were more specifically adapted to E2 site while G19, G21, G28 and G30 were more favorable to sites E4 and E5. No any genotypes specifically adapted to sites E1 and E3. Genotypes, G36, G40, G24, G32, G10, G38, G4, G11, G2, G20, G28 and G12 were located near to central line of IPCA1 scores which indicates, these genotypes have highest additive main effect. In the present investigation, G36 was stable with highest average oil content whereas G4, G20, G28, G2 and G12 were most stable with low oil content. Among all, G16, G13, G7, G8, G1, G22, G14, G23 and G37 were located far from central line of IPCA1 score which were indicating the maximum interaction between genotype and environment.

In AMMI2 biplot (Figure 16.2), IPCA2 was plotted against IPCA1 which explained the GE interaction, making it a useful test for interaction. It was found that most of the genotypes and environments were sparged around the biplot. Genotypes farther from the center of biplot show specific adaptation. In the present study, G38, G36, G3, G24, G11, G21, G6, G39 and G20 were more stable than the

other genotypes since they were found near to the origin and have general adaptability. However, G36 was stable with highest oil content than grand mean. The other genotypes showed specific to the certain environments. for example, G35, G25, G22, G33 and G4 were more adapted to E4 site whereas G9, G7, G1 and G40 were specifically adapted to site E2. The G16 was more favorable to site E1. Also, no any environment fell into sector with G22, G12, G34, G37 and G14 vertex, it implies that, these are the poorest genotypes in some or all of the locations. In the present investigation, G16 was the good at E1, G9 was better at E2 and in E4, G35 and G25 was the best (Fig. 16.2), suggesting that these genotype won to which environment lie. These genotypes positioned on the polygon vertex might be have the longest distance from biplot origin, supposed to the most responsive and have highest interaction between genotype and environment.

Among tested environments, E1, E4 and E3 were the most discriminating environments that provided adequate information on the performance of the genotypes. Further explanation, E1, E4 and E3 environments were powerful for genotype evaluation and interesting sites to identify superior genotypes. On other hand, E2 and E5 environments falls close to the bi-plot origin and the least discriminating environment (Fig. 16.2) and it provided little information about the performance difference of genotypes.

13. Protein content (%)

Considering all the stability parameters (Table 32), genotype, G36 (GM=22.13%, bi=1.383, S^2di =0.022, IPCA1=0.22, IPCA2=0.011, ASV=0.45, GSI=16) observed more stable for higher protein content followed by the genotype, G32 (GM=20.87%, bi=0.948, S^2di =-0.182, IPCA1=0.34, IPCA2=0.039, ASV=0.69, GSI=24), G24 (GM=20.80%, bi=0.998, S^2di =-0.165, IPCA1=-0.17, IPCA2=0.059, ASV=0.35, GSI=15), G10 (GM=19.63%, bi=0.873, S^2di =0.450, IPCA1=-0.21, IPCA2=0.018, ASV=0.43, GSI=22) and G34 (GM=19.53%, bi=1.048, S^2di =-0.044, IPCA1=0.12, IPCA2=0.009, ASV=0.24, GSI=16) while genotype, G27 (GM=18.20%, bi=1.303, S^2di =0.773, IPCA1=0.29, IPCA2=0.017, ASV=0.59, GSI=47) registered highly stable for lower protein content followed by G14 (GM=18.23%, bi=0.938, S^2di =0.504, IPCA1=0.31, IPCA2=-0.017, ASV=0.63, GSI=48).

Table 32: Estimation of stability parameters of 40 Niger genotypes for protein content (%).

Sr. No.	Genotype code	Protein content (%)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	18.03	31	0.147	-0.130	-0.02	0.040	0.06	3	34
2.	G 2	18.47	27	0.789	-0.343*	-0.71	0.013	1.44	29	56
3.	G 3	18.73	21	-0.375*	-0.187	0.21	0.038	0.43	14	35
4.	G 4	19.40	10	0.813	0.561	-0.51	0.038	1.03	27	37
5.	G 5	18.50	26	0.127	-0.435	0.81	0.039	1.64	30	56
6.	G 6	19.00	16	0.595	-0.430	-0.41	0.004	0.83	24	40
7.	G 7	18.83	20	0.212	0.118	-0.32	0.025	0.65	20	40
8.	G 8	18.70	22	-0.028	-0.346	0.81	-0.019	1.64	30	52
9.	G 9	18.97	17	0.642	0.424	-0.19	-0.020	0.38	12	29
10.	G 10	19.63	8	0.873	0.450	-0.21	0.018	0.43	14	22
11.	G 11	19.30	12	1.789	-0.023	-0.51	0.015	1.03	27	39
12.	G 12	19.13	14	0.972	-0.353*	-0.17	0.010	0.34	10	24
13.	G 13	19.20	13	0.114	0.540	0.51	-0.001	1.03	27	40
14.	G 14	18.23	29	0.938	0.504	0.31	-0.017	0.63	19	48
15.	G 15	18.67	23	0.973	-0.231	-0.10	0.020	0.20	5	28
16.	G 16	18.23	29	2.114*	0.358	-0.40	-0.009	0.81	23	52
17.	G 17	18.40	28	1.403	0.214	-0.34	-0.210	0.72	22	50
18.	G 18	19.30	12	3.004**	0.504	-0.41	-0.038	0.83	24	36
19.	G 19	19.20	13	1.862	-0.090	-0.14	-0.029	0.28	8	21
20.	G 20	18.87	19	2.316**	0.351	0.09	0.044	0.19	4	23
21.	G 21	19.33	11	0.074	0.025	0.22	-0.021	0.45	15	26
22.	G 22	19.13	14	0.262	0.399	-0.45	-0.011	0.91	26	40
23.	G 23	18.73	21	-0.314	-0.338*	0.30	-0.019	0.61	18	39
24.	G 24	20.80	4	0.998	-0.165	-0.17	0.059	0.35	11	15
25.	G 25	18.60	25	-0.529	-0.198	-0.35	-0.490	0.86	25	50
26.	G 26	18.93	18	1.521*	-0.329	0.71	-0.017	1.44	29	47
27.	G 27	18.20	30	1.303	0.773	0.29	0.017	0.59	17	47
28.	G 28	18.63	24	1.032	-0.362	0.15	0.016	0.30	9	33
29.	G 29	18.63	24	1.187	-0.260	0.61	-0.008	1.23	28	52
30.	G 30	18.87	19	1.288	-0.239	0.009	0.013	0.02	1	20
31.	G 31	18.50	26	0.512*	-0.282	-0.51	0.016	1.03	27	53
32.	G 32	20.87	3	0.948	-0.182	0.34	0.039	0.69	21	24
33.	G 33	19.07	15	1.53	-0.385	-0.22	-0.021	0.45	15	30
34.	G 34	19.53	9	1.048	-0.044	0.12	0.009	0.24	7	16
35.	G 35	20.07	7	1.266	-0.137*	-0.11	-0.041	0.23	6	13
36.	G 36	22.13	1	1.383	0.022	0.22	0.011	0.45	15	16
37.	G 37	18.70	22	1.314	0.445	-0.21	-0.009	0.42	13	35
38.	G 38	20.53	5	1.868*	-2.03**	0.00	-0.028	0.03	2	7
39.	G 39	20.30	6	2.622*	1.77**	0.14	0.019	0.28	8	14
40.	G 40	21.37	2	0.758	-1.07*	0.25	0.025	0.51	16	18

*Significant at 5% level of significance

**Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression Coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI Stability Value, RASVi: Rank of ASV, GSI: Genotype Selection Index

In AMMI1 (Figure 17.1), IPCA1 was plotted against mean protein content, the vertical line passing through the origin is the grand mean. Accordingly, those genotypes which were noticed in the right side of the vertical line were observed more average protein content than grand mean. Among all, genotypes, G36, G40, and G32 have positive IPCA1 score with highest average protein content while G24 have negative IPCA1 score with more average protein content. On the other hand, the mean performance for most of the genotypes were noticed below the grand mean and which were located to left side of the vertical line. Among all, genotypes, G1, G27, G14, G16 and G17 were located extreme left side of the biplot which indicates, these genotypes had lowest average protein content. The lowest protein content was observed in all the environment than grand mean hence they were found in the left side of the Figure 17.1. Genotypes, G26 and G13 were more specifically adapted to E4 site while G35 was more favorable to site E3. No any genotypes specifically adapted to sites E1, E2 and E5. Genotypes, G36, G38, G24, G35, G3, G20 and G15 were located near to central line of IPCA1 scores which indicates, these genotypes have highest additive main effect. In the present investigation, G36 and G24 were stable with highest average protein content whereas G15, G20, G3 and G35 were most stable with low protein content. Among all, G2, G31, G11, G14, G22, G18, G5, G26, G28 and G13 were located far from central line of IPCA1 score which were indicating the maximum interaction between genotype and environment.

In Figure 17.2 where IPCA2 was plotted against IPCA1 which elucidated the GE interaction, making it a useful test for interaction. It was found that most of the genotypes and environments were scattered around the biplot. Genotypes farther from the center of biplot show specific adaptation. In the present study, G36, G12, G37, G15, G10 and G34 were more stable than the other genotypes since they were found near to the origin and have general adaptability. However, G36 was stable with highest protein content than grand mean. The other genotypes showed specific to the certain environments. for instance, G2, G31 and G11 were more adapted to E2 site whereas G24 and G1 were specifically adapted to site E4. The G26, G29, G13 and G14 were more favorable to site E1 while G20, G25, G18, G35

and G22 were more suited for E3 and E5 sites. Also, no any environment fell into sector with G4 and G5 vertex, it implies that, these are the poorest genotypes in some or all of the locations. In the present investigation, G26 was the best at E1, G2 was good at E2, G25 and G20 were the better in E3 and E5, and G24 was the best at E4 (Fig. 17.2), suggesting that these genotype won to which environment lie. These genotypes positioned on the polygon vertex might be have the longest distance from biplot origin, supposed to the most responsive and have highest interaction between genotype and environment.

Among tested environments, E1, E4, E3 and E5 were the most discriminating environments that provided adequate information on the performance of the genotypes. Further explanation, E1, E4, E3 and E5 environments were powerful for genotype evaluation and interesting sites to identify superior genotypes. On other hand, E2 environment falls close to the bi-plot origin and the least discriminating environment (Fig. 17.2) and it provided little information about the performance difference of genotypes.

CHAPTER - V

DISCUSSION

Niger crop is though cumbersome for genetic improvement and it would prove readily adaptable genetic options for sustaining self-sufficiency and mitigating the future needs of oil seeds in the country. The ultimate goal of the plant breeder is to develop promising cultivars with some improved economic features. This goal can be achieved only by carefully planned collection, evaluation and selection procedures through well established and clearly defined objectives. The hereditary variations are of major interest to the plant breeder. The plant breeder's particular task is to sort out these heritable variations which will be useful for the improvement of crop plants and congregate them in a variety. However, the major problem of the plant breeder here is to know at what extent a character is heritable and to what extent it influences by the environment. As the fixable genetic component of variance can be exploited, the non-additive component which is not fixable, can be effective only when there is presence of genetic variability and diversity among the population. The effectiveness of selection depends upon the extent to which variability is present in the population. The selection of desirable genotypes among the widely related primary lines can be made through evaluating the ability of these genotypes to genetic variability and diversity for a solitary character. Concerted research efforts are needed to identify the variable and diverse genotypes for yield and yield contributing traits. Development and evaluation of high yielding genotypes and studying their stability over different seasons and locations will go a long way in identifying the appropriate genotypes to meet the research gaps. However, plateauing trend in yields, declining and degrading resources and increasing population warrant another mini-green revolution in agriculture. The genetic models for estimation of variability, diversity and stability have widely been reported by several scientists in self- and cross-pollinated crops.

The present investigation was undertaken to study the nature and extent of genetic variability, diversity, stability and genotype x environment interaction

(GEI) with different biometrical techniques involving forty genotypes of Niger (*Guizotia abyssinica* L.).

The results obtained in the present study were discussed under the following head:

5.1. Analysis of variance

In the present investigation, the mean sum of squares among the genotypes were statistically significant for all the characters under study except capitulum diameter and 1000 seed weight. Results showed that all the characters under study have significant variation. The similar results were also reported by Adhanom (1985), Pradhan *et. al.* (1995), Patil (1999), Patil and Duhoon (2005), Panda and Sial (2012) and Ahmad *et. al.* (2016).

5.2. Mean performance

Among all, G1, G2, G4, G8, G9, G10, G24, G25, G26, G28, G32, G35, G36, G39 and G40 were genetically variable and diverse genotypes. These genotypes were reported desirable for future breeding programme. The tantamount findings were also reported by Bagari (1973), Goyal and Sudhir (1985), Payasi *et. al.* (1987), Pradhan *et. al.* (1995), Mishra (1995), Patil (1999), Kenjale *et. al.* (2003), Patil and Duhoon (2005), Rani *et. al.* (2010), Panda and Sial (2012), Yadav *et. al.* (2012), Ahmad *et. al.* (2016), Benelli *et. al.* (2017), Jay Laxami (2017) and Kusumlata *et. al.* (2018).

5.3. Genetic variability

Genetic variability is the prime requirement for crop breeding programme. Hence, plant breeder always interested in collecting or creating variability through exploration and recombination. Moreover, plant breeder should have in-depth knowledge of nature and expression of different characters and range of variability present in the population of crop before adopting different methods. Assessment of variability in the population, therefore becomes the basic requirement for any breeding programme.

5.3.1. Components of variation

The total variability in each character could be partitioned into three components *viz.*, phenotypic, genotypic and environmental. This helps to determine heritable and non-heritable portion of variation in respect of characters.

In general, the magnitudes of phenotypic variances were greater than genotypic variances for all the traits. In the present study, the highest genotypic, phenotypic and environmental variances were found in number of primary and secondary branches plant⁻¹, number of capitula plant⁻¹, number of seeds capitulum⁻¹, seed yield plant⁻¹, seed yield plot⁻¹ while lowest in capitulum diameter. This is because of the addition of environmental variance into the phenotypic variance. These findings were in conformity to those of Bagari (1973), Adhanom (1985), Goyal and Sudhir (1985), Bilaiya (1987), Payasi *et. al.* (1987), Mishra (1995), Pradhan *et. al.* (1995), Patil (2000), Kenjale *et. al.* (2003), Rani *et. al.* (2010), Yadav *et. al.* (2012), Ahmad *et. al.* (2016), Benelli *et. al.* (2017), Kusumlata *et. al.* (2018) and Fekadu (2020).

5.3.2. Coefficient of variation

Phenotypic and genotypic coefficients of variation measure the extent of variation present in the population for particular character.

In general, phenotypic coefficients of variation (PCV) were found to be maximum than corresponding genotypic coefficients of variation (GCV) for all the characters. In the present investigation, the high magnitude of genotypic coefficient of variation was noticed for number of primary and secondary branches plant⁻¹, number of capitulum plant⁻¹, number of seeds plant⁻¹, seed yield plant⁻¹ and seed yield plot⁻¹ revealed the presence of high genetic variability. In the present study, the highest GCV and PCV were found in number of primary and secondary branches plant⁻¹ while lowest in days to maturity. This is because of the insertion of environmental coefficient of variation into the phenotypic coefficient of variation. The simulative results were also reported by Bagari (1973), Goyal and Sudhir (1985), Channarayappa (1987), Bilaiya (1987), Mishra (1995), Pradhan *et. al.* (1995), Borole and Patil (1997), Patil (1999), Ahmad *et. al.* (2003), Sreedhar (2003), Patil and Duhoon (2005), Panda and Sial (2012), Ahmad *et. al.*

(2016), Dudhe *et. al.* (2017), Kusumlata *et. al.* (2018), Suryanarayana *et. al.* (2018a) and Fekadu (2020).

5.4. Heritability

The genotypic coefficient of variation does not offer full scope to estimate the heritable variation and hence, estimates of heritability becomes most necessary. Heritability in broad sense is a measure of heritable variation and may fluctuate from season to season. Moreover, heritability is a property not only of a character but also of a population and of the environmental circumstances to which the individuals are subjected (Falconer, 1960).

Heritability is the good index of the transmission of characters from parents to their offspring (Falconer, 1960). The heritability of a character has a major impact on methods chosen for population improvement, inbreeding and other aspect of selection. It may be effective for a character with low heritability (5-10%), medium heritability (10-30%) and high heritability (30 to 60%) and above (60%) very high (Robinson, 1966). The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic populations.

In the present investigation, the highest heritability was found in number of capitula⁻¹, days to 50 per cent flowering, number of primary and secondary branches plant⁻¹ while lowest in oil content and protein content. These traits were governed by additive genes and selection for improvement of these traits may useful. The tantamount findings were also reported by Nema and Singh (1965), Nayakar (1976), Goyal and Sudhir (1985), Channarayappa (1987), Bilaiya (1987), Abraham and Gupta (1989), Patel *et. al.* (1993), Pradhan *et. al.* (1995), Patil (2000), Kenjale *et. al.* (2003), Mehta *et. al.* (2003), Sreedhar (2003), Rani *et. al.* (2010), Ahmad *et. al.* (2016), Dudhe *et. al.* (2017), Kusumlata *et. al.* (2018), Suryanarayana *et. al.* (2018a) and Fekadu (2020).

5.5. Genetic advance and genetic advance per cent mean

Genetic advance is a measure of expected progress under selection scheme. The heritability estimates provide the information on the magnitude of inheritance of quantitative characters, but it does not indicate the magnitude of genetic gain obtained by selection of best individual from the best population. So,

heritability along with genetic advance is more useful for selection than the heritability alone.

In the present investigation, the maximum genetic advance and genetic advance per cent mean was found in number of primary and secondary branches plant⁻¹, number of capitula⁻¹, number of seeds capitulum⁻¹, seed yield plant⁻¹ and seed yield plot⁻¹. These genotypes were controlled by additive genes and selection is beneficial for such traits. These findings were in conformity to those of Channarayappa (1987), Mathur and Gupta (1993), Pradhan *et. al.* (1995), Borole and Patil (1997), Patil (1999), Patil (2000), Ahmad *et. al.* (2003), Sreedhar (2003), Rani *et. al.* (2010), Panda and Sial (2012), Ahmad *et. al.* (2016), Dudhe *et. al.* (2017), Kusumlata *et. al.* (2018), Suryanarayana *et. al.* (2018a) and Fekadu (2020).

5.6. Gene action studies

Heritability alone can't provide information on the amount of genetic progress that would result from the selection. It is therefore advocated to use appropriate selection procedure for improvement of these characters in general and yield in particular since high heritability coupled with high genetic advance reveals the presence of lesser environmental influence and prevalence of additive gene action. The high heritability accompanied with low genetic advance indicates, that the character is under the control of non-additive gene effects, low heritability accompanied with high genetic advance indicates, that the character is under the control of additive gene effects and a low heritability accompanied with low genetic advance indicates, that the character is highly influenced by environmental effects.

In the present study, most of the characters *i.e.*, days to 50 per cent flowering, plant height, number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of capitula plant⁻¹, number of seeds capitulum⁻¹, 1000 seed weight, seed yield plant⁻¹, seed yield plot⁻¹ and days to maturity were under the control of additive gene action. Therefore, improvement of these traits having high heritability along with and high genetic advance would be more effective through selection in the present material. These results are in harmony with the findings of Patel *et. al.* (1993), Pradhan *et. al.* (1995), Patil (1999), Patil (2000),

Patil and Duhoon (2005), Rani *et. al.* (2010), Yadav *et. al.* (2012), Dudhe *et. al.* (2017) and Suryanarayana *et. al.* (2018a).

On the other hand, characters *viz.*, capitulum diameter, oil content and protein content showed high heritability coupled with low genetic advance, indicating substantial contribution of non-additive gene action in the expression of these traits. Therefore, improvement of these traits having high heritability along with and low genetic advance would be less effective if the selection in the present material could be rigorously applied. The simulative quests were also reported by Mathur and Gupta (1993), Pradhan *et. al.* (1995) and Borole and Patil (1997).

5.7. Genetic diversity

The appreciable amount of variability in the quantitative characters appears to lead the wide range of genetic diversity among the biological genotypes under study.

5.7.1. Clustering pattern of genotypes

Analysis of genetic diversity based on Mahalanobis D^2 statistics (Mahalanobis, 1936b) was done to quantify the degree of divergence among the Niger (*Guizotia abyssinica* L.) genotypes to assess the relative contribution of different components to the total divergence at inter and intra cluster levels.

The high level of D^2 value indicated wide range of divergence among the population of Niger. The magnitude of D^2 values of pooled data, forty genotypes were grouped in 5, 4, 4, 8 and 4 clusters for E1, E2, E3, E4 and E5, respectively it considers the environment wise.

The pooled results of ARS, Phondaghat revealed that the forty genotypes were grouped in 5 clusters on the basis of magnitude of D^2 values. Cluster I with 24 genotypes emerged as the largest cluster followed by cluster IV with 10 genotypes, cluster II with 4 genotypes whereas the cluster III and V contained only single genotype, thus these clusters remained solitary.

On the basis pooled magnitude of D^2 values, the forty genotypes were grouped into 4 clusters during the experiment at ARS, Shirgaon. Cluster I with 30

genotypes emerged as the largest cluster followed by cluster III with 5 genotypes, cluster II with 4 genotypes while the cluster IV was solitary.

In the investigation of Department of Agril. Botany, the forty genotypes were grouped in 4 clusters on the basis of magnitude of D^2 values. Cluster I with 32 genotypes emerged as the largest cluster followed by cluster II with 5 genotypes, cluster III with 2 genotypes whereas the cluster IV was solitary.

On the basis of magnitude of D^2 values, the forty genotypes were grouped in 8 clusters during conducted the experiment at RARS, Karjat. Cluster I with 20 genotypes emerged as the largest cluster followed by cluster III with 7 genotypes, cluster II with 5 genotypes cluster VII with 3 genotypes and cluster VIII with 2 genotypes whereas the cluster IV, V and VI were solitary in regard to the multi-varietal composition.

The results of ARS, Palghar exhibited that the forty genotypes were grouped in 4 clusters on the basis of magnitude of D^2 values. Cluster I with 27 genotypes emerged as the largest cluster followed by cluster III with 7 genotypes, cluster II with 5 genotypes while the cluster IV was solitary.

The solitary clusters indicating their independent identity and importance due to the unique characters constituted by those genotypes. These genotypes may serve as potential parents for breeding programme.

These results are in harmony with the findings of Chatterjee (1983), Sohan (1987), Mehta (1989), Chatterjee *et. al.* (1991), Jagdev and Samal (1991), Biswas *et. al.* (1993), Ravanappa *et. al.* (1994), Kumar (1999), Sreedhar *et. al.* (2006), Patil (2007), Parameshwarappa *et. al.* (2009), Parameshwarappa *et. al.* (2011), Sangita *et. al.* (2012), Goyal and Bisen (2017), Misganaw (2017), Naik *et. al.* (2018), Ram *et. al.* (2018), Suryanarayana *et. al.* (2018b) and Suryanarayana *et. al.* (2019).

5.7.2. Intra and Inter cluster divergence

The intra-cluster distance is another parameter, besides cluster mean for particular character, as it indicated the extent of variability existed in the genotypes comprised in a particular cluster.

On the basis of pooled data, location wise the highest intra cluster distance was observed for cluster IV ($D=4.69$), I ($D=3.04$), II ($D=4.12$), VIII ($D=3.10$) and III

($D=3.61$) for E1, E2, E3, E4 and E5, respectively. The high intra cluster distance within a cluster indicated high degree of variability within the cluster offers scope for improvement by various selection methods.

The similar results were also reported by Sohan (1987), Mehta (1989), Chatterjee *et. al.* (1991), Jagdev and Samal (1991), Biswas *et. al.* (1993), Ravanappa *et. al.* (1994), Kumar (1999), Sreedhar *et. al.* (2006), Patil (2007), Parameshwarappa *et. al.* (2009), Parameshwarappa *et. al.* (2011), Sangita *et. al.* (2012), Goyal and Bisen (2017), Misganaw (2017), Naik *et. al.* (2018), Ram *et. al.* (2018), Suryanarayana *et. al.* (2018b) and Suryanarayana *et. al.* (2019).

The inter-cluster studies indicated magnitude of genetic divergence between the clusters. It showed that, how much this clusters were genetically diverse from each other.

In the present investigation, environment wise the highest inter cluster distance for pooled data was observed between cluster II and V ($D=13.26$), II and III ($D=7.28$), III and IV ($D=7.89$), IV and VIII ($D=8.45$), and I and IV ($D=7.54$) for E1, E2, E3, E4 and E5, respectively. These clusters were found genetically diverse. Those genotypes reported maximum inter cluster distance indicated that these genotypes were included in these clusters will give high heterotic response and better segregants. The genotypes which included in that genetically diverse clusters could be used in hybridization programme for future crop improvement in niger. The lowest inter cluster distance was observed between cluster III and IV ($D=4.52$), I and II ($D=4.88$), I and IV ($D=4.75$), I and IV ($D=3.20$), and I and II ($D=4.59$) for E1, E2, E3, E4 and E5, respectively. It indicating that genotypes present in these cluster might have genetical similarities with one another and appeared to have evolved from common gene pool.

These results are in harmony with the findings of Sohan (1987), Jagdev and Samal (1991), Biswas *et. al.* (1993), Ravanappa *et. al.* (1994), Kumar (1999), Sreedhar *et. al.* (2006), Patil (2007), Parameshwarappa *et. al.* (2009), Parameshwarappa *et. al.* (2011), Goyal and Bisen (2017), Naik *et. al.* (2018), Ram *et. al.* (2018), Suryanarayana *et. al.* (2018b) and Suryanarayana *et. al.* (2019).

5.7.3. Cluster means

Genotypes from cluster III, III, VII showed earliness for flowering and maturity with dwarf plant stature in E1, E3 and E4, respectively. In E2, early flowering and maturity of genotypes from cluster IV and dwarf plant height observed in cluster III. Also, in E5, genotypes found early flowering and dwarf statured plants in cluster IV and early matured genotypes reported in cluster II. The highest number of primary and secondary branches plant⁻¹, number of capitula plant⁻¹, capitulum diameter, number of seeds capitulum⁻¹, 1000 seed weight, seed yield plant⁻¹, seed yield plot⁻¹, oil content and protein content were found in genotypes consisted the cluster V (E1), clusters II and IV (E2 and E3), clusters VI and VIII (E4), and clusters III and IV (E5).

D² analysis revealed that geographical distribution had no relation to genetic diversity as similar findings were in conformity with previous workers *viz.*, Sohan (1987), Jagdev and Samal (1991), Biswas *et. al.* (1993), Ravanappa *et. al.* (1994), Kumar (1999), Sreedhar *et. al.* (2006), Patil (2007), Parameshwarappa *et. al.* (2009), Parameshwarappa *et. al.* (2011), Goyal and Bisen (2017), Naik *et. al.* (2018), Ram *et. al.* (2018), Suryanarayana *et. al.* (2018b) and Suryanarayana *et. al.* (2019).

5.7.4. Per cent contribution for divergence

D² values tell us the magnitude of divergence between two clusters. The question arises that which are the characters responsible for divergence between the genotypes. By studying the contribution of different characters towards the total divergence, breeder can get an idea about the characters, which are mainly responsible for the total divergence. This is important while selecting the parents in breeding programme.

On the basis of pooled data, location wise the contribution of various traits towards divergence was ranged from 0.00% (oil content) to 32.44% (number of capitula plant⁻¹), 1.28% (number of secondary branches plant⁻¹) to 26.28% (capitulum diameter), 0.26% (1000 seed weight) to 30.13% (days to 50 per cent flowering), 0.13% (protein content) to 33.59% (days to 50 per cent flowering) and 0.77% (1000 seed weight) to 32.56% (days to 50 per cent flowering) for E1, E2, E3, E4 and E5, respectively.

It is obvious the yield is the dependent character governed by several other yield contributing characters, which are affected by different environments in different locations. Therefore, changes in variability in character among genotypes for breeding cannot be made only on the basis of yield potential. Hence to improve it, selection must be done considering plant height, number of primary and secondary branches plant⁻¹, number of capitulum plant⁻¹, capitulum diameter, number of seeds capitulum⁻¹, 1000 seed weight as their contribution towards total divergence is more.

The similar results were also reported by Jagadev and Samal (1991), Biswas *et. al.* (1993), Ravanappa *et. al.* (1994), Sohan and Kerketta (1998), Kumar (1999), Sreedhar *et. al.* (2006), Parmeshwarappa *et. al.* (2009), Parmeshwarappa *et. al.* (2011), Goyal and Bisen (2017), Naik *et. al.* (2018), Ram *et. al.* (2018), Suryanarayana *et. al.* (2018b) and Suryanarayana *et. al.* (2019).

5.8. Stability and Genotype x Environment interaction (GEI)

AMMI model has been popularized as additive main effects and multiplicative interaction and a number of applications have been found (Gauch, 1988; 1992). It combines a univariate technique (ANOVA) for the main effects and a multivariate technique (PCA) for GEI. Crossa (1990) suggests that the use of multivariate techniques permits a better use of information than the regression models in the MET analysis. It can be used to understand and structure interactions between genotypes and environments. The GGE biplot provides a capacity to evaluate genotypes for their yielding ability, adaptability and stability.

The combined analysis of variance showed that mean squares due to genotype, environment and genotype x environment interaction (GEI) highly significant ($p < 0.01$) for all the traits under study. This showed that environments were diverse and affects the performance of genotypes. The similar conclusion was reported by Patil and Purkar (2000), Salah *et. al.* (2008), Igor *et. al.* (2010), Marinkovic *et. al.* (2011), Tadesse and Abay (2011), Hossein (2012), Milan *et. al.* (2012), Igor *et. al.* (2013), Muhammad *et. al.* (2013), Miroslav *et. al.* (2013), Pourdard and Moghaddam (2013), Abeya *et. al.* (2014), Patil *et. al.* (2014), Abate *et. al.* (2015), Mekonnen *et. al.* (2015), Marisol *et. al.* (2016), Seyed *et. al.* (2016), Bhavsar (2017),

Ali and Mohammadi (2017), Boureima *et. al.* (2017), Jay Laxami (2017), Baraki and Gebremariam (2018), Tadele *et. al.* (2018), Baraki *et. al.* (2019) and Abdelsatar *et. al.* (2020).

In the present study, the analysis of variance for AMMI model revealed significant difference for genotypes, environment, GEI interaction and its Interaction Principal Components (IPCA1, IPCA2 and IPCA3) for all the traits. The first two PCAs are used to represent environment as well as genotypes. It shows the relative performance, so that one genotype does not better than other in an environment and permits the estimation of interaction effect of a genotype in each location. The significance of genotype x environment interaction was further decomposed into three interaction principal component analysis (IPCA). In this study, contribution of per cent variance of first three IPCAs for seed yield plant⁻¹ and seed yield plot⁻¹ was 40.26, 32.61, 21.41 and 62.52, 32.40, 3.21, respectively; and the cumulative variance was 94.28 and 98.13, respectively. It demonstrated that genotypes may be selected for adaptation to specific environments. Such tantamount findings were observed by previous workers *viz.*, Patil and Purkar (2000), Salah *et. al.* (2008), Igor *et. al.* (2010), Marinkovic *et. al.* (2011), Tadesse and Abay (2011), Hossein (2012), Milan *et. al.* (2012), Igor *et. al.* (2013), Muhammad *et. al.* (2013), Miroslav *et. al.* (2013), Pourdad and Moghaddam (2013), Abeya *et. al.* (2014), Patil *et. al.* (2014), Abate *et. al.* (2015), Mekonnen *et. al.* (2015), Marisol *et. al.* (2016), Seyed *et. al.* (2016), Ali and Mohammadi (2017), Bhavsar (2017), Boureima *et. al.* (2017), Jay Laxami (2017), Baraki and Gebremariam (2018), Tadele *et. al.* (2018), Baraki *et. al.* (2019) and Abdelsatar *et. al.* (2020). Gauch and Zobel (1996) suggested that the most accurate model for AMMI can be predicted by using first two principal component analyses.

AMMI and GGE models were considered as an emerging novel and prestigious models for data analysis of multi-location trials (Yan and Kang, 2003). AMMI biplots were recently preferred biplots to visualize adaptability and stability of genotypes across tested environments (Gauch and Zobel, 1997; Gauch, 2006). Moreover, the model also useful on grouping similar performance

genotypes and/or environments and also provide some information about GEI in order to identify the genotypes adapted to specific environment.

Purchase *et. al.* (2000) developed the AMMI stability value (ASV) based on the AMMI model's IPCA1 and IPCA2 (Interaction Principal Components Axes 1 and 2, respectively) scores for each genotype. Since ASV only consider the IPCA score without taking into account the mean performance of the genotypes, stable genotypes identified using ASV may gave inferior performance. A new approach known as genotype selection index (GSI) was recommended by Farshadfar (2008). Using AMMI stability value and mean performance, GSI incorporates both mean and stability in a single criterion. Low value of this parameter shows desirable genotypes with high mean and stability. The selection of stable genotypes decided by those genotypes gives higher mean performance and deviated non-significantly to zero, regression coefficient near to one (Regression model), IPCA1 score close to zero, low ASV with less GSI (AMMI model) (Farshadfar *et. al.*, 2011 and Tadele *et. al.*, 2018).

With considering stability parameters as per Regression model, the results relanced, 13 genotypes were stable for days to 50 per cent flowering. Seven genotypes were stable for plant height, 5 for number of primary branches plant⁻¹, 7 for number of secondary branches plant⁻¹, 5 for number of capitula plant⁻¹ and 7 for capitulum diameter. Eight genotypes had non-significant regression coefficient and deviation mean squares with high mean for number of seeds capitulum⁻¹ indicating their stability across the environments. Similarly, 8 genotypes for 1000 seed weight, 12 for seed yield plant⁻¹, 5 for seed yield plot⁻¹ and 8 for days to maturity were found stable. On the other hand, 4 and 6 genotypes had high mean, non-significant regression coefficient and deviation from regression for oil and protein content. The simulative results were in conformity with the findings of Patil and Purkar (2000), Salah *et. al.* (2008), Tadesse and Abay (2011), Hossein (2012), Igor *et. al.* (2013), Muhammad *et. al.* (2013), Patil *et. al.* (2014), Bhavsar (2017), Tadale *et. al.* (2018), Abdelsatar *et. al.* (2020) and Ansarifard *et. al.* (2020).

Stability parameters as per AMMI model for competent traits revealed, 14 genotypes were stable for days to 50 per cent flowering. The 11 genotypes were stable for plant height, 9 for number of primary branches plant⁻¹, 7 for number of secondary branches plant⁻¹, 9 for number of capitula plant⁻¹ and 13 for capitulum diameter. Nine genotypes had IPCA1 score close to zero, low ASV value, less GSI index with high mean for number of seeds capitulum⁻¹ indicating their stability across the environments. Similarly, 18 genotypes for 1000 seed weight, 14 for seed yield plant⁻¹, 6 for seed yield plot⁻¹ and 12 genotypes for days to maturity were found to be stable across the environments. On the other hand, 8 and 7 genotypes had high mean, IPCA1 score close to zero, low ASV value and less GSI index for oil and protein content. These results were in conformity with the findings of Igor *et. al.* (2010), Marinkovic *et. al.* (2011), Milan *et. al.* (2012), Igor *et. al.* (2013), Muhammad *et. al.* (2013), Miroslav *et. al.* (2013), Pourdad and Moghaddam (2013), Abeya *et. al.* (2014), Abate *et. al.* (2015), Mekonnen *et. al.* (2015), Marisol *et. al.* (2016), Seyed *et. al.* (2016), Ali and Mohammadi (2017), Boureima *et. al.* (2017), Jay Laxami (2017), Baraki and Gebremariam (2018), Tadale *et. al.* (2018), Baraki *et. al.* (2019) and Abdelsatar *et. al.* (2020).

With considering all the stability parameters (Regression and AMMI model) the results exhibited, 7 genotypes were stable for days to 50 per cent flowering. Four genotypes were stable for plant height and 5 for number of primary branches plant⁻¹, 4 for number of secondary branches plant⁻¹, 5 for number of capitula plant⁻¹ and 7 for capitulum diameter. Seven genotypes deviated non-significantly to zero, regression coefficient near to one, IPCA1 score close to zero, low ASV value, less GSI index with high mean for number of seeds capitulum⁻¹, indicating their stability across the environments. Similarly, 8 genotypes for 1000 seed weight, 11 for seed yield plant⁻¹, 5 for seed yield plot⁻¹ and 6 genotypes for days to maturity were found more stable. On the other hand, five genotypes each deviated non-significantly to zero, regression coefficient near to one, IPCA1 score close to zero, low ASV value, less GSI index with high mean for oil and protein content. The similar results were in harmony with the findings of Patil and Purkar (2000), Salah *et. al.* (2008), Igor *et. al.* (2010), Marinkovic *et. al.* (2011), Tadesse and

Abay (2011), Hossein (2012), Milan *et. al.* (2012), Igor *et. al.* (2013), Muhammad *et. al.* (2013), Miroslav *et. al.* (2013), Pourdad and Moghaddam (2013), Abeya *et. al.* (2014), Patil *et. al.* (2014), Abate *et. al.* (2015), Mekonnen *et. al.* (2015), Marisol *et. al.* (2016), Seyed *et. al.* (2016), Ali and Mohammadi (2017), Bhavsar (2017), Boureima *et. al.* (2017), Jay Laxami (2017), Baraki and Gebremariam (2018), Tadale *et. al.* (2018), Baraki *et. al.* (2019) and Abdelsatar *et. al.* (2020).

5.9. AMMI GGE biplots

Stable and best genotypes were identified by graphical representation of AMMI biplots which uses genotype and G x E components and identifies G x E interaction pattern of multi-environment data and clearly shows stable genotype and best performer in which environment (Lakew *et. al.*, 2014). Vijaykumar *et. al.*, (2001) ascribed that these biplots helps in visual interpretation of GE patterns and identify genotypes or environments that exhibit low, medium and high interaction effects. Genotypes or environments with large negative or positive IPCA scores have high interaction and those with IPCA scores near to zero have little interaction across environment and *vice versa* for environments (Crossa *et. al.*, 1990).

In AMMI1 biplot for various traits for pooled data evinced, seven genotypes were stable with high additive main effect for days to 50 per cent flowering while 11 genotypes had IPCA1 score (positive or negative) which were indicating the maximum interaction between genotype and environment. Four genotypes were suited for favorable environments while three genotypes were suited for unfavorable environments. Similarly, environments E2, E3 and E5 showed little interaction and environments E1 and E4 were exert maximum interaction. Eight genotypes were stable with high additive main effect for plant height while 8 genotypes had IPCA1 score (positive or negative) which were indicating the maximum interaction between genotype and environment. Three genotypes each were suited for favorable and unfavorable environments. Similarly, environments E2 and E4 showed little interaction and environments E1, E3 and E5 were exert maximum interaction. Five genotypes were stable with high additive main effect for number of primary branches plant⁻¹ while 9 genotypes had IPCA1 score

(positive or negative) which were indicating the maximum interaction between genotype and environment. Three genotypes were suited for unfavorable and only one suited for favorable environments. Similarly, environments E3 and E5 showed little interaction and environments E1, E2 and E4 were exert maximum interaction. Three genotypes were stable with high additive main effect for number of secondary branches plant⁻¹ while 10 genotypes had IPCA1 score (positive or negative) which were indicating the maximum interaction between genotype and environment. Four genotypes were suited for unfavorable while two for favorable environments. Similarly, environments E2 and E4 showed little interaction and environments E1, E3 and E4 were exert maximum interaction. Five genotypes were stable with high additive main effect for number of capitula plant⁻¹ while 12 genotypes had IPCA1 score (positive or negative) which were indicating the maximum interaction between genotype and environment. Four genotypes were suited for favorable environments and three for unfavorable environments. Similarly, environment E3, E4 and E5 showed little interaction and environments E1 and E2 were exert maximum interaction. Seven genotypes were stable with high additive main effect for capitulum diameter while 10 genotypes had IPCA1 score (positive or negative) which were indicating the maximum interaction between genotype and environment. Four genotypes were suited to unfavorable and two for favorable environments. Similarly, environment E4 showed little interaction and environments E1, E2, E3 and E5 were exert maximum interaction. Five genotypes were stable with high additive main effect for number of seeds capitulum⁻¹ while 12 genotypes had IPCA1 score (positive or negative) which were indicating the maximum interaction between genotype and environment. Three genotypes each were suited for favorable and unfavorable environments. Similarly, environments E4 and E5 showed little interaction and environments E1, E2 and E3 were exert maximum interaction. Most of the genotypes except few were stable with high additive main effect for 1000 seed weight while 4 genotypes had IPCA1 score (positive or negative) which were indicating the maximum interaction between genotype and environment. Three genotypes were suited for unfavorable and only one for favorable environments.

Similarly, environments E1, E3 and E5 showed little interaction and environments E2 and E4 were exert maximum interaction. Four genotypes were stable with high additive main effect for seed yield plant⁻¹ while 10 genotypes had IPCA1 score (positive or negative) which were indicating the maximum interaction between genotype and environment. Four genotypes were suited for favorable and two for unfavorable environments. Similarly, environments E1, E2 and E4 showed little interaction and environments E3 and E5 were exert maximum interaction. Six genotypes were stable with high additive main effect for seed yield plot⁻¹ while 11 genotypes had IPCA1 score (positive or negative) which were indicating the maximum interaction between genotype and environment. Five genotypes each were suited for favorable and unfavorable environments. Similarly, environments E1, E2 and E4 showed little interaction and environments E3 and E5 were exert maximum interaction. Eight genotypes were stable with high additive main effect for days to maturity while 9 genotypes had IPCA1 score (positive or negative) which were indicating the maximum interaction between genotype and environment. A single genotype each was suited for favorable and unfavorable environments. Similarly, all the environments had more IPCA score indicating maximum interaction. Six genotypes were stable with high additive main effect for oil content while 9 genotypes had IPCA1 score (positive or negative) which were indicating the maximum interaction between genotype and environment. Four genotypes were suited for unfavorable and three for favorable environments. Similarly, environments E4 and E5 showed little interaction and environments E1, E2 and E3 were exert maximum interaction. Four genotypes were stable with high additive main effect for protein content while 10 genotypes had IPCA1 score (positive or negative) which were indicating the maximum interaction between genotype and environment. Four genotypes each were suited for favorable and unfavorable environments. Similarly, environments E2, E3 and E5 showed little interaction and environments E1 and E4 were exert maximum interaction.

These results are in conformity with the findings of Patil and Purkar (2000), Salah *et. al.* (2008), Igor *et. al.* (2010), Marinkovic *et al.* (2011), Tadesse and Abay

(2011), Hossein (2012), Milan *et. al.* (2012), Igor *et. al.* (2013), Muhammad *et. al.* (2013), Miroslav *et. al.* (2013), Pourdad and Moghaddam (2013), Abeya *et. al.* (2014), Patil *et. al.* (2014), Abate *et. al.* (2015), Mekonnen *et. al.* (2015), Marisol *et. al.* (2016), Seyed *et. al.* (2016), Ali and Mohammadi (2017), Bhavsar (2017), Boureima *et. al.* (2017), Jay Laxami (2017), Baraki and Gebremariam (2018), Tadele *et. al.* (2018), Baraki *et. al.* (2019) and Abdelsatar *et. al.* (2020).

In AMMI2 biplot, genotypes located on the vertices of the polygon performed either the best or the poorest in one or more environments (Yan and Kang, 2003). The equality lines divide the biplot into sectors, and the winning genotype for each sector is the one located on the respective vertex (Yan *et. al.*, 2007). The environmental scores were joined to the origin by site lines, site with short spokes didn't exert strong interactive forces, while those with long spokes exerted strong interaction (Crossa *et. al.*, 1990).

In AMMI2 biplot of various traits for pooled data evinced, G22 was the best at E1, G3 was winning genotype at E2, G24 and G29 were the pre-eminent at E4 and G4, G5 and G2 were the excellent in E5 and E3 for days to 50 per cent flowering. No any environment felt in genotype G32 located on the vertices of the polygon performed either the best or the poorest in one or more environments. Discriminating environments were ranked from top to bottom as E1>E4>E3>E5>E2. Environments, E1, E4 and E3 were received as ideal environments for discrimination of superior genotypes. For plant height, G2 and G3 were the pre-eminent at E5, G39 was the best at E1, G33 was the classiest in E3 and G20 was winning genotype at E2 and E4. No any environment felt in genotypes G40 and G27 were located on the vertices of the polygon performed either the best or the poorest in one or more environments. Discriminating environments were ranked from top to bottom as E1>E4>E3>E2>E5. Environments, E1, E4 and E3 were exhibited as ideal environments for discrimination of superior genotypes. The genotype G26 was the winning genotype at E1, G13 and G17 were pre-eminent at E2 and E4; G9 and G18 were the excellent in E5; and at E3, G33 and G32 were the best for number of primary branches plant⁻¹. No any environment felt in genotypes G12, G4 and G31 located

on the vertices of the polygon performed either the best or the poorest in one or more environments. Discriminating environments were ranked from top to bottom as $E1 > E3 > E4 > E2 > E5$. Environments, E1, E3 and E4 were observed as ideal environments for discrimination of superior genotypes. For number of secondary branches plant⁻¹, G3 and G4 were the best at E1, G30 and G17 were excellent at E2 and E3, G26 was the classiest in E4 and G16 was the winning genotype at E5. Discriminating environments were ranked from top to bottom as $E1 > E3 > E5 > E4 > E2$. Environments, E1, E3 and E5 were found to be as ideal environments for discrimination of superior genotypes. The genotype, G18 and G32 were the excellent at E1, G2 and G30 were pre-eminent at E3, G4 was the classiest in E2, and G15, G25 and G26 were the best at E4 and E5 for number of capitula plant⁻¹. No any environment felt in genotypes G31 and G13 located on the vertices of the polygon performed either the best or the poorest in one or more environments. Discriminating environments were ranked from top to bottom as $E1 > E3 > E2 > E4 > E5$. Environments, E1, E3, E2 and E4 were received as ideal environments for discrimination of superior genotypes. For capitulum diameter, G1 was the best at E1, G8 was winning genotype at E2; G20, G26 and G19 were the pre-eminent in E4 and G28 and G33 were the classiest at E3 and E5. No any environment felt in genotype G24 located on the vertices of the polygon performed either the best or the poorest in one or more environments. Discriminating environments were ranked from top to bottom as $E4 > E1 > E3 > E5 > E2$. Environments, E1, E3 and E4 were exhibited as ideal environments for discrimination of superior genotypes. The genotypes, G9 and G12 were the excellent at E1 and E2, G27 was winning genotype at E3, G22 was the excellent in E4 and E5 for number of seeds capitulum⁻¹. No any environment felt in genotypes G10, G19 and G24 located on the vertices of the polygon performed either the best or the poorest in one or more environments. Discriminating environments were ranked from top to bottom as $E3 > E4 > E1 > E2 > E5$. Environments, E1, E2, E3 and E4 were found as ideal environments. For 1000 seed weight, G26 and G16 were the pre-eminent at E1 and E3; G27 and G21 were excellent at E4, G28 and G29 were the best in E2 and E5.

Discriminating environments were ranked from top to bottom as $E4 > E3 > E2 > E5 > E1$. Environments, E3, E4 and E2 were observed as ideal environments for discrimination of superior genotypes. The genotype, G38 was the classiest at E1 and E2, G28 and G18 were excellent at E5, G5 and G8 were the best at E4 and G32 was the winning genotype in E3 for seed yield plant⁻¹. No any environment felt in genotypes G25, G11 and G18 located on the vertices of the polygon performed either the best or the poorest in one or more environments.

Discriminating environments were ranked from top to bottom as $E4 > E1 > E3 > E2 > E5$. Environments, E1, E4 and E3 were found as ideal environments for discrimination of superior genotypes. For seed yield plot⁻¹, G14 was the winning genotype at E5, G8 was classiest at E2, G17 and G23 were the pre-eminent in E4, G25 and G1 were the excellent at E1 and G6 was best in E3. No any environment felt in genotypes G20, G27 and G8 located on the vertices of the polygon performed either the best or the poorest in one or more environments.

Discriminating environments were ranked from top to bottom as $E4 > E3 > E1 > E2 > E5$. Environments, E4, E3 and E1 were observed to be as ideal environments for discrimination of superior genotypes. The genotypes, G4 and G34 were excellent at E1 and E2, G22 and G9 were the pre-eminent at E4 and G31 was the best in E3 and E5 for days to maturity. No any environment felt in genotypes G2 and G5 located on the vertices of the polygon performed either the best or the poorest in one or more environments.

Discriminating environments were ranked from top to bottom as $E3 > E4 > E1 > E5 > E2$. Environments, E1, E4 and E3 were reported as ideal environments for discrimination of superior genotypes. For oil content, G16 was winning genotype at E1, G9 was excellent at E2; and in E4, G35 and G25 was the best. No any environment felt in genotypes G22, G12, G34, G37 and G14 located on the vertices of the polygon performed either the best or the poorest in one or more environments.

Discriminating environments were ranked from top to bottom as $E3 > E4 > E1 > E2 > E5$. Environments, E3, E4 and E1 were found as ideal environments for discrimination of superior genotypes. The genotypes, G26 was the best at E1, G2 was winning genotype at E2, G25 and G20 were the excellent in E3 and E5, and G24 was the classiest at E4 for protein

content. No any environment felt in genotypes G4 and G5 located on the vertices of the polygon performed either the best or the poorest in one or more environments. Discriminating environments were ranked from top to bottom as $E1 > E5 > E4 > E2 > E3$. Environments, E1, E5 and E4 were observed as ideal environments for discrimination of superior genotypes.

These results are in conformity with the findings of Patil and Purkar (2000), Salah *et. al.* (2008), Igor *et. al.* (2010), Marinkovic *et. al.* (2011), Tadesse and Abay (2011), Hossein (2012), Milan *et. al.* (2012), Igor *et. al.* (2013), Muhammad *et. al.* (2013), Miroslav *et. al.* (2013), Pourdad and Moghaddam (2013), Abeya *et. al.* (2014), Patil *et. al.* (2014), Abate *et. al.* (2015), Mekonnen *et. al.* (2015), Marisol *et. al.* (2016), Seyed *et. al.* (2016), Ali and Mohammadi (2017), Bhavsar (2017), Boureima *et. al.* (2017), Jay Laxami (2017), Baraki and Gebremariam (2018), Tadele *et. al.* (2018), Baraki *et. al.* (2019) and Abdelsatar *et. al.* (2020).

The study of all the stability parameters and AMMI GGE biplots, genotypes, G36, G32, G24 and G10 were highly stable for most of the yield and yield contributing traits. The genotypes, G6, G8, G22 and G28 were suitable for favorable/rich environments while G2, G4, G7, G23 and G31 for unfavorable/poor environments in most of the traits. The genotypes, G4, G17, G25 and G28 were best performers in some environments for few yield contributing traits. These genotypes behaved as a potential breeding materials stock for future crop improvement. As per AMMI GGE biplots, two different mega-environments (METs) were identified, the first MET consists E1, E3 and E4 which are potential and excellent sites for discrimination of superior genotypes and second MET includes E2 and E5 were stable places for most of the characters.

Therefore, evaluation of multi-environment experiments for distinguishing the effects of the genotype and the environment, and then assess the $G \times E$ interaction in a reduced dimensional space with minimum error, AMMI stability model is the best and more efficient than joint regression model.

Table 33: Summary of genetically variable, diverse and promising genotypes of Niger for yield and yield contributing traits.

Sr. No.	Genotype code	Diverse	Mean performance								
			Flowering and Maturity (days)	Plant Stature	Primary and secondary branches plant ⁻¹	Number of capitula plant ⁻¹	Number of seeds capitulum ⁻¹	Seed yield plant ⁻¹ (g)	Seed yield plot ⁻¹ (g)	Oil content (%)	Protein content (%)
1.	G1	✓	MLF & MLM	SD	G	M	G	G	M	M	P
2.	G2	✓	LF & LM	SD	G	G	G	G	M	G	G
3.	G4	✓	LF & LM	T	G	G	G	G	G	G	G
4.	G8	✓	LF & LM	D	P	P	G	P	P	M	M
5.	G9	✓	LF & LM	SD	P	G	G	P	M	M	M
6.	G10	✓	MLF & LM	T	G	G	G	G	G	G	G
7.	G24	✓	EF & EM	D	G	G	G	G	G	G	G
8.	G25	✓	EF & EM	D	M	P	P	P	G	M	M
9.	G26	✓	EF & EM	D	P	P	P	G	M	M	M
10.	G28	✓	MLF & MLM	SD	P	P	M	P	P	P	P
11.	G32	✓	MLF & MLM	SD	G	G	G	G	G	G	G
12.	G35	✓	LF & LM	T	G	G	M	G	M	M	M
13.	G36	✓	MLF & LM	SD	G	G	G	G	G	G	G
14.	G39	✓	MLF & MLM	T	M	G	M	G	M	G	G
15.	G40	✓	MLF & MLM	T	G	G	G	G	M	G	G

EF: Early Flowering, MLF: Mid-late Flowering, LF: Late Flowering, EM: Early Maturity, MLM: Mid-late Maturity, LM: Late Maturity
D: Dwarf, SD: Semi-dwarf, T: Tall, G: Good, M: Medium, P: Poor

Table 34: Summary of promising and stable genotypes of Niger by regression and AMMI model for different qualitative and quantitative traits.

Sr. No.	Environments Characters	Regression Model (Eberhart and Russell model, 1966)	AMMI model (Gauch, 1992)
1.	Days to 50 per cent flowering	G1, G4, G10, G11, G12, G16, G20, G23, G24, G25, G32, G35, G36	G7, G10, G14, G16, G20, G21, G23, G24, G25, G26, G30, G31, G35, G40
2.	Plant height (cm)	G4, G8, G16, G24, G28, G32, G36	G4, G7, G8, G11, G14, G17, G24, G25, G28, G32, G40
3.	Number of primary branches plant ⁻¹	G10, G24, G32, G35, G36	G2, G4, G6, G10, G24, G32, G34, G36, G40
4.	Number of secondary branches plant ⁻¹	G10, G24, G30, G32, G33, G35, G36	G10, G24, G32, G33, G36, G39, G40
5.	Number of capitula plant ⁻¹	G14, G24, G32, G35, G36	G1, G14, G24, G32, G35, G36, G38, G39, G40
6.	Capitulum diameter (cm)	G2, G10, G15, G30, G32, G36, G39	G2, G10, G15, G30, G31, G32, G33, G34, G35, G36, G38, G39, G40
7.	Number of seeds capitulum ⁻¹	G24, G31, G32, G36, G37, G38, G39, G40	G18, G24, G31, G32, G35, G36, G38, G39, G40
8.	1000 seed weight (g)	G3, G4, G7, G10, G12, G24, G36, G37	G3, G4, G7, G10, G12, G17, G22, G24, G31, G32, G33, G35, G36, G37, G38, G39, G40
9.	Seed yield plant ⁻¹ (g)	G1, G2, G6, G10, G24, G26, G32, G33, G35, G36, G38, G40	G1, G6, G10, G21, G23, G24, G26, G32, G33, G35, G36, G38, G39, G40
10.	Seed yield plot ⁻¹ (g)	G4, G10, G24, G32, G36	G2, G4, G10, G24, G32, G36
11.	Days to maturity	G8, G9, G10, G24, G26, G28, G32, G36	G8, G10, G13, G14, G19, G23, G24, G26, G27, G28, G35, G36
12.	Oil content (%)	G10, G32, G36, G40	G4, G10, G11, G24, G32, G36, G39, G40
13.	Protein content (%)	G4, G10, G24, G32, G34, G36	G10, G24, G32, G34, G36, G38, G40

Table 35: Summary of stable genotypes of Niger over all the environments, favorable and unfavorable environments for different qualitative and quantitative traits.

Sr. No.	Characters	Stable genotypes (Considering both the stability models)	Genotypes suitable for favorable environments	Genotypes suitable for unfavorable environments
1.	Days to 50 per cent flowering	G10, G16, G20, G23, G24, G25, G35	G3, G11, G22, G9	G5, G32, G2
2.	Plant height (cm)	G8, G24, G28, G32	G39, G38, G35	G3, G2, G20
3.	Number of primary branches plant ⁻¹	G10, G24, G32, G35, G36	G26	G13, G18, G9
4.	Number of secondary branches plant ⁻¹	G10, G24, G32, G36	G16, G6	G4, G2, G11, G25
5.	Number of capitula plant ⁻¹	G14, G24, G32, G35, G36	G18, G10, G20, G9	G31, G4, G2
6.	Capitulum diameter (cm)	G2, G10, G15, G30, G32, G36, G39	G8, G12	G28, G24, G27, G5
7.	Number of seeds capitulum ⁻¹	G24, G31, G32, G36, G38, G39, G40	G19, G1, G24	G12, G9, G16
8.	1000 seed weight (g)	G3, G4, G7, G10, G12, G24, G36, G37	G27	G28, G26, G15
9.	Seed yield plant ⁻¹ (g)	G1, G6, G10, G24, G26, G32, G33, G35, G36, G38, G40	G28, G37, G18, G22	G4, G7
10.	Seed yield plot ⁻¹ (g)	G4, G10, G24, G32, G36	G6, G33, G8, G17, G3	G27, G20, G1, G37, G25
11.	Days to maturity	G8, G10, G24, G26, G28, G36	G29	G9
12.	Oil content (%)	G10, G24, G32, G36, G40	G14, G23, G37	G18, G13, G8, G1
13.	Protein content (%)	G10, G24, G32, G34, G36	G5, G26, G28, G13	G2, G31, G11, G4

Table 36: Summary of environment wise best Niger genotypes for different qualitative and quantitative traits.

Sr. No.	Environments	E1	E2	E3	E4	E5	Best / Poorest for specific or all the environments	Discriminating environments
	Characters							
1.	Days to 50 per cent flowering	G22	G3	G4, G2, G5	G24, G29	G4, G2, G5	G32	E1, E3, E4
2.	Plant height (cm)	G39	G20	G33	G20	G2, G3	G40, G27	E1, E3, E4
3.	Number of primary branches plant ⁻¹	G26	G13, G17	G33, G32	G13, G17	G9, G18	G12, G4, G31	E1, E3, E4
4.	Number of secondary branches plant ⁻¹	G3, G4	G30, G17	G30, G17	G26	G16	-	E1, E3, E5
5.	Number of capitula plant ⁻¹	G18, G32	G4	G2, G30	G15, G25, G26	G15, G25, G26	G31, G13	E1, E2, E3, E4
6.	Capitulum diameter (cm)	G1	G8	G28, G33	G20, G26, G19	G28, G33	G24	E1, E3, E4
7.	Number of seeds capitulum ⁻¹	G9, G12	G9, G12	G27	G22	G22	G10, G19, G24	E1, E2, E3, E4
8.	1000 seed weight (g)	G26, G16	G28, G29	G26, G16	G27, G21	G28, G29	-	E2, E3, E4
9.	Seed yield plant ⁻¹ (g)	G38	G38	G32	G5, G8	G28, G18	G25, G11, G18	E1, E3, E4
10.	Seed yield plot ⁻¹ (g)	G14	G8	G6	G17, G23	G25, G1	G20, G27, G8	E1, E3, E4
11.	Days to maturity	G4, G34	G4, G34	G31	G22, G9	G31	G2, G5	E1, E3, E4
12.	Oil content (%)	G16	G9	-	G35, G25	-	G22, G12, G34, G37, G14	E1, E3, E4
13.	Protein content (%)	G26	G2	G25, G20	G24	G25, G20	G4, G5	E1, E5, E4

E1: ARS, Phondaghat; E2: ARS, Shirgaon; E3: Department of Agril. Botany, Dapoli; E4: RARS, Karjat; E5: ARS, Palghar

Table 37: Summary of highly stable Niger genotypes for seed yield and other characters to overall and specific environment.

Sr. No.	Genotype code	Seed yield plot ¹ (g)	Average stable for the traits	Traits for favorable/rich environment	Traits for unfavorable/ poor environment
1.	G36	265	NPBPP, NSBPP, NCPP, CD, NSPC, 1000 SW, SYPp, SYPP, DM, OC, PC	DFPF, PH	-
2.	G24	260	DFPF, PH, NPBPP, NSBPP, NCPP, NSPC, 1000 SW, SYPp, SYPP, DM, OC, PC	-	CD
3.	G32	257	PH, NPBPP, NSBPP, NCPP, CD, NSPC, SYPp, SYPP, DM, OC, PC	DM, 1000 SW	DFPF
4.	G10	257	DFPF, NPBPP, NSBPP, CD, 1000 SW, SYPp, SYPP, DM, OC, PC	NCPP	PH, NSPC

DFPF: Days to 50 per cent flowering
 NCPP: No. of capitula plant⁻¹
 SYPp: Seed yield plant⁻¹
 PC: Protein content

PH: Plant height
 CD: Capitulum diameter
 SYPP: Seed yield plot⁻¹

NPBPP: No. of primary branches plant⁻¹
 NSPC: No. of seeds capitulum⁻¹
 DM: Days to maturity

NSBPP: No. of secondary branches plant⁻¹
 SW: Seed weight
 OC: Oil content

CHAPTER - VI

SUMMARY AND CONCLUSION

The present investigation entitled “**Genetic variability, diversity and stability study in Niger (*Guizotia abyssinica* L.)**” through different biometrical techniques was undertaken at five environments *viz.*, ARS, Phondaghat (E1); ARS, Shirgaon (E2); Department of Agril. Botany, Dapoli (E3); RARS, Karjat (E4) and ARS, Palghar (E5) during *Kharif* 2018 and *Kharif* 2019.

The principles of the investigation were,

1. To study the nature and extent of genetic variability in yield and yield contributing traits,
2. To measure the divergence between different genotypes by D² statistics,
3. To study the stability of Niger genotypes under different environments, and
4. To study the G x E interaction for yield and yield contributing traits.

The material for the present study comprised of forty genotypes of niger collected from all over Maharashtra state. Evaluation of these collected genotypes of niger grown in Randomized Block Design with three replications was done during *Kharif* 2018 and *Kharif*, 2019. The genetic variability, genetic parameters, gene action, genetic diversity, genotype x environment interaction and stability for thirteen yield and yield contributing traits were assessed.

The observations were recorded on 13 characters *viz.*, days to 50 per cent flowering, plant height (cm), number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of capitula plant⁻¹, capitulum diameter (cm), number of seeds capitulum⁻¹, 1000 seed weight (g), seed yield plant⁻¹ (g), seed yield plot⁻¹ (g), days to maturity, oil content (%), protein content (%) etc. The results are summarized in this chapter.

The important findings are given below:

1. Sufficient variability was present among the genotypes studied for all the traits in this study except capitulum diameter and 1000 seed weight.

2. On overall mean basis, among all, G36, G24, G32, G40, G38, G10, G4 were recorded highest mean performance in most of the characters *viz.*, number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of capitula plant⁻¹ (%), capitulum diameter (cm), number seeds capitulum⁻¹, 1000 seed weight (g), seed yield plant⁻¹ (g), seed yield plot⁻¹ (g), oil content (%) and protein content (%). The genotypes G24, G25 and G26 were early. The G1, G10, G28, G32, G36, G39 and G40 were mid-late genotypes. The genotypes, G2, G4, G8, G9 and G35 were late.
3. The phenotypic coefficient of variation was slightly more than genotypic coefficient of variation for all the traits, indicating the role of environment in the expression of these traits.
4. Heritability in broad sense was highest for days to 50 per cent flowering followed by number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of capitula plant⁻¹, capitulum diameter and days to maturity indicating these traits were least influenced by environments and selection for improvement of such characters may be useful.
5. The highest genetic advance and genetic advance per cent mean was observed in seed yield plant⁻¹, seed yield plot⁻¹, number of capitula plant⁻¹ and number of seeds capitula⁻¹. These traits were governed by additive genes and selection for improvement is beneficial for these traits.
6. Most of the yield contributing traits exhibited high heritability coupled with high genetic advance and which were under control of additive gene action, indicating more effective if the selection in the present material could be rigorously applied.
7. On overall basis, inter and intra-cluster distance coupled with cluster means of different traits, the genotypes classified in clusters IV, V and III in E1; clusters III and IV in E2; clusters II and IV in E3; clusters VIII, III, VI and VII in E4, and III and IV in E5 were found to be superior and genotypes from that clusters should utilized for hybridization program to achieve novel recombinants.

8. Among all, G1, G2, G4, G8, G9, G10, G24, G25, G26, G28, G32, G35, G36, G39 and G40 were identified as diverse in all tested environments as per D^2 statistics and these were suggested as potential parents in future crop improvement programme.
9. The highest contributors towards the genetic divergence were days to 50 per cent flowering, number of primary and secondary branches plant⁻¹, number of capitula plant⁻¹ and capitulum diameter.
10. The combined analysis of variance was highly significant for genotype, environment and their interaction (GEI) for all the traits except capitulum diameter and 1000 seed weight.
11. The analysis of variance for AMMI model due to genotype, environment and their interaction (GEI), IPCA1, IPCA2 and IPCA3 were highly significant for all the characters under study.
12. The study of both Regression and AMMI stability model, among all, genotypes, G36, G32, G24 and G10 were noticed the most stable and ideal genotypes with highest mean seed yield and maximum additive main effect with least interaction between genotype x environment.
13. On overall, the genotypes located on vertex of GGE biplot polygon, G25 and G1 were the best at E1; G8 was classiest at E2; G6 was the excellent at E3; G23 and G17 were the pre-eminent in E4, and G14 was the winning genotype at E5, suggesting highest interaction between genotype and environment for seed yield plot⁻¹. While no any environment felt in genotypes, G20, G27 and G8 located on the vertices of the polygon performed either the best or the poorest in one or more environments.
14. The genotypes, G6, G8, G22 and G28 were suitable for favorable/rich environments while G2, G4, G7, G23 and G31 for unfavorable/poor environments in most of the traits. The genotypes, G4, G17, G25 and G28 were best performers in some environments for few yield contributing traits. These genotypes behaved as a potential breeding materials stock for future crop

improvement programme.

15. The consideration of overall data of stability parameters (IPCA scores) and AMMI GGE biplots, two different mega-environments (METs) were identified, the first MET consists E1, E3 and E4 which are potential and favorable sites for discrimination of genotypes and second MET includes E2 and E5 were stable places for most of the characters.

Conclusion

From the present study it was concluded that, the high estimates of genotypic coefficient of variation among the genotypes indicated sufficient amount of variability for the characters *viz.*, number of primary and secondary branches plant⁻¹, number of capitula plant⁻¹, number of seeds capitulum⁻¹, seed yield plant⁻¹ and seed yield plot⁻¹. Most of the yield and yield contributing traits showed high estimates of genetic advance and genetic advance per cent mean. High heritability coupled with high genetic advance indicated preponderance of additive gene action in the inheritance of most of the yield contributing traits and these were used for future crop improvement. On the basis of intra and inter cluster distances, cluster mean and *per se* performance, the genotypes *viz.*, G1, G2, G4, G8, G9, G10, G24, G25, G26, G28, G32, G35, G36, G39 and G40 were found to be superior. These genotypes may be used in future hybridization programme. The yield performance of Niger genotypes was highly influenced by GE interaction effects. Environments, E1, E3 and E4 which are potential and excellent sites for discrimination of superior genotypes among all tested environments. The study of stability parameters *viz.*, high mean, regression coefficient (bi), deviation from regression (S²di), IPCA1 scores, ASV, GSI revealed that the genotypes, G36, G32, G24 and G10 were found highly stable for yield and yield contributing traits over the seasons and the environments. Therefore, these four genotypes were identified as candidate genotypes and are recommended for future investigations.

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*Original not seen.

APPENDIX – I

Metrological data of Agriculture Research Station, Phondaghat for *Kharif*, 2018

Months Parameter		MONTHLY WEATHER DATA 2018 (Kharif season)							
		June	July	Aug.	Sep.	Oct.	Nov.	Mean	Total / Range
No. of rainy days		29	30	26	15	09	05	19.0	114
Total Rainfall (mm)		1091	1384	855.4	239	113	8.3	614.9	3689.5
Avg. Max. Temp. (°C)		33.1	29.5	29.5	30.2	33.0	35.5	26.9	29.5-35.5
Avg. Min. Temp. (° C)		24.0	22.1	22.4	22.8	21.8	17.9	21.8	17.9- 24.4
Humidity (%)	Morning	89.8	95.5	96.9	96.5	88.1	61.3	88.0	61.3- 96.9
	Evening	71.7	88.3	89.3	88.6	64.8	40.1	58.9	40.1-89.3

WEATHER DATA DURING GROWTH PERIOD <i>Kharif</i> 2018							
Met. Week No.	Metrological Period	Rainfall (mm)	Rainy days	Max. Temp. (°C)	Mini. Temp. (°C)	Humidity (%)	
						Morning	Evening
21	21-05-18 to 27-05-18	0.0	0.0	37.9	26.3	79.1	49.7
22	28-05-18 to 03-06-18	13.8	2	38.1	24.7	82.4	47.3
23	04-06-18 to 10-06-18	319.5	5	34.1	24.1	93.4	71.0
24	11-06-18 to 17-06-18	169.5	7	30.4	23.9	92.6	82.7
25	18-06-18 to 24-06-18	237.3	7	30.2	23.0	95.4	89.4
26	25-06-18 to 01-07-18	350.5	6	28.2	22.2	95.9	90.6
27	02-07-18 to 08-07-18	407.9	7	29.2	23.7	95.9	91.9
28	09-07-18 to 15-07-18	475.9	7	28.5	23.6	95.9	88.6
29	16-07-18 to 22-07-18	371.8	7	28.7	23.0	97.0	93.4
30	23-07-18 to 29-07-18	128.1	7	28.8	15.7	99.0	93.0
31	30-07-18 to 05-08-18	100.7	5	27.9	17.5	97.9	93.0
32	06-08-18 to 12-08-18	91.5	7	29.7	23.7	97.0	90.3
33	13-08-18 to 19-08-18	242.9	7	30.0	24.1	96.3	82.6
34	20-08-18 to 26-08-18	203.6	7	30.9	23.5	98.4	87.7
35	27-08-18 to 02-09-18	216.7	7	29.1	23.5	94.9	93.3
36	03-09-18 to 09-09-18	68.7	6	31.1	22.7	93.3	87.9
37	10-09-18 to 16-09-18	10.2	1	30.6	23.1	96.3	85.4
38	17-09-18 to 23-09-18	85.6	2	28.8	22.6	98.1	94.6
39	24-09-18 to 30-09-18	74.0	3	30.6	22.8	98.4	86.8
40	01-10-18 to 07-10-18	6.1	2	30.6	22.1	94.6	81.7
41	09-10-18 to 14-10-18	73.3	2	31.7	23.4	94.4	78.6
42	15-10-18 to 21-10-18	6.6	3	35.5	20.8	82.0	51.1
43	22-10-18 to 28-10-18	27.0	2	34.3	21.0	81.6	47.9
44	29-10-18 to 04-11-18	3.0	1	35.7	19.6	62.9	41.6
45	05-11-18 to 11-11-18	2.0	1	34.0	16.1	70.4	32.4
46	12-11-18 to 18-11-18	0.0	0	35.6	19.6	70.7	46.0
47	19-11-18 to 25-11-18	3.3	3	35.5	18.0	48.9	31.4
48	26-11-18 to 02-12-18	0.0	0	36.6	16.2	53.9	49.0
Total / Average		3689.5	114	31.9	22.0	87.7	73.5

APPENDIX – II

Metrological data of Agriculture Research Station, Shirgaon for *Kharif*, 2018

Months Parameter		MONTHLY WEATHER DATA 2018 (Kharif season)							
		June	July	Aug.	Sep.	Oct.	Nov.	Mean	Total / Range
No. of rainy days		35	24	28	2	2	0	14.2	91
Total Rainfall (mm)		2055.9	666.6	407.3	45.2	50.3	0.0	536.8	3225.3
Avg. Max. Temp. (°C)		31.6	30.2	29.7	31.7	35.1	35.8	32.4	29.7-35.8
Avg. Min. Temp. (° C)		24.9	24.8	24.4	23.2	23.1	21.0	23.6	21.0-26.5
Humidity (%)	Morning	93.3	91.5	95.4	96.2	92.6	90.0	92.9	88.4-96.2
	Evening	91.0	90.8	90.8	89.0	81.4	61.2	83.8	61.2-91.0

WEATHER DATA DURING GROWTH PERIOD <i>Kharif</i> 2018							
Met. Week No.	Metrological Period	Rainfall (mm)	Rainy days	Max. Temp. (°C)	Mini. Temp. (°C)	Humidity (%)	
						Morning	Evening
21	21-05-18 to 27-05-18	0.0	0.0	36.8	27.1	90.3	86.7
22	28-05-18 to 03-06-18	23.6	4.0	35.0	27.8	92.9	90.7
23	04-06-18 to 10-06-18	1014.2	7.0	31.1	24.8	91.4	92.9
24	11-06-18 to 17-06-18	166.5	7.0	32.8	25.5	95.6	87.6
25	18-06-18 to 24-06-18	697.2	7.0	29.1	23.4	93.3	93.3
26	25-06-18 to 01-07-18	240.4	7.0	30.9	24.2	93.6	92.3
27	02-07-18 to 08-07-18	174.0	5.0	30.3	24.3	91.0	91.9
28	09-07-18 to 15-07-18	239.9	3.0	30.0	24.5	91.1	92.6
29	16-07-18 to 22-07-18	130.8	5.0	29.5	24.8	91.6	89.3
30	23-07-18 to 29-07-18	24.7	7.0	30.5	25.6	92.6	86.4
31	30-07-18 to 05-08-18	61.7	7.0	30.5	25.4	93.3	95.1
32	06-08-18 to 12-08-18	77.4	5.0	30.2	24.7	95.3	89.7
33	13-08-18 to 19-08-18	82.9	7.0	28.8	24.0	95.9	91.4
34	20-08-18 to 26-08-18	141.1	6.0	29.5	24.0	96.1	93.3
35	27-08-18 to 02-09-18	60.8	5.0	30.3	24.2	95.4	85.9
36	03-09-18 to 09-09-18	19.8	1.0	30.6	23.4	95.4	88.0
37	10-09-18 to 16-09-18	0.0	0.0	31.7	22.7	96.3	89.0
38	17-09-18 to 23-09-18	18.6	1.0	31.4	23.4	95.9	92.4
39	24-09-18 to 30-09-18	0.0	0.0	33.3	23.0	97.1	86.9
40	01-10-18 to 07-10-18	0.0	0.0	35.6	24.7	92.9	83.7
41	09-10-18 to 14-10-18	26.0	1.0	34.0	24.5	96.3	86.9
42	15-10-18 to 21-10-18	24.3	1.0	34.2	23.7	96.1	84.1
43	22-10-18 to 28-10-18	0.0	0.0	36.2	21.6	94.3	78.6
44	29-10-18 to 04-11-18	0.0	0.0	36.4	20.8	84.0	67.0
45	05-11-18 to 11-11-18	0.0	0.0	36.1	23.7	94.9	76.1
46	12-11-18 to 18-11-18	0.0	0.0	35.9	20.6	83.7	61.9
47	19-11-18 to 25-11-18	0.0	0.0	34.9	21.0	91.3	60.9
48	26-11-18 to 02-12-18	0.0	0.0	35.4	16.9	80.7	33.9
Total / Average		3225.3	91	32.4	23.6	92.9	83.8

APPENDIX – III

Metrological data of Department of Agril Botany, Dapoli for *Kharif*, 2018

Months Parameter	MONTHLY WEATHER DATA 2018 (<i>Kharif season</i>)							
	June	July	Aug.	Sep.	Oct.	Nov.	Mean	Total / Range
No. of rainy days	23	27	34	10	04	0.0	16.34	98
Total Rainfall (mm)	1090.6	1098.9	722.4	117.5	37.0	0.0	510.97	3065.8
Avg. Max. Temp. (°C)	30.82	27.88	27.64	29.68	33.64	33.98	30.7	26.7-34.6
Avg. Min. Temp. (°C)	23.8	23.6	23.3	21.85	20.34	16.8	21.8	14.0-25.4
Humidity (%)	Morning	94.6	97.25	94.8	90.0	89.2	88.25	92.4
	Evening	89.2	95.0	91.6	80.5	65.2	66.03	81.0

WEATHER DATA DURING GROWTH PERIOD <i>Kharif</i> 2018							
Met. Week No.	Metrological Period	Rainfall (mm)	Rainy days	Max. Temp. (°C)	Mini. Temp. (°C)	Humidity (%)	
						Morning	Evening
21	21-05-18 to 27-05-18	0.0	0.0	33.7	24.5	90	71
22	28-05-18 to 03-06-18	10.2	1.0	33.9	25.4	89	76
23	04-06-18 to 10-06-18	135.2	5.0	32.2	23.6	95	89
24	11-06-18 to 17-06-18	96.6	4.0	31.2	24.5	97	90
25	18-06-18 to 24-06-18	642.8	6.0	28.4	22.4	96	96
26	25-06-18 to 01-07-18	205.9	7.0	28.4	23.1	96	95
27	02-07-18 to 08-07-18	545.4	7.0	28.1	22.9	98	96
28	09-07-18 to 15-07-18	316.9	7.0	27.7	23.6	99	95
29	16-07-18 to 22-07-18	203.4	7.0	27.7	23.7	98	95
30	23-07-18 to 29-07-18	33.2	6.0	28.0	24.2	94	94
31	30-07-18 to 05-08-18	100.6	6.0	28.3	24.1	93	90
32	06-08-18 to 12-08-18	92.0	7.0	28.1	23.9	96	90
33	13-08-18 to 19-08-18	194.4	7.0	26.7	23.1	97	94
34	20-08-18 to 26-08-18	205.6	7.0	27.1	22.8	96	92
35	27-08-18 to 02-09-18	129.8	7.0	28.0	22.6	92	92
36	03-09-18 to 09-09-18	52.2	6.0	28.3	22.0	91	85
37	10-09-18 to 16-09-18	0.0	0.0	29.5	20.8	87	81
38	17-09-18 to 23-09-18	49.2	2.0	29.8	22.1	89	79
39	24-09-18 to 30-09-18	15.4	2.0	31.1	22.5	93	77
40	01-10-18 to 07-10-18	28.2	3.0	34.1	21.7	91	64
41	09-10-18 to 14-10-18	0.0	0.0	33.2	22.5	90	73
42	15-10-18 to 21-10-18	8.8	1.0	33.4	21.0	90	69
43	22-10-18 to 28-10-18	0.0	0.0	33.9	19.5	89	60
44	29-10-18 to 04-11-18	0.0	0.0	33.6	17.0	86	60
45	05-11-18 to 11-11-18	0.0	0.0	34.6	19.6	85	68
46	12-11-18 to 18-11-18	0.0	0.0	34.6	15.2	90	65
47	19-11-18 to 25-11-18	0.0	0.0	33.5	18.4	88	65
48	26-11-18 to 02-12-18	0.0	0.0	33.2	14.0	90	66.1
Total / Average		3065.8	98	30.7	21.8	92.4	81.0

APPENDIX – IV

Metrological data of Regional Agriculture Research Station, Karjat for *Kharif*, 2018

Months Parameter		MONTHLY WEATHER DATA 2018 (Kharif season)							
		June	July	Aug.	Sep.	Oct.	Nov.	Mean	Total / Range
No. of rainy days		18	26	28	10	02	11	15.83	87.00
Total Rainfall (mm)		885.7	1605.4	752.5	199.7	21.8	207.1	612.03	3558.3
Avg. Max. Temp. (°C)		32.70	28.55	29.03	30.92	35.53	31.91	31.44	28.55-35.53
Avg. Min. Temp. (° C)		25.01	24.08	23.70	22.96	24.70	23.75	24.03	22.96- 25.01
Humidity (%)	Morning	86.73	90.48	91.42	90.50	88.35	93.60	90.18	86.73- 91.42
	Evening	69.23	88.03	82.19	66.23	44.90	68.60	69.86	44.90-88.03

WEATHER DATA DURING GROWTH PERIOD <i>Kharif</i> 2018							
Met. Week No.	Metrological Period	Rainfall (mm)	Rainy days	Max. Temp. (°C)	Mini. Temp. (°C)	Humidity (%)	
						Morning	Evening
21	21-05-18 to 27-05-18	0.0	0.0	39.3	26.9	67.1	39.0
22	28-05-18 to 03-06-18	1.3	0.0	38.5	27.3	73.4	45.6
23	04-06-18 to 10-06-18	60.0	3.0	35.1	25.4	87.0	62.0
24	11-06-18 to 17-06-18	39.7	4.0	33.5	25.9	82.6	64.0
25	18-06-18 to 24-06-18	386.9	5.0	31.3	23.8	89.6	77.4
26	25-06-18 to 01-07-18	417.0	7.0	29.3	24.0	91.9	82.3
27	02-07-18 to 08-07-18	616.4	6.0	28.4	23.5	93.4	94.9
28	09-07-18 to 15-07-18	540.5	7.0	27.6	23.8	92.6	91.1
29	16-07-18 to 22-07-18	396.6	7.0	28.2	24.0	91.7	89.7
30	23-07-18 to 29-07-18	30.8	5.0	28.7	24.9	86.3	83.6
31	30-07-18 to 05-08-18	98.5	5.0	29.8	24.5	86.1	82.6
32	06-08-18 to 12-08-18	77.3	7.0	29.4	24.4	87.1	86.4
33	13-08-18 to 19-08-18	246.9	7.0	27.7	23.6	93.3	88.3
34	20-08-18 to 26-08-18	330.9	7.0	27.8	23.3	95.6	86.0
35	27-08-18 to 02-09-18	90.8	6.0	29.0	23.5	95.0	73.9
36	03-09-18 to 09-09-18	59.6	4.0	29.9	23.4	90.4	70.3
37	10-09-18 to 16-09-18	5.2	1.0	31.0	21.9	87.9	63.1
38	17-09-18 to 23-09-18	47.7	2.0	31.8	22.4	89.7	65.1
39	24-09-18 to 30-09-18	61.4	1.0	32.8	23.3	92.4	65.4
40	01-10-18 to 07-10-18	8.4	1.0	35.2	23.4	90.1	52.9
41	09-10-18 to 14-10-18	0.0	0.0	35.2	23.9	92.4	54.4
42	15-10-18 to 21-10-18	13.4	1.0	35.6	22.0	87.6	45.9
43	22-10-18 to 28-10-18	0.0	0.0	34.8	19.2	88.0	34.1
44	29-10-18 to 04-11-18	0.2	0.0	35.5	17.2	80.0	37.1
45	05-11-18 to 11-11-18	27.6	1.0	35.4	18.9	86.1	33.4
46	12-11-18 to 18-11-18	0.0	0.0	36.1	16.2	88.1	31.6
47	19-11-18 to 25-11-18	1.2	0.0	36.2	19.0	91.0	36.3
48	26-11-18 to 02-12-18	0.0	0.0	35.0	14.8	91.7	27.3
Total / Average		3558.3	87.0	34.5	20.6	82.8	46.0

APPENDIX – V

Metrological data of Agriculture Research Station, Palghar for *Kharif*, 2018

Months Parameter		MONTHLY WEATHER DATA 2018 (Kharif season)							
		June	July	Aug.	Sep.	Oct.	Nov.	Mean	Total / Range
No. of rainy days		12	21	21	04	00	00	9.67	58
Total Rainfall (mm)		679.1	1453.4	192.8	26.0	0.0	0.0	391.89	2351.3
Avg. Max. Temp. (°C)		32.84	29.18	29.7	30.98	35.12	35.1	32.26	28.4-38.8
Avg. Min. Temp. (° C)		27.06	25.2	25.48	24.1	22.54	19.15	24.15	17.4-28.2
Humidity (%)	Morning	83.22	90.18	89.06	87.33	80.64	83.3	85.24	64.5-92.0
	Evening	74.02	89.38	82.58	74.75	49.98	41.33	68.68	32.8-91.8

WEATHER DATA DURING GROWTH PERIOD <i>Kharif</i> 2018							
Met. Week No.	Metrological Period	Rainfall (mm)	Rainy days	Max. Temp. (°C)	Mini. Temp. (°C)	Humidity (%)	
						Morning	Evening
21	21-05-18 to 27-05-18	0.0	0	33.9	26.9	79.8	68.1
22	28-05-18 to 03-06-18	0.0	0	34.0	27.4	80.1	66.1
23	04-06-18 to 10-06-18	0.0	0	34.4	28.2	80.4	70.5
24	11-06-18 to 17-06-18	43.0	3	33.4	28.1	85.1	74.0
25	18-06-18 to 24-06-18	191.4	3	32.3	26.5	84.1	77.4
26	25-06-18 to 01-07-18	445.0	6	30.1	25.1	86.4	82.1
27	02-07-18 to 08-07-18	512.6	7	29.9	24.8	92.0	89.5
28	09-07-18 to 15-07-18	699.8	7	28.4	25.0	91.5	91.8
29	16-07-18 to 22-07-18	229.0	6	29.0	25.0	91.0	89.4
30	23-07-18 to 29-07-18	12.0	1	29.4	26.0	86.2	86.8
31	30-07-18 to 05-08-18	42.0	3	30.1	26.0	87.4	81.0
32	06-08-18 to 12-08-18	38.4	4	29.7	25.8	87.1	86.8
33	13-08-18 to 19-08-18	55.4	6	29.4	25.6	90.7	84.5
34	20-08-18 to 26-08-18	42.6	6	29.6	25.1	91.1	82.0
35	27-08-18 to 02-09-18	14.4	2	29.7	24.9	89.0	78.8
36	03-09-18 to 09-09-18	16.4	3	30.1	24.5	87.4	77.8
37	10-09-18 to 16-09-18	9.6	1	30.3	23.0	86.5	77.8
38	17-09-18 to 23-09-18	0.0	0	31.1	24.4	87.4	71.0
39	24-09-18 to 30-09-18	0.0	0	32.4	24.5	88.0	72.4
40	01-10-18 to 07-10-18	0.0	0	35.5	25.1	81.8	60.5
41	09-10-18 to 14-10-18	0.0	0	34.4	23.8	89.7	63.8
42	15-10-18 to 21-10-18	0.0	0	34.6	23.0	85.0	58.0
43	22-10-18 to 28-10-18	0.0	0	35.4	20.1	82.2	33.8
44	29-10-18 to 04-11-18	0.0	0	35.7	20.7	64.5	33.8
45	05-11-18 to 11-11-18	0.0	0	34.5	20.6	84.4	42.1
46	12-11-18 to 18-11-18	0.0	0	38.8	18.3	83.1	46.2
47	19-11-18 to 25-11-18	0.0	0	33.6	20.3	85.5	44.2
48	26-11-18 to 02-12-18	0.0	0	33.5	17.4	80.2	32.8
Total / Average		2351.6	58	32.3	24.1	85.3	68.7

APPENDIX – VI

Metrological data of Agriculture Research Station, Phondaghat for *Kharif*, 2019

Months Parameter		MONTHLY WEATHER DATA 2019 (Kharif season)							
		June	July	Aug.	Sep.	Oct.	Nov.	Mean	Total / Range
No. of rainy days		31	30	31	18	16	00	21.0	126
Total Rainfall (mm)		1719	1850	1360	327	54.1	0.00	893.0	5358
Avg. Max. Temp. (°C)		33.4	27.5	29.0	28.7	31.4	34.2	30.7	27.5-34.2
Avg. Min. Temp. (° C)		24.1	23.2	23.3	22.2	22.5	22.3	22.9	22.2- 24.1
Humidity (%)	Morning	87.7	94.8	94.9	93.9	92.6	78.5	90.4	78.5- 94.9
	Evening	73.8	94.1	87.9	84.9	80.5	61.4	80.4	61.4-94.1

WEATHER DATA DURING GROWTH PERIOD <i>Kharif</i> 2019							
Met. Week No.	Metrological Period	Rainfall (mm)	Rainy days	Max. Temp. (°C)	Mini. Temp. (°C)	Humidity (%)	
						Morning	Evening
21	21-05-19 to 27-05-19	172.1	7.0	37.8	24.1	83.3	63.7
22	28-05-19 to 03-06-19	519.8	7.0	37.7	24.5	83.1	67.1
23	04-06-19 to 10-06-19	359.0	7.0	35.1	23.5	90.1	62.6
24	11-06-19 to 17-06-19	431.7	7.0	32.3	25.9	89.6	74.0
25	18-06-19 to 24-06-19	236.7	8.0	29.1	24.4	89.1	83.1
26	25-06-19 to 01-07-19	411.4	7.0	28.2	22.4	90.9	92.3
27	02-07-19 to 08-07-19	534.6	9.0	28.0	22.9	92.6	91.1
28	09-07-19 to 15-07-19	647.2	7.0	27.0	23.3	96.0	92.3
29	16-07-19 to 22-07-19	122.2	7.0	28.6	23.3	93.0	94.0
30	23-07-19 to 29-07-19	134.6	9.0	26.2	23.2	97.7	98.9
31	30-07-19 to 05-08-19	136.7	7.0	26.8	23.1	96.7	94.0
32	06-08-19 to 12-08-19	634.4	7.0	27.1	23.1	98.3	92.7
33	13-08-19 to 19-08-19	159.8	6.0	29.5	23.8	89.1	84.1
34	20-08-19 to 26-08-19	127.3	6.0	32.6	23.2	93.6	80.9
35	27-08-19 to 02-09-19	301.6	4.0	29.1	23.4	96.6	87.9
36	03-09-19 to 09-09-19	28.1	3.0	25.9	19.9	97.6	96.9
37	10-09-19 to 16-09-19	108.6	6.0	28.6	23.3	89.9	86.3
38	17-09-19 to 23-09-19	117.7	4.0	28.3	23.0	97.1	78.1
39	24-09-19 to 30-09-19	72.1	5.0	32.1	22.5	90.9	78.1
40	01-10-19 to 07-10-19	12.0	4.0	33.1	23.0	96.9	78.4
41	09-10-19 to 14-10-19	52.1	7.0	32.0	22.2	94.9	79.0
42	15-10-19 to 21-10-19	20.0	5.0	31.3	23.2	88.9	82.4
43	22-10-19 to 28-10-19	0.0	0.0	29.3	21.7	89.7	82.0
44	29-10-19 to 04-11-19	0.0	0.0	34.3	23.8	77.4	64.3
45	05-11-19 to 11-11-19	0.0	0.0	33.6	22.0	88.7	63.3
46	12-11-19 to 18-11-19	0.0	0.0	34.3	21.8	80.3	65.4
47	19-11-19 to 25-11-19	0.0	0.0	34.6	21.7	77.9	58.1
48	26-11-19 to 02-12-19	0.0	0.0	34.0	22.0	68.4	55.7
Total / Average		5358	126	27.6	20.6	77.5	62.2

APPENDIX – VII

Metrological data of Agriculture Research Station, Shirgaon for *Kharif*, 2019

Months Parameter		MONTHLY WEATHER DATA 2019 (Kharif season)							
		June	July	Aug.	Sep.	Oct.	Nov.	Mean	Total / Range
No. of rainy days		19	31	26	24	11	0	17.5	110
Total Rainfall (mm)		674.1	1281.3	774.9	875.9	269.9	1.2	646.2	3877.3
Avg. Max. Temp. (°C)		32.7	30.8	30.3	30.2	32.1	34.1	31.7	28.2-35.5
Avg. Min. Temp. (° C)		25.7	24.0	24.5	23.9	23.2	22.3	23.9	17.3-27.6
Humidity (%)	Morning	86.5	90.6	90.0	93.8	93.0	89.8	90.6	78.4-95.1
	Evening	75.6	84.1	81.6	81.5	73.8	59.0	75.9	46.9-90.0

WEATHER DATA DURING GROWTH PERIOD <i>Kharif</i> 2019							
Met. Week No.	Metrological Period	Rainfall (mm)	Rainy days	Max. Temp. (°C)	Mini. Temp. (°C)	Humidity (%)	
						Morning	Evening
21	21-05-19 to 27-05-19	459.0	6.0	37.8	27.1	75.3	43.7
22	28-05-19 to 03-06-19	102.9	7.0	32.9	26.6	78.4	64.7
23	04-06-19 to 10-06-19	276.0	7.0	34.4	27.6	85.0	65.0
24	11-06-19 to 17-06-19	245.8	7.0	33.0	25.7	86.5	80.5
25	18-06-19 to 24-06-19	552.0	7.0	31.9	24.6	90.8	76.8
26	25-06-19 to 01-07-19	527.2	7.0	30.8	23.9	89.9	84.8
27	02-07-19 to 08-07-19	95.0	7.0	31.3	25.1	89.4	80.5
28	09-07-19 to 15-07-19	96.4	7.0	30.6	24.0	89.3	87.3
29	16-07-19 to 22-07-19	50.5	7.0	31.0	23.4	91.2	80.0
30	23-07-19 to 29-07-19	188.9	4.0	30.1	23.8	90.8	89.3
31	30-07-19 to 05-08-19	475.6	5.0	29.7	23.5	90.3	87.6
32	06-08-19 to 12-08-19	62.6	7.0	29.2	24.4	91.5	88.0
33	13-08-19 to 19-08-19	110.8	4.0	31.0	24.8	89.3	77.0
34	20-08-19 to 26-08-19	118.4	4.0	31.4	25.2	89.9	74.0
35	27-08-19 to 02-09-19	0.0	3.0	29.6	23.6	90.8	84.7
36	03-09-19 to 09-09-19	29.2	0.0	28.2	23.3	93.8	90.0
37	10-09-19 to 16-09-19	51.5	4.0	31.1	24.9	92.8	80.4
38	17-09-19 to 23-09-19	189.2	5.0	30.9	24.1	94.8	77.1
39	24-09-19 to 30-09-19	1.2	0.0	30.9	23.5	94.3	76.1
40	01-10-19 to 07-10-19	0.0	0.0	32.0	24.0	92.4	69.0
41	09-10-19 to 14-10-19	0.0	0.0	32.2	23.2	92.9	69.0
42	15-10-19 to 21-10-19	0.0	0.0	33.6	24.0	93.7	76.4
43	22-10-19 to 28-10-19	0.0	0.0	29.7	21.8	93.5	84.9
44	29-10-19 to 04-11-19	0.0	0.0	33.6	22.9	91.8	70.6
45	05-11-19 to 11-11-19	0.0	0.0	32.2	22.6	95.1	64.9
46	12-11-19 to 18-11-19	0.0	0.0	34.5	22.0	89.5	58.3
47	19-11-19 to 25-11-19	0.0	0.0	35.5	23.4	88.9	53.3
48	26-11-19 to 02-12-19	0.0	0.0	35.0	20.7	84.9	46.9
Total / Average		3878.3	110	31.81	22.46	89.15	64.48

APPENDIX – VIII

Metrological data of Department of Agril Botany, Dapoli for *Kharif*, 2019

Months Parameter		MONTHLY WEATHER DATA 2019 (Kharif season)							
		June	July	Aug.	Sep.	Oct.	Nov.	Mean	Total / Range
No. of rainy days		17	27	33	23	10	02	18.67	112
Total Rainfall (mm)		737.9	1571.4	1607.6	1047.2	154.6	12.2	855.15	5130.9
Avg. Max. Temp. (°C)		32.18	28.85	28.14	28.40	30.96	32.65	30.4	26.5-34.5
Avg. Min. Temp. (° C)		24.66	23.95	23.40	23.60	21.88	20.03	23.0	18.9-25.9
Humidity (%)	Morning	89.4	96.25	96.2	96.0	91.8	91.73	93.1	81.0-99.0
	Evening	74.8	90.75	89.0	89.25	73.0	58.1	78.2	51.4-96.0

WEATHER DATA DURING GROWTH PERIOD <i>Kharif</i> 2019							
Met. Week No.	Metrological Period	Rainfall (mm)	Rainy days	Max. Temp. (°C)	Mini. Temp. (°C)	Humidity (%)	
						Morning	Evening
21	21-05-19 to 27-05-19	0.0	0.0	33.9	23.7	83	56
22	28-05-19 to 03-06-19	0.0	0.0	34.0	23.9	81	57
23	04-06-19 to 10-06-19	10.0	1.0	34.5	25.9	86	61
24	11-06-19 to 17-06-19	110.4	5.0	32.6	25.1	91	81
25	18-06-19 to 24-06-19	162.3	5.0	31.1	24.2	94	84
26	25-06-19 to 01-07-19	455.2	6.0	28.7	24.2	95	91
27	02-07-19 to 08-07-19	294.2	7.0	29.1	24.2	95	89
28	09-07-19 to 15-07-19	399.4	7.0	29.1	23.9	98	92
29	16-07-19 to 22-07-19	118.2	6.0	29.6	24.1	94	86
30	23-07-19 to 29-07-19	759.6	7.0	27.6	23.6	98	96
31	30-07-19 to 05-08-19	719.2	7.0	26.9	23.5	98	96
32	06-08-19 to 12-08-19	353.8	7.0	27.2	24.6	96	93
33	13-08-19 to 19-08-19	112.6	7.0	29.1	24.3	95	86
34	20-08-19 to 26-08-19	103.6	6.0	29.1	20.9	95	83
35	27-08-19 to 02-09-19	318.4	6.0	28.4	23.7	97	87
36	03-09-19 to 09-09-19	771.6	7.0	26.5	23.1	99	96
37	10-09-19 to 16-09-19	167.2	7.0	28.3	23.8	97	90
38	17-09-19 to 23-09-19	53.4	6.0	29.1	24.1	95	86
39	24-09-19 to 30-09-19	55.0	3.0	29.7	23.4	93	85
40	01-10-19 to 07-10-19	0.2	0.0	30.7	22.7	92	75
41	09-10-19 to 14-10-19	29.8	2.0	31.7	19.8	94	71
42	15-10-19 to 21-10-19	63.4	3.0	31.7	23.0	89	73
43	22-10-19 to 28-10-19	61.2	5.0	28.8	21.9	94	79
44	29-10-19 to 04-11-19	2.6	1.0	31.9	22.0	90	67
45	05-11-19 to 11-11-19	9.6	1.0	31.0	21.5	94	71
46	12-11-19 to 18-11-19	0.0	0.0	33.3	20.6	89	55
47	19-11-19 to 25-11-19	0.0	0.0	33.0	19.1	93	55
48	26-11-19 to 02-12-19	0.0	0.0	33.3	18.9	90.9	51.4
Total / Average		5130.9	112.0	30.4	23.0	93.1	78.2

APPENDIX – IX

Metrological data of Regional Agriculture Research Station, Karjat for *Kharif*, 2019

Months Parameter		MONTHLY WEATHER DATA 2019 (Kharif season)							
		June	July	Aug.	Sep.	Oct.	Nov.	Mean	Total / Range
No. of rainy days		11	28	26	25	14	1	17.5	105
Total Rainfall (mm)		536.8	1985.2	1111.5	1267.4	293.7	2.6	866.2	5197.2
Avg. Max. Temp. (°C)		34.29	29.54	29.47	29.28	32.22	33.72	31.42	29.28-34.29
Avg. Min. Temp. (° C)		25.97	24.20	24.45	23.59	22.72	20.91	23.64	20.91- 25.97
Humidity (%)	Morning	81.23	91.52	90.68	92.20	90.42	90.13	89.36	81.23- 92.20
	Evening	62.27	87.03	82.48	85.63	67.68	49.10	72.37	49.10-87.03

WEATHER DATA DURING GROWTH PERIOD <i>Kharif</i> 2019							
Met. Week No.	Metrological Period	Rainfall (mm)	Rainy days	Max. Temp. (°C)	Mini. Temp. (°C)	Humidity (%)	
						Morning	Evening
21	21-05-19 to 27-05-19	18.8	2	39.6	26.2	71.9	37.9
22	28-05-19 to 03-06-19	531.4	6	39.3	26.3	70.9	39.0
23	04-06-19 to 10-06-19	469.2	7	38.0	27.4	76.6	46.7
24	11-06-19 to 17-06-19	363.4	7	33.8	25.2	80.3	65.7
25	18-06-19 to 24-06-19	43.2	5	33.6	26.0	85.3	62.9
26	25-06-19 to 01-07-19	737.2	6	29.0	24.2	88.9	86.1
27	02-07-19 to 08-07-19	978.8	7	29.0	24.2	92.1	88.6
28	09-07-19 to 15-07-19	253.6	7	30.5	24.5	91.0	82.7
29	16-07-19 to 22-07-19	54.9	6	31.8	24.7	89.0	82.3
30	23-07-19 to 29-07-19	72.7	5	28.1	24.0	93.7	91.4
31	30-07-19 to 05-08-19	128.9	5	27.7	23.5	90.3	92.6
32	06-08-19 to 12-08-19	546.5	7	28.6	25.1	89.9	89.7
33	13-08-19 to 19-08-19	345.7	7	30.1	24.6	92.0	76.3
34	20-08-19 to 26-08-19	182.4	6	30.0	24.2	92.6	77.0
35	27-08-19 to 02-09-19	104.2	3	29.9	24.3	89.0	81.9
36	03-09-19 to 09-09-19	77.4	3	28.2	23.7	91.9	90.1
37	10-09-19 to 16-09-19	90.4	4	27.8	23.5	94.6	89.1
38	17-09-19 to 23-09-19	33.7	3	29.9	23.3	91.3	85.3
39	24-09-19 to 30-09-19	92.2	4	31.4	23.8	91.0	77.0
40	01-10-19 to 07-10-19	2.6	1	32.4	23.3	91.9	70.0
41	09-10-19 to 14-10-19	0	0	33.5	22.4	93.4	60.4
42	15-10-19 to 21-10-19	0	0	31.2	21.7	86.4	74.3
43	22-10-19 to 28-10-19	0	0	31.2	23.5	91.1	71.1
44	29-10-19 to 04-11-19	0	0	33.2	23.0	90.1	57.9
45	05-11-19 to 11-11-19	0	0	32.9	22.2	92.1	56.3
46	12-11-19 to 18-11-19	0	0	34.1	20.9	89.7	44.3
47	19-11-19 to 25-11-19	0	0	34.2	19.3	88.6	43.1
48	26-11-19 to 02-12-19	0	0	34.3	19.7	88.9	45.3
Total / Average		5197.2	105	31.42	23.64	89.36	72.37

APPENDIX – X

Metrological data of Agriculture Research Station, Palghar for *Kharif*, 2019

Months Parameter		MONTHLY WEATHER DATA 2019 (Kharif season)							
		June	July	Aug.	Sep.	Oct.	Nov.	Mean	Total / Range
No. of rainy days		09	25	21	26	05	03	14.84	89
Total Rainfall (mm)		965.4	1148	781.6	1278.6	27.6	61.2	710.4	4262.4
Avg. Max. Temp. (°C)		33.12	30.48	29.82	29.98	32.5	33.3	31.66	28.7-34.0
Avg. Min. Temp. (° C)		26.52	25.3	25.5	25.3	25.2	23.24	25.20	22.5-28.2
Humidity (%)	Morning	84.16	90.08	89.26	92.28	81.84	85.65	86.63	77.2-93.8
	Evening	75.68	84.30	82.48	84.10	62.86	50.75	73.18	43.8-92.2

WEATHER DATA DURING GROWTH PERIOD <i>Kharif</i> 2019							
Met. Week No.	Metrological Period	Rainfall (mm)	Rainy days	Max. Temp. (°C)	Mini. Temp. (°C)	Humidity (%)	
						Morning	Evening
21	21-05-19 to 27-05-19	0.0	0.0	33.6	26.0	77.2	67.4
22	28-05-19 to 03-06-19	0.0	0.0	33.7	26.5	76.4	68.7
23	04-06-19 to 10-06-19	0.0	0.0	33.5	28.2	80.5	70.5
24	11-06-19 to 17-06-19	83.2	5.0	33.2	25.9	84.7	81.4
25	18-06-19 to 24-06-19	17.4	1.0	33.8	26.6	86.0	70.8
26	25-06-19 to 01-07-19	864.8	4.0	31.4	25.4	93.2	87.0
27	02-07-19 to 08-07-19	617.6	7.0	28.7	25.0	93.8	92.2
28	09-07-19 to 15-07-19	177.4	7.0	30.6	25.5	90.5	85.0
29	16-07-19 to 22-07-19	55.6	3.0	31.7	26.0	88.0	77.5
30	23-07-19 to 29-07-19	297.4	5.0	30.9	24.7	88.0	82.5
31	30-07-19 to 05-08-19	597.4	7.0	28.7	24.9	91.5	87.2
32	06-08-19 to 12-08-19	49.6	5.0	28.9	26.0	86.8	84.0
33	13-08-19 to 19-08-19	33.0	5.0	30.3	25.8	90.0	81.5
34	20-08-19 to 26-08-19	27.0	4.0	30.8	25.3	88.2	76.2
35	27-08-19 to 02-09-19	74.6	4.0	30.4	25.5	89.8	83.5
36	03-09-19 to 09-09-19	616.4	7.0	29.7	24.9	93.8	91.5
37	10-09-19 to 16-09-19	467.4	7.0	29.0	25.1	92.5	86.5
38	17-09-19 to 23-09-19	134.4	5.0	30.3	25.4	91.8	80.0
39	24-09-19 to 30-09-19	60.4	5.0	30.9	25.8	91.0	78.4
40	01-10-19 to 07-10-19	11.8	2.0	31.7	25.7	85.4	71.1
41	09-10-19 to 14-10-19	0.0	0.0	33.8	26.2	84.5	59.1
42	15-10-19 to 21-10-19	4.4	1.0	32.9	24.9	77.4	59.5
43	22-10-19 to 28-10-19	11.4	2.0	31.6	24.0	81.2	68.2
44	29-10-19 to 04-11-19	20.0	1.0	34.0	24.2	80.7	56.4
45	05-11-19 to 11-11-19	41.2	2.0	32.0	23.2	89.5	63.5
46	12-11-19 to 18-11-19	0.0	0.0	33.4	23.5	80.8	50.5
47	19-11-19 to 25-11-19	0.0	0.0	33.4	22.8	84.8	43.8
48	26-11-19 to 02-12-19	0.0	0.0	33.7	22.5	87.5	45.2
Total / Average		4262.4	89	31.66	25.20	86.63	73.18

APPENDIX - XI

Environment wise analysis of variance for quantitative and qualitative traits in Niger for Kharif, 2018 and Kharif, 2019

ARS, Phondaghat (E1)							
Sr. No.	Characters	Kharif, 2018			Kharif, 2019		
		Replication	Treatment	Error	Replication	Treatment	Error
	DF	2	39	78	2	39	78
1.	DFFP	27.30	34.46**	3.58	14.41	48.45**	3.73
2.	PH (cm)	140.40	223.34**	58.15	236.26	661.60**	93.34
3.	NPBPP	1.90	19.84**	1.54	1.43	15.17**	2.49
4.	NSBPP	28.06	74.37**	3.29	40.86	66.29**	10.19
5.	NCP	23.76	361.54**	8.92	30.81	736.60**	45.42
6.	CD (cm)	0.01	0.03	0.001	0.01	0.07	0.01
7.	NSPC	20.77	30.63**	15.19	13.86	99.41**	22.41
8.	1000 SW (g)	0.05	0.09	0.03	0.04	0.03	0.02
9.	SYPP (g)	0.41	0.27**	0.09	0.17	0.23**	0.09
10.	SYPP (g)	278.03	1189.24**	460.75	2031.46	1408.49**	753.73
11.	DM	5.03	39.45**	7.70	18.53	58.87**	8.77
12.	OC (%)	2.86	12.27**	5.75	2.06	8.53**	4.29
13.	PC (%)	0.63	4.59*	1.43	1.61	4.07*	1.07
ARS, Shirgaon (E2)							
Sr. No.	Characters	Kharif, 2018			Kharif, 2019		
		Replication	Treatment	Error	Replication	Treatment	Error
	DF	2	39	78	2	39	78
1.	DFFP	1.07	22.51**	3.14	18.96	44.25**	5.09
2.	PH (cm)	117.01	141.91**	59.01	241.61	187.90**	105.60
3.	NPBPP	5.58	16.22**	3.12	0.81	7.35**	2.47
4.	NSBPP	21.83	45.02**	10.98	5.20	37.91**	9.41
5.	NCP	42.06	111.95**	33.92	3.91	167.69**	50.34
6.	CD (cm)	0.001	0.02	0.01	0.02	0.05	0.01
7.	NSPC	3.31	24.00**	13.54	20.01	78.22**	16.09
8.	1000 SW (g)	0.01	0.11	0.03	0.09	0.06	0.03
9.	SYPP (g)	0.07	0.21**	0.07	0.03	0.28**	0.13
10.	SYPP (g)	3037.30	1908.27**	865.06	405.23	1058.96**	405.81
11.	DM	3.31	18.96**	6.19	2.77	48.66**	9.44
12.	OC (%)	4.82	7.96**	4.23	3.86	7.25**	2.92
	PC (%)	2.51	3.35*	1.74	3.48	5.30**	2.83
Dept. of Agril. Botany, Dapoli (E3)							
Sr. No.	Characters	Kharif, 2018			Kharif, 2019		
		Replication	Treatment	Error	Replication	Treatment	Error
	DF	2	39	78	2	39	78
1.	DFFP	0.36	26.09**	3.42	8.56	64.87**	4.27
2.	PH (cm)	64.61	150.00**	69.57	10.98	705.47**	121.16
3.	NPBPP	2.56	5.93**	1.15	4.66	17.02**	2.16
4.	NSBPP	0.23	20.10**	2.51	8.40	57.37**	10.64
5.	NCP	10.86	56.62**	6.05	27.07	585.79**	47.86
6.	CD (cm)	0.001	0.02	0.01	0.01	0.07	0.01
7.	NSPC	2.28	23.76**	13.46	6.31	104.82**	26.43
8.	1000 SW (g)	0.04	0.11	0.06	0.001	0.13*	0.05
9.	SYPP (g)	0.32	0.21**	0.09	0.23	0.47**	0.23
10.	SYPP (g)	4326.01	1874.63**	1037.79	1366.41	1440.81**	519.49
11.	DM	14.23	15.47**	7.26	36.11	119.13**	30.21
12.	OC (%)	0.93	6.78**	3.05	1.31	6.75**	3.62
	PC (%)	2.61	2.53*	1.05	1.03	3.18*	1.53

(Table Contd...)

RARS, Karjat (E4)							
Sr. No.	Characters	Kharif, 2018			Kharif, 2019		
		Replication	Treatment	Error	Replication	Treatment	Error
	DF	2	39	78	2	39	78
1.	DFFP	1.31	48.80**	3.74	2.42	38.63**	5.26
2.	PH (cm)	19.43	122.50**	63.46	83.13	118.06**	72.07
3.	NPBPP	1.46	14.51**	1.42	0.31	14.62**	1.07
4.	NSBPP	4.26	38.60**	3.99	4.36	26.73**	6.62
5.	NCPP	10.43	109.48**	8.72	88.56	130.26**	30.05
6.	CD (cm)	0.02	0.03	0.01	0.01	0.02	0.01
7.	NSPC	1.73	12.87**	7.96	3.56	21.45**	8.93
8.	1000 SW (g)	0.03	0.12*	0.06	0.02	0.12*	0.06
9.	SYPP (g)	0.01	0.11*	0.04	0.02	0.13*	0.04
10.	SYPP (g)	263.56	564.53**	248.95	46.23	574.44**	272.28
11.	DM	7.56	27.18**	8.55	6.47	30.03**	9.90
12.	OC (%)	2.56	8.09**	2.53	3.90	8.92**	3.05
	PC (%)	2.41	3.94*	2.04	2.77	4.36*	2.30
ARS, Plaghar (E5)							
Sr. No.	Characters	Kharif, 2018			Kharif, 2019		
		Replication	Treatment	Error	Replication	Treatment	Error
	DF	2	39	78	2	39	78
1.	DFFP	3.56	33.75**	4.26	8.63	52.70**	3.67
2.	PH (cm)	23.16	115.38**	61.15	4.26	342.00**	102.14
3.	NPBPP	4.26	14.30**	3.01	1.31	12.82**	0.90
4.	NSBPP	15.10	65.20**	11.80	17.31	26.69**	6.58
5.	NCPP	10.83	141.63**	8.37	6.91	114.94**	25.51
6.	CD (cm)	0.001	0.02	0.01	0.01	0.05	0.01
7.	NSPC	17.31	33.06**	9.89	0.21	35.21**	12.70
8.	1000 SW (g)	0.08	0.10	0.06	0.06	0.09	0.05
9.	SYPP (g)	0.05	0.22**	0.12	0.09	0.14**	0.07
10.	SYPP (g)	226.42	1183.35**	598.37	408.40	1234.89**	401.66
11.	DM	11.03	69.17**	12.40	15.21	45.10**	10.89
12.	OC (%)	4.66	6.94**	3.31	3.10	8.21**	3.65
13.	PC (%)	1.08	3.08*	1.47	14.93	4.61**	2.44

APPENDIX – XII

Mean performance of various traits for *kharif*, 2018 and *kharif*, 2019 in 40 genotypes of Niger

S. No.	Genotype code	Days to 50 per cent flowering											
		<i>Kharif</i> , 2018						<i>Kharif</i> , 2019					
		E1	E2	E3	E4	E5	GM	E1	E2	E3	E4	E5	GM
1	G 1	47	46	47	43	47	46	55	54	52	54	53	54
2	G 2	49	48	48	44	51	48	58	57	54	54	54	55
3	G 3	40	48	48	48	42	45	50	51	58	58	57	55
4	G 4	49	46	48	43	43	46	57	56	57	54	58	56
5	G 5	42	46	47	43	45	44	62	61	50	53	51	55
6	G 6	48	45	45	44	47	46	49	49	50	52	49	50
7	G 7	47	47	48	44	46	46	52	51	52	54	53	53
8	G 8	46	48	47	45	46	46	57	56	56	55	55	56
9	G 9	41	47	47	53	43	46	55	54	60	59	60	58
10	G 10	41	45	45	44	43	43	54	53	55	53	53	54
11	G 11	40	48	46	51	49	47	52	51	55	59	53	54
12	G 12	51	45	46	47	43	46	55	54	55	52	56	54
13	G 13	50	47	45	51	43	47	57	56	55	57	54	55
14	G 14	50	47	47	50	41	47	58	56	56	59	56	57
15	G 15	51	47	46	49	43	47	58	57	53	59	56	57
16	G 16	50	47	47	49	44	47	58	57	55	60	56	57
17	G 17	44	48	47	51	43	46	52	51	56	60	54	55
18	G 18	46	46	45	51	42	46	57	56	52	58	54	55
19	G 19	48	47	47	52	45	48	49	50	44	52	52	50
20	G 20	50	48	47	50	44	48	51	51	55	54	53	53
21	G 21	50	45	47	51	45	48	58	58	53	56	54	56
22	G 22	48	47	47	52	49	48	46	46	53	59	51	51
23	G 23	50	47	46	52	42	47	51	49	49	53	50	50
24	G 24	48	39	38	41	37	40	45	44	41	48	45	45
25	G 25	48	39	38	40	38	41	45	44	42	49	43	45
26	G 26	45	38	39	42	40	41	45	44	43	46	41	44
27	G 27	45	41	40	44	38	42	50	49	46	50	46	48
28	G 28	46	42	40	43	39	42	50	49	47	54	48	49
29	G 29	47	42	40	45	39	43	51	50	46	57	45	50
30	G 30	41	46	48	45	41	44	54	54	49	58	51	53
31	G 31	40	47	46	48	42	45	56	55	49	54	49	52
32	G 32	51	46	45	44	41	45	54	53	50	56	51	53
33	G 33	42	47	46	54	48	47	55	55	47	56	55	54
34	G 34	49	48	47	52	48	49	52	52	57	60	58	56
35	G 35	47	50	49	52	48	49	55	54	56	61	57	56
36	G 36	44	46	44	53	47	47	54	54	56	58	55	56
37	G 37	49	51	50	54	48	50	53	53	55	61	57	56
38	G 38	45	45	44	50	46	46	54	53	54	57	54	54
39	G 39	44	47	47	51	46	47	53	53	52	57	54	54
40	G 40	47	45	44	49	45	46	53	52	49	56	53	53
	GM	46	46	45	48	44	46	53	53	52	55	53	53
	Range	40-51	38-51	38-50	40-54	37-51	37-50	45-62	44-61	41-60	46-61	41-60	44-57
	S.E. $\pm$	1.55	1.45	1.51	1.58	1.69		1.58	1.84	1.69	1.87	1.56	
	C.D. (5%)	3.08	2.88	3.01	3.15	3.35		3.14	3.67	3.36	3.73	3.11	

Note: GM – Grand Mean

(Table Contd...)

S. No.	Genotype code	Plant height (cm)											
		<i>Kharif, 2018</i>						<i>Kharif, 2019</i>					
		E1	E2	E3	E4	E5	GM	E1	E2	E3	E4	E5	GM
1	G 1	127	138	130	134	135	133	158	113	152	145	142	142
2	G 2	140	136	127	132	134	134	154	119	141	148	130	138
3	G 3	143	133	131	130	130	133	134	120	125	125	108	122
4	G 4	138	137	137	136	135	137	136	112	149	142	145	137
5	G 5	137	135	132	131	131	133	137	94	155	140	144	134
6	G 6	150	135	137	135	133	138	130	110	155	134	135	133
7	G 7	138	141	138	138	141	139	119	98	142	139	140	128
8	G 8	135	133	128	127	135	131	115	108	112	131	120	117
9	G 9	147	128	128	127	125	131	123	110	141	135	141	130
10	G 10	148	133	134	131	131	135	141	97	155	145	143	136
11	G 11	144	143	140	140	141	142	127	111	137	132	130	127
12	G 12	146	132	129	127	127	132	137	109	142	140	143	134
13	G 13	142	148	143	146	142	144	146	101	141	137	135	132
14	G 14	136	151	133	148	143	142	124	131	146	144	142	138
15	G 15	131	131	130	128	130	130	131	111	139	136	141	132
16	G 16	158	138	135	132	136	140	124	106	147	137	143	131
17	G 17	143	132	130	132	136	134	122	120	176	136	154	142
18	G 18	154	142	139	141	139	143	131	122	139	136	137	133
19	G 19	147	135	135	134	136	137	128	115	146	141	139	134
20	G 20	152	132	131	132	132	136	156	119	175	148	155	150
21	G 21	133	138	137	139	139	137	142	107	154	141	142	137
22	G 22	143	140	136	139	138	139	137	105	136	136	139	131
23	G 23	134	139	140	137	139	138	122	108	142	133	134	128
24	G 24	133	133	142	137	143	138	114	110	120	140	121	121
25	G 25	121	127	133	125	123	126	119	100	116	127	121	117
26	G 26	125	130	136	128	131	130	97	100	113	127	129	113
27	G 27	130	131	134	129	132	131	128	108	162	132	154	137
28	G 28	129	131	145	135	135	135	135	110	136	139	142	132
29	G 29	128	132	137	131	134	133	113	115	150	137	153	134
30	G 30	127	135	143	143	139	137	132	115	161	140	149	140
31	G 31	129	136	150	135	131	136	112	117	154	140	143	133
32	G 32	127	132	133	136	134	132	142	115	125	131	125	128
33	G 33	135	148	136	151	133	141	116	120	131	148	138	131
34	G 34	135	148	148	139	140	142	115	115	131	139	140	128
35	G 35	133	148	147	143	136	142	109	120	162	145	142	136
36	G 36	133	142	143	142	141	140	106	113	150	141	135	129
37	G 37	140	145	145	142	131	141	97	111	142	144	140	127
38	G 38	136	149	152	141	149	145	112	122	154	147	153	138
39	G 39	132	153	155	146	147	147	106	113	148	151	153	134
40	G 40	129	145	145	141	154	143	135	123	172	147	158	147
	GM	137	138	138	136	136	137	127	112	144	139	139	132
	Range	121-154	127-153	127-155	125-151	123-154	126-156	97-158	94-131	112-176	125-151	108-158	117-150
	S.E. $\pm$	6.23	6.27	6.81	6.50	6.38		7.89	8.39	8.99	6.93	8.25	
	C.D. (5%)	12.40	12.49	13.56	12.95	12.71		15.70	16.70	17.89	13.80	16.43	

Note: GM – Grand Mean

(Table Contd...)

S. No.	Genotype code	Number of primary branches plant ⁻¹											
		<i>Kharif, 2018</i>						<i>Kharif, 2019</i>					
		E1	E2	E3	E4	E5	GM	E1	E2	E3	E4	E5	GM
1	G 1	12	11	10	9	12	11	12	9	12	9	9	10
2	G 2	10	12	12	11	15	12	11	9	12	8	10	10
3	G 3	5	9	7	6	11	8	8	8	6	5	6	6
4	G 4	8	13	11	10	15	12	11	13	12	9	10	11
5	G 5	7	9	8	7	9	8	8	7	9	5	6	7
6	G 6	11	9	11	8	12	10	7	8	8	8	8	8
7	G 7	10	12	7	6	7	8	7	10	12	7	5	8
8	G 8	8	8	8	6	9	8	9	7	7	6	5	7
9	G 9	11	8	8	7	10	9	11	9	8	7	8	8
10	G 10	13	13	10	7	15	12	12	11	11	9	9	10
11	G 11	9	10	9	11	11	10	7	9	9	4	5	7
12	G 12	7	9	8	7	9	8	7	8	11	5	9	8
13	G 13	9	8	9	5	10	8	10	8	10	5	4	7
14	G 14	9	10	8	7	10	9	9	7	9	8	6	8
15	G 15	7	9	7	6	9	8	9	9	4	6	5	7
16	G 16	14	9	9	8	10	10	7	9	8	5	7	7
17	G 17	8	7	7	7	12	8	7	7	11	5	5	7
18	G 18	12	8	9	6	8	8	9	8	7	7	6	7
19	G 19	10	8	8	6	9	8	6	10	5	6	5	6
20	G 20	10	10	7	7	9	9	10	8	8	8	7	8
21	G 21	9	9	7	5	10	8	6	8	9	4	6	7
22	G 22	8	9	8	6	9	8	10	8	6	6	6	7
23	G 23	9	9	7	8	9	8	6	12	8	7	5	8
24	G 24	15	16	12	14	15	14	10	11	9	11	12	11
25	G 25	7	10	8	9	12	9	6	7	7	8	6	7
26	G 26	5	11	7	6	9	8	4	8	5	6	7	6
27	G 27	7	9	8	8	10	8	5	9	7	7	6	7
28	G 28	7	9	8	9	10	9	5	7	7	4	5	6
29	G 29	7	8	7	7	10	8	5	8	8	7	7	7
30	G 30	7	11	7	7	9	8	8	10	11	5	6	8
31	G 31	7	9	7	5	9	7	5	10	8	5	8	7
32	G 32	14	14	11	12	15	13	11	12	9	12	9	11
33	G 33	11	12	9	12	13	11	8	10	5	8	5	7
34	G 34	10	11	8	9	11	10	10	10	9	9	7	9
35	G 35	9	14	9	9	13	11	10	12	12	9	9	10
36	G 36	16	15	9	11	14	13	10	10	13	12	14	12
37	G 37	10	7	7	10	10	9	6	9	9	9	6	8
38	G 38	11	14	9	9	12	11	9	11	11	10	9	10
39	G 39	11	13	9	11	12	11	7	11	12	10	9	10
40	G 40	11	12	9	11	13	11	10	11	13	11	9	11
	GM	10	10	8	8	11	9	8	9	9	7	7	8
	Range	5-16	7-16	7-12	5-14	7-15	7-14	4-12	7-13	5-13	4-12	4-14	6-12
	S.E. $\pm$	1.01	1.44	0.87	0.97	1.42		1.29	1.28	1.20	0.84	0.77	
	C.D. (5%)	2.02	2.87	1.74	1.94	2.82		2.57	2.56	2.39	1.68	1.54	

Note: GM-Grand Mean

(Table Contd...)

S. No.	Genotype code	Number of secondary branches plant ⁻¹											
		<i>Kharif, 2018</i>						<i>Kharif, 2019</i>					
		E1	E2	E3	E4	E5	GM	E1	E2	E3	E4	E5	GM
1	G 1	17	21	18	15	17	18	26	20	25	15	11	19
2	G 2	17	21	15	19	24	19	26	28	23	15	13	21
3	G 3	8	18	9	11	22	14	16	19	15	12	11	15
4	G 4	14	25	17	18	28	20	22	27	19	15	12	19
5	G 5	9	18	11	12	13	13	14	23	20	10	15	17
6	G 6	20	18	14	14	16	16	13	18	14	15	14	15
7	G 7	13	23	9	13	17	15	15	19	16	14	11	15
8	G 8	11	16	12	12	18	14	14	20	24	11	13	17
9	G 9	16	16	12	14	21	16	21	21	20	10	17	18
10	G 10	21	24	17	19	24	21	27	19	23	17	14	20
11	G 11	11	17	12	13	18	14	14	17	16	12	11	14
12	G 12	11	19	11	13	16	14	20	19	17	12	19	17
13	G 13	14	15	12	11	18	14	21	17	19	11	10	16
14	G 14	12	19	10	13	16	14	16	18	25	13	12	17
15	G 15	9	17	13	12	17	14	17	17	14	14	14	15
16	G 16	26	18	11	14	18	17	14	19	22	11	15	16
17	G 17	10	15	10	13	23	14	16	15	27	10	11	16
18	G 18	22	16	10	12	16	15	21	15	20	12	10	16
19	G 19	17	16	9	11	17	14	16	25	15	14	9	16
20	G 20	20	20	10	13	16	16	22	20	19	16	15	19
21	G 21	14	17	9	11	18	14	13	21	22	10	14	16
22	G 22	11	18	9	13	16	13	16	20	17	13	12	15
23	G 23	12	20	9	15	14	14	14	21	16	12	13	15
24	G 24	15	30	19	26	31	24	18	22	23	20	20	21
25	G 25	9	20	12	18	25	17	13	16	16	14	10	14
26	G 26	9	20	11	12	17	14	10	17	14	10	15	13
27	G 27	10	18	11	15	17	14	11	18	22	12	12	15
28	G 28	11	20	11	14	16	14	10	14	22	10	10	13
29	G 29	12	14	12	13	16	13	10	17	18	13	11	14
30	G 30	11	21	9	14	14	14	15	24	32	10	11	18
31	G 31	11	16	9	11	17	13	12	24	21	14	14	17
32	G 32	22	25	15	23	30	23	23	26	28	20	13	22
33	G 33	16	22	11	16	23	18	14	19	17	15	13	16
34	G 34	12	20	11	15	18	15	19	19	16	15	14	17
35	G 35	14	26	10	15	25	18	22	22	28	15	17	21
36	G 36	27	28	13	21	27	23	22	27	26	21	21	23
37	G 37	14	13	10	14	22	15	12	21	18	14	12	15
38	G 38	22	24	13	17	23	20	18	24	23	17	17	20
39	G 39	18	22	13	20	25	20	21	22	23	18	18	20
40	G 40	22	24	13	21	25	21	22	26	24	18	20	22
	GM	15	20	12	15	20	16	17	20	20	14	14	17
	Range	9-27	13-30	9-19	11-26	13-31	13-24	10-27	14-28	14-32	10-21	9-21	13-23
	S.E. $\pm$	1.48	2.71	1.29	1.63	2.80		2.61	2.51	2.66	2.10	2.09	
	C.D. (5%)	2.95	5.39	2.57	3.25	5.58		5.19	4.99	5.30	4.18	4.17	

Note: GM-Grand Mean

(Table Contd...)

S. No.	Genotype code	Total number of capitula plant ⁻¹											
		<i>Kharif, 2018</i>						<i>Kharif, 2019</i>					
		E1	E2	E3	E4	E5	GM	E1	E2	E3	E4	E5	GM
1	G 1	44	44	44	38	45	43	53	42	52	52	42	48
2	G 2	28	39	43	42	30	37	47	45	75	51	37	51
3	G 3	32	33	31	28	33	31	36	40	42	40	31	38
4	G 4	39	48	44	41	45	43	33	45	45	52	42	43
5	G 5	31	34	32	33	33	32	27	46	41	43	32	38
6	G 6	38	33	35	32	34	35	20	34	42	40	32	34
7	G 7	38	41	35	31	32	35	26	36	48	37	30	35
8	G 8	32	32	34	30	32	32	22	39	36	38	37	34
9	G 9	39	30	34	34	33	34	68	31	52	46	37	47
10	G 10	51	44	41	43	42	44	73	37	46	52	46	51
11	G 11	32	34	35	32	34	33	27	34	38	38	31	33
12	G 12	28	35	36	31	31	32	40	32	37	41	40	38
13	G 13	37	30	32	27	32	32	62	26	65	35	30	44
14	G 14	37	36	33	31	30	33	42	34	58	40	36	42
15	G 15	28	35	32	32	31	32	40	46	23	42	36	37
16	G 16	58	34	34	28	32	37	28	33	51	37	34	36
17	G 17	30	31	34	24	30	30	34	38	61	34	30	39
18	G 18	50	32	32	28	32	35	68	36	39	37	37	43
19	G 19	49	33	32	27	33	35	41	46	39	38	26	38
20	G 20	51	38	32	25	31	36	63	42	54	41	42	48
21	G 21	33	35	33	27	27	31	41	47	41	34	38	40
22	G 22	28	30	34	26	31	30	39	37	34	32	32	35
23	G 23	33	35	33	33	31	33	29	41	30	39	35	35
24	G 24	67	49	49	50	52	53	49	39	46	56	47	47
25	G 25	29	38	33	32	37	34	26	26	25	40	35	30
26	G 26	27	33	32	25	30	29	21	34	27	36	40	32
27	G 27	28	36	31	29	33	31	31	29	37	34	34	33
28	G 28	27	27	30	27	30	28	26	25	52	33	30	33
29	G 29	30	29	34	27	30	30	26	21	32	34	36	30
30	G 30	27	41	31	28	30	32	36	30	74	36	29	41
31	G 31	31	32	36	24	27	30	24	56	50	39	37	41
32	G 32	62	42	42	44	49	48	51	44	46	57	47	49
33	G 33	39	36	31	32	32	34	36	42	33	35	32	36
34	G 34	32	39	32	32	32	33	44	36	33	41	35	38
35	G 35	31	49	31	31	37	36	65	42	64	47	38	51
36	G 36	66	35	32	38	58	46	69	50	70	48	50	57
37	G 37	32	26	31	30	32	30	31	42	54	36	34	40
38	G 38	42	45	34	32	40	38	42	46	69	46	41	49
39	G 39	38	41	32	38	39	38	63	41	64	46	49	52
40	G 40	42	49	37	39	45	42	63	46	70	47	50	55
	GM	38	37	35	32	35	35	41	38	47	41	37	41
	Range	27-67	26-49	30-49	24-50	27-58	28-53	20-69	21-56	23-75	32-56	29-50	30-57
	S.E. ±	2.44	4.76	2.01	2.41	2.36		5.50	5.79	5.65	4.48	4.12	
	C.D. (5%)	4.86	9.47	4.00	4.80	4.70		10.96	11.53	11.25	8.91	8.21	

Note: GM-Grand Mean

(Table Contd...)

S. No.	Genotype code	Capitulum diameter (cm)											
		<i>Kharif, 2018</i>						<i>Kharif, 2019</i>					
		E1	E2	E3	E4	E5	GM	E1	E2	E3	E4	E5	GM
1	G 1	1.17	1.13	1.07	1.00	0.97	1.07	1.13	1.27	1.13	0.90	1.03	1.09
2	G 2	1.13	1.03	1.17	1.20	1.07	1.12	0.97	1.03	1.07	0.97	0.93	0.99
3	G 3	1.07	1.17	1.13	1.07	1.00	1.09	1.07	1.10	1.03	1.07	0.97	1.05
4	G 4	1.33	1.00	1.20	0.93	1.13	1.12	1.13	1.07	0.93	1.13	0.90	1.03
5	G 5	1.13	1.00	1.13	0.93	1.03	1.05	0.87	0.83	1.10	1.00	1.03	0.97
6	G 6	1.13	1.07	1.07	1.00	1.00	1.05	1.13	1.10	1.10	0.93	0.87	1.03
7	G 7	1.03	0.93	0.97	0.87	1.03	0.97	0.87	0.90	0.97	1.03	0.87	0.93
8	G 8	1.07	0.97	1.03	0.93	0.97	0.99	1.27	1.33	0.93	0.97	0.83	1.07
9	G 9	0.97	1.00	0.97	0.93	1.00	0.97	1.07	1.17	1.03	1.00	0.93	1.04
10	G 10	1.17	1.13	1.17	1.03	1.07	1.11	0.93	0.97	0.97	0.97	0.87	0.94
11	G 11	1.13	1.03	1.00	1.03	0.97	1.03	1.10	1.07	0.97	0.93	0.97	1.01
12	G 12	1.23	1.07	1.00	1.00	0.93	1.05	1.10	1.17	0.93	0.90	0.93	1.01
13	G 13	1.07	1.00	0.90	0.93	1.03	0.99	1.07	1.13	1.07	0.97	0.97	1.04
14	G 14	1.13	1.07	0.93	0.97	0.93	1.01	1.13	1.13	1.07	0.90	0.97	1.04
15	G 15	1.27	1.17	1.00	1.13	1.13	1.14	1.03	1.13	1.17	1.07	1.03	1.09
16	G 16	1.27	1.10	1.07	0.93	1.00	1.07	1.10	1.07	1.03	0.93	0.87	1.00
17	G 17	1.07	1.03	0.97	0.93	0.93	0.99	0.97	1.00	1.27	0.97	1.10	1.06
18	G 18	1.03	1.00	1.07	1.03	0.97	1.02	1.13	1.13	0.93	1.00	0.87	1.01
19	G 19	1.23	1.07	1.03	1.17	1.13	1.13	0.80	0.90	1.10	0.93	0.97	0.94
20	G 20	1.13	1.03	0.93	1.03	0.93	1.01	0.87	0.97	0.97	0.97	0.80	0.91
21	G 21	1.23	1.07	1.03	0.97	0.97	1.05	0.77	0.87	1.23	0.93	1.07	0.97
22	G 22	1.07	1.13	1.00	0.93	1.00	1.03	1.17	1.30	1.17	1.07	1.03	1.15
23	G 23	1.13	1.03	1.00	0.97	0.93	1.01	1.00	0.90	1.07	0.93	0.90	0.96
24	G 24	1.07	1.10	1.17	0.93	1.17	1.09	0.83	1.03	1.27	1.13	0.93	1.04
25	G 25	1.00	1.00	1.03	0.87	0.93	0.97	0.87	1.00	0.97	0.93	0.90	0.93
26	G 26	1.03	0.97	1.00	0.97	0.93	0.98	0.73	0.83	0.83	0.93	0.77	0.82
27	G 27	1.07	0.93	0.97	0.93	0.97	0.97	0.80	0.83	1.13	0.87	1.03	0.93
28	G 28	1.03	0.97	0.93	0.83	0.93	0.94	0.83	0.90	1.30	0.90	1.17	1.02
29	G 29	0.93	0.87	0.90	0.87	0.97	0.91	1.03	1.07	1.27	1.03	1.13	1.11
30	G 30	1.03	0.97	0.97	0.93	0.93	0.97	1.17	1.13	1.33	1.00	1.07	1.14
31	G 31	1.13	1.13	1.03	0.93	0.97	1.04	1.07	1.17	1.27	1.00	1.10	1.12
32	G 32	1.03	1.00	1.07	0.90	1.10	1.02	1.10	1.13	1.07	0.97	0.93	1.04
33	G 33	1.17	1.07	1.07	1.00	1.03	1.07	1.03	0.93	1.33	0.93	1.07	1.06
34	G 34	0.97	0.83	1.00	0.93	1.07	0.96	1.23	1.10	1.23	1.07	1.17	1.16
35	G 35	1.17	1.00	1.13	1.03	1.03	1.07	1.17	1.17	1.33	1.10	1.13	1.18
36	G 36	1.27	1.23	1.23	1.20	1.23	1.23	1.27	1.23	1.40	1.17	1.27	1.27
37	G 37	1.13	1.00	1.03	1.00	1.00	1.03	0.87	0.83	1.00	0.97	1.00	0.93
38	G 38	1.20	1.10	1.17	1.13	1.17	1.15	1.17	1.13	1.37	1.13	1.17	1.19
39	G 39	1.17	1.10	1.07	1.07	1.13	1.11	1.20	1.07	1.33	1.10	1.20	1.18
40	G 40	1.23	1.20	1.13	1.17	1.20	1.19	1.17	1.20	1.37	1.13	1.27	1.23
	GM	1.12	1.04	1.04	0.99	1.02	1.04	1.03	1.06	1.13	1.00	1.00	1.04
	Range	0.93-1.33	0.83-1.23	0.90-1.23	0.83-1.20	0.93-1.23	0.91-1.23	0.73-1.27	0.83-1.33	0.83-1.40	0.87-1.17	0.77-1.27	0.91-1.27
	S.E. $\pm$	0.05	0.06	0.07	0.07	0.07		0.06	0.07	0.07	0.08	0.07	
	C.D. (5%)	0.10	0.13	0.13	0.13	0.13		0.12	0.14	0.14	0.16	0.15	

Note: GM-Grand Mean

(Table Contd...)

S. No.	Genotype code	Number of seeds capitulum ⁻¹											
		<i>Kharif, 2018</i>						<i>Kharif, 2019</i>					
		E1	E2	E3	E4	E5	GM	E1	E2	E3	E4	E5	GM
1	G 1	38	31	33	22	28	30	21	23	36	18	23	24
2	G 2	44	37	37	25	29	35	28	22	22	23	24	24
3	G 3	39	35	35	25	25	32	21	24	36	19	19	24
4	G 4	41	36	36	23	30	33	24	25	28	22	25	25
5	G 5	38	33	33	26	26	31	27	32	34	20	21	27
6	G 6	38	33	33	25	27	31	25	25	32	19	19	24
7	G 7	35	30	30	25	27	29	28	25	23	16	15	21
8	G 8	38	33	33	22	27	31	31	29	27	17	19	25
9	G 9	37	31	31	23	30	31	32	33	22	19	22	25
10	G 10	41	36	36	25	29	33	24	28	21	23	25	24
11	G 11	36	30	30	24	25	29	21	22	32	20	20	23
12	G 12	37	32	32	23	24	30	29	28	21	20	17	23
13	G 13	36	31	31	23	28	30	24	24	27	20	21	23
14	G 14	36	31	31	22	25	29	26	33	27	20	17	25
15	G 15	41	36	36	23	31	33	25	24	32	23	26	26
16	G 16	40	35	35	22	25	31	29	30	25	17	19	24
17	G 17	36	31	31	21	26	29	20	24	35	16	16	22
18	G 18	42	36	36	22	28	33	28	30	36	20	21	27
19	G 19	41	34	34	22	29	32	19	21	37	19	22	23
20	G 20	36	31	31	21	23	29	25	31	29	17	18	24
21	G 21	40	35	35	24	27	32	21	24	32	16	19	22
22	G 22	39	34	34	23	27	31	34	38	34	13	17	27
23	G 23	37	32	32	20	26	30	28	25	27	20	21	24
24	G 24	43	38	38	23	31	35	28	23	41	21	27	28
25	G 25	37	32	32	21	27	30	27	22	27	19	22	23
26	G 26	37	31	31	20	25	29	27	25	30	17	19	24
27	G 27	34	29	29	22	26	28	20	18	30	16	21	21
28	G 28	39	30	30	21	24	29	27	24	30	15	21	23
29	G 29	35	28	28	21	24	27	17	30	32	13	18	22
30	G 30	36	31	31	21	27	29	35	26	26	21	22	26
31	G 31	41	33	33	20	31	32	28	36	32	20	26	28
32	G 32	45	36	36	22	34	35	31	24	37	22	29	28
33	G 33	36	31	31	21	27	29	32	28	30	19	22	26
34	G 34	36	31	31	23	28	29	33	29	36	21	23	28
35	G 35	38	34	34	20	29	31	39	31	38	21	24	31
36	G 36	48	40	40	28	38	39	37	38	43	23	28	34
37	G 37	37	31	31	18	27	29	30	21	32	18	22	25
38	G 38	45	38	38	26	34	36	38	35	41	22	26	32
39	G 39	41	32	32	21	32	31	38	32	39	21	26	31
40	G 40	44	38	38	27	36	37	39	38	42	23	26	34
	GM	39	33	33	23	28	31	28	28	31	19	22	26
	Range	35-48	28-40	28-40	20-28	24-38	27-39	17-39	18-38	21-43	13-23	15-28	21-34
	S.E. $\pm$	3.18	3.00	3.00	2.30	2.57		3.86	3.28	4.20	2.44	2.91	
	C.D. (5%)	6.34	5.98	5.96	4.58	5.11		7.69	6.52	8.36	4.86	5.79	

Note: GM-Grand Mean

(Table Contd...)

S. No.	GC	1000 Seed weight (g)											
		<i>Kharif, 2018</i>						<i>Kharif, 2019</i>					
		E1	E2	E3	E4	E5	GM	E1	E2	E3	E4	E5	GM
1	G 1	2.60	2.50	2.57	2.38	2.47	2.51	2.56	2.58	2.64	2.50	2.55	2.56
2	G 2	2.74	2.62	2.72	2.56	2.61	2.65	2.70	2.52	2.70	2.65	2.67	2.65
3	G 3	2.74	2.62	2.71	2.51	2.60	2.64	2.70	2.60	2.81	2.59	2.66	2.67
4	G 4	2.71	2.58	2.70	2.66	2.56	2.64	2.71	2.60	2.64	2.73	2.63	2.66
5	G 5	2.66	2.56	2.64	2.46	2.53	2.57	2.64	2.52	2.63	2.55	2.62	2.59
6	G 6	2.60	2.55	2.57	2.38	2.45	2.51	2.58	2.44	2.61	2.44	2.54	2.52
7	G 7	2.66	2.59	2.65	2.44	2.51	2.57	2.63	2.62	2.63	2.53	2.60	2.60
8	G 8	2.44	2.37	2.40	2.23	2.29	2.34	2.52	2.48	2.11	2.33	2.41	2.37
9	G 9	2.53	2.56	2.56	2.38	2.45	2.50	2.53	2.53	2.68	2.45	2.56	2.55
10	G 10	2.79	2.63	2.73	2.64	2.62	2.68	2.74	2.56	2.70	2.69	2.68	2.67
11	G 11	2.60	2.59	2.57	2.38	2.45	2.52	2.61	2.46	2.43	2.47	2.52	2.50
12	G 12	2.82	2.65	2.73	2.54	2.62	2.67	2.76	2.66	2.68	2.62	2.71	2.69
13	G 13	2.62	2.37	2.47	2.26	2.36	2.42	2.62	2.59	2.71	2.35	2.47	2.55
14	G 14	2.64	2.52	2.54	2.32	2.44	2.49	2.63	2.67	2.48	2.40	2.55	2.55
15	G 15	2.62	2.44	2.47	2.24	2.36	2.42	2.59	2.76	2.38	2.33	2.75	2.56
16	G 16	2.63	2.59	2.62	2.41	2.51	2.55	2.63	2.63	2.27	2.46	2.57	2.51
17	G 17	2.67	2.67	2.68	2.48	2.56	2.61	2.65	2.70	2.82	2.55	2.65	2.67
18	G 18	2.64	2.51	2.54	2.37	2.43	2.50	2.63	2.62	2.41	2.43	2.51	2.52
19	G 19	2.58	2.46	2.53	2.33	2.41	2.46	2.62	2.76	2.58	2.41	2.52	2.58
20	G 20	2.63	2.51	2.55	2.32	2.43	2.49	2.58	2.58	2.55	2.43	2.51	2.53
21	G 21	2.69	2.53	2.67	2.45	2.55	2.58	2.67	2.33	2.67	2.53	2.56	2.55
22	G 22	2.66	2.57	2.61	2.42	2.51	2.55	2.65	2.61	2.82	2.53	2.63	2.65
23	G 23	2.62	2.52	2.53	2.31	2.41	2.48	2.61	2.47	2.69	2.40	2.45	2.52
24	G 24	2.71	2.67	2.75	2.64	2.63	2.68	2.67	2.80	2.78	2.73	2.71	2.74
25	G 25	2.43	2.34	2.30	2.14	2.19	2.28	2.48	2.47	2.16	2.19	2.23	2.31
26	G 26	2.16	2.18	2.21	2.00	2.42	2.19	2.52	2.79	2.12	2.13	2.50	2.41
27	G 27	2.03	1.79	1.90	2.38	1.80	1.98	2.64	2.52	2.55	2.49	2.03	2.45
28	G 28	2.32	2.10	2.16	1.61	2.05	2.05	2.33	2.48	2.30	1.73	2.12	2.19
29	G 29	2.45	2.05	2.13	1.89	2.02	2.11	2.48	2.54	2.45	2.02	2.16	2.33
30	G 30	2.51	2.38	2.44	2.23	2.33	2.38	2.50	2.28	2.56	2.33	2.44	2.42
31	G 31	2.71	2.55	2.67	2.44	2.55	2.59	2.72	2.55	2.74	2.51	2.51	2.61
32	G 32	2.64	2.54	2.62	2.42	2.49	2.54	2.64	2.58	2.76	2.57	2.60	2.63
33	G 33	2.68	2.54	2.63	2.42	2.51	2.55	2.64	2.71	2.70	2.50	2.62	2.63
34	G 34	2.60	2.52	2.56	2.36	2.43	2.49	2.66	2.75	2.61	2.42	2.52	2.59
35	G 35	2.70	2.59	2.65	2.48	2.55	2.59	2.75	2.91	2.91	2.59	2.62	2.76
36	G 36	2.87	2.68	2.80	2.61	2.69	2.73	2.89	2.88	2.78	2.74	2.80	2.82
37	G 37	2.68	2.59	2.65	2.44	2.54	2.58	2.66	2.67	2.52	2.50	2.63	2.60
38	G 38	2.86	2.70	2.78	2.58	2.67	2.72	2.82	2.86	2.87	2.72	2.73	2.80
39	G 39	2.70	2.52	2.54	2.33	2.44	2.51	2.81	2.81	2.81	2.66	2.60	2.74
40	G 40	2.87	2.72	2.77	2.60	2.66	2.72	2.85	2.82	2.90	2.73	2.79	2.82
	GM	2.62	2.50	2.56	2.38	2.45	2.50	2.64	2.62	2.60	2.47	2.55	2.58
	Range	2.03-2.87	1.79-2.72	1.90-2.80	1.61-2.61	1.80-2.69	1.98-2.73	2.33-2.89	2.28-2.91	2.11-2.91	1.73-2.74	2.03-2.80	2.19-2.82
	S.E. $\pm$	0.14	0.13	0.20	0.20	0.20		0.11	0.15	0.18	0.19	0.18	
	C.D. (5%)	0.28	0.27	0.39	0.40	0.40		0.22	0.30	0.35	0.38	0.35	

Note: GC – Genotype code & GM – Grand Mean

(Table Contd...)

S. No.	GC	Seed yield plant ¹											
		<i>Kharif, 2018</i>						<i>Kharif, 2019</i>					
		E1	E2	E3	E4	E5	GM	E1	E2	E3	E4	E5	GM
1	G 1	2.71	2.90	3.35	2.36	2.53	2.77	2.61	2.74	3.38	2.60	2.43	2.75
2	G 2	2.96	3.10	3.61	2.58	2.83	3.02	2.87	2.92	3.56	2.37	2.37	2.82
3	G 3	2.60	2.74	3.56	2.36	2.33	2.72	2.57	2.65	3.31	2.20	2.21	2.59
4	G 4	3.01	3.15	3.64	2.63	2.32	2.95	2.93	2.75	3.44	2.52	2.23	2.78
5	G 5	2.45	2.62	3.40	2.67	2.43	2.72	2.54	2.49	3.77	2.57	2.33	2.74
6	G 6	2.74	2.92	3.38	2.33	2.79	2.83	2.62	2.75	3.55	2.18	2.68	2.76
7	G 7	2.30	2.55	3.23	2.31	2.21	2.52	2.34	2.43	3.26	2.07	2.13	2.45
8	G 8	2.58	2.69	3.48	2.49	2.34	2.71	2.42	2.55	3.60	2.43	2.21	2.64
9	G 9	2.42	2.57	3.35	2.43	2.33	2.62	2.36	2.46	3.29	2.30	2.20	2.52
10	G 10	2.93	3.08	3.52	2.71	2.49	2.95	2.78	2.63	3.43	2.61	2.74	2.84
11	G 11	2.69	2.85	3.63	2.37	2.91	2.89	2.64	2.75	3.14	2.10	2.66	2.66
12	G 12	2.51	2.68	3.57	2.13	2.42	2.66	2.47	2.61	3.18	2.03	2.35	2.53
13	G 13	2.58	2.71	3.54	2.27	2.61	2.74	2.62	2.59	3.01	2.23	2.52	2.59
14	G 14	2.66	2.79	3.63	2.47	2.59	2.83	2.60	2.69	3.07	2.35	2.49	2.64
15	G 15	2.56	2.72	3.55	2.31	2.69	2.77	2.51	2.62	3.33	2.17	2.30	2.59
16	G 16	2.72	2.74	3.61	2.26	2.46	2.76	2.62	2.75	3.39	2.22	2.35	2.67
17	G 17	2.87	3.04	3.40	2.31	2.68	2.86	2.50	2.58	3.06	2.18	2.60	2.58
18	G 18	2.47	2.98	3.43	2.33	2.83	2.81	2.74	2.54	2.85	2.22	2.65	2.60
19	G 19	2.46	2.60	3.49	2.30	2.45	2.66	2.43	2.48	3.67	2.19	2.30	2.62
20	G 20	2.30	2.64	3.27	2.35	2.23	2.56	2.40	2.37	3.25	2.29	2.18	2.50
21	G 21	2.95	2.75	3.81	2.32	2.73	2.91	2.80	2.67	3.40	2.27	2.57	2.74
22	G 22	2.60	2.73	3.55	2.46	2.84	2.84	2.51	2.65	3.03	2.33	2.72	2.65
23	G 23	2.66	3.05	4.03	2.24	2.76	2.95	2.59	2.73	3.38	2.16	2.76	2.72
24	G 24	3.20	3.27	4.19	2.82	3.13	3.32	2.97	3.50	4.05	2.74	3.02	3.25
25	G 25	2.85	2.94	3.43	2.16	2.77	2.83	2.68	2.57	3.04	2.06	2.36	2.54
26	G 26	2.85	2.96	3.76	2.43	2.74	2.95	2.67	3.30	3.44	2.29	2.66	2.87
27	G 27	2.60	2.88	3.53	2.40	2.50	2.78	2.60	2.57	3.06	2.34	2.45	2.60
28	G 28	2.23	2.34	3.23	2.43	2.67	2.58	2.11	2.22	2.73	2.25	2.60	2.38
29	G 29	2.70	2.93	3.55	2.28	2.62	2.82	2.59	2.66	2.82	2.11	2.49	2.53
30	G 30	2.62	2.71	3.57	2.46	2.53	2.78	2.54	2.54	2.79	2.35	2.45	2.53
31	G 31	2.72	2.87	3.64	2.59	2.31	2.83	2.63	2.70	2.91	2.48	2.21	2.59
32	G 32	3.18	3.29	4.04	2.70	2.70	3.18	3.42	3.50	4.03	2.79	2.82	3.31
33	G 33	2.77	2.89	3.64	2.32	2.68	2.86	2.73	2.73	3.45	2.29	2.57	2.75
34	G 34	2.44	2.84	3.42	2.52	2.41	2.73	2.52	2.61	2.95	2.41	2.66	2.63
35	G 35	2.60	2.91	3.55	2.56	2.49	2.82	2.90	2.63	3.82	2.52	2.60	2.89
36	G 36	3.70	3.61	4.32	2.92	3.47	3.60	3.43	3.52	4.05	2.77	2.86	3.33
37	G 37	2.50	2.79	3.50	2.43	2.67	2.78	2.68	2.78	2.47	2.31	2.51	2.55
38	G 38	3.32	3.47	4.24	2.86	3.21	3.42	3.13	3.18	3.97	2.60	2.72	3.12
39	G 39	2.45	2.92	3.47	2.47	2.71	2.80	2.65	2.88	3.83	2.50	2.70	2.91
40	G 40	3.15	3.52	4.11	2.76	3.12	3.33	3.29	3.30	3.93	2.69	2.82	3.20
	GM	2.72	2.89	3.61	2.45	2.64	2.86	2.67	2.74	3.34	2.35	2.51	2.72
	Range	2.23-3.70	2.34-3.61	3.23-4.32	2.13-2.92	2.21-3.47	2.52-3.60	2.11-3.43	2.22-3.52	2.73-4.05	2.06-2.77	2.18-3.02	2.38-3.33
	S.E. $\pm$	0.25	0.22	0.24	0.17	0.28		0.25	0.29	0.39	0.17	0.21	
	C.D. (5%)	0.50	0.44	0.49	0.33	0.55		0.50	0.58	0.78	0.34	0.42	

Note: GC – Genotype code & GM-Grand Mean

(Table Contd...)

S. No.	Genotype code	Seed yield plot ¹											
		<i>Kharif, 2018</i>						<i>Kharif, 2019</i>					
		E1	E2	E3	E4	E5	GM	E1	E2	E3	E4	E5	GM
1	G 1	223	256	261	196	217	231	243	224	257	192	219	227
2	G 2	250	262	267	223	238	248	249	246	261	227	240	245
3	G 3	234	209	213	190	222	213	201	233	211	192	233	214
4	G 4	261	269	275	226	252	257	257	254	262	222	254	250
5	G 5	216	218	223	191	201	210	208	213	219	193	209	208
6	G 6	235	184	188	192	211	202	185	220	186	196	229	203
7	G 7	246	222	227	188	235	223	215	238	224	190	237	221
8	G 8	246	205	211	180	234	215	202	245	205	179	234	213
9	G 9	221	235	240	205	210	222	225	219	236	207	215	220
10	G 10	266	273	279	220	255	258	266	260	272	223	257	256
11	G 11	225	221	226	202	214	217	214	223	222	200	218	215
12	G 12	238	224	229	199	226	223	224	230	226	200	228	222
13	G 13	238	214	218	190	226	217	214	231	215	193	231	217
14	G 14	230	238	245	181	220	223	228	223	239	182	227	220
15	G 15	229	233	240	190	216	222	226	226	234	196	223	221
16	G 16	205	221	226	193	188	206	217	202	222	191	195	205
17	G 17	213	194	198	202	200	201	188	213	194	204	204	201
18	G 18	212	217	221	191	202	209	210	206	219	188	201	205
19	G 19	231	207	213	187	217	211	200	225	208	189	222	209
20	G 20	199	234	236	186	181	207	228	196	235	190	192	208
21	G 21	210	229	234	181	194	210	219	208	232	184	206	210
22	G 22	213	226	231	191	200	212	217	207	223	193	204	209
23	G 23	193	212	215	188	183	198	216	195	216	196	186	202
24	G 24	275	273	276	220	257	260	266	270	263	234	264	260
25	G 25	226	267	248	194	216	230	260	227	266	195	220	233
26	G 26	210	253	255	203	199	224	247	212	220	207	200	217
27	G 27	204	254	259	185	190	218	245	204	223	187	192	210
28	G 28	209	211	217	190	199	205	211	209	212	192	198	204
29	G 29	214	249	254	198	202	223	238	210	215	197	205	213
30	G 30	231	206	211	189	210	209	212	234	208	193	225	214
31	G 31	217	218	224	183	204	209	214	214	219	190	206	209
32	G 32	265	278	281	218	246	258	268	268	267	220	259	256
33	G 33	229	192	202	188	217	205	208	230	196	190	217	208
34	G 34	222	215	220	180	211	210	225	226	219	185	225	216
35	G 35	229	205	210	199	217	212	242	232	241	204	236	231
36	G 36	271	283	299	227	258	268	268	266	272	235	268	262
37	G 37	215	241	247	180	201	217	227	221	243	188	209	218
38	G 38	235	238	245	181	226	225	222	227	231	189	225	219
39	G 39	213	234	231	185	201	213	240	216	242	193	221	222
40	G 40	236	240	241	174	223	223	233	229	236	198	231	226
	GM	228	232	236	195	216	221	227	226	230	198	221	220
	Range	193-271	184-283	188-299	174-227	181-258	198-268	185-268	196-270	186-272	182-235	186-268	201-262
	S.E. $\pm$	17.53	24.01	26.30	12.88	19.97		22.42	16.45	18.61	13.47	16.36	
	C.D. (5%)	34.89	47.81	52.37	25.65	39.76		44.63	32.75	37.05	26.82	32.58	

Note: GM – Grand Mean

(Table Contd...)

S. No.	Genotype code	Days to maturity											
		<i>Kharif, 2018</i>						<i>Kharif, 2019</i>					
		E1	E2	E3	E4	E5	GM	E1	E2	E3	E4	E5	GM
1	G 1	87	83	81	84	82	83	86	86	82	86	85	85
2	G 2	90	83	82	85	83	84	89	90	84	87	84	87
3	G 3	89	83	81	85	82	84	82	84	88	89	86	86
4	G 4	88	83	81	84	87	85	88	87	86	88	88	88
5	G 5	86	83	81	86	89	85	93	90	80	86	81	86
6	G 6	87	83	81	93	90	87	79	81	81	83	80	81
7	G 7	87	83	81	90	90	86	83	82	83	85	83	83
8	G 8	87	83	81	89	90	86	88	88	86	88	85	87
9	G 9	86	83	81	90	88	85	85	85	92	90	90	89
10	G 10	87	80	78	89	86	84	84	86	85	86	83	85
11	G 11	87	81	79	86	91	85	83	85	85	91	83	85
12	G 12	86	80	78	90	87	84	85	86	86	88	86	86
13	G 13	86	81	79	89	87	84	87	87	86	88	84	86
14	G 14	87	81	79	89	85	84	89	85	86	90	87	87
15	G 15	86	82	79	87	87	84	90	89	83	89	86	88
16	G 16	87	81	79	88	83	84	93	88	86	90	86	89
17	G 17	86	80	78	88	84	83	82	81	86	91	84	85
18	G 18	86	80	78	88	84	83	87	86	82	89	85	86
19	G 19	85	78	78	89	85	83	79	80	75	86	82	81
20	G 20	86	79	77	91	85	84	83	83	85	84	83	84
21	G 21	85	80	78	90	88	84	90	92	83	86	85	87
22	G 22	87	83	81	92	89	86	76	77	84	91	81	82
23	G 23	86	84	81	90	83	85	82	82	79	88	80	82
24	G 24	75	73	71	81	77	76	75	76	71	80	79	76
25	G 25	77	73	72	81	72	75	75	74	71	80	75	75
26	G 26	76	78	79	81	74	78	75	75	70	79	73	74
27	G 27	78	81	79	85	74	79	79	81	76	82	76	79
28	G 28	78	83	81	89	76	81	80	81	76	83	77	79
29	G 29	85	81	81	88	75	82	81	81	74	88	75	80
30	G 30	83	83	80	89	79	83	85	86	80	90	81	84
31	G 31	85	80	78	88	78	82	86	85	59	89	79	79
32	G 32	89	80	79	84	78	82	85	84	81	87	81	84
33	G 33	85	82	80	91	82	84	86	87	77	87	85	84
34	G 34	88	84	81	84	81	84	83	84	88	89	89	87
35	G 35	85	82	80	86	83	83	85	84	86	89	86	86
36	G 36	87	84	82	85	81	84	83	86	87	89	86	86
37	G 37	86	84	82	87	82	84	84	83	85	91	87	86
38	G 38	80	81	79	83	81	81	84	86	84	88	85	85
39	G 39	83	82	80	85	81	82	83	84	83	86	85	84
40	G 40	86	83	81	84	82	83	83	83	84	84	85	84
	GM	85	81	79	87	83	83	84	84	82	87	83	84
	Range	75-90	73-84	71-82	81-91	72-91	75-87	75-93	74-92	70-92	79-91	73-90	74-89
	S.E. $\pm$	2.27	2.03	2.20	2.39	2.88		2.42	2.51	4.49	2.57	2.69	
	C.D. (5%)	4.51	4.04	4.38	4.75	5.72		4.81	4.99	8.93	5.12	5.36	

Note: GM - Grand Mean

(Table Contd...)

S. No.	Genotype code	Oil content (%)											
		<i>Kharif, 2018</i>						<i>Kharif, 2019</i>					
		E1	E2	E3	E4	E5	GM	E1	E2	E3	E4	E5	GM
1	G 1	37	39	39	37	36	38	39	40	37	38	38	38
2	G 2	37	38	40	37	37	38	38	39	40	39	38	39
3	G 3	36	37	37	35	36	36	37	38	39	37	37	38
4	G 4	37	39	40	36	38	38	39	39	41	37	38	39
5	G 5	37	38	38	37	37	37	38	39	40	38	38	39
6	G 6	37	38	39	37	37	38	39	40	40	38	38	39
7	G 7	37	38	37	37	37	37	39	39	39	38	38	38
8	G 8	37	38	37	36	37	37	38	39	38	38	39	38
9	G 9	38	38	38	38	37	38	39	39	40	39	38	39
10	G 10	39	40	41	38	38	39	40	41	42	40	40	41
11	G 11	37	38	40	37	37	38	38	39	41	38	38	39
12	G 12	33	35	36	35	35	35	35	36	38	37	37	37
13	G 13	37	39	37	37	37	37	38	40	38	38	38	38
14	G 14	32	34	39	33	33	34	34	36	41	35	35	36
15	G 15	35	36	38	36	35	36	36	38	40	37	36	37
16	G 16	37	38	36	37	37	37	38	39	38	38	39	38
17	G 17	36	37	39	36	36	37	38	39	41	38	38	39
18	G 18	34	36	39	35	36	36	36	38	41	36	37	38
19	G 19	36	38	37	36	37	37	37	39	39	37	38	38
20	G 20	34	37	38	35	35	36	36	38	38	36	37	37
21	G 21	36	37	38	36	36	36	37	38	39	37	37	38
22	G 22	35	37	36	34	36	36	36	39	37	36	37	37
23	G 23	33	35	40	35	35	35	35	36	41	36	37	37
24	G 24	38	39	41	39	39	39	41	41	43	41	41	41
25	G 25	34	36	39	34	36	36	36	38	40	36	38	37
26	G 26	35	36	39	35	36	36	37	38	39	36	37	37
27	G 27	33	36	40	35	36	36	36	37	40	36	38	37
28	G 28	35	36	37	35	35	36	37	37	39	37	36	37
29	G 29	33	35	40	34	34	35	36	37	39	36	36	37
30	G 30	35	37	36	35	35	36	36	38	38	36	37	37
31	G 31	35	37	40	36	37	37	37	39	41	38	38	39
32	G 32	38	38	41	39	39	39	40	41	43	41	41	41
33	G 33	35	37	39	35	36	37	37	39	40	37	38	38
34	G 34	33	35	39	35	35	35	37	37	41	37	36	37
35	G 35	35	37	39	35	37	37	38	38	40	36	39	38
36	G 36	40	40	42	40	40	40	41	42	43	42	42	42
37	G 37	32	34	39	34	34	35	35	36	40	37	36	37
38	G 38	37	39	40	37	38	38	39	40	41	40	40	40
39	G 39	39	40	40	39	39	39	39	41	42	40	41	41
40	G 40	39	39	41	39	40	40	40	41	42	41	41	41
	GM	36	37	39	36	37	37	38	39	40	38	38	38
	Range	32-40	34-40	36-42	33-40	34-40	34-40	34-41	36-42	37-43	35-42	35-42	36-42
	S.E. $\pm$	1.96	1.68	1.43	1.30	1.49		1.69	1.39	1.55	1.43	1.56	
	C.D. (5%)	3.90	3.34	2.84	2.59	2.96		3.37	2.78	3.09	2.84	3.10	

Note: GM - Grand Mean

(Table Contd...)

S. No.	Genotype code	Protein content (%)											
		<i>Kharif, 2018</i>						<i>Kharif, 2019</i>					
		E1	E2	E3	E4	E5	GM	E1	E2	E3	E4	E5	GM
1	G 1	17	19	19	19	16	18	17	18	19	19	17	18
2	G 2	18	18	19	18	17	18	20	18	19	20	18	19
3	G 3	16	19	18	19	19	18	19	19	20	20	18	19
4	G 4	20	19	19	19	19	19	19	19	19	21	19	20
5	G 5	15	18	19	20	20	18	16	19	21	18	19	19
6	G 6	18	18	20	19	19	19	19	18	21	20	18	19
7	G 7	18	18	19	20	18	19	19	18	20	19	18	19
8	G 8	18	18	20	18	18	19	16	20	20	18	19	19
9	G 9	19	19	19	18	19	19	19	19	20	19	18	19
10	G 10	19	19	19	19	20	19	19	20	20	21	19	20
11	G 11	19	19	20	20	18	19	19	18	21	20	19	19
12	G 12	19	19	19	19	19	19	18	19	20	19	20	19
13	G 13	18	20	20	19	20	19	18	19	19	19	20	19
14	G 14	15	18	20	17	18	18	18	18	20	19	19	19
15	G 15	19	19	19	19	19	19	18	19	19	19	18	19
16	G 16	18	18	19	18	19	18	18	17	20	18	17	18
17	G 17	19	19	19	18	19	19	18	18	20	18	16	18
18	G 18	20	20	20	19	19	19	19	18	21	19	19	19
19	G 19	19	19	20	19	19	19	19	19	21	19	19	19
20	G 20	19	19	19	17	19	19	18	19	20	19	19	19
21	G 21	19	20	20	18	19	19	18	20	20	19	19	19
22	G 22	19	19	19	19	20	19	20	18	21	20	18	19
23	G 23	17	18	19	18	19	18	18	21	21	18	18	19
24	G 24	20	20	21	22	20	21	19	21	22	22	20	21
25	G 25	18	18	19	18	19	18	20	18	20	18	19	19
26	G 26	18	19	18	18	19	19	17	21	20	18	20	19
27	G 27	17	19	19	18	19	18	16	18	19	19	18	18
28	G 28	16	19	18	18	19	18	18	20	20	19	18	19
29	G 29	18	19	19	18	19	19	17	20	21	18	18	19
30	G 30	18	19	19	19	19	19	18	19	20	19	18	19
31	G 31	18	19	19	19	18	19	19	17	20	19	17	18
32	G 32	20	21	21	21	21	21	19	22	22	22	21	21
33	G 33	19	19	19	19	19	19	19	19	20	19	19	19
34	G 34	19	19	20	19	20	19	18	20	21	20	19	20
35	G 35	20	20	20	20	20	20	20	20	22	19	21	20
36	G 36	21	23	22	22	22	22	21	22	24	22	22	22
37	G 37	18	19	19	19	19	19	18	18	20	19	18	19
38	G 38	20	21	21	20	20	20	20	21	22	20	20	21
39	G 39	19	20	20	20	20	20	20	21	22	21	21	21
40	G 40	20	22	21	21	21	21	21	22	23	22	21	22
	GM	18	19	19	19	19	19	19	19	21	19	19	19
	Range	15-21	18-23	18-22	17-22	17-22	18-22	16-21	17-22	19-24	18-22	17-22	18-22
	S.E. $\pm$	0.98	1.08	0.84	1.17	0.99		0.84	1.37	1.01	1.24	1.27	
	C.D. (5%)	1.94	2.14	1.67	2.32	1.97		1.68	2.73	2.01	2.47	2.54	

Note: GM – Grand Mean

APPENDIX – XIII

Environment wise components of variation of different traits in Niger for *kharif*, 2018 and *kharif*, 2019

ARS, Phondaghat (E1)

Sr. No.	Characters	<i>kharif</i> , 2018			<i>kharif</i> , 2019		
		Phenotypic variance (σ^2_p)	Genotypic variance (σ^2_g)	Environmental variance (σ^2_e)	Phenotypic variance (σ^2_p)	Genotypic variance (σ^2_g)	Environmental variance (σ^2_e)
1.	DFPF	13.88	10.29	3.58	18.64	14.90	3.73
2.	PH (cm)	113.21	55.06	58.15	282.76	189.42	93.34
3.	NPBPP	7.64	6.10	1.54	6.72	4.23	2.49
4.	NSBPP	26.98	23.69	3.29	28.89	18.70	10.19
5.	NCPP	126.46	117.54	8.92	275.81	230.39	45.42
6.	CD (cm)	0.01	0.01	0.00	0.03	0.02	0.01
7.	NSPC	20.34	5.14	15.19	48.07	25.67	22.41
8.	1000 SW (g)	0.05	0.02	0.03	0.02	0.01	0.02
9.	SYPP (g)	0.15	0.06	0.09	0.14	0.04	0.09
10.	SYPP (g)	703.58	242.83	460.75	971.98	218.25	753.73
11.	DM	18.28	10.58	7.70	25.47	16.70	8.77
12.	OC (%)	7.92	2.17	5.75	5.70	1.41	4.29
13.	PC (%)	2.48	1.06	1.43	2.07	1.00	1.07

ARS, Shirgaon (E2)

Sr. No.	Characters	<i>kharif</i> , 2018			<i>kharif</i> , 2019		
		Phenotypic variance (σ^2_p)	Genotypic variance (σ^2_g)	Environmental variance (σ^2_e)	Phenotypic variance (σ^2_p)	Genotypic variance (σ^2_g)	Environmental variance (σ^2_e)
1.	DFPF	9.60	6.45	3.14	18.14	13.05	5.09
2.	PH (cm)	86.64	27.63	59.01	133.03	27.43	105.60
3.	NPBPP	7.49	4.37	3.12	4.10	1.62	2.47
4.	NSBPP	22.33	11.35	10.98	18.91	9.50	9.41
5.	NCPP	59.93	26.01	33.92	89.46	39.12	50.34
6.	CD (cm)	0.01	0.01	0.01	0.02	0.02	0.01
7.	NSPC	17.03	3.49	13.54	36.80	20.71	16.09
8.	1000 SW (g)	0.05	0.03	0.03	0.04	0.01	0.03
9.	SYPP (g)	0.12	0.05	0.07	0.18	0.05	0.13
10.	SYPP (g)	1212.80	347.74	865.06	623.53	217.71	405.81
11.	DM	10.45	4.26	6.19	22.51	13.07	9.44
12.	OC (%)	5.47	1.25	4.23	4.36	1.44	2.92
13.	PC (%)	2.28	0.54	1.74	3.65	0.82	2.83

Dept. of Agril. Botany, Dapoli (E3)

Sr. No.	Characters	<i>kharif</i> , 2018			<i>kharif</i> , 2019		
		Phenotypic variance (σ^2_p)	Genotypic variance (σ^2_g)	Environmental variance (σ^2_e)	Phenotypic variance (σ^2_p)	Genotypic variance (σ^2_g)	Environmental variance (σ^2_e)
1.	DFPF	10.98	7.56	3.42	24.47	20.20	4.27
2.	PH (cm)	96.38	26.81	69.57	315.93	194.77	121.16
3.	NPBPP	2.74	1.59	1.15	7.12	4.95	2.16
4.	NSBPP	8.37	5.86	2.51	26.21	15.58	10.64
5.	NCPP	22.90	16.86	6.05	227.17	179.31	47.86
6.	CD (cm)	0.01	0.00	0.01	0.03	0.02	0.01
7.	NSPC	16.89	3.43	13.46	52.56	26.13	26.43
8.	1000 SW (g)	0.08	0.02	0.06	0.07	0.03	0.05
9.	SYPP (g)	0.13	0.04	0.09	0.31	0.08	0.23
10.	SYPP (g)	1316.73	278.95	1037.79	826.59	307.11	519.49
11.	DM	10.00	2.74	7.26	59.85	29.64	30.21
12.	OC (%)	4.29	1.24	3.05	4.66	1.04	3.62
13.	PC (%)	1.54	0.49	1.05	2.08	0.55	1.53

(Table Contd...)

RARS, Karjat (E4)

Sr. No.	Characters	<i>kharif, 2018</i>			<i>kharif, 2019</i>		
		Phenotypic variance (σ^2_p)	Genotypic variance (σ^2_g)	Environmental variance (σ^2_e)	Phenotypic variance (σ^2_p)	Genotypic variance (σ^2_g)	Environmental variance (σ^2_e)
1.	DFPF	18.76	15.02	3.74	16.39	11.12	5.26
2.	PH (cm)	83.14	19.68	63.46	87.40	15.33	72.07
3.	NPBPP	5.79	4.36	1.42	5.59	4.52	1.07
4.	NSBPP	15.53	11.54	3.99	13.33	6.70	6.62
5.	NCPP	42.31	33.58	8.72	63.46	33.40	30.05
6.	CD (cm)	0.01	0.01	0.01	0.01	0.00	0.01
7.	NSPC	9.59	1.64	7.96	13.11	4.17	8.93
8.	1000 SW (g)	0.08	0.02	0.06	0.08	0.02	0.06
9.	SYPP (g)	0.06	0.02	0.04	0.07	0.03	0.04
10.	SYPP (g)	354.14	105.19	248.95	373.00	100.72	272.28
11.	DM	14.76	6.21	8.55	16.61	6.71	9.90
12.	OC (%)	4.38	1.85	2.53	5.01	1.96	3.05
13.	PC (%)	2.67	0.63	2.04	2.99	0.68	2.30

ARS, Palghar (E5)

Sr. No.	Characters	<i>kharif, 2018</i>			<i>kharif, 2019</i>		
		Phenotypic variance (σ^2_p)	Genotypic variance (σ^2_g)	Environmental variance (σ^2_e)	Phenotypic variance (σ^2_p)	Genotypic variance (σ^2_g)	Environmental variance (σ^2_e)
1.	DFPF	14.09	9.83	4.26	20.01	16.34	3.67
2.	PH (cm)	79.23	18.08	61.15	182.09	79.95	102.14
3.	NPBPP	6.77	3.76	3.01	4.87	3.97	0.90
4.	NSBPP	29.60	17.80	11.80	13.29	6.70	6.58
5.	NCPP	52.79	44.42	8.37	55.32	29.81	25.51
6.	CD (cm)	0.012	0.005	0.01	0.02	0.01	0.01
7.	NSPC	17.61	7.72	9.89	20.20	7.51	12.70
8.	1000 SW (g)	0.07	0.01	0.06	0.06	0.01	0.05
9.	SYPP (g)	0.15	0.04	0.12	0.09	0.03	0.07
10.	SYPP (g)	793.36	194.99	598.37	679.41	277.74	401.66
11.	DM	31.32	18.92	12.40	22.29	11.40	10.89
12.	OC (%)	4.52	1.21	3.31	5.17	1.52	3.65
13.	PC (%)	2.01	0.54	1.47	3.16	0.72	2.44

DFPF: Days to 50 per cent flowering

NCPP: No. of capitula plant⁻¹

SYPP: Seed yield plant⁻¹

PC: Protein content

PH: Plant height

CD: Capitulum diameter

SYPP: Seed yield plot⁻¹

NPBPP: No. of primary branches plant⁻¹

NSPC: No. of seeds capitulum⁻¹

DM: Days to maturity

NSBPP: No. of secondary branches plant⁻¹

SW: Seed weight

OC: Oil content

APPENDIX – XIV

Estimates of genetic parameters for quantitative and qualitative traits in Niger for *Kharif, 2018 and Kharif, 2019* ARS, Phondaghat (E1)

Sr. No.	Characters	<i>kharif, 2018</i>						<i>kharif, 2019</i>					
		PCV	GCV	H ² b	GA	GAM	Ga	PCV	GCV	H ² b	GA	GAM	Ga
1.	DFPF	8.03	6.92	74.19	5.69	12.28	A	8.11	7.25	79.97	7.11	13.36	A
2.	PH (cm)	7.75	5.41	48.64	10.66	7.77	A	13.28	10.87	66.99	23.20	18.32	A
3.	NPBPP	29.02	25.93	79.84	4.55	47.73	A	31.51	24.99	62.89	8.36	40.83	A
4.	NSBPP	35.24	33.02	87.81	9.40	63.74	A	31.33	25.20	64.72	7.17	41.77	A
5.	NCP	29.65	28.58	92.95	21.53	56.76	A	40.03	36.59	83.53	28.58	68.89	A
6.	CD (cm)	9.49	7.72	66.19	0.14	12.93	NA	15.51	13.65	77.46	0.25	24.76	NA
7.	NSPC	11.60	5.83	35.29	12.35	6.04	A	24.87	18.17	53.39	7.63	27.35	A
8.	1000 SW (g)	8.41	5.18	37.91	10.17	6.57	A	5.85	2.80	33.01	10.07	2.77	A
9.	SYPP (g)	14.37	8.96	38.89	10.31	11.52	A	13.90	7.90	32.32	10.25	9.25	A
10.	SYPP (g)	11.61	6.82	34.51	18.86	8.26	A	13.73	6.51	32.45	14.42	6.35	A
11.	DM	5.03	3.82	57.88	5.10	5.99	A	6.02	4.87	65.56	6.82	8.13	A
12.	OC (%)	7.85	4.11	27.45	1.59	4.44	NA	6.35	3.16	24.77	1.22	3.24	NA
13.	PC (%)	8.53	5.56	42.50	1.38	7.47	NA	7.75	5.39	48.33	1.43	7.72	NA
ARS, Shirgaon (E2)													
Sr. No.	Characters	<i>kharif, 2018</i>						<i>kharif, 2019</i>					
		PCV	GCV	H ² b	GA	GAM	Ga	PCV	GCV	H ² b	GA	GAM	Ga
1.	DFPF	6.75	5.54	67.25	4.29	9.36	A	8.09	6.87	71.96	6.31	12.00	A
2.	PH (cm)	6.75	3.81	31.89	6.12	4.43	A	10.32	4.68	30.62	4.90	4.38	A
3.	NPBPP	26.57	20.29	58.30	8.29	31.91	A	22.29	14.03	39.62	7.65	18.19	A
4.	NSBPP	23.96	17.08	50.83	4.95	25.08	A	21.29	15.09	50.23	4.50	22.03	A
5.	NCP	21.19	13.96	43.40	6.92	18.94	A	24.64	16.29	43.72	8.52	22.19	A
6.	CD (cm)	10.23	6.84	44.64	0.10	9.41	NA	14.23	11.81	68.81	0.21	20.18	NA
7.	NSPC	12.44	5.63	30.48	11.74	5.25	A	22.05	16.54	56.27	7.03	25.56	A
8.	1000 SW (g)	9.23	6.45	48.80	10.23	9.28	A	7.96	3.86	33.48	10.10	3.85	A
9.	SYPP (g)	11.97	7.53	39.55	10.28	9.75	A	15.48	8.26	48.49	10.25	9.08	A
10.	SYPP (g)	15.04	8.05	38.67	20.57	8.88	A	11.06	6.53	34.92	17.96	7.95	A
11.	DM	3.98	2.54	40.76	2.71	3.34	A	5.65	4.30	58.06	5.68	6.75	A
12.	OC (%)	6.28	2.99	22.76	1.10	2.94	NA	5.40	3.11	33.09	1.42	3.68	NA
13.	PC (%)	7.85	3.81	23.63	0.73	3.82	NA	9.91	4.71	22.58	0.89	4.61	NA
Dept. of Agril. Botany, Dapoli (E3)													
Sr. No.	Characters	<i>kharif, 2018</i>						<i>kharif, 2019</i>					
		PCV	GCV	H ² b	GA	GAM	Ga	PCV	GCV	H ² b	GA	GAM	Ga
1.	DFPF	7.30	6.05	68.86	4.70	10.35	A	9.55	8.67	82.56	8.41	16.24	A
2.	PH (cm)	7.14	3.76	37.82	6.63	4.09	A	12.31	9.67	61.65	22.57	15.64	A
3.	NPBPP	19.57	14.92	58.11	7.98	23.43	A	30.09	25.10	69.61	8.83	43.14	A
4.	NSBPP	24.49	20.49	70.06	4.18	35.34	A	25.01	19.28	59.41	6.27	30.61	A
5.	NCP	13.85	11.88	73.60	7.26	21.00	A	31.83	28.28	78.93	24.51	51.76	A
6.	CD (cm)	10.38	6.66	41.22	0.09	8.81	NA	15.05	12.89	73.39	0.26	22.75	NA
7.	NSPC	12.38	5.58	30.31	11.72	5.18	A	23.03	16.24	49.72	7.42	23.58	A
8.	1000 SW (g)	10.72	5.11	32.68	10.13	5.01	A	10.43	6.21	35.41	10.20	7.61	A
9.	SYPP (g)	10.04	5.67	31.89	10.24	6.59	A	16.70	8.39	35.26	10.29	8.69	A
10.	SYPP (g)	15.38	7.08	41.18	15.84	6.71	A	12.51	7.63	37.15	22.00	9.58	A
11.	DM	3.98	2.08	37.38	1.78	2.24	A	9.48	6.67	49.52	7.89	9.67	A
12.	OC (%)	5.34	2.87	28.92	1.23	3.18	NA	5.40	2.56	22.41	1.00	2.49	NA
13.	PC (%)	6.38	3.60	31.85	0.82	4.19	NA	7.00	3.60	26.41	0.78	3.81	NA

(Table Contd...)

RARS, Karjat (E4)

Sr. No.	Characters	kharif, 2018						kharif, 2019					
		PCV	GCV	H ² b	GA	GAM	Ga	PCV	GCV	H ² b	GA	GAM	Ga
1.	DFPF	9.05	8.10	80.05	7.14	14.93	A	7.30	6.01	67.88	5.66	10.20	A
2.	PH (cm)	6.70	3.26	33.67	4.45	3.27	A	6.73	2.82	17.54	8.38	2.43	A
3.	NPBPP	29.57	25.68	75.39	8.74	45.93	A	32.46	29.19	80.87	6.94	54.07	A
4.	NSBPP	26.46	22.81	74.29	6.03	40.50	A	26.47	18.77	50.30	7.78	27.42	A
5.	NCP	20.33	18.11	79.38	10.64	33.25	A	19.30	14.01	52.64	8.64	20.93	A
6.	CD (cm)	11.57	8.03	48.22	0.11	11.49	NA	11.22	5.66	25.43	0.06	5.88	NA
7.	NSPC	13.66	5.64	37.08	11.09	4.80	A	18.86	10.64	31.83	7.37	12.37	A
8.	1000 SW (g)	12.09	6.03	34.90	10.15	6.20	A	11.27	6.00	38.35	10.16	6.58	A
9.	SYPP (g)	10.30	6.04	34.34	10.18	7.29	A	11.31	7.02	38.52	10.21	8.98	A
10.	SYPP (g)	9.67	5.27	39.70	11.51	5.92	A	9.75	5.07	37.00	10.74	5.42	A
11.	DM	4.41	2.86	42.07	8.33	3.82	A	4.68	2.97	40.38	8.39	3.89	A
12.	OC (%)	5.79	3.76	42.22	1.82	5.04	NA	5.93	3.71	39.04	1.80	4.77	NA
13.	PC (%)	8.63	4.20	23.63	0.80	4.20	NA	8.90	4.26	22.90	0.82	4.20	NA

ARS, Palghar (E5)

Sr. No.	Characters	kharif, 2018						kharif, 2019					
		PCV	GCV	H ² b	GA	GAM	Ga	PCV	GCV	H ² b	GA	GAM	Ga
1.	DFPF	8.54	7.14	69.77	5.39	12.28	A	8.49	7.68	81.67	7.53	14.29	A
2.	PH (cm)	6.54	3.13	32.82	6.18	3.08	A	9.68	6.41	43.91	12.21	8.75	A
3.	NPBPP	23.84	17.77	55.56	8.98	27.29	A	30.69	27.72	81.56	6.71	51.57	A
4.	NSBPP	27.41	21.25	60.13	6.74	33.95	A	26.69	18.96	50.46	8.79	27.74	A
5.	NCP	20.80	19.08	84.14	12.59	36.06	A	20.17	14.81	53.89	8.26	22.40	A
6.	CD (cm)	10.57	6.83	41.71	0.09	9.08	NA	14.54	11.33	20.75	0.18	18.20	NA
7.	NSPC	14.94	9.90	43.85	8.79	13.50	A	20.73	12.63	37.15	8.44	15.87	A
8.	1000 SW (g)	10.98	4.58	37.37	10.10	3.93	A	9.57	4.54	32.46	10.11	4.43	A
9.	SYPP (g)	14.74	7.21	43.94	10.19	7.27	A	12.11	6.43	38.23	10.18	7.04	A
10.	SYPP (g)	13.07	6.48	44.58	14.26	6.62	A	11.76	7.52	40.88	21.95	9.91	A
11.	DM	6.74	5.24	60.41	6.97	8.39	A	5.69	4.07	51.14	4.97	5.99	A
12.	OC (%)	5.82	3.01	26.79	1.17	3.21	NA	5.98	3.24	29.44	1.38	3.63	NA
13.	PC (%)	7.41	3.84	26.80	0.78	4.09	NA	9.43	4.51	22.92	0.84	4.45	NA

PCV: Phenotypic Coefficient of Variation
 GAM: Genetic Advance Per Cent Mean
 DFPF: Days to 50 per cent flowering
 NCP: No. of capitula plant⁻¹
 SYPP: Seed yield plant⁻¹
 PC: Protein content

GCV: Genotypic Coefficient of Variation
 Ga: Gene Action
 PH: Plant height
 CD: Capitulum diameter
 SYPP: Seed yield plot⁻¹

H²b: Heritability (Broad Sense)
 NA: Non-Additive
 NPBPP: No. of primary branches plant⁻¹
 NSPC: No. of seeds capitulum⁻¹
 DM: Days to maturity

GA: Genetic Advance
 A: Additive
 NSBPP: No. of secondary branches plant⁻¹
 SW: Seed weight
 OC: Oil content

APPENDIX – XV

**Environment wise grouping of 40 Niger genotypes into different clusters by Tochers’ method during *Kharif, 2018* and *Kharif, 2019*
ARS, Phondaghat (E1)**

Cluster No.	<i>Kharif, 2018</i>		<i>Kharif, 2019</i>		
	Number of Genotypes	Name of the Genotypes	Cluster No.	Number of Genotypes	Name of the Genotypes
I	36	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G17, G18, G19, G20, G21, G22, G23, G25, G26, G27, G28, G29, G30, G31, G33, G34, G35, G37, G38, G39, G40	I	16	G3, G4, G6, G7, G8, G11, G12, G14, G15, G16, G17, G23, G30, G31, G33, G34
II	1	G16	II	11	G2, G9, G10, G13, G18, G32, G35, G36, G38, G39, G40
III	3	G32, G36, G24	III	1	G19
			IV	1	G1
			V	1	G37
			VI	1	G28
			VII	4	G25, G26, G27, G29
			VIII	1	G20
			XI	2	G5, G21
			X	1	G22
			XI	1	G24
ARS, Shirgaon (E2)					
Cluster No.	<i>Kharif, 2018</i>		<i>Kharif, 2019</i>		
	Number of Genotypes	Name of the Genotypes	Cluster No.	Number of Genotypes	Name of the Genotypes
I	31	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G30, G31, G32, G33, G34, G35, G37, G39	I	24	G1, G3, G6, G7, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G23, G24, G29, G30, G33, G34, G35, G37, G39
II	5	G25, G26, G27, G28, G29	II	8	G2, G4, G8, G31, G32, G36, G38, G40
III	3	G36, G38, G40	III	4	G25, G26, G27, G28
IV	1	G24	IV	1	G21
			V	1	G5
			VI	1	G22
			VII	1	G24

(Table Contd...)

Dept. of Agril. Botany, Dapoli (E3)

Cluster No.	<i>Kharif, 2018</i>		<i>Kharif, 2019</i>		
	Number of Genotypes	Name of the Genotypes	Cluster No.	Number of Genotypes	Name of the Genotypes
I	32	G3, G5, G6, G7, G8, G9, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G26, G27, G28, G29, G30, G31, G33, G34, G35, G37, G38, G39, G40	I	8	G1, G17, G21, G35, G36, G38, G39, G40
II	5	G1, G2, G4, G10, G32	II	20	G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G16, G18, G20, G22, G23, G34, G37
III	1	G36	III	10	G15, G19, G25, G26, G27, G28, G29, G31, G32, G33
IV	1	G25	IV	1	G30
V	1	G24	V	1	G24

RARS, Karjat (E4)

Cluster No.	<i>Kharif, 2018</i>		<i>Kharif, 2019</i>		
	Number of Genotypes	Name of the Genotypes	Cluster No.	Number of Genotypes	Name of the Genotypes
I	25	G1, G3, G5, G6, G7, G8, G9, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G27, G29, G30, G31, G34, G35	I	26	G3, G5, G6, G7, G8, G9, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G27, G29, G30, G31, G33, G34, G37
II	1	G37	II	10	G1, G2, G4, G10, G32, G35, G36, G38, G39, G40
III	1	G33	III	1	G25
IV	1	G28	IV	1	G26
V	1	G26	V	1	G28
VI	5	G2, G4, G10, G24, G32	VI	1	G24
VII	1	G25			
VIII	4	G36, G38, G39, G40			
IX	1	G11			

ARS, Palghar (E5)

Cluster No.	<i>Kharif, 2018</i>		<i>Kharif, 2019</i>		
	Number of Genotypes	Name of the Genotypes	Cluster No.	Number of Genotypes	Name of the Genotypes
I	30	G3, G5, G6, G7, G8, G9, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G26, G27, G28, G29, G30, G31, G33, G34, G35, G37, G39	I	32	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G30, G31, G33, G34, G35, G37, G38, G39, G40
II	6	G4, G10, G24, G32, G38, G40	II	5	G25, G26, G27, G28, G29
III	1	G2	III	1	G32
IV	1	G25	IV	1	G24
V	1	G1	V	1	G36
VI	1	G36			

APPENDIX - XVI

Environment wise average intra and inter cluster divergence (D & D²) in 40 genotypes of Niger during *Kharif* 2018 and *Kharif*, 2019

ARS, Phondaghat (E1)

<i>Kharif</i> , 2018				<i>Kharif</i> , 2019											
Cluster	I	II	III	Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	4.13 (17.06)	6.79 (46.10)	8.24 (67.90)	I	2.90 (8.41)	5.01 (25.10)	3.75 (14.06)	5.05 (25.50)	3.60 (12.96)	3.97 (15.76)	4.53 (20.52)	5.20 (27.04)	3.95 (15.60)	3.93 (15.44)	4.87 (23.72)
II		0.00 (0.00)	6.35 (40.32)	II		3.39 (11.49)	5.49 (30.14)	4.20 (17.64)	6.14 (37.70)	6.79 (46.10)	7.29 (53.14)	4.30 (18.49)	5.92 (35.05)	4.74 (22.47)	4.83 (23.33)
III			6.18 (38.19)	III			0.00 (0.00)	5.60 (31.36)	3.55 (12.60)	2.58 (6.66)	3.69 (13.62)	4.23 (17.89)	4.03 (16.24)	4.24 (17.98)	3.79 (14.36)
				IV				0.00 (0.00)	7.10 (40.41)	6.68 (44.62)	7.53 (56.70)	2.99 (8.94)	5.65 (31.92)	4.97 (24.70)	5.88 (34.57)
				V					0.00 (0.00)	3.46 (11.97)	3.16 (9.99)	6.45 (41.60)	4.02 (16.16)	5.13 (26.32)	4.45 (19.80)
				VI						0.00 (0.00)	3.07 (9.42)	5.68 (32.26)	4.23 (17.89)	4.63 (21.44)	4.97 (24.70)
				VII							3.13 (9.80)	6.83 (46.65)	5.18 (26.83)	5.30 (28.09)	4.90 (24.01)
				VIII								0.00 (0.00)	5.36 (28.73)	4.68 (21.90)	4.92 (24.21)
				IX									2.50 (6.25)	6.14 (37.70)	5.97 (35.64)
				X										0.00 (0.00)	3.97 (15.76)
				XI											0.00 (0.00)
ARS, Shirgaon (E2)															
<i>Kharif</i> , 2018					<i>Kharif</i> , 2019										
Cluster	I	II	III	IV	Cluster	I	II	III	IV	V	VI	VII			
	2.28 (5.20)	3.90 (15.21)	4.22 (17.81)	5.03 (25.30)	I	2.63 (6.92)	3.67 (13.47)	3.94 (15.52)	3.44 (11.83)	4.22 (17.81)	4.08 (16.65)	4.27 (18.23)			
II		2.69 (7.24)	5.78 (33.41)	4.87 (23.72)	II		3.04 (9.24)	5.82 (33.87)	4.34 (18.84)	4.46 (19.89)	4.59 (21.07)	4.63 (21.44)			
III			2.85 (8.12)	4.27 (18.23)	III			2.60 (6.76)	4.79 (22.94)	5.72 (32.72)	4.88 (23.81)	4.06 (16.48)			
IV				0.00 (0.00)	IV				0.00 (0.00)	2.73 (7.45)	6.19 (38.32)	5.68 (32.26)			
					V					0.00 (0.00)	6.09 (37.09)	6.38 (40.70)			
					VI						0.00 (0.00)	4.69 (22.00)			
					VII							0.00 (0.00)			

(Table Contd...)

Department of Agril. Botany, Dapoli (E3)

Kharif, 2018										Kharif, 2019						
Cluster		I	II	III	IV	V		Cluster	I	II	III	IV	V			
		2.63 (6.92)	4.36 (19.01)	4.40 (19.36)	3.93 (15.44)	6.18 (38.19)			3.08 (9.49)	4.84 (23.43)	5.37 (28.84)	3.99 (15.92)	5.61 (31.47)			
II			2.12 (4.49)	4.33 (18.75)	5.74 (32.95)	4.17 (17.39)		II		3.36 (11.29)	4.84 (23.43)	5.54 (30.69)	6.90 (47.61)			
III				0.00 (0.00)	5.81 (33.76)	5.46 (29.81)		III			3.89 (15.13)	5.80 (33.64)	4.83 (23.33)			
IV					0.00 (0.00)	5.72 (32.72)		IV				0.00 (0.00)	6.43 (41.34)			
V						0.00 (0.00)		V					0.00 (0.00)			
RARS, Karjat (E4)																
Kharif, 2018										Kharif, 2019						
Cluster	I	II	III	IV	V	VI	VII	VIII	IX	Cluster	I	II	III	IV	V	VI
	2.73 (7.45)	3.54 (12.53)	4.32 (18.66)	3.90 (15.21)	3.64 (13.25)	5.33 (28.41)	3.96 (15.68)	4.64 (21.53)	3.79 (14.36)	I	2.37 (5.62)	3.97 (15.76)	3.01 (9.06)	3.63 (13.18)	2.99 (8.94)	5.85 (34.22)
II		0.00 (0.00)	1.81 (3.28)	4.44 (19.71)	4.92 (24.21)	6.07 (36.84)	5.16 (26.63)	4.56 (20.79)	2.78 (7.73)	II		2.52 (6.35)	3.95 (15.60)	4.84 (23.43)	5.31 (28.20)	3.46 (11.97)
III			0.00 (0.00)	4.81 (23.14)	5.96 (35.52)	6.26 (39.19)	5.93 (35.16)	4.90 (24.01)	2.57 (6.60)	III			0.00 (0.00)	1.75 (3.06)	3.44 (11.83)	4.88 (23.81)
IV				0.00 (0.00)	2.89 (8.35)	6.29 (39.56)	3.41 (11.63)	6.34 (40.20)	4.37 (19.10)	IV				0.00 (0.00)	3.27 (10.69)	5.38 (28.94)
V					0.00 (0.00)	6.06 (36.72)	2.52 (6.35)	6.09 (37.09)	4.81 (23.14)	V					0.00 (0.00)	6.92 (47.89)
VI						3.30 (10.89)	4.89 (23.91)	4.26 (18.15)	5.52 (30.47)	VI						0.00 (0.00)
VII							0.00 (0.00)	5.74 (32.95)	5.11 (26.11)							
VIII								2.76 (7.62)	4.52 (20.43)							
IX								0.00 (0.00)								
ARS, Palghar (E5)																
Kharif, 2018								Kharif, 2019								
Cluster	I	II	III	IV	V	VI	Cluster	I	II	III	IV	V				
I	2.58 (6.66)	4.93 (24.30)	3.87 (14.98)	4.03 (16.24)	3.69 (13.62)	7.30 (53.29)	I	3.05 (9.30)	4.25 (18.06)	3.95 (15.60)	5.77 (33.29)	5.91 (34.93)				
II		3.13 (9.80)	5.73 (32.83)	4.35 (18.92)	4.15 (17.22)	4.01 (16.08)	II		2.83 (8.01)	4.74 (22.47)	5.67 (32.15)	7.10 (50.41)				
III			0.00 (0.00)	5.43 (29.48)	3.71 (13.76)	7.60 (57.76)	III			0.00 (0.00)	3.18 (10.11)	3.83 (14.67)				
IV				0.00 (0.00)	4.23 (17.89)	6.67 (44.49)	IV				0.00 (0.00)	3.87 (14.98)				
V					0.00 (0.00)	5.56 (30.91)	V					0.00 (0.00)				
VI						0.00 (0.00)										

(Figures in parenthesis indicate D² values)

APPENDIX – XVII

**Environment wise cluster mean performance for 13 characters in 40 genotypes of Niger during *Kharif*, 2018 and *Kharif*, 2019
ARS, Phondaghat (E1)**

Sr. No.	Characters	Kharif, 2018				Kharif, 2019											
		Clusters				Clusters											
		I	II	III	PM	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	PM
1.	DFFP	46.16	49.67	47.89	47.91	54.17	54.79	49.33	55.33	52.67	49.67	47.58	51.33	60.17	45.67	45.33	51.46
2.	PH (cm)	137.19	157.67	130.78	141.88	124.81	127.73	128.33	158.33	97.33	135.00	114.50	156.33	139.33	137.33	114.00	130.27
3.	NPBPP	8.94	14.33	15.00	12.76	7.69	10.18	6.00	12.33	6.33	5.33	4.92	10.33	7.00	9.67	10.33	8.19
4.	NSBPP	13.87	26.33	21.33	20.51	15.75	22.15	16.33	26.00	11.67	10.00	11.00	22.33	13.33	15.67	18.00	16.57
5.	NCPP	35.12	57.67	65.11	52.63	32.27	60.88	41.00	53.33	30.67	26.33	26.00	63.33	33.67	38.67	48.67	41.35
6.	CD (cm)	1.12	1.27	1.12	1.17	1.09	1.11	0.80	1.13	0.87	0.83	0.86	0.87	0.82	1.17	0.83	0.94
7.	NSPC	38.32	40.00	45.11	41.14	27.13	32.48	19.00	21.00	30.00	26.67	23.08	24.67	24.00	34.00	28.33	26.40
8.	1000 SW (g)	2.61	2.63	2.74	2.66	2.63	2.73	2.62	2.56	2.66	2.33	2.53	2.58	2.65	2.65	2.67	2.60
9.	SYPP (g)	2.66	2.72	3.36	2.91	2.58	2.93	2.43	2.61	2.68	2.11	2.63	2.40	2.67	2.51	2.97	2.59
10.	SYPP (g)	225.56	204.67	270.56	233.60	214.56	239.73	199.67	243.00	226.67	211.00	247.58	228.00	213.67	217.33	266.33	227.96
11.	DM	85.14	87.00	83.78	85.31	85.17	85.06	79.33	86.33	83.67	79.67	77.50	82.67	91.50	75.67	75.33	81.99
12.	OC (%)	35.37	37.00	38.89	37.09	37.08	39.00	37.33	38.67	35.33	37.00	36.17	36.00	37.50	36.33	40.67	37.37
13.	PC (%)	18.33	17.67	20.33	18.78	18.31	19.67	19.00	17.00	18.33	18.00	17.42	18.00	17.33	19.67	19.00	18.34
ARS, Shirgaon (E2)																	
Sr. No.	Characters	Kharif, 2018					Kharif, 2019										
		Clusters					Clusters										
		I	II	III	IV	PM	I	II	III	IV	V	VI	VII	PM			
1.	DFFP	47.00	40.53	45.56	38.67	42.94	52.96	54.63	46.75	58.00	61.33	46.00	44.33	52.00			
2.	PH (cm)	138.56	130.33	145.44	133.33	136.92	112.92	116.04	104.58	106.67	94.33	104.67	110.38	107.08			
3.	NPBPP	9.91	9.60	13.56	16.00	12.27	9.07	10.29	7.58	8.00	6.67	7.67	10.67	8.56			
4.	NSBPP	19.04	18.47	25.44	30.00	23.24	19.35	25.33	16.17	20.67	23.33	19.67	21.67	20.88			
5.	NCPP	36.14	32.67	42.89	49.00	40.18	36.78	46.38	28.50	46.67	45.67	37.00	38.67	39.95			
6.	CD (cm)	1.04	0.95	1.18	1.10	1.07	1.06	1.16	0.89	0.87	0.83	1.30	1.03	1.02			
7.	NSPC	32.99	30.00	38.67	38.00	34.92	26.97	30.83	22.25	24.00	32.00	38.33	23.33	28.24			
8.	1000 SW (g)	2.54	2.09	2.70	2.67	2.50	2.62	2.66	2.57	2.33	2.52	2.61	2.80	2.59			
9.	SYPP (g)	2.83	2.81	3.53	3.27	3.11	2.63	3.05	2.66	2.67	2.49	2.65	3.50	2.81			
10.	SYPP (g)	225.58	246.80	253.89	273.33	249.90	222.28	243.75	212.75	208.33	213.33	206.67	270.00	225.30			
11.	DM	81.76	79.20	82.78	72.67	79.10	84.47	86.21	77.58	91.67	90.00	77.33	75.67	83.28			
12.	OC (%)	37.25	35.73	39.56	39.00	37.89	38.31	40.04	37.50	38.33	39.33	38.67	41.33	39.07			
13.	PC (%)	18.99	18.93	21.89	20.33	20.04	18.97	20.13	19.08	20.33	18.67	18.00	21.33	19.50			

(Table Contd...)

Dept. of Agril. Botany, Dapoli (E3)

Sr. No.	Characters	<i>Kharif, 2018</i>						<i>Kharif, 2019</i>					
		Clusters						Clusters					
		I	II	III	IV	V	Population Mean	I	II	III	IV	V	Population Mean
1.	DFPF	45.76	46.40	44.00	38.33	37.67	42.43	53.42	54.42	46.70	49.33	40.67	48.91
2.	PH (cm)	138.28	132.13	142.67	132.67	142.33	137.62	158.42	142.68	137.30	161.00	120.00	143.88
3.	NPBPP	7.96	10.93	8.67	8.33	12.00	9.58	11.54	8.90	6.47	10.67	9.00	9.32
4.	NSBPP	10.84	16.33	13.33	11.67	19.00	14.23	24.58	19.03	18.70	31.67	23.00	23.40
5.	NCP	32.95	42.80	31.67	33.33	49.00	37.95	61.33	45.97	36.43	74.00	45.67	52.68
6.	CD (cm)	1.02	1.13	1.23	1.03	1.17	1.12	1.30	1.03	1.14	1.33	1.27	1.21
7.	NSPC	32.52	35.60	39.67	31.67	38.00	35.49	38.08	28.57	31.63	26.00	41.00	33.06
8.	1000 SW (g)	2.54	2.67	2.80	2.30	2.75	2.61	2.80	2.58	2.47	2.56	2.78	2.64
9.	SYPP (g)	3.57	3.63	4.32	3.43	4.19	3.83	3.68	3.25	3.25	2.79	4.05	3.40
10.	SYPP (g)	226.55	272.60	298.67	247.67	275.67	264.23	238.13	227.77	226.00	207.67	263.33	232.58
11.	DM	79.82	80.13	81.67	71.67	71.33	76.92	84.42	84.85	74.10	79.67	71.33	78.87
12.	OC (%)	38.40	40.07	42.00	39.00	41.33	40.16	40.71	39.63	39.93	38.33	42.67	40.25
13.	PC (%)	19.36	19.47	22.33	19.00	21.00	20.23	21.54	20.33	20.23	20.00	22.00	20.82

RARS, Karjat (E4)

Sr. No.	Characters	<i>Kharif, 2018</i>										<i>Kharif, 2019</i>						
		Clusters										Clusters						
		I	II	III	IV	V	VI	VII	VIII	IX	PM	I	II	III	IV	V	VI	PM
1.	DFPF	48.43	53.67	54.33	43.00	41.67	43.13	40.00	50.92	51.00	47.35	56.21	56.07	49.33	45.67	53.67	48.33	51.55
2.	PH (cm)	135.05	142.00	151.00	134.67	127.67	134.53	125.33	142.67	140.33	137.03	137.72	144.27	127.33	127.33	139.00	140.00	135.94
3.	NPBPP	6.89	9.67	11.67	8.67	6.33	11.07	9.00	10.33	11.00	9.40	6.27	9.90	7.67	6.33	4.33	11.00	7.58
4.	NSBPP	12.99	14.33	15.67	14.33	12.00	21.07	18.00	19.58	13.00	15.66	12.50	17.20	14.33	10.33	9.67	20.33	14.06
5.	NCP	29.36	29.67	32.00	27.33	24.67	44.20	32.33	36.67	32.00	32.03	37.99	49.80	40.00	36.33	33.00	55.67	42.13
6.	CD (cm)	0.97	1.00	1.00	0.83	0.97	1.00	0.87	1.14	1.03	0.98	0.98	1.06	0.93	0.93	0.90	1.13	0.99
7.	NSPC	22.43	18.00	21.33	21.33	20.33	23.73	21.33	25.33	24.33	22.02	18.41	21.73	19.00	16.67	14.67	21.33	18.64
8.	1000 SW (g)	2.36	2.44	2.42	1.61	2.00	2.59	2.14	2.53	2.38	2.27	2.44	2.66	2.19	2.13	1.73	2.73	2.31
9.	SYPP (g)	2.38	2.43	2.32	2.43	2.43	2.69	2.16	2.75	2.37	2.40	2.26	2.60	2.06	2.29	2.25	2.74	2.37
10.	SYPP (g)	190.19	179.67	188.00	190.33	203.00	221.27	194.33	191.75	202.00	195.62	192.04	210.40	195.00	206.67	192.33	234.33	205.13
11.	DM	88.36	87.33	90.67	89.33	81.33	84.60	81.33	84.42	85.67	85.89	88.09	87.07	80.33	78.67	83.33	79.67	82.86
12.	OC (%)	35.69	34.33	35.00	35.33	34.67	37.80	34.00	38.75	36.67	35.80	37.06	39.50	36.00	35.67	37.33	41.33	37.82
13.	PC (%)	18.57	18.67	19.00	17.67	18.00	19.80	18.00	20.75	19.67	18.90	18.92	20.73	18.00	18.33	19.33	22.00	19.55

ARS, Palghar (E5)

Sr. No.	Characters	<i>Kharif, 2018</i>								<i>Kharif, 2019</i>						
		Clusters								Clusters						
		I	II	III	IV	V	VI	PM		I	II	III	IV	V	PM	
1.	DFPF	43.94	42.56	51.33	38.33	47.33	46.67	45.03		54.14	44.60	51.00	45.00	55.33	50.01	
2.	PH (cm)	135.38	141.00	134.33	123.33	135.33	141.00	135.06		140.55	139.67	125.00	120.67	135.00	132.18	
3.	NPBPP	9.96	14.17	14.67	12.00	12.00	14.33	12.86		6.92	6.20	9.33	12.33	13.67	9.69	
4.	NSBPP	17.98	26.83	24.33	25.33	17.33	26.67	23.08		13.58	11.73	12.67	19.67	20.67	15.66	
5.	NCP	31.84	45.28	30.00	37.00	45.33	57.67	41.19		36.15	34.80	46.67	47.00	50.33	42.99	
6.	CD (cm)	1.00	1.14	1.07	0.93	0.97	1.23	1.06		1.00	1.00	0.93	0.93	1.27	1.03	
7.	NSPC	26.89	32.33	29.33	27.33	27.67	38.33	30.31		21.30	20.53	28.67	26.67	27.67	24.97	
8.	1000 SW (g)	2.42	2.61	2.61	2.19	2.47	2.69	2.50		2.59	2.20	2.60	2.71	2.80	2.58	
9.	SYPP (g)	2.57	2.83	2.83	2.77	2.53	3.47	2.83		2.47	2.51	2.82	3.02	2.86	2.74	
10.	SYPP (g)	207.72	243.22	238.00	216.33	217.33	258.33	230.16		220.52	203.00	259.00	264.33	268.00	242.97	
11.	DM	83.70	81.94	82.67	72.33	81.67	81.00	80.55		84.33	75.40	81.33	79.00	85.67	81.15	
12.	OC (%)	36.01	38.61	36.67	35.67	36.33	40.00	37.22		37.86	36.93	41.00	41.33	42.33	39.89	
13.	PC (%)	18.98	20.17	16.67	19.00	16.33	21.67	18.80		18.71	18.60	21.00	20.33	21.67	20.06	

APPENDIX – XVIII

Season wise and environment wise contribution of various characters towards divergence in 40 genotypes of Niger

Sr. No.	Environments	ARS, Phondaghat (E1)				ARS, Shirgaon (E2)				Dept. of Agril. Botany, Dapoli (E3)				RARS, Karjat (E4)				ARS, Phondaghat (E5)			
	Seasons	2018		2019		2018		2019		2018		2019		2018		2019		2018		2019	
	Characters	TRF	% C	TRF	% C	TRF	% C	TRF	% C	TRF	% C	TRF	% C	TRF	% C	TRF	% C	TRF	% C	TRF	% C
1.	DFPF	136	17.44%	160	20.51%	129	16.54%	152	19.49%	148	18.97%	202	25.90%	254	32.56%	198	25.38%	163	20.90%	257	32.95%
2.	PH (cm)	14	1.79%	50	6.41%	45	5.77%	9	1.15%	50	6.41%	41	5.26%	12	1.54%	13	1.67%	13	1.67%	36	4.62%
3.	NPBPP	70	8.97%	5	0.64%	129	16.54%	28	3.59%	53	6.79%	81	10.38%	157	20.13%	334	42.82%	48	6.15%	245	31.41%
4.	NSBPP	147	18.85%	17	2.18%	9	1.15%	28	3.59%	156	20.00%	30	3.85%	36	4.62%	6	0.77%	31	3.97%	32	4.10%
5.	NCPP	228	29.23%	306	39.23%	12	1.54%	44	5.64%	79	10.13%	103	13.21%	107	13.72%	68	8.72%	256	32.82%	19	2.44%
6.	CD (cm)	78	10.00%	134	17.18%	94	12.05%	212	27.18%	57	7.31%	172	22.05%	36	4.62%	19	2.44%	34	4.36%	90	11.54%
7.	NSPC	0	0.00%	39	5.00%	9	1.15%	121	15.51%	10	1.28%	20	2.56%	20	2.56%	38	4.87%	13	1.67%	22	2.82%
8.	1000 SW (g)	24	3.08%	4	0.51%	61	7.82%	20	2.56%	2	0.26%	5	0.64%	16	2.05%	29	3.72%	22	2.82%	10	1.28%
9.	SYPP (g)	8	1.03%	21	2.69%	50	6.41%	24	3.08%	36	4.62%	23	2.95%	13	1.67%	23	2.95%	20	2.56%	5	0.64%
10.	SYPP (g)	10	1.28%	3	0.38%	24	3.08%	92	11.79%	14	1.79%	26	3.33%	15	1.92%	17	2.18%	14	1.79%	34	4.36%
11.	DM	33	4.23%	2	0.26%	72	9.23%	7	0.90%	25	3.21%	37	4.74%	71	9.10%	7	0.90%	111	14.23%	0	0.00%
12.	OC (%)	1	0.13%	9	1.15%	61	7.82%	34	4.36%	62	7.95%	19	2.44%	21	2.69%	17	2.18%	16	2.05%	10	1.28%
13.	PC (%)	31	3.97%	30	3.85%	85	10.90%	9	1.15%	88	11.28%	21	2.69%	22	2.82%	11	1.41%	39	5.00%	20	2.56%

E1: ARS, Phondaghat; E2 : ARS, Shirgaon; E3 : Department of Agril. Botany, Dapoli; E4 : RARS, Karjat; E5 : ARS, Palghar

TRF : Times ranked 1st, % C : Per Cent contribution

DFPF: Days to 50 per cent flowering

PH: Plant height

NPBPP: No. of primary branches plant⁻¹

NSBPP: No. of secondary branches plant⁻¹

NCPP: No. of capitula plant⁻¹

CD: Capitulum diameter

NSPC: No. of seeds capitulum⁻¹

SW: Seed weight

SYPP: Seed yield plant⁻¹

SYPP: Seed yield plot⁻¹

DM: Days to maturity

OC: Oil content

PC: Protein content

APPENDIX - XIX

ANOVA for AMMI model for different traits of 40 Niger genotypes tested at five environments for *Kharif, 2018* and *Kharif, 2019*

Character	Days to 50 per cent flowering									
	<i>Kharif, 2018</i>					<i>Kharif, 2019</i>				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	1056.89	27.09**	3.85	42.66	39	2309.90	59.22**	9.98	65.18
Environment (E)	4	324.19	81.04**	11.53	13.09	4	308.30	77.07**	12.98	8.70
Genotype x Environment	156	1096.11	7.02**	-	44.25	156	925.78	5.93**	-	26.12
IPCA1	42	626.64	14.92**	2.12	25.30	42	591.68	14.08**	82.29	16.70
IPCA2	40	300.40	7.51**	1.06	12.13	40	241.93	6.04**	35.33	6.83
IPCA3	38	154.34	4.06**	0.57	6.23	38	85.99	2.26**	13.22	2.43
Residual	36	14.71	0.40	0.058		36	6.16	0.17	1.00	
Pooled Residual	156	1096.11	7.02	-		36	6.16	0.17	-	
Total	199	2477.20	12.44	1.77		199	3543.99	17.80	3.00	
Character	Plant height (cm)									
	<i>Kharif, 2018</i>					<i>Kharif, 2019</i>				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	4453.82	114.20**	3.33	44.91	39	10951.86	280.81**	2.87	20.33
Environment (E)	4	126.15	31.53**	0.92	1.27	4	27679.96	6919.99**	70.81	51.38
Genotype x Environment	156	5336.77	34.21**	-	53.82	156	15243.50	97.71**	-	28.29
IPCA1	42	3736.90	88.97**	6.34	37.68	42	8032.74	191.25**	3.02	14.91
IPCA2	40	814.85	20.37**	1.45	8.22	40	5076.35	126.90**	2.00	9.42
IPCA3	38	577.14	15.18**	1.08	5.82	38	1498.77	39.44**	0.62	2.78
Residual	36	207.86	5.77	0.41		36	635.62	17.65	0.27	
Pooled Residual	114	1599.86	14.03	-		114	7210.75	63.25	-	
Total	199	9916.75	49.83	1.45		199	53875.33	270.73	2.77	
Character	Number of primary branches plant ⁻¹									
	<i>Kharif, 2018</i>					<i>Kharif, 2019</i>				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	621.64	15.93**	8.32	62.69	39	520.53	13.34**	5.94	52.42
Environment (E)	4	223.79	55.94**	29.21	22.57	4	122.31	30.57**	13.62	12.32
Genotype x Environment	156	298.78	1.91**	-	30.13	156	350.21	2.24**	-	35.27
IPCA1	42	136.30	3.24**	3.38	13.74	42	125.85	2.99**	1.33	12.67
IPCA2	40	74.90	1.87**	1.95	7.55	40	109.19	2.72**	1.21	11.00
IPCA3	38	53.00	1.39**	1.45	5.34	38	72.60	1.91**	0.85	7.31
Residual	36	34.56	0.96	1.00		36	42.55	1.18	0.52	
Pooled Residual	36	34.56	0.96	-		36	350.21	2.24	-	
Total	199	991.67	4.98	3.00		199	993.06	4.99	2.22	

(Table Contd...)

Character	Number of secondary branches plant ⁻¹									
	<i>Kharif, 2018</i>					<i>Kharif, 2019</i>				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	1934.50	49.60**	6.30	37.82	39	1365.55	35.01**	3.82	29.66
Environment (E)	4	1952.00	488.00**	61.97	38.16	4	1809.59	452.39**	49.37	39.30
Genotype x Environment	156	1228.30	7.87**	-	24.01	156	1429.34	9.16**	-	31.04
IPCA1	42	672.45	16.01**	8.38	13.15	42	540.89	12.87**	2.41	11.75
IPCA2	40	285.44	7.13**	3.73	5.58	40	494.28	12.35**	2.32	10.73
IPCA3	38	201.66	5.30**	2.77	3.94	38	255.21	6.71**	1.26	5.54
Residual	36	68.74	1.90	1.00		36	138.95	3.85	0.72	
Pooled Residual	36	68.74	1.90	-		74	394.16	5.32	-	
Total	199	5114.81	25.70	3.26		199	4604.48	23.13	2.52	
Character	Number of capitula plant ⁻¹									
	<i>Kharif, 2018</i>					<i>Kharif, 2019</i>				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	6139.27	157.41**	6.11	56.03	39	10277.12	263.51**	3.34	40.88
Environment (E)	4	801.15	200.28**	7.77	7.31	4	2579.57	644.89**	8.19	10.26
Genotype x Environment	156	4016.58	25.74**	-	36.66	156	12281.49	78.72**	-	48.86
IPCA1	42	2734.39	65.10**	5.78	24.96	42	6028.59	143.53**	11.71	23.98
IPCA2	40	564.08	14.10**	1.25	5.15	40	4658.76	116.46**	9.50	18.53
IPCA3	38	506.14	13.31**	1.18	4.62	38	1153.07	30.34**	2.47	4.59
Residual	36	211.95	5.88	0.52		36	441.05	12.25	1.00	
Pooled Residual	114	1282.18	11.24	-		36	441.05	12.25	-	
Total	199	10957.01	55.06	2.13		199	25138.19	126.32	1.60	
Character	Capitulum diameter (cm)									
	<i>Kharif, 2018</i>					<i>Kharif, 2019</i>				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	0.96	0.024**	7.12	51.06	39	1.78	0.045**	4.64	47.21
Environment (E)	4	0.36	0.091**	26.35	19.15	4	0.45	0.11**	11.48	11.94
Genotype x Environment	156	0.54	0.003*	-	28.72	156	1.53	0.009*	-	40.58
IPCA1	42	0.20	0.004**	1.69	10.64	42	1.06	0.025**	2.58	28.12
IPCA2	40	0.14	0.003*	1.20	7.45	40	0.27	0.006*	0.69	7.16
IPCA3	38	0.11	0.002*	0.98	5.85	38	0.11	0.003*	0.31	2.92
Residual	36	0.08	0.002	0.78		36	0.07	0.002	0.22	
Pooled Residual	114	0.33	0.003	-		156	1.53	0.009	-	
Total	199	1.88	0.009	2.71		199	3.77	0.018	1.92	

(Table Contd...)

Character	Number of seeds capitulum ⁻¹									
	Kharif, 2018					Kharif, 2019				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	1265.26	32.44**	14.42	16.70	39	2004.89	51.40**	3.33	23.86
Environment (E)	4	5960.82	1490.20**	662.73	78.67	4	3995.85	998.96**	64.83	47.55
Genotype x Environment	156	350.77	2.24**	-	4.63	156	2403.61	15.40**	-	28.60
IPCA1	42	190.05	4.52**	2.01	2.51	42	1106.88	26.35**	2.31	13.17
IPCA2	40	134.37	3.35**	1.49	1.77	40	779.97	19.49**	1.71	9.28
IPCA3	38	25.45	0.66*	0.29	0.34	38	432.78	11.38**	1.00	5.15
Residual	36	0.90	0.02	0.011		36	83.96	2.33	0.20	
Pooled Residual	156	350.77	2.24	-		114	1296.73	11.37	-	
Total	199	7576.86	38.07	16.93		199	8404.35	42.23	2.74	
Character	1000 seed weight (g)									
	Kharif, 2018					Kharif, 2019				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	5.96	0.15**	29.38	72.95	39	3.67	0.09**	7.56	57.89
Environment (E)	4	1.40	0.35**	67.39	17.14	4	0.72	0.18**	14.47	11.36
Genotype x Environment	156	0.81	0.005*	-	9.91	156	1.94	0.01*	-	30.60
IPCA1	42	0.54	0.01**	5.67	6.61	42	0.97	0.02**	4.30	15.30
IPCA2	40	0.17	0.004*	1.91	2.08	40	0.57	0.01**	2.68	8.99
IPCA3	38	0.066	0.001*	0.76	0.81	38	0.28	0.007*	1.41	4.42
Residual	36	0.019	0.0005	0.23		36	0.10	0.003	0.56	
Pooled Residual	114	0.26	0.002	-		74	0.39	0.005	-	
Total	199	8.17	0.041	7.89		199	6.34	0.031	2.55	
Character	Seed yield plant ⁻¹ (g)									
	Kharif, 2018					Kharif, 2019				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	10.18	0.26**	12.65	22.56	39	10.62	0.27**	7.57	27.26
Environment (E)	4	31.72	7.93**	384.23	70.30	4	22.73	5.68**	158.01	58.34
Genotype x Environment	156	3.21	0.02*	-	7.11	156	5.61	0.03*	-	14.40
IPCA1	42	1.27	0.03**	3.38	2.81	42	3.08	0.07**	2.04	7.91
IPCA2	40	1.04	0.02**	2.90	2.30	40	1.21	0.03*	0.84	3.11
IPCA3	38	0.57	0.01*	1.68	1.26	38	0.88	0.02*	0.64	2.26
Residual	36	0.32	0.008	1.00		36	0.42	0.01	0.32	
Pooled Residual	36	0.32	0.008	-		156	5.61	0.03	-	
Total	199	45.12	0.22	10.98		199	38.96	0.19	5.44	

(Table Contd...)

Character	Seed yield plot ¹ (g)									
	Kharif, 2018					Kharif, 2019				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	60610.97	1554.12**	9.06	45.97	39	53359.51	1368.19**	10.17	53.01
Environment (E)	4	44487.46	11121.86**	64.86	33.74	4	26334.49	6583.62**	48.97	26.16
Genotype x Environment	156	26749.14	171.46**	-	20.29	156	20969.11	134.41**	-	20.83
IPCA1	42	20810.55	495.48**	2.89	15.78	42	14566.85	346.82**	2.58	14.47
IPCA2	40	5299.90	132.49**	0.77	4.02	40	4310.51	107.76**	0.80	4.28
IPCA3	38	403.51	10.61**	0.062	0.31	38	1669.76	43.94**	0.32	1.66
Residual	36	235.16	6.53	0.038		36	421.96	11.72	0.08	
Pooled Residual	156	26749.14	171.63	-		156	20969.11	134.41	-	
Total	199	131847.59	662.55	3.86		199	100663.11	134.41	3.76	
Character	Days to maturity									
	Kharif, 2018					Kharif, 2019				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	1251.88	32.09**	5.21	34.10	39	2530.45	64.88**	7.26	55.41
Environment (E)	4	1457.93	364.48**	59.16	39.72	4	643.63	160.90**	18.02	14.09
Genotype x Environment	156	961.04	6.16**	-	26.18	156	1392.67	8.92**	-	30.49
IPCA1	42	540.64	12.87**	2.08	14.73	42	918.41	21.86**	2.44	20.11
IPCA2	40	266.52	6.66**	1.08	7.26	40	318.35	7.95**	0.89	6.97
IPCA3	38	144.74	3.80**	0.61	3.94	38	113.35	2.98**	0.33	2.48
Residual	36	9.14	0.25	0.041		36	42.54	1.18	0.13	
Pooled Residual	156	961.04	6.16	-		156	1392.67	8.92	-	
Total	199	3670.86	18.44	2.99		199	4566.96	22.94	2.57	
Character	Oil content (%)									
	Kharif, 2018					Kharif, 2019				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	420.59	10.78**	13.36	54.96	39	409.95	10.51**	15.53	61.42
Environment (E)	4	218.71	54.67**	67.75	28.58	4	151.91	37.97**	56.13	22.76
Genotype x Environment	156	125.90	0.80*	-	16.45	156	105.55	0.67*	-	15.81
IPCA1	42	99.53	2.36**	17.07	13.01	42	69.83	1.66**	2.45	10.46
IPCA2	40	12.70	0.31*	2.28	1.66	40	17.95	0.44*	0.66	2.69
IPCA3	38	8.66	0.22*	1.64	1.13	38	12.09	0.31*	0.47	1.81
Residual	36	4.99	0.13	1.00		36	5.66	0.15	0.23	
Pooled Residual	36	4.99	0.13	-		156	105.55	0.67	-	
Total	199	765.22	3.84	4.76		199	667.41	3.35	4.95	
Character	Protein content (%)									
	Kharif, 2018					Kharif, 2019				
Source	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	152.42	3.90**	8.13	60.84	39	184.33	4.72**	7.73	49.17
Environment (E)	4	23.10	5.77**	12.01	9.22	4	95.17	23.79**	38.92	25.39
Genotype x Environment	156	74.98	0.48*	-	29.93	156	95.35	0.61*	-	25.44
IPCA1	42	28.56	0.68*	1.41	11.40	42	50.71	1.20**	1.97	13.53
IPCA2	40	22.98	0.57*	1.19	9.17	40	22.34	0.55*	0.91	5.96
IPCA3	38	13.27	0.34*	0.72	5.30	38	13.84	0.36*	0.59	3.69
Residual	36	10.15	0.28	0.58		36	8.45	0.23	0.38	
Pooled Residual	156	74.98	0.48	-		156	95.35	0.61	-	
Total	199	250.51	1.25	2.61		199	374.86	1.88	3.08	

APPENDIX – XX

Estimation of stability parameters of 40 Niger genotypes for various traits during Kharif, 2018

Sr. No.	Genotype code	Days to 50 per cent flowering								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	46.07	21	-0.855*	-1.077	-0.19	0.032	0.39	4	25
2.	G 2	48.00	5	1.004	-3.435**	-0.42	0.045	0.87	13	18
3.	G 3	45.40	24	2.203**	-0.956*	1.21	0.03	2.52	30	54
4.	G 4	45.80	23	0.688	-1.692	-0.70	0.022	1.46	22	45
5.	G 5	44.47	26	2.223**	-3.955**	0.51	0.028	1.06	17	43
6.	G 6	45.80	23	1.538	1.061	-0.40	0.024	0.83	11	34
7.	G 7	46.20	19	1.331	9.025**	-0.20	0.03	0.41	5	24
8.	G 8	46.07	21	1.818*	-1.412	0.01	0.025	0.03	2	23
9.	G 9	46.27	18	1.261	4.768**	1.40	-0.012	2.92	33	51
10.	G 10	43.40	28	1.750	2.935	0.60	0.018	1.25	19	47
11.	G 11	46.67	15	1.445	-1.402	1.70	0.008	3.54	36	51
12.	G 12	46.33	17	1.588	-1.284	-0.80	-0.004	1.66	28	45
13.	G 13	47.13	12	1.835*	-3.026**	-0.51	-0.018	1.06	17	29
14.	G 14	46.80	14	1.057	-2.058	-0.50	-0.014	1.04	16	30
15.	G 15	47.33	10	1.550	-3.485**	-0.56	-0.007	1.16	18	28
16.	G 16	47.27	11	0.962	1.029	-0.49	-0.004	1.02	15	26
17.	G 17	46.40	16	0.740	-1.733	0.70	-0.081	1.46	25	41
18.	G 18	46.13	20	1.356	-3.252**	0.32	-0.016	0.66	9	29
19.	G 19	47.93	6	0.965*	-1.145	0.21	-0.005	0.43	6	12
20.	G 20	47.67	7	1.629	-2.984*	-0.67	-0.002	1.39	21	28
21.	G 21	47.53	8	1.365	-1.133	0.04	-0.011	0.62	7	15
22.	G 22	48.33	4	1.412	3.847**	-0.30	-0.002	0.93	14	18
23.	G 23	47.27	11	1.614	1.889	-0.45	-0.022	0.73	10	21
24.	G 24	40.47	33	1.041	-2.740*	-1.35	-0.021	3.12	35	68
25.	G 25	40.87	31	1.730*	-1.914	-1.50	-0.06	0.62	8	39
26.	G 26	40.73	32	0.237	-1.945	-0.30	0.001	1.29	20	52
27.	G 27	41.87	30	1.460	1.035	-0.62	0.004	1.62	27	57
28.	G 28	41.87	30	0.237	-1.250	-0.78	-0.017	1.48	26	56
29.	G 29	42.73	29	0.622*	0.445	-0.71	-0.042	1.46	24	53
30.	G 30	44.33	27	0.164	2.142*	-0.70	-0.012	2.29	31	58
31.	G 31	44.80	25	0.392	2.829*	1.10	-0.011	2.71	32	57
32.	G 32	45.40	24	1.137	-0.924	-1.30	0.004	3.06	34	58
33.	G 33	47.47	9	0.433	0.412	1.47	0.002	0.35	3	12
34.	G 34	49.07	3	0.483	-2.003*	0.17	-0.004	1.16	18	21
35.	G 35	49.27	2	0.141	-3.797**	0.56	0.001	1.62	27	29
36.	G 36	46.80	14	-0.570	0.005	0.78	-0.012	0.85	12	26
37.	G 37	50.27	1	0.155	6.258**	0.41	-0.006	1.66	28	29
38.	G 38	46.27	18	-0.250	9.629**	0.80	-0.006	1.85	29	47
39.	G 39	47.00	13	0.370	0.505	0.89	-0.006	0.05	1	14
40.	G 40	46.00	22	0.036	11.264**	0.00	-0.006	0.06	1	23

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Plant height (cm)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	132.73	30	1.020	-18.734**	-0.74	0.020	3.39	16	46
2.	G 2	134.07	27	1.085	1.267	0.98	0.014	4.49	21	48
3.	G 3	133.33	28	1.627	-23.118**	1.29	0.080	5.91	27	55
4.	G 4	136.73	22	1.367	-2.432	0.19	0.001	0.87	3	25
5.	G 5	133.27	29	1.673	-18.093**	0.57	0.051	2.61	10	39
6.	G 6	138.13	16	2.004**	16.222	1.67	-0.008	7.65	32	48
7.	G 7	138.93	15	0.256	-5.923	-0.18	0.006	0.82	2	17
8.	G 8	131.47	34	1.230	-5.235	0.54	0.670	2.56	9	43
9.	G 9	131.00	36	1.328	42.895**	2.26	0.006	10.36	37	73
10.	G 10	135.47	24	1.719*	-8.298	1.71	-0.019	7.84	33	57
11.	G 11	141.60	8	1.588	-16.241**	0.34	0.052	1.56	8	16
12.	G 12	132.47	32	0.388	31.233**	1.94	-0.004	8.89	34	66
13.	G 13	144.33	3	1.310	-12.618*	-0.31	0.012	1.42	6	9
14.	G 14	142.07	7	1.151	-0.955	-0.60	0.044	2.75	11	18
15.	G 15	129.93	38	0.978	-17.353**	0.16	-0.012	0.73	1	39
16.	G 16	139.67	13	1.242	-14.629**	2.52	-0.007	11.55	39	52
17.	G 17	134.47	26	0.809	-8.458	1.19	0.047	5.45	25	51
18.	G 18	143.13	4	-0.268	11.665**	1.58	0.042	7.24	31	35
19.	G 19	137.33	20	-0.063*	11.057**	1.30	-0.090	5.96	28	48
20.	G 20	135.80	23	0.539	-9.995	2.28	-0.009	10.45	38	61
21.	G 21	137.07	21	1.115	-8.038	-0.62	0.090	2.84	13	34
22.	G 22	139.20	14	0.049	29.754**	0.61	0.081	2.79	12	26
23.	G 23	137.93	17	1.009	50.153**	-0.55	0.019	2.52	7	24
24.	G 24	137.60	18	1.334	-9.735	-0.81	-0.013	3.71	18	36
25.	G 25	125.93	39	0.883	-22.113**	-0.84	-0.012	3.85	19	58
26.	G 26	129.80	37	0.927	-15.773**	-0.86	-0.014	3.94	20	57
27.	G 27	131.07	35	0.244	-20.973**	-0.28	-0.008	1.28	5	40
28.	G 28	135.13	25	1.167	9.351	-1.04	-0.024	4.76	22	47
29.	G 29	132.60	31	1.550*	-7.685	-0.71	-0.010	3.25	15	46
30.	G 30	137.40	19	0.106	3.811	-1.53	-0.006	7.01	30	49
31.	G 31	136.13	23	0.938	55.237**	-1.24	-0.013	5.68	26	49
32.	G 32	132.40	33	0.862	3.436	-0.77	0.008	3.53	17	50
33.	G 33	140.60	11	-0.740*	14.596**	-0.63	0.036	2.88	14	25
34.	G 34	142.27	6	0.143	2.519	-1.13	-0.004	5.18	24	30
35.	G 35	141.53	9	2.105**	16.18**	-1.24	0.042	5.68	26	35
36.	G 36	140.20	12	1.262	1.159	-1.10	0.056	5.04	23	35
37.	G 37	140.67	10	1.037	4.661	-0.25	-0.009	1.14	4	14
38.	G 38	145.27	2	0.935	-8.631	-1.46	-0.011	6.69	29	31
39.	G 39	146.60	1	1.722**	22.263**	-2.24	-0.007	10.27	36	37
40.	G 40	142.73	5	0.889	-6.341	-1.99	0.051	9.12	35	40

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Number of primary branches plant ⁻¹								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	11	4	1.383	0.754	0.309	-0.093	0.570	17	21
2.	G 2	12	3	1.194	-0.818	-0.568	-0.677	1.236	30	33
3.	G 3	8	7	1.169	0.534	-0.760	-0.390	1.437	31	38
4.	G 4	12	3	1.790*	0.941	-1.129	-0.310	2.078	38	41
5.	G 5	8	7	1.547	-0.676	-0.220	-0.132	0.422	6	13
6.	G 6	10	5	-0.603	1.875	0.462	-0.819	1.174	29	34
7.	G 7	8	7	1.728*	7.357**	0.484	1.169	1.464	32	39
8.	G 8	8	7	0.623	2.210*	0.087	-0.469	0.495	11	18
9.	G 9	9	6	0.121*	2.664*	0.784	-0.360	1.471	33	39
10.	G 10	12	3	0.826	-4.414	0.309	-0.087	0.569	16	19
11.	G 11	10	5	0.254	0.045	-0.380	-0.216	0.724	20	25
12.	G 12	8	7	1.621*	4.941**	-0.303	-0.094	0.559	15	22
13.	G 13	8	7	1.497	2.929*	0.495	-0.648	1.110	28	35
14.	G 14	9	6	1.174	-1.341	-0.034	0.040	0.074	1	7
15.	G 15	8	7	0.859	-1.470	-0.229	0.142	0.440	7	14
16.	G 16	10	5	2.988**	0.182	1.483	-0.165	2.704	40	45
17.	G 17	8	7	2.804**	0.804	-0.084	-0.955	0.967	25	32
18.	G 18	8	7	1.541	-0.010*	1.158	-0.249	2.122	39	46
19.	G 19	8	7	3.544**	0.761	0.533	-0.150	0.981	26	33
20.	G 20	9	6	1.311	1.714	0.427	0.501	0.925	23	29
21.	G 21	8	7	-0.062	-0.735	0.271	-0.051	0.496	12	19
22.	G 22	8	7	0.509	-0.351	-0.058	-0.017	0.107	2	9
23.	G 23	8	7	0.144	-1.489	0.218	0.198	0.443	8	8
24.	G 24	14	1	0.205	-0.766	0.051	0.520	0.528	14	15
25.	G 25	9	6	0.768	-0.681	-0.882	-0.254	1.625	37	43
26.	G 26	8	7	1.154	-0.962	-0.837	0.452	1.589	36	43
27.	G 27	8	7	1.221	-0.901	-0.351	-0.277	0.696	19	26
28.	G 28	9	7	1.089	-1.110	-0.537	-0.151	0.989	27	34
29.	G 29	8	6	2.632**	-1.068	-0.210	-0.295	0.483	10	16
30.	G 30	8	7	0.919	-0.001*	-0.340	0.503	0.797	22	29
31.	G 31	7	8	1.264	-0.914	-0.263	0.049	0.481	9	17
32.	G 32	13	2	1.105	-1.316	0.278	0.087	0.513	13	15
33.	G 33	11	4	2.571**	-1.460	-0.130	0.323	0.400	5	9
34.	G 34	10	5	2.690**	-1.354	0.078	0.328	0.357	4	9
35.	G 35	11	4	1.740*	-0.426	-0.798	0.635	1.585	35	39
36.	G 36	13	2	0.991	-0.008	0.656	0.963	1.534	34	36
37.	G 37	9	6	-1.396	8.311**	0.411	-0.549	0.928	24	30
38.	G 38	11	4	-1.529	4.362**	-0.043	0.743	0.747	21	25
39.	G 39	11	4	-0.916*	12.952**	-0.202	0.529	0.644	18	22
40.	G 40	11	4	-0.889	4.785**	-0.136	0.222	0.332	3	7

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Number of secondary branches plant ⁻¹								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	18	6	0.949	0.083	0.33	-1.20	1.43	24	30
2.	G 2	19	5	0.013	-6.882**	-0.20	0.42	0.63	8	13
3.	G 3	14	10	0.396	-0.353	-0.98	0.83	2.45	30	40
4.	G 4	20	4	0.729	-0.097	-1.15	0.34	2.73	32	36
5.	G 5	13	11	0.718	-8.539**	-0.21	-1.26	1.35	21	32
6.	G 6	16	8	-0.483	0.486	1.33	-0.58	3.19	33	41
7.	G 7	15	9	0.280	14.293**	-0.07	-0.60	0.62	7	16
8.	G 8	14	10	-0.582	8.688**	-0.18	-0.15	0.45	4	14
9.	G 9	16	8	-1.002*	1.743	0.33	0.57	0.96	14	22
10.	G 10	21	3	0.014	2.051	0.24	0.00	0.57	6	9
11.	G 11	14	10	0.475	-1.804	-0.35	-0.25	0.86	12	22
12.	G 12	14	10	1.971*	-7.573**	-0.33	-0.66	1.02	16	26
13.	G 13	14	10	0.922	-6.808**	0.34	0.08	0.80	11	21
14.	G 14	14	10	1.747	-6.714**	-0.07	-0.47	0.50	5	15
15.	G 15	14	10	0.710	-7.783**	-0.52	-0.62	1.37	22	32
16.	G 16	17	7	2.600	-2.362	2.27	0.39	5.36	38	45
17.	G 17	14	10	2.935**	1.666	-0.69	1.15	1.99	28	38
18.	G 18	15	9	1.828	-6.960**	1.82	0.26	4.30	37	46
19.	G 19	14	10	3.251**	-5.049*	1.03	0.26	2.44	29	39
20.	G 20	16	8	2.205**	3.080	1.37	-0.26	3.24	34	42
21.	G 21	14	10	-0.164	-6.329*	0.30	0.20	0.73	10	20
22.	G 22	13	11	0.990	-4.049	-0.13	-0.28	0.41	3	14
23.	G 23	14	10	0.063	-8.714**	-0.03	-0.86	0.86	12	22
24.	G 24	24	1	0.029	-1.358	-1.82	0.08	4.29	36	37
25.	G 25	17	7	0.905	-6.580**	-1.46	0.76	3.52	35	42
26.	G 26	14	10	1.812*	-5.472*	-0.67	-0.69	1.72	25	35
27.	G 27	14	10	2.127**	-6.807**	-0.56	-0.46	1.40	23	33
28.	G 28	14	10	1.735*	-4.948	-0.37	-0.74	1.14	18	28
29.	G 29	13	11	2.596**	-5.831*	0.06	-0.31	0.34	2	13
30.	G 30	14	10	1.043	-7.247**	-0.21	-1.16	1.26	19	29
31.	G 31	13	11	1.556	-7.535**	-0.10	0.12	0.26	1	12
32.	G 32	23	2	1.031	-1.481	-0.01	1.12	1.12	17	19
33.	G 33	18	6	1.939*	-8.365**	-0.22	0.46	0.69	9	15
34.	G 34	15	9	2.536**	-8.153**	-0.31	-0.46	0.86	12	21
35.	G 35	18	6	1.354	-8.250**	-0.74	0.41	1.79	26	32
36.	G 36	23	2	0.928	-2.785	1.02	0.66	2.49	31	33
37.	G 37	15	9	0.283	19.622**	0.02	1.33	1.33	20	29
38.	G 38	20	4	-0.814	15.779**	0.75	0.32	1.80	27	31
39.	G 39	20	4	0.537	10.121**	-0.21	0.71	0.87	13	17
40.	G 40	21	3	-0.660*	35.059**	0.36	0.51	0.99	15	18

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Number of capitula plant ⁻¹								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	43	5	1.564	8.146	-0.22	0.001	1.07	6	11
2.	G 2	37	8	1.212	22.772**	-1.99	-0.026	9.65	34	42
3.	G 3	31	14	-0.282	13.004	-0.27	0.005	1.31	7	21
4.	G 4	43	5	1.123	3.885	-1.05	0.008	5.09	25	30
5.	G 5	32	13	0.063	22.079**	-0.59	-0.004	2.86	18	31
6.	G 6	35	10	1.176	48.724**	0.18	-0.011	0.87	4	14
7.	G 7	35	10	1.047	27.641**	-0.20	0.011	0.97	5	15
8.	G 8	32	13	1.023	40.939**	-0.42	-0.008	2.04	13	26
9.	G 9	34	11	-0.619	32.581**	0.38	-0.019	1.84	11	22
10.	G 10	44	4	0.474	3.395	0.57	-0.002	2.76	17	21
11.	G 11	33	12	0.653	6.257	-0.63	-0.009	3.05	19	31
12.	G 12	32	13	0.638	-5.455	-1.11	-0.008	5.38	28	41
13.	G 13	32	13	0.787	-2.631*	0.48	-0.009	2.33	27	40
14.	G 14	33	12	1.572	-4.785	0.02	-0.001	0.10	1	13
15.	G 15	32	13	-0.149	-9.999	-0.94	-0.001	4.56	23	36
16.	G 16	37	8	5.013**	-7.051	2.58	-0.005	12.51	36	44
17.	G 17	30	15	5.886**	6.189	-0.37	-0.008	1.79	10	25
18.	G 18	35	10	2.236**	28.966**	1.81	-0.008	8.77	33	43
19.	G 19	35	10	5.531**	7.405	1.72	-0.003	8.34	31	41
20.	G 20	36	9	3.025**	10.334	1.80	0.012	8.73	32	41
21.	G 21	31	14	0.119	1.230	-0.29	-0.006	1.41	8	22
22.	G 22	30	15	0.047	-7.485	-0.66	-0.012	3.20	20	35
23.	G 23	33	12	-0.595*	-7.718	-0.50	-0.008	2.42	16	28
24.	G 24	53	1	0.992	-1.936	1.72	-0.008	8.34	31	32
25.	G 25	34	11	0.297	-11.515	-1.09	0.012	5.28	26	37
26.	G 26	29	16	0.819	-10.660	-0.78	-0.004	3.78	22	38
27.	G 27	31	14	1.723	0.6810	-0.98	0.011	4.75	24	38
28.	G 28	28	17	1.990*	-7.993	-0.45	-0.013	2.18	15	32
29.	G 29	30	15	1.603	4.267	-0.41	-0.016	1.99	12	27
30.	G 30	32	13	1.097	-9.130	-1.24	0.018	6.01	29	42
31.	G 31	30	15	1.825*	3.369	-0.43	-0.011	2.08	14	29
32.	G 32	48	2	1.722	-5.110	2.00	-0.004	9.70	35	37
33.	G 33	34	11	1.873*	-10.168	0.35	0.006	1.70	9	20
34.	G 34	33	12	1.741	-12.05**	-0.73	0.012	3.54	21	33
35.	G 35	36	9	0.680	-10.388	-1.25	0.046	6.06	30	39
36.	G 36	46	3	1.104	0.631	3.47	0.020	16.82	37	40
37.	G 37	30	15	-2.75**	93.827**	0.04	-0.017	0.19	2	17
38.	G 38	38	7	-0.259	67.345**	0.06	0.031	0.29	3	10
39.	G 39	38	7	-1.697	73.098**	-0.22	0.016	1.07	6	13
40.	G 40	42	6	-1.194	79.767**	-0.38	0.030	1.84	11	17

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Capitulum diameter (cm)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	1.07	9	1.576	-0.001	-0.126	0.002	0.186	26	35
2.	G 2	1.12	6	1.433	0.000	0.085	-0.009	0.126	19	25
3.	G 3	1.09	8	-0.015	0.003	-0.005	0.000	0.007	1	9
4.	G 4	1.12	6	0.995	0.000	0.066	0.190	0.214	29	35
5.	G 5	1.05	10	0.181	-0.002	0.091	0.009	0.135	22	32
6.	G 6	1.05	10	-0.229	0.009*	-0.03	0.002	0.044	10	20
7.	G 7	0.97	17	0.023	0.009*	0.112	0.001	0.165	24	41
8.	G 8	0.99	15	0.217	0.005	0.040	0.002	0.059	13	28
9.	G 9	0.97	17	0.168	0.001	0.085	0.002	0.126	19	36
10.	G 10	1.11	7	0.328	0.01	0.022	0.001	0.033	8	15
11.	G 11	1.03	12	0.913	0.000	-0.087	-0.003	0.129	20	32
12.	G 12	1.05	10	0.595	0.004	-0.21	0.003	0.310	34	44
13.	G 13	0.99	15	1.301	-0.002	-0.007	0.004	0.011	3	18
14.	G 14	1.01	14	-0.088	0.000	-0.170	-0.010	0.251	32	46
15.	G 15	1.14	4	1.382	0.004	-0.139	-0.005	0.205	28	32
16.	G 16	1.07	9	1.992*	0.003	-0.145	0.130	0.251	32	41
17.	G 17	0.99	15	2.472**	0.000	-0.072	0.001	0.106	18	33
18.	G 18	1.02	13	2.631**	0.005*	0.054	-0.003	0.080	17	30
19.	G 19	1.13	5	1.346	0.000	-0.036	-0.008	0.054	12	17
20.	G 20	1.01	14	2.043*	-0.002	-0.160	-0.005	0.236	31	45
21.	G 21	1.05	10	1.511	0.003	-0.155	0.006	0.229	30	40
22.	G 22	1.03	12	0.812	-0.002	-0.052	-0.011	0.078	16	28
23.	G 23	1.01	14	0.812	-0.002	-0.107	0.001	0.158	23	37
24.	G 24	1.09	8	1.717*	0.000	0.222	0.006	0.328	35	43
25.	G 25	0.97	17	0.414	0.000	0.052	0.004	0.077	15	32
26.	G 26	0.98	16	1.425	0.000	0.011	0.000	0.016	4	20
27.	G 27	0.97	17	1.458	0.001	0.018	-0.001	0.027	7	24
28.	G 28	0.94	19	1.551	-0.001	-0.013	0.005	0.020	6	25
29.	G 29	0.91	20	0.926*	-0.001	0.129	-0.002	0.191	27	47
30.	G 30	0.97	17	1.669	0.001	-0.006	0.001	0.009	2	19
31.	G 31	1.04	11	0.032	0.013	-0.112	0.005	0.166	25	36
32.	G 32	1.02	13	0.680	0.002	0.190	0.004	0.281	33	46
33.	G 33	1.07	9	-0.332	0.001	-0.027	0.001	0.040	9	18
34.	G 34	0.96	18	0.701	0.008*	0.266	0.001	0.393	36	54
35.	G 35	1.07	9	0.867	0.000	0.051	0.002	0.075	14	23
36.	G 36	1.23	1	0.975	0.001	0.050	0.020	0.077	15	16
37.	G 37	1.03	12	1.107	0.002	-0.012	-0.001	0.018	5	17
38.	G 38	1.15	3	1.646*	0.002	0.090	-0.002	0.133	21	24
39.	G 39	1.11	7	1.105	0.001	0.032	-0.002	0.047	11	18
40.	G 40	1.19	2	1.059	0.006*	0.007	-0.004	0.011	3	5

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Number of seeds capitulum ⁻¹								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	30	8	-1.812*	-9.20	0.10	-0.001	0.141	1	9
2.	G 2	35	4	-0.290	-10.52**	0.10	0.028	0.144	3	7
3.	G 3	32	6	-0.144	-10.37**	-0.90	0.026	1.273	16	22
4.	G 4	33	5	0.496	-1.45	0.20	0.014	0.283	7	12
5.	G 5	31	7	0.428	-10.16**	-0.90	0.004	1.273	16	23
6.	G 6	31	7	0.844	29.90**	-0.70	0.001	0.990	14	21
7.	G 7	29	9	1.000	1.69	-0.90	-0.031	1.273	16	25
8.	G 8	31	7	-0.286	4.86	-0.20	0.001	0.283	7	14
9.	G 9	31	7	-1.006	-12.60**	-0.10	-0.032	0.145	4	11
10.	G 10	33	5	0.410	-6.43	-0.11	0.013	0.156	6	11
11.	G 11	29	9	3.074**	-6.70	-1.00	-0.011	1.414	17	26
12.	G 12	30	8	1.112	-10.77**	-0.80	0.021	1.132	15	23
13.	G 13	30	8	2.269**	-13.82**	-0.40	-0.016	0.566	10	18
14.	G 14	29	9	-0.345	-9.18	-0.50	0.003	0.707	11	20
15.	G 15	33	5	0.090	-5.53	0.40	0.004	0.566	10	15
16.	G 16	31	7	2.908**	5.07	-0.10	0.036	0.146	5	12
17.	G 17	29	9	4.663**	-4.61	-0.20	-0.002	0.283	7	16
18.	G 18	33	5	3.736**	6.419	0.30	0.029	0.425	9	14
19.	G 19	32	6	3.080**	-8.42	0.40	0.002	0.566	10	16
20.	G 20	29	9	2.618**	-10.48	-0.20	0.021	0.284	8	17
21.	G 21	32	6	1.372	15.01**	-0.40	-0.003	0.566	10	16
22.	G 22	31	7	0.211	-7.40	-0.20	0.019	0.284	8	15
23.	G 23	30	8	-0.403	1.94	0.10	0.016	0.142	2	10
24.	G 24	35	4	1.747	-9.20	0.50	0.025	0.708	12	16
25.	G 25	30	8	0.297	-10.17	0.10	-0.006	0.142	2	10
26.	G 26	29	9	0.054	-2.19	-0.10	0.015	0.142	2	11
27.	G 27	28	10	1.221	-12.36**	-0.40	-0.028	0.566	10	20
28.	G 28	29	9	2.786**	-8.77	-0.20	0.012	0.283	7	16
29.	G 29	27	11	1.922	-5.01	-0.70	0.013	0.990	14	25
30.	G 30	29	9	3.678**	-9.63	0.10	-0.015	0.142	2	11
31.	G 31	32	6	0.367	16.49**	1.10	-0.007	1.556	18	24
32.	G 32	35	4	0.756	-5.79	1.30	-0.001	1.839	20	24
33.	G 33	29	9	-0.665*	-5.31	-0.10	-0.008	0.142	2	11
34.	G 34	29	9	-1.338	-8.58	-0.40	-0.022	0.566	10	19
35.	G 35	31	7	-1.296	-13.47**	0.50	0.005	0.707	11	18
36.	G 36	39	1	1.353	-1.23	0.90	-0.016	1.273	16	17
37.	G 37	29	9	0.330	-1.45	0.70	0.003	0.990	14	23
38.	G 38	36	3	1.017	-14.42**	0.60	-0.003	0.849	13	16
39.	G 39	31	7	-0.840	-2.15	1.11	-0.025	1.570	19	26
40.	G 40	37	2	0.583	-15.95**	0.50	-0.014	0.707	11	13

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	1000 seed weight (g)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	2.51	14	1.24	0.031*	0.006	0.001	0.019	4	18
2.	G 2	2.65	5	1.59	0.029	0.051	0.017	0.160	21	26
3.	G 3	2.64	6	0.79	0.024	0.007	0.005	0.022	5	11
4.	G 4	2.64	6	0.53	-0.009	0.193	0.001	0.602	30	36
5.	G 5	2.57	10	0.081	0.04	0.023	0.001	0.072	16	26
6.	G 6	2.51	13	1.20	0.007	-0.005	0.001	0.016	3	16
7.	G 7	2.57	10	1.59	0.039	0.002	0.001	0.006	1	11
8.	G 8	2.34	21	1.68*	0.071	0.008	-0.002	0.025	6	27
9.	G 9	2.50	15	0.21	-0.002	0.012	-0.007	0.038	11	26
10.	G 10	2.68	3	1.10	0.007	0.110	-0.004	0.343	28	31
11.	G 11	2.52	13	0.85*	-0.002	-0.023	0.000	0.072	16	29
12.	G 12	2.67	4	1.22	-0.006	-0.013	0.004	0.041	12	16
13.	G 13	2.42	19	1.56	0.022	-0.038	-0.006	0.119	20	39
14.	G 14	2.49	16	3.31**	0.005	-0.069	-0.004	0.215	24	40
15.	G 15	2.42	19	2.50**	0.020	-0.086	-0.002	0.268	26	45
16.	G 16	2.55	11	2.02**	0.053*	-0.026	0.001	0.081	17	28
17.	G 17	2.61	7	1.85*	0.017	-0.010	0.005	0.032	8	15
18.	G 18	2.50	15	1.89*	0.020	-0.011	-0.003	0.034	9	24
19.	G 19	2.46	18	1.52	0.001	-0.01	-0.007	0.031	7	25
20.	G 20	2.49	16	2.48**	0.031*	-0.057	-0.002	0.178	22	38
21.	G 21	2.58	9	1.70*	0.028	0.007	0.004	0.022	5	14
22.	G 22	2.55	11	2.08**	0.018	-0.016	0.001	0.050	14	25
23.	G 23	2.48	17	0.64	0.006	-0.059	0.003	0.184	23	40
24.	G 24	2.68	3	1.23	-0.008	0.117	0.006	0.365	29	32
25.	G 25	2.28	22	1.51	-0.007	-0.027	-0.001	0.084	18	40
26.	G 26	2.19	24	1.41	0.036*	-0.076	0.021	0.310	27	51
27.	G 27	1.98	26	1.04	0.032*	0.675	-0.007	2.104	33	59
28.	G 28	2.05	25	-0.04	0.005	-0.407	-0.005	1.269	31	56
29.	G 29	2.11	23	0.54	0.001	-0.128	-1.40	1.456	32	55
30.	G 30	2.38	20	0.80	0.110	-0.033	0.001	0.103	19	39
31.	G 31	2.59	8	-0.74	0.026	-0.019	0.003	0.059	15	23
32.	G 32	2.54	12	-0.51	0.026	0.006	0.005	0.019	4	16
33.	G 33	2.55	11	0.35	0.009	-0.006	0.004	0.019	4	15
34.	G 34	2.49	16	-0.01	-0.004	-0.012	-0.007	0.037	10	26
35.	G 35	2.59	8	-0.38	0.011	0.015	0.004	0.047	13	21
36.	G 36	2.73	1	0.94	0.001	0.010	0.003	0.031	7	8
37.	G 37	2.58	9	0.66	0.032*	-0.016	0.001	0.050	14	23
38.	G 38	2.72	2	-0.37*	0.039*	-0.015	0.007	0.047	13	15
39.	G 39	2.51	14	-0.15	0.033*	-0.073	-0.003	0.228	25	39
40.	G 40	2.72	2	-0.01	0.053*	-0.004	0.0009	0.013	2	4

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Seed yield plant ⁻¹ (g)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	2.8	7	1.82*	-0.037	0.008	-0.066	0.067	3	10
2.	G 2	3.0	5	0.51	-0.054	-0.040	-0.025	0.055	1	6
3.	G 3	2.7	8	0.81	-0.068	0.102	-0.125	0.177	13	21
4.	G 4	2.9	6	0.02	-0.062	0.240	-0.414	0.507	36	42
5.	G 5	2.7	8	-0.19*	-0.066	0.342	0.177	0.454	35	43
6.	G 6	2.8	7	-0.85	-0.014	-0.151	0.084	0.203	19	26
7.	G 7	2.5	10	1.17	-0.071*	0.211	0.043	0.261	21	31
8.	G 8	2.7	8	-0.70	-0.082*	0.213	-0.044	0.264	22	30
9.	G 9	2.6	9	-1.69	-0.089*	0.210	0.075	0.267	23	32
10.	G 10	2.9	6	-1.44	-0.071*	0.249	-0.188	0.358	31	37
11.	G 11	2.9	6	-0.32	-0.039	-0.195	0.193	0.307	28	34
12.	G 12	2.7	8	0.55	-0.088*	-0.106	-0.064	0.144	9	17
13.	G 13	2.7	8	0.70	-0.058	-0.092	0.065	0.130	7	15
14.	G 14	2.8	7	-0.05	-0.032	0.047	0.029	0.064	2	9
15.	G 15	2.8	7	-0.59	-0.058	-0.101	0.141	0.187	16	23
16.	G 16	2.8	7	2.90**	0.177*	-0.061	-0.139	0.158	12	19
17.	G 17	2.9	6	4.17**	-0.003	-0.136	-0.112	0.200	18	24
18.	G 18	2.8	7	3.08**	0.036	-0.130	0.226	0.276	24	31
19.	G 19	2.7	8	3.23**	-0.026	0.033	0.065	0.076	5	13
20.	G 20	2.6	9	2.39**	-0.042	0.228	0.033	0.280	26	35
21.	G 21	2.9	6	1.92*	-0.052	-0.206	-0.090	0.267	23	29
22.	G 22	2.8	7	0.77	-0.022	-0.063	0.266	0.277	25	32
23.	G 23	2.9	6	0.81	-0.070	-0.266	-0.058	0.330	30	36
24.	G 24	3.3	3	1.50	-0.055	-0.108	-0.008	0.132	8	11
25.	G 25	2.8	7	-1.21	-0.079*	-0.293	-0.055	0.362	33	40
26.	G 26	2.9	6	1.63	-0.004	-0.112	-0.048	0.145	10	16
27.	G 27	2.8	7	3.87**	-0.014	0.054	-0.036	0.075	4	11
28.	G 28	2.6	9	3.99**	-0.079*	0.099	0.498	0.512	37	46
29.	G 29	2.8	7	0.25	-0.070	-0.119	-0.056	0.156	11	18
30.	G 30	2.8	7	1.71	-0.085*	0.085	0.038	0.111	6	13
31.	G 31	2.8	7	-0.41	-0.007	0.261	-0.191	0.372	32	39
32.	G 32	3.2	4	0.94	-0.073	0.032	-0.315	0.317	29	33
33.	G 33	2.9	6	0.87	-0.068	-0.141	-0.043	0.178	14	20
34.	G 34	2.7	8	1.57	-0.033	0.232	0.057	0.289	27	35
35.	G 35	2.8	7	0.09	-0.075	0.180	-0.011	0.220	20	27
36.	G 36	3.6	1	1.45	0.005	-0.294	-0.139	0.385	34	35
37.	G 37	2.8	7	1.64	-0.038	0.021	0.179	0.181	15	22
38.	G 38	3.4	2	1.99*	-0.061	-0.142	-0.080	0.191	17	19
39.	G 39	2.8	7	2.95**	-0.054	0.040	0.215	0.220	20	27
40.	G 40	3.3	3	1.73	-0.040	-0.131	-0.077	0.178	14	17

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Seed yield plot ¹ (g)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	231	6	3.60**	2.89**	-0.22	-0.004	0.86	10	16
2.	G 2	248	5	0.44	2.24	-0.61	0.002	2.40	13	18
3.	G 3	213	15	2.36*	0.79	0.12	-0.002	0.47	6	21
4.	G 4	257	4	1.31	0.82	-2.40	-0.004	9.42	27	31
5.	G 5	210	18	2.48*	0.91	0.20	0.008	0.79	9	27
6.	G 6	202	23	1.16	3.21**	4.40	0.009	17.28	33	56
7.	G 7	223	10	3.50**	0.37	2.10	-0.002	8.25	24	34
8.	G 8	215	14	0.69	1.56	3.60	-0.005	14.14	31	45
9.	G 9	222	11	4.53**	0.20	-0.16	0.029	0.63	8	19
10.	G 10	258	3	1.24	0.09	-0.40	-0.010	1.57	11	14
11.	G 11	217	13	-0.45	0.89	0.81	0.200	3.19	14	27
12.	G 12	223	10	-1.24	0.33	1.40	0.001	5.50	21	31
13.	G 13	217	13	0.54	4.56**	2.20	-0.005	8.64	25	38
14.	G 14	223	10	1.11	0.56	-1.90	-0.004	7.46	22	32
15.	G 15	222	11	2.14*	2.15*	-0.011	-0.005	0.05	1	12
16.	G 16	206	21	0.42	4.24**	-1.10	0.014	4.32	17	38
17.	G 17	201	24	1.47	1.34	2.20	0.023	8.64	25	49
18.	G 18	209	19	1.81	0.99	0.13	0.008	0.51	7	26
19.	G 19	211	17	4.12**	6.91**	2.10	-0.001	8.25	24	41
20.	G 20	207	20	3.44**	3.01**	-2.61	0.021	10.25	29	49
21.	G 21	210	18	1.48	0.35	-1.40	0.001	5.50	21	39
22.	G 22	212	16	0.40*	0.78	-0.91	0.007	3.57	15	31
23.	G 23	198	25	-1.33	5.04**	-1.10	0.016	4.32	18	43
24.	G 24	260	2	1.10	0.01	0.10	-0.003	0.39	4	6
25.	G 25	230	7	0.56	1.11	-2.30	-0.005	9.03	26	33
26.	G 26	224	9	-1.25	0.71	-3.10	0.021	12.17	30	39
27.	G 27	218	12	0.39	0.44	-4.10	0.001	16.10	32	44
28.	G 28	205	22	-0.04	0.23	0.42	0.021	1.65	12	34
29.	G 29	223	10	0.22	1.05*	-2.41	0.006	9.46	28	38
30.	G 30	209	19	0.04	1.10	2.00	0.002	7.85	23	42
31.	G 31	209	19	4.29**	0.90	0.11	0.010	0.43	5	24
32.	G 32	258	3	1.81	0.08	-1.30	-0.001	5.10	20	23
33.	G 33	205	22	-0.52	1.08	3.60	0.003	14.14	31	53
34.	G 34	210	18	3.26**	1.45	0.92	-0.004	3.61	16	34
35.	G 35	212	16	0.74	0.12	2.40	0.009	9.42	27	43
36.	G 36	268	1	1.22	0.06	-1.13	-0.032	4.44	19	20
37.	G 37	217	13	-3.58**	0.87	-2.20	-0.006	8.64	25	38
38.	G 38	225	8	-3.49**	0.56	-0.02	-0.006	0.09	2	10
39.	G 39	213	15	-3.98**	0.23	-1.12	0.001	4.40	18	33
40.	G 40	223	10	-4.67**	0.98	-0.05	0.021	0.20	3	13

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Days to maturity								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	83	5	1.25	-3.838**	0.41	-0.027	0.832	6	11
2.	G 2	84	4	2.01**	0.709	0.34	-0.035	0.691	3	7
3.	G 3	84	4	1.45	0.374	0.52	-0.028	1.055	12	16
4.	G 4	85	3	2.46**	-0.943	-0.51	-0.030	1.035	11	14
5.	G 5	85	3	2.64**	1.239	-0.6	-0.020	1.217	14	17
6.	G 6	87	1	1.39	-5.744**	-0.71	0.018	1.440	18	19
7.	G 7	86	2	2.74**	-4.703**	-0.80	0.001	1.623	19	21
8.	G 8	86	2	0.75	-3.980**	-0.90	-0.005	1.826	20	22
9.	G 9	85	3	1.64	-1.989	-0.50	0.005	1.014	8	11
10.	G 10	84	4	0.95	-6.576**	-0.30	0.004	0.609	2	6
11.	G 11	85	3	1.55	-5.524**	-1.40	-0.002	2.840	23	26
12.	G 12	84	4	1.19	-4.031**	-0.59	0.012	1.197	13	17
13.	G 13	84	4	-0.36*	-5.193**	-0.70	0.001	1.420	17	21
14.	G 14	84	4	1.93*	-5.329**	-0.50	0.004	1.014	8	12
15.	G 15	84	4	1.19	-2.090	-0.70	-0.010	1.420	17	21
16.	G 16	84	4	0.62	-3.877**	-0.30	0.000	0.609	2	6
17.	G 17	83	5	1.58	-2.476	-0.40	0.001	0.811	5	10
18.	G 18	83	5	-0.17	-2.255	0.60	8.000	8.092	25	30
19.	G 19	83	5	1.44	-2.715	-0.08	0.012	0.162	1	6
20.	G 20	84	4	-0.14	-4.474**	-0.60	0.019	1.217	14	18
21.	G 21	84	4	0.25	-1.377	-1.10	0.015	2.231	21	25
22.	G 22	86	2	0.95	-6.103**	-0.61	0.013	1.237	16	18
23.	G 23	85	3	-0.02	-1.952	0.30	0.001	0.609	2	5
24.	G 24	76	10	1.80*	-1.667	-0.50	0.014	1.014	8	18
25.	G 25	75	11	1.00	1.578	0.40	0.011	0.811	4	15
26.	G 26	78	9	1.16	-5.536**	1.40	0.006	2.840	23	32
27.	G 27	79	8	1.38	1.972	1.50	0.008	3.043	24	32
28.	G 28	81	7	0.98	0.478	1.40	0.034	2.840	23	30
29.	G 29	82	6	0.46	3.443**	1.30	0.007	2.637	22	28
30.	G 30	83	5	0.75	5.714**	0.80	0.015	1.623	19	24
31.	G 31	82	6	0.27	-2.837	0.50	0.009	1.014	9	15
32.	G 32	82	6	0.46	-2.965	0.60	-0.032	1.218	15	21
33.	G 33	84	4	0.70	2.924	0.40	0.018	0.812	5	9
34.	G 34	84	4	1.22	-6.486**	0.60	-0.031	1.217	14	18
35.	G 35	83	5	1.11	-0.862	0.20	-0.005	0.406	1	6
36.	G 36	84	4	1.03	0.935	0.70	-0.025	1.420	17	21
37.	G 37	84	4	0.57	20.936**	0.49	-0.005	0.994	7	11
38.	G 38	81	7	0.98	-9.353**	0.30	-0.004	0.609	2	9
39.	G 39	82	6	1.14	16.193**	0.40	-0.005	0.811	4	10
40.	G 40	83	5	2.26**	0.304	0.50	-0.026	1.015	10	15

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Oil content (%)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	37.93	8	1.79	6.688**	-0.27	-0.31	2.138	19	27
2.	G 2	37.53	11	0.33	6.035**	0.04	-0.14	0.343	2	13
3.	G 3	36.13	21	0.17	-0.225	-0.29	-0.31	2.293	20	41
4.	G 4	37.87	9	0.58	-0.909	-0.09	-0.62	0.939	9	18
5.	G 5	37.47	12	0.40	-1.244	-0.38	0.22	2.985	24	36
6.	G 6	37.73	10	-1.46	-0.337	-0.27	-0.09	2.117	18	28
7.	G 7	37.47	12	-0.70	3.129*	-0.82	0.24	6.428	34	46
8.	G 8	36.87	16	-0.46	8.182**	-0.75	-0.03	5.875	32	48
9.	G 9	37.87	9	0.94	6.137**	-0.57	0.18	4.469	30	39
10.	G 10	39.13	5	0.71	0.691	-0.18	-0.12	1.415	14	19
11.	G 11	37.73	10	-0.55*	-0.422	-0.01	-0.14	0.160	1	11
12.	G 12	34.87	29	-0.07	-0.064	0.01	0.81	0.810	7	36
13.	G 13	37.40	13	0.68	1.481	-0.9	0.20	7.053	36	49
14.	G 14	34.33	31	0.99	1.710	0.95	-0.45	7.456	39	70
15.	G 15	35.87	24	-0.36	1.820	0.07	0.15	0.569	3	27
16.	G 16	37.00	15	3.33**	2.230	-0.90	0.12	7.051	35	50
17.	G 17	37.00	15	3.32**	1.891	0.10	-0.32	0.846	8	23
18.	G 18	36.20	20	1.86	1.392	0.52	0.03	4.074	28	48
19.	G 19	36.67	17	4.17**	-0.423	-0.43	-0.20	3.374	26	43
20.	G 20	35.67	26	4.18**	-1.085	0.17	-0.29	1.363	13	39
21.	G 21	36.33	19	0.16	-0.103	-0.21	0.18	1.655	15	34
22.	G 22	35.53	27	0.64	5.608**	-0.50	-0.31	3.929	27	54
23.	G 23	35.33	28	0.93	2.071	0.93	0.24	7.289	38	66
24.	G 24	39.47	3	1.36	-3.456*	0.06	0.53	0.708	6	9
25.	G 25	35.67	26	-0.26	-0.894	0.56	-0.39	4.404	29	55
26.	G 26	36.07	22	-0.16	-0.800*	0.23	0.30	1.827	16	38
27.	G 27	35.93	23	1.96	-0.284	0.77	0.12	6.033	33	56
28.	G 28	35.80	25	3.99**	1.027	-0.12	0.17	0.955	10	35
29.	G 29	35.13	29	3.58**	4.292**	0.99	0.11	7.756	40	69
30.	G 30	35.53	27	2.55*	-0.336	-0.38	-0.19	2.983	23	50
31.	G 31	37.07	14	1.53	-1.124	0.31	-0.08	2.430	22	36
32.	G 32	39.00	6	1.62	0.262	0.05	0.44	0.589	4	10
33.	G 33	36.60	18	0.89	3.532*	0.29	-0.41	2.308	21	39
34.	G 34	35.47	28	4.09**	4.211**	0.66	0.32	5.180	31	59
35.	G 35	36.67	17	1.63	0.465	0.25	-0.06	1.959	17	34
36.	G 36	40.40	1	0.99	0.717	-0.13	0.10	1.023	11	12
37.	G 37	34.80	30	-1.47	2.913	0.91	0.40	7.140	37	67
38.	G 38	38.27	7	-1.42	3.928*	-0.17	-0.15	1.340	12	19
39.	G 39	39.20	4	1.04	-1.196	-0.40	0.00	3.133	25	29
40.	G 40	39.73	2	3.28*	1.511	-0.07	0.39	0.673	5	7

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Protein content (%)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	18.07	22	0.86	0.010	-0.02	0.065	0.070	4	26
2.	G 2	18.00	23	1.47	-0.442	-0.30	0.035	0.374	14	37
3.	G 3	18.40	20	0.12	0.084	0.80	-0.013	0.994	22	42
4.	G 4	19.13	11	0.97	0.323	-0.40	-0.002	0.497	18	29
5.	G 5	18.47	19	0.32	-0.254	1.30	0.024	1.616	23	42
6.	G 6	18.60	18	-0.25	-0.266	0.01	0.013	0.013	1	19
7.	G 7	18.73	16	0.23	-0.305	0.20	0.039	0.252	11	27
8.	G 8	18.60	18	0.43	-0.28	0.10	0.010	0.125	6	24
9.	G 9	18.80	15	1.72	1.776*	-0.30	-0.029	0.374	14	29
10.	G 10	19.40	7	1.34	0.611	-0.20	-0.039	0.252	11	18
11.	G 11	19.20	10	2.06**	-0.386	-0.40	0.049	0.499	19	29
12.	G 12	19.00	13	1.55	-0.359*	-0.30	0.011	0.373	13	26
13.	G 13	19.27	9	-0.57	0.207	0.30	-0.023	0.374	14	23
14.	G 14	17.53	24	1.35	0.046	0.70	0.019	0.870	21	45
15.	G 15	18.73	16	1.05	-0.412	-0.20	0.015	0.249	10	26
16.	G 16	18.40	20	1.85	2.023**	0.10	0.000	0.124	5	25
17.	G 17	18.73	16	1.76	0.143	-0.10	-0.028	0.127	7	23
18.	G 18	19.33	8	3.45	0.969*	-0.40	-0.011	0.497	18	26
19.	G 19	19.00	13	2.16**	-0.142	-0.20	0.008	0.249	10	23
20.	G 20	18.87	14	1.86	0.938	-0.11	-0.049	0.145	9	23
21.	G 21	19.27	9	0.84	0.595	-0.41	-0.011	0.510	20	29
22.	G 22	19.07	12	0.29	0.865	0.00	-0.020	0.020	3	15
23.	G 23	18.33	21	-0.33*	-0.403	0.40	-0.011	0.497	17	38
24.	G 24	20.67	3	0.99	-0.126	-0.30	0.031	0.374	14	17
25.	G 25	18.40	20	-0.70	0.323	0.01	-0.018	0.018	2	22
26.	G 26	18.67	17	1.68	-0.235	-0.10	-0.038	0.130	7	24
27.	G 27	18.33	21	1.60	1.418*	0.30	-0.030	0.374	14	35
28.	G 28	18.07	22	0.82	-0.427	0.70	-0.027	0.870	21	43
29.	G 29	18.60	18	1.61	0.440	-0.10	-0.016	0.125	6	24
30.	G 30	18.73	16	1.11	-0.183	-0.21	-0.007	0.261	12	28
31.	G 31	18.60	18	-0.11	0.544	-0.32	0.012	0.398	15	33
32.	G 32	20.67	3	0.92	-0.066	0.20	0.010	0.249	10	13
33.	G 33	19.07	12	0.96	-0.322	-0.30	-0.008	0.373	13	25
34.	G 34	19.40	7	1.29	-0.303	-0.11	-0.009	0.137	8	15
35.	G 35	19.80	5	1.08	-0.141	-0.30	0.003	0.373	13	18
36.	G 36	22.00	1	1.19	-0.201	-0.41	0.009	0.510	20	21
37.	G 37	18.73	16	0.69	0.103	-0.34	-0.006	0.423	16	32
38.	G 38	20.27	4	1.00	3.467**	-0.11	0.007	0.137	8	12
39.	G 39	19.73	6	2.61**	1.921*	0.10	0.008	0.125	6	12
40.	G 40	21.07	2	0.99	4.573**	0.30	0.010	0.373	13	15

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

APPENDIX - XXII

Estimation of stability parameters of 40 Niger genotypes for various traits during Kharif, 2019

Sr. No.	Genotype Code	Days to 50 per cent flowering								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	54	5	1.770*	-1.89	0.45	-0.33	1.15	16	21
2.	G 2	55	4	1.610	10.95**	0.94	-0.74	2.42	28	32
3.	G 3	55	4	1.386	15.75**	-1.64	-0.67	4.07	32	36
4.	G 4	56	3	1.717*	-0.83	0.23	-1.42	1.53	24	27
5.	G 5	55	4	1.650	7.68	2.40	-0.31	5.88	34	38
6.	G 6	50	9	1.320	11.20**	-0.21	-0.29	0.59	5	14
7.	G 7	53	6	1.399	7.66	-0.19	-0.47	0.66	7	13
8.	G 8	56	3	1.490	6.15	0.39	-0.87	1.29	19	22
9.	G 9	58	1	1.559	22.24**	-1.09	-0.86	2.80	29	30
10.	G 10	54	5	1.672	13.61**	-0.01	-0.85	0.85	13	18
11.	G 11	54	5	1.017	5.53	-0.73	0.30	1.81	25	30
12.	G 12	54	5	0.871	-1.69	0.07	-1.32	1.33	21	26
13.	G 13	55	4	1.592	0.77	0.31	-0.23	0.79	12	16
14.	G 14	57	2	0.959	-1.65	0.05	-0.06	0.14	1	3
15.	G 15	57	2	1.627	1.85	0.52	0.28	1.30	20	22
16.	G 16	57	2	1.375	1.11	0.18	0.16	0.47	4	6
17.	G 17	55	4	0.769	-1.30*	-1.18	0.41	2.91	30	34
18.	G 18	55	4	0.590	-0.01	0.51	0.46	1.33	21	25
19.	G 19	50	9	1.207	-0.64	0.23	0.39	0.68	8	17
20.	G 20	53	6	0.805	-1.80	-0.51	-0.75	1.46	23	29
21.	G 21	56	3	0.518	8.49*	0.90	-0.33	2.23	27	30
22.	G 22	51	8	0.656	2.77	-1.81	0.69	4.48	33	41
23.	G 23	50	9	0.988	-1.83	-0.17	0.00	0.42	3	12
24.	G 24	45	12	0.861	-0.45	0.20	0.57	0.75	11	23
25.	G 25	45	12	0.990	-7.23**	-0.02	0.72	0.72	9	21
26.	G 26	44	13	0.909	-9.78**	0.37	-0.05	0.91	14	27
27.	G 27	48	11	-0.008	4.67	0.55	0.10	1.35	22	33
28.	G 28	49	10	0.166	2.92	0.13	0.66	0.73	10	20
29.	G 29	50	9	0.651	9.25**	0.28	1.69	1.82	26	35
30.	G 30	53	6	0.546	7.92	0.39	0.85	1.28	18	24
31.	G 31	52	7	0.471	1.90	1.14	0.23	2.80	29	36
32.	G 32	53	6	0.592	-1.50	0.40	0.56	1.13	15	21
33.	G 33	54	5	0.733	0.66	0.72	0.44	1.81	25	30
34.	G 34	56	3	0.407	17.04**	-1.33	-0.21	3.26	31	34
35.	G 35	56	3	0.820	-2.60	-0.72	0.44	1.81	25	28
36.	G 36	56	3	1.209	0.50	-0.51	-0.14	1.26	17	20
37.	G 37	56	3	0.787	17.87**	-0.98	0.36	2.42	28	31
38.	G 38	54	5	0.821	15.92**	-0.24	-0.09	0.59	5	10
39.	G 39	54	5	0.881	8.15	-0.11	0.11	0.29	2	7
40.	G 40	53	6	0.917	23.39**	0.11	0.55	0.61	6	12

*Significant at 5% level of significance **Significant at 1% level of significance

Rmi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype Code	Plant height (cm)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	142	3	3.247**	97.667**	2.41	0.009	3.81	31	34
2.	G 2	138	5	1.151	50.549**	2.89	-0.005	4.57	37	42
3.	G 3	122	16	4.992**	-69.718**	2.61	-0.015	4.13	34	50
4.	G 4	137	6	1.950	-3.365	0.38	0.005	0.60	5	11
5.	G 5	134	8	5.797**	-8.743	0.46	0.020	0.73	7	15
6.	G 6	133	9	3.973*	68.959**	0.13	0.008	0.21	3	12
7.	G 7	128	14	4.023**	-48.159**	-0.51	0.005	0.81	9	23
8.	G 8	117	18	2.845	-44.221**	1.01	-0.018	1.58	20	38
9.	G 9	130	12	0.846	-4.023	-0.22	0.001	0.35	4	16
10.	G 10	136	7	1.091	-13.306	0.77	0.016	1.22	15	22
11.	G 11	127	15	-0.714	-72.946**	0.75	-0.003	1.19	14	29
12.	G 12	134	8	0.900	25.023**	0.92	0.004	1.46	19	27
13.	G 13	132	10	0.602	-56.713**	2.17	0.008	3.43	28	38
14.	G 14	138	5	-1.185	-63.234**	-0.57	-0.017	0.90	10	15
15.	G 15	132	10	0.548	92.168**	0.58	-0.001	0.92	11	21
16.	G 16	131	11	1.705	-49.455**	-0.43	0.005	0.68	6	17
17.	G 17	142	3	1.063	89.927**	-2.21	0.014	3.50	29	32
18.	G 18	133	9	4.880**	-8.026	0.68	-0.004	1.08	13	22
19.	G 19	134	8	0.518	-8.621	0.04	-0.002	0.06	2	10
20.	G 20	150	1	1.490	-88.346**	0.84	0.018	1.33	16	17
21.	G 21	137	6	2.084	-6.801	0.90	0.011	1.42	18	24
22.	G 22	131	11	-0.642	-37.731**	1.39	-0.004	2.20	24	35
23.	G 23	128	14	-1.839	-98.032**	-0.02	0.001	0.03	1	15
24.	G 24	121	17	1.035	-9.602	0.49	-0.018	0.78	8	25
25.	G 25	117	18	1.743	-5.546	1.29	-0.009	2.04	23	41
26.	G 26	113	19	1.981	-9.983	-0.89	-0.015	1.41	17	36
27.	G 27	137	6	0.722	-84.621**	-1.04	0.015	1.65	21	27
28.	G 28	132	10	0.623	-71.078**	1.01	-0.002	1.58	20	30
29.	G 29	134	8	-1.819	-61.693**	-1.94	0.001	3.07	27	35
30.	G 30	140	4	-1.786	25.238	-0.51	0.009	0.81	9	13
31.	G 31	133	9	0.049	-105.65**	-1.82	-0.002	2.88	25	34
32.	G 32	128	14	-0.339	-3.244	2.71	-0.009	4.29	36	50
33.	G 33	131	11	-1.236	-79.068**	-0.51	-0.017	0.81	9	20
34.	G 34	128	14	0.736	-67.626**	-0.63	-0.014	1.00	12	26
35.	G 35	136	7	1.251	-3.137	-2.51	-0.001	3.97	32	39
36.	G 36	129	13	0.164	-3.537	-1.93	-0.004	3.05	26	39
37.	G 37	127	15	-1.144	24.640	-2.63	-0.009	4.16	35	50
38.	G 38	138	5	1.976	47.057**	-2.38	-0.005	3.77	30	35
39.	G 39	134	8	1.172	46.693**	-2.56	-0.006	4.05	33	41
40.	G 40	147	2	4.082**	-10.162	-1.15	0.101	1.82	22	24

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Number of primary branches plant ⁻¹								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	10	3	-0.521	1.962	-0.35	0.029	0.40	13	16
2.	G 2	10	3	-0.046	3.416**	-0.40	0.014	0.46	14	17
3.	G 3	6	7	0.691	-0.563	0.40	0.010	0.46	14	21
4.	G 4	11	2	0.987	-2.384	-0.44	0.006	0.51	16	18
5.	G 5	7	6	0.119	3.581**	-0.42	0.011	0.48	15	21
6.	G 6	8	5	0.452	4.333**	0.01	-0.012	0.02	1	6
7.	G 7	8	5	1.178	4.516**	-0.81	-0.010	0.93	25	30
8.	G 8	7	6	1.148	0.890	0.18	0.022	0.21	6	12
9.	G 9	8	5	0.968*	1.224	0.51	0.031	0.59	20	25
10.	G 10	10	3	1.124	2.345	0.17	0.023	0.20	5	8
11.	G 11	7	6	1.827*	-0.400	-0.8	0.007	0.92	24	30
12.	G 12	8	5	1.638	0.564	-0.6	-0.003	0.69	22	27
13.	G 13	7	6	2.053**	2.478	-0.52	0.039	0.60	21	27
14.	G 14	8	5	1.160	-1.006	0.17	0.009	0.20	5	10
15.	G 15	7	6	1.583	0.151	1.30	0.021	1.50	29	35
16.	G 16	7	6	2.145**	-0.765	-0.19	-0.006	0.22	7	13
17.	G 17	7	6	2.447**	-0.362	-1.00	0.012	1.15	27	33
18.	G 18	7	6	2.248**	0.751	0.42	0.018	0.48	15	21
19.	G 19	6	7	1.952*	5.152**	0.60	-0.004	0.69	22	29
20.	G 20	8	5	3.212**	-0.730	0.47	0.019	0.54	18	23
21.	G 21	7	6	0.232	-0.611	-0.71	0.001	0.82	23	29
22.	G 22	7	6	0.434	-0.894	0.50	0.025	0.58	19	25
23.	G 23	8	5	0.915	-0.175*	0.11	-0.017	0.13	3	8
24.	G 24	11	2	0.949	-1.213	0.80	-0.012	0.92	24	26
25.	G 25	7	6	0.721	-0.965	0.42	-0.010	0.48	15	21
26.	G 26	6	7	1.154	-0.694	0.40	-0.031	0.46	14	21
27.	G 27	7	6	0.564	-0.445	0.32	-0.022	0.37	11	17
28.	G 28	6	7	1.363	2.618	-0.31	-0.002	0.36	10	17
29.	G 29	7	6	0.842	-1.249	-0.21	-0.022	0.24	8	14
30.	G 30	8	5	0.986	-0.963	-0.71	0.009	0.82	23	28
31.	G 31	7	6	1.221	1.424	-0.33	-0.021	0.38	12	18
32.	G 32	11	2	0.897	-1.132	0.90	-0.002	1.04	26	28
33.	G 33	7	6	1.580	-0.860	1.10	-0.003	1.27	28	34
34.	G 34	9	4	0.418	-0.746	0.23	0.009	0.27	9	13
35.	G 35	10	3	2.018**	0.608	-0.31	0.000	0.36	10	13
36.	G 36	12	1	1.016	0.649	-0.11	-0.018	0.13	3	4
37.	G 37	8	5	-0.733	3.905**	0.12	-0.021	0.14	4	9
38.	G 38	10	3	0.356	7.545**	0.09	-0.012	0.10	2	5
39.	G 39	10	3	-0.281	3.820**	-0.41	-0.230	0.53	17	20
40.	G 40	11	2	0.382	7.583**	-0.52	-0.006	0.60	21	23

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Number of secondary branches plant ⁻¹								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	19	5	0.067	15.912**	0.40	1.89	1.94	36	41
2.	G 2	21	3	-0.813*	-1.616	-0.09	1.07	1.07	24	27
3.	G 3	15	9	1.318	-7.004	-0.68	0.04	0.75	10	19
4.	G 4	19	5	0.438	-0.100	-0.60	0.53	0.84	17	22
5.	G 5	17	7	0.222	-5.672	0.18	-0.81	0.83	16	23
6.	G 6	15	9	0.601	24.002**	-1.10	-0.77	1.43	32	41
7.	G 7	15	9	0.579	9.009**	-0.46	-0.06	0.51	7	16
8.	G 8	17	7	0.024	8.069**	1.01	-0.46	1.20	28	35
9.	G 9	18	6	0.033	-2.184	-0.21	0.38	0.44	5	11
10.	G 10	20	4	1.624	-2.540	-0.23	1.82	1.84	34	38
11.	G 11	14	10	3.027**	-4.252	-0.31	-0.06	0.34	1	11
12.	G 12	17	7	1.988	-6.790	-0.88	0.14	0.97	21	28
13.	G 13	16	8	1.303	-1.583	-0.13	1.26	1.27	29	37
14.	G 14	17	7	1.276	-4.962	1.03	0.24	1.15	25	32
15.	G 15	15	9	1.290	-3.936	-1.21	0.20	1.34	30	39
16.	G 16	16	8	2.071*	-5.052	0.58	-0.41	0.76	11	19
17.	G 17	16	8	3.221**	2.429	1.64	0.59	1.89	35	43
18.	G 18	16	8	2.023*	-5.254	0.01	1.44	1.44	33	41
19.	G 19	16	8	3.416**	-0.041	-0.72	-0.12	0.80	14	22
20.	G 20	19	5	2.526*	-8.863	-0.86	0.67	1.16	26	31
21.	G 21	16	8	0.804	0.815	0.65	-0.75	1.03	22	30
22.	G 22	15	9	0.001	-7.781	-0.33	-0.07	0.37	2	11
23.	G 23	15	9	0.132	-7.584	-0.47	-0.57	0.77	12	21
24.	G 24	21	3	1.157	-4.949	-0.32	-0.64	0.73	9	12
25.	G 25	14	10	0.192	-6.666*	-0.41	-0.12	0.46	6	16
26.	G 26	13	11	0.841	-0.550	-0.61	-1.16	1.34	30	41
27.	G 27	15	9	1.742	-4.172	0.85	-0.74	1.19	27	36
28.	G 28	13	11	0.940	-11.99**	1.20	-0.36	1.36	31	42
29.	G 29	14	10	0.915	-6.509	0.19	-0.78	0.81	15	25
30.	G 30	18	6	1.026	-1.651	2.46	-0.14	2.70	37	43
31.	G 31	17	7	1.167	-4.922	0.27	-1.15	1.19	27	34
32.	G 32	22	2	1.564	-6.976	0.67	0.60	0.95	19	21
33.	G 33	16	8	0.736	1.354	-0.45	-0.60	0.78	13	21
34.	G 34	17	7	0.960	-1.942	-0.93	0.26	1.05	23	30
35.	G 35	21	3	2.046**	-3.660	0.78	0.45	0.96	20	23
36.	G 36	23	1	0.922	-4.553	-0.18	-0.32	0.38	3	4
37.	G 37	15	9	1.295	4.477	-0.07	-0.91	0.91	18	27
38.	G 38	20	4	0.314	-0.955	-0.06	-0.53	0.53	8	12
39.	G 39	20	4	-0.290	5.374	-0.29	0.13	0.34	1	5
40.	G 40	22	2	0.685	16.599**	-0.31	-0.19	0.39	4	6

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Number of capitula plant ⁻¹								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	48	6	0.713	88.38**	0.39	-0.60	0.78	4	10
2.	G 2	51	4	0.153	98.09**	0.87	2.18	2.45	29	33
3.	G 3	38	14	0.249	42.59**	-0.53	0.04	0.69	3	17
4.	G 4	43	9	0.039	4.70	-1.61	0.09	2.09	21	30
5.	G 5	38	14	-0.175	15.55	-1.7	0.51	2.26	25	39
6.	G 6	34	18	0.622	90.46**	-1.43	1.03	2.12	22	40
7.	G 7	35	17	0.162	60.80**	-0.67	1.27	1.54	15	32
8.	G 8	34	18	-0.218	97.12**	-1.96	0.22	2.55	30	48
9.	G 9	47	7	0.908	65.52**	2.47	-1.39	3.49	35	42
10.	G 10	51	4	1.047	-5.90	1.85	-2.54	3.49	35	39
11.	G 11	33	19	1.380	-22.17	-0.99	0.19	1.30	10	29
12.	G 12	38	14	2.141*	-1.61	-0.25	-0.96	1.01	8	22
13.	G 13	44	8	2.098*	-28.23**	3.47	0.48	4.52	38	46
14.	G 14	42	10	1.597	-27.67**	0.78	1.08	1.48	14	24
15.	G 15	37	15	1.079	-36.80**	-1.57	-2.21	3.00	33	48
16.	G 16	36	16	2.464*	16.51	-0.31	1.36	1.42	12	28
17.	G 17	39	13	2.303*	-7.54	0.48	2.12	2.21	24	37
18.	G 18	43	9	1.184	-17.58	1.94	-2.55	3.58	36	45
19.	G 19	38	14	2.660*	-8.02	-0.37	-0.45	0.66	2	16
20.	G 20	48	6	2.110*	-20.81**	1.60	-0.92	2.27	26	32
21.	G 21	40	12	0.386	-7.46	-0.58	-0.43	0.86	5	17
22.	G 22	35	17	0.072	-12.10	-0.26	-0.92	0.98	7	24
23.	G 23	35	17	1.485	-10.55	-1.75	-0.85	2.42	28	45
24.	G 24	47	7	1.313	-8.31	-0.33	-1.05	1.13	9	16
25.	G 25	30	21	0.906	-17.37	-1.38	-1.07	2.08	20	41
26.	G 26	32	20	-0.124	44.92**	-2.15	-0.66	2.86	32	52
27.	G 27	33	19	0.715	-28.86**	-0.35	-0.17	0.48	1	20
28.	G 28	33	19	1.047	24.35**	0.30	1.68	1.72	18	37
29.	G 29	30	21	1.460	-32.92**	-0.61	-0.43	0.90	6	27
30.	G 30	41	11	1.284	7.52	1.62	3.16	3.79	37	48
31.	G 31	41	11	0.939	4.56	-2.16	1.53	3.19	34	45
32.	G 32	49	5	1.258	-6.79	-0.50	-1.14	1.31	11	16
33.	G 33	36	16	-0.105	93.17**	-0.93	-0.85	1.47	13	29
34.	G 34	38	14	1.475	1.38	-0.21	-1.54	1.56	16	30
35.	G 35	51	4	1.453	11.80	2.05	-0.04	2.65	31	35
36.	G 36	57	1	1.054	-4.05	1.76	0.06	2.28	27	28
37.	G 37	40	12	0.071	77.43**	-0.52	1.51	1.65	17	29
38.	G 38	49	5	1.096	12.07	0.27	2.01	2.04	19	24
39.	G 39	52	3	0.203	58.33**	1.67	-0.13	2.16	23	26
40.	G 40	55	2	0.889	34.34**	1.61	0.39	2.12	12	14

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Capitulum diameter (cm)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	1.09	10	-0.218	0.009*	0.14	-0.070	0.55	18	28
2.	G 2	0.99	19	0.697	-0.002	0.02	0.018	0.08	5	24
3.	G 3	1.05	13	0.021	-0.001	0.12	0.040	0.47	16	29
4.	G 4	1.03	15	-0.247	0.005	0.20	0.009	0.78	22	37
5.	G 5	0.97	20	0.826	-0.004	-0.18	-0.002	0.71	21	41
6.	G 6	1.03	15	1.952*	0.008	0.11	-0.034	0.43	15	30
7.	G 7	0.93	23	0.713	0.001	-0.01	0.100	0.11	8	31
8.	G 8	1.07	11	1.033	-0.002	0.44	-0.001	1.72	29	40
9.	G 9	1.04	14	2.024**	0.007*	0.15	-0.003	0.59	20	34
10.	G 10	0.94	22	1.065	0.003	0.04	0.050	0.16	9	31
11.	G 11	1.01	17	1.521	-0.003	0.13	-0.010	0.51	17	34
12.	G 12	1.01	17	1.491	-0.003	0.22	-0.020	0.86	24	41
13.	G 13	1.04	14	1.275	-0.002	0.12	-0.010	0.47	16	30
14.	G 14	1.04	14	1.167	-0.003	0.01	-0.050	0.06	3	17
15.	G 15	1.09	10	2.095**	-0.003	0.00	0.030	0.03	1	11
16.	G 16	1.00	18	2.133**	0.001	0.14	-0.020	0.55	18	36
17.	G 17	1.06	12	2.535**	-0.001	-0.02	-0.010	0.07	4	16
18.	G 18	1.01	17	2.454**	-0.004	0.24	0.030	0.94	25	42
19.	G 19	0.94	22	1.906*	-0.004	-0.14	0.040	0.55	18	40
20.	G 20	0.91	24	1.315	0.004	0.04	0.070	0.17	10	34
21.	G 21	0.97	20	-0.885	0.009*	0.31	0.020	1.22	27	47
22.	G 22	1.15	6	-0.713	-0.005	0.14	-0.020	0.55	18	24
23.	G 23	0.96	21	-0.635	0.003	-0.02	0.010	0.08	5	26
24.	G 24	1.04	14	-0.887	-0.001	-0.14	0.090	0.56	19	33
25.	G 25	0.93	23	-0.040	0.000	0.02	0.040	0.09	6	29
26.	G 26	0.82	25	0.957	-0.004	0.00	0.110	0.11	8	33
27.	G 27	0.93	23	0.853	-0.003	-0.26	0.000	1.02	26	49
28.	G 28	1.02	16	1.137	0.002	-0.34	-0.040	1.33	28	44
29.	G 29	1.11	9	0.448	0.001	-0.12	-0.030	0.47	16	25
30.	G 30	1.14	7	0.489	0.005	-0.02	-0.067	0.10	7	14
31.	G 31	1.12	8	1.140	0.007*	-0.04	-0.010	0.16	9	17
32.	G 32	1.04	14	1.118	-0.002	0.12	0.012	0.47	16	30
33.	G 33	1.06	12	0.595	0.002	-0.20	-0.060	0.79	23	35
34.	G 34	1.16	5	1.612	0.009*	-0.01	-0.030	0.05	2	7
35.	G 35	1.18	4	1.419	0.006	-0.05	-0.040	0.20	11	15
36.	G 36	1.27	1	1.182	-0.002	-0.06	-0.013	0.24	12	13
37.	G 37	0.93	23	1.270	-0.004	-0.11	0.050	0.43	15	38
38.	G 38	1.19	3	1.608	-0.005	-0.09	-0.030	0.35	13	16
39.	G 39	1.18	4	1.625	-0.003	-0.11	-0.010	0.43	15	19
40.	G 40	1.23	2	1.250	0.010**	-0.09	-0.040	0.36	14	16

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Number of seeds capitulum ⁻¹								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	24	8	1.231	-13.116**	1.52	0.001	2.16	31	39
2.	G 2	24	8	0.408	-5.361	-0.58	-0.032	0.82	15	23
3.	G 3	24	8	-0.352	-13.634**	1.29	0.007	1.83	30	38
4.	G 4	25	7	0.402	5.676	0.23	-0.020	0.33	9	16
5.	G 5	27	5	0.197	-7.574	0.00	0.009	0.01	1	6
6.	G 6	24	8	1.072	-9.869	0.39	0.001	0.55	13	21
7.	G 7	21	11	1.156	-13.804**	-1.14	0.001	1.62	25	36
8.	G 8	25	7	0.369	-8.095	-1.11	0.002	1.58	23	30
9.	G 9	25	7	0.904	-13.564**	-1.88	-0.008	2.67	34	41
10.	G 10	24	8	1.206	-4.698	-0.80	-0.028	1.14	19	27
11.	G 11	23	9	2.123**	-10.821	1.06	-0.0067	1.50	22	31
12.	G 12	23	9	2.079	-17.052**	-1.64	-0.012	2.33	33	42
13.	G 13	23	9	1.184	-11.908	0.01	-0.016	0.02	2	11
14.	G 14	25	7	1.224	-11.075	-0.84	0.007	1.19	20	27
15.	G 15	26	6	-0.028	-12.729*	0.78	-0.018	1.11	18	24
16.	G 16	24	8	2.298**	-12.593*	-1.15	0.0017	1.63	26	34
17.	G 17	22	10	1.274	-12.728*	1.13	0.014	1.60	24	34
18.	G 18	27	5	2.301**	-15.589*	0.40	0.011	0.57	14	19
19.	G 19	23	9	0.875	-16.479**	1.93	0.001	2.74	35	44
20.	G 20	24	8	1.948*	-15.710*	-0.36	0.01	0.51	11	19
21.	G 21	22	10	-0.089	-15.383*	0.80	0.003	1.14	19	29
22.	G 22	27	5	0.931	-4.275	-1.27	0.038	1.80	29	34
23.	G 23	24	8	-0.527	-10.581	-0.34	-0.013	0.48	10	18
24.	G 24	28	4	0.201	-4.105	1.62	0.001	2.30	32	36
25.	G 25	23	9	-0.056	-8.601	-0.09	-0.016	0.13	6	15
26.	G 26	24	8	1.545	4.007	0.02	0.002	0.03	3	11
27.	G 27	21	11	0.723*	-9.025	1.18	-0.012	1.67	27	38
28.	G 28	23	9	1.281	-11.096	0.07	0.001	0.10	4	13
29.	G 29	22	10	2.045**	-12.677*	0.70	0.017	0.99	17	27
30.	G 30	26	6	0.847	-16.580**	-1.22	-0.014	1.73	28	34
31.	G 31	28	4	1.822*	-13.594*	-0.37	0.004	0.53	12	16
32.	G 32	28	4	1.080	-1.793	0.91	-0.014	1.29	21	25
33.	G 33	26	6	1.148	-2.580	-0.63	0.002	0.89	16	22
34.	G 34	28	4	0.860	-9.862*	0.12	0.008	0.17	7	11
35.	G 35	31	3	0.682	5.566	-0.39	0.013	0.55	13	16
36.	G 36	34	1	1.062	-1.152	0.08	0.019	0.12	5	6
37.	G 37	25	7	0.808	-8.448	0.39	-0.004	0.55	13	20
38.	G 38	32	2	1.525	-9.916	-0.22	0.018	0.31	8	10
39.	G 39	31	3	1.341	-15.706**	-0.22	0.013	0.31	8	11
40.	G 40	34	1	1.014	-7.425	-0.37	0.021	0.53	12	13

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	1000 seed weight (g)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	2.56	14	0.917	0.020	-0.069	-0.005	0.12	6	20
2.	G 2	2.65	8	1.553	0.035*	-0.167	-0.135	0.31	18	26
3.	G 3	2.67	6	1.152	0.003	-0.157	0.016	0.26	16	22
4.	G 4	2.66	7	0.743	-0.010	-0.111	-0.174	0.26	16	23
5.	G 5	2.59	12	1.384	-0.012	-0.104	-0.100	0.20	11	23
6.	G 6	2.52	17	1.309	-0.006	-0.127	-0.047	0.22	12	29
7.	G 7	2.60	11	0.256	0.025*	-0.029	-0.047	0.26	16	27
8.	G 8	2.37	23	0.551	0.012	0.205	-0.252	0.35	20	43
9.	G 9	2.55	15	-0.284*	-0.008	-0.112	0.022	0.24	14	29
10.	G 10	2.67	6	1.084	-0.003	-0.147	-0.149	0.30	17	23
11.	G 11	2.50	19	1.372	0.010	-0.015	-0.166	0.11	5	24
12.	G 12	2.69	5	0.306	-0.005	-0.035	-0.109	0.19	10	15
13.	G 13	2.55	15	0.194	-0.011	-0.043	0.177	0.08	2	17
14.	G 14	2.55	15	1.727	-0.009	0.132	-0.029	0.26	16	31
15.	G 15	2.56	14	1.523	0.027*	0.303	-0.138	0.56	25	39
16.	G 16	2.51	18	1.377	0.015	0.210	-0.244	0.36	21	39
17.	G 17	2.67	6	2.296**	0.021	-0.079	0.091	0.16	9	15
18.	G 18	2.52	17	2.769**	0.018	0.122	-0.093	0.22	12	29
19.	G 19	2.58	13	1.033	-0.010	0.136	0.092	0.23	13	26
20.	G 20	2.53	16	2.813**	0.012	0.008	-0.009	0.10	4	20
21.	G 21	2.55	15	-0.992	-0.002	-0.259	-0.103	0.44	23	38
22.	G 22	2.65	8	1.948*	0.041*	-0.139	0.073	0.25	15	23
23.	G 23	2.52	17	0.874	-0.003	-0.142	0.102	0.24	14	31
24.	G 24	2.74	4	0.782	-0.009	-0.050	-0.043	0.09	3	7
25.	G 25	2.31	25	1.917*	0.010	0.203	-0.037	0.35	20	45
26.	G 26	2.41	22	1.424	-0.010	0.511	-0.060	0.89	26	48
27.	G 27	2.45	20	1.446	0.015	-0.107	0.216	0.42	22	42
28.	G 28	2.19	26	0.969	0.009	0.262	0.383	0.55	24	50
29.	G 29	2.33	24	1.285	-0.007	0.138	0.334	0.23	13	37
30.	G 30	2.42	21	1.386	0.075	-0.194	-0.02	0.33	19	40
31.	G 31	2.61	10	0.399	-0.004	-0.130	0.076	0.22	12	22
32.	G 32	2.63	9	0.051	-0.009	-0.148	0.010	0.25	15	24
33.	G 33	2.63	9	0.494	0.000	0.004	0.047	0.10	4	13
34.	G 34	2.59	12	0.487	0.015	0.113	0.101	0.30	17	29
35.	G 35	2.76	3	0.469	0.027	0.013	0.231	0.06	1	4
36.	G 36	2.82	1	0.996	0.005	0.047	-0.060	0.13	7	8
37.	G 37	2.60	11	1.223	0.022	0.083	-0.103	0.15	8	19
38.	G 38	2.80	2	0.298	0.066**	-0.029	0.043	0.11	5	7
39.	G 39	2.74	4	0.334	-0.002	-0.032	0.094	0.06	1	5
40.	G 40	2.82	1	0.337	0.063**	-0.067	0.018	0.11	5	6

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Seed yield plant ⁻¹ (g)								
		Mean	RYi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	2.8	6	1.051	-0.070*	-0.002	0.025	0.03	3	9
2.	G 2	2.9	5	1.079	-0.003	-0.180	-0.046	0.46	15	20
3.	G 3	2.6	8	1.343	-0.035	-0.120	-0.021	0.30	11	19
4.	G 4	2.8	6	0.342	-0.079*	-0.130	-0.030	0.33	12	18
5.	G 5	2.8	6	-0.402	-0.059	-0.350	0.070	0.89	25	31
6.	G 6	2.8	6	-0.949	0.151**	-0.009	0.009	0.02	2	8
7.	G 7	2.5	9	-0.314	-0.054	-0.190	0.008	0.48	16	25
8.	G 8	2.7	7	-0.777*	-0.048	-0.310	0.040	0.79	23	30
9.	G 9	2.5	9	-1.359	-0.080	-0.140	0.038	0.36	13	22
10.	G 10	2.8	6	-0.247	-0.074	0.006	0.060	0.06	5	11
11.	G 11	2.7	7	0.366	-0.064	0.130	-0.022	0.33	12	19
12.	G 12	2.5	9	1.028	-0.081	-0.003	-0.002	0.01	1	10
13.	G 13	2.6	8	1.483	-0.023	0.200	-0.007	0.51	17	25
14.	G 14	2.7	7	0.883	0.005	0.130	-0.002	0.33	12	19
15.	G 15	2.7	7	1.231	-0.053	-0.100	-0.001	0.25	8	15
16.	G 16	2.7	7	4.847**	-0.033	-0.009	-0.025	0.03	3	10
17.	G 17	2.6	8	3.284**	-0.060*	0.340	0.015	0.86	24	32
18.	G 18	2.6	8	1.125	0.033	0.380	-0.004	0.96	26	34
19.	G 19	2.6	8	2.438**	-0.056	-0.340	0.039	0.86	24	32
20.	G 20	2.5	9	3.321**	-0.054	-0.110	0.040	0.28	10	19
21.	G 21	2.8	6	-0.655	-0.025	-0.003	-0.009	0.01	1	7
22.	G 22	2.7	7	0.292	-0.025	0.260	0.039	0.66	19	26
23.	G 23	2.7	7	-0.079	-0.029	0.005	0.012	0.02	2	9
24.	G 24	3.3	2	1.140	-0.007	-0.012	-0.020	0.04	4	6
25.	G 25	2.6	8	-0.933	-0.059	0.100	-0.037	0.26	9	17
26.	G 26	2.9	5	2.816**	0.008	0.004	-0.062	0.06	5	10
27.	G 27	2.6	8	2.393**	-0.049	0.120	0.014	0.30	11	19
28.	G 28	2.4	10	1.689	-0.034	0.340	0.090	0.86	24	34
29.	G 29	2.6	8	1.011	-0.061	0.300	-0.030	0.76	22	30
30.	G 30	2.6	8	1.235	-0.047	0.290	0.014	0.73	21	29
31.	G 31	2.6	8	1.817	-0.051	-0.002	-0.021	0.02	2	10
32.	G 32	3.3	2	0.840	-0.001	-0.018	-0.072	0.09	7	9
33.	G 33	2.8	6	0.867	0.005	-0.004	-0.007	0.01	1	7
34.	G 34	2.6	8	1.399*	-0.027	0.300	0.040	0.76	22	30
35.	G 35	2.9	5	1.412	-0.040	-0.270	0.041	0.68	20	25
36.	G 36	3.4	1	1.061	0.002	-0.160	0.070	0.41	14	15
37.	G 37	2.6	8	1.021	0.022	0.590	-0.042	1.49	27	35
38.	G 38	3.2	4	-0.408	0.230**	-0.025	-0.038	0.07	6	10
39.	G 39	2.9	5	2.738**	0.091*	-0.250	0.037	0.63	18	23
40.	G 40	3.3	2	1.069	-0.059	-0.011	-0.049	0.06	5	7

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Seed yield plot ¹ (g)								
		Mean	RYi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	227	8	2.956**	0.021	-2.40	-0.002	8.11	22	30
2.	G 2	244	6	-0.366	1.04	-0.40	0.003	1.35	7	13
3.	G 3	212	18	-0.620	1.78*	3.10	-0.003	10.48	25	43
4.	G 4	250	5	1.636	0.08	-0.10	-0.006	0.34	3	8
5.	G 5	207	22	1.910*	0.99	0.40	0.006	1.35	7	29
6.	G 6	200	27	1.658	4.01**	4.20	0.013	14.19	28	55
7.	G 7	220	11	2.023**	5.06**	2.00	-0.012	6.76	19	30
8.	G 8	213	17	0.869	1.10	3.80	-0.014	12.84	27	44
9.	G 9	219	12	3.026**	0.96	0.08	0.008	0.27	2	14
10.	G 10	255	3	1.126	0.06	-0.60	-0.012	2.03	9	12
11.	G 11	215	16	2.593**	0.24	0.80	0.006	2.70	11	27
12.	G 12	221	10	1.273	0.93	0.81	0.001	2.74	12	22
13.	G 13	216	15	-0.253	1.04	1.80	-0.003	6.08	18	33
14.	G 14	218	13	0.953	4.67**	-0.40	-0.017	1.35	7	20
15.	G 15	220	11	2.513**	1.09	-0.11	-0.003	0.37	4	15
16.	G 16	204	24	3.043**	2.01*	-1.40	0.009	4.73	16	40
17.	G 17	200	27	1.021	0.98	2.20	0.026	7.43	21	48
18.	G 18	205	24	2.906**	0.45	-0.40	0.006	1.35	7	31
19.	G 19	208	21	6.313**	0.27	2.40	0.001	8.11	22	43
20.	G 20	206	23	4.690**	0.91	-0.30	0.006	1.01	6	29
21.	G 21	208	21	2.133**	17.35**	-1.20	-0.004	4.06	14	35
22.	G 22	208	21	-1.134*	0.47	1.10	0.027	3.72	13	34
23.	G 23	201	26	0.917	3.01**	-1.80	0.021	6.08	18	44
24.	G 24	258	2	0.954	0.09	0.60	-0.003	2.03	9	11
25.	G 25	233	7	0.170	0.24	-3.20	-0.015	10.81	26	33
26.	G 26	217	14	-0.163	0.14	-2.10	0.020	7.10	20	34
27.	G 27	210	20	0.462	1.10	-3.00	0.006	10.14	24	44
28.	G 28	205	24	0.864	13.95**	-0.20	0.012	0.68	5	29
29.	G 29	213	17	1.001	1.32	-1.30	0.012	4.39	15	32
30.	G 30	211	19	0.536	0.87	2.41	0.002	8.14	23	42
31.	G 31	208	21	4.626**	0.24	-0.11	0.004	0.37	4	25
32.	G 32	254	4	0.930	0.01	-0.10	-0.014	0.34	3	7
33.	G 33	208	21	0.583	3.79**	2.40	0.006	8.11	22	43
34.	G 34	213	17	2.065**	0.99	0.70	-0.008	2.37	10	27
35.	G 35	227	8	1.010	2.76*	-0.41	-0.004	1.39	8	16
36.	G 36	260	1	1.047	0.02	0.20	-0.005	0.68	5	6
37.	G 37	216	15	-5.27**	0.76	-1.40	-0.008	4.73	16	31
38.	G 38	219	12	-2.35**	3.90**	0.40	-0.009	1.35	7	19
39.	G 39	218	13	-3.31**	2.65*	-1.50	-0.007	5.07	17	30
40.	G 40	224	9	-5.54**	14.89**	0.01	-0.006	0.01	1	10

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Days to maturity								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	85	5	2.956*	39.05**	0.20	-0.010	0.58	3	8
2.	G 2	87	3	-0.366	42.20**	0.50	-0.020	1.44	16	19
3.	G 3	86	4	-0.620	85.76**	-0.42	0.004	1.21	12	16
4.	G 4	88	2	1.636	-8.95	-0.20	-0.013	0.58	3	5
5.	G 5	86	4	1.910	-38.24**	1.50	-0.030	4.33	28	32
6.	G 6	81	9	2.658*	66.32**	-0.50	-0.004	1.44	16	25
7.	G 7	83	7	2.023*	43.22**	-0.49	-0.008	1.41	15	22
8.	G 8	87	3	0.869	14.45	0.00	-0.015	0.02	1	4
9.	G 9	89	1	3.026*	26.89**	-1.56	-0.001	4.50	29	30
10.	G 10	85	5	3.126*	5.81	-0.41	-0.014	1.18	11	16
11.	G 11	85	5	2.593*	28.19	-0.45	0.010	1.30	14	19
12.	G 12	86	4	1.273	35.13**	-0.80	-0.027	2.31	26	30
13.	G 13	86	4	-0.253	-61.86**	-0.30	-0.011	0.87	7	11
14.	G 14	87	3	0.953	-53.81**	-0.40	-0.001	1.15	10	13
15.	G 15	88	2	2.513*	-46.18**	0.60	-0.011	1.73	21	23
16.	G 16	89	1	3.043*	89.18**	0.52	-0.017	1.50	17	18
17.	G 17	85	5	4.021**	34.80**	-1.00	0.021	2.88	27	32
18.	G 18	86	4	2.906*	7.720	0.55	-0.001	1.59	18	22
19.	G 19	81	9	6.313**	49.68**	0.58	0.024	1.67	19	28
20.	G 20	84	6	4.690**	57.24**	-0.71	-0.014	2.05	25	31
21.	G 21	87	3	2.133*	-81.89**	0.70	-0.028	2.02	24	27
22.	G 22	82	8	-1.134	-8.84	-1.50	0.040	4.33	28	36
23.	G 23	82	8	0.517	-6.41	0.10	0.011	0.29	2	10
24.	G 24	76	12	0.654	-4.75	0.22	0.012	0.63	5	17
25.	G 25	75	13	0.170	38.5**	0.21	0.016	0.61	4	17
26.	G 26	74	14	1.163	-8.18	0.59	0.006	1.70	20	34
27.	G 27	79	11	0.462	-56.18	0.31	-0.032	0.89	8	19
28.	G 28	79	11	0.864	-89.63**	0.27	0.002	0.78	6	17
29.	G 29	80	10	1.001	-9.25	0.70	0.019	2.02	24	34
30.	G 30	84	6	0.536	1.98	0.59	0.009	1.70	20	26
31.	G 31	79	11	4.626**	-45.42**	3.20	0.034	9.23	30	41
32.	G 32	84	6	0.930	-6.71	0.20	-0.003	0.58	3	9
33.	G 33	84	6	0.583	-87.09**	1.00	0.003	2.88	27	33
34.	G 34	87	3	2.065*	-70.53**	-0.43	0.008	1.24	13	16
35.	G 35	86	4	1.010	-8.04	-0.45	0.021	1.30	14	18
36.	G 36	86	4	-1.047	8.82	-0.65	0.000	1.88	23	27
37.	G 37	86	4	-5.27**	99.37**	-0.41	0.018	1.18	11	15
38.	G 38	85	5	-2.35*	-28.38	0.39	-0.002	1.13	9	14
39.	G 39	84	6	-3.31**	42.70**	-0.31	-0.003	0.89	8	14
40.	G 40	84	6	-5.54**	71.95**	-0.62	-0.010	1.79	22	28

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Oil content (%)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	38.40	14	1.837*	-1.886	1.10	-0.020	4.28	25	39
2.	G 2	38.73	10	1.542*	4.950*	0.00	-0.024	0.02	2	12
3.	G 3	37.80	17	1.379*	5.003*	0.40	0.014	1.56	16	33
4.	G 4	38.80	9	1.094	-0.443	-0.09	0.0144	0.35	5	14
5.	G 5	38.67	11	1.514*	3.367	0.17	-0.006	0.66	9	20
6.	G 6	38.93	7	1.547*	5.146*	0.20	-0.008	0.78	11	18
7.	G 7	38.47	13	1.310	1.654	0.61	-0.020	2.37	20	33
8.	G 8	38.47	13	1.760*	1.815	0.71	0.020	2.76	21	34
9.	G 9	39.00	6	1.657*	7.564**	0.60	-0.048	2.33	19	25
10.	G 10	40.67	4	1.350	0.990	-0.09	-0.021	0.35	5	9
11.	G 11	38.87	8	1.083	4.887*	-0.08	-0.009	0.31	4	12
12.	G 12	36.60	28	0.822	-5.379*	-0.20	-0.018	0.78	11	39
13.	G 13	38.40	14	1.306	-3.487	0.72	-0.016	2.80	22	36
14.	G 14	36.33	29	0.915	-6.165*	-1.10	0.010	4.28	25	54
15.	G 15	37.27	23	1.204	-3.718*	-0.50	-0.028	1.95	17	40
16.	G 16	38.40	14	1.132	-5.079*	0.80	0.015	3.11	23	37
17.	G 17	38.67	11	0.619	-7.359**	-0.31	0.003	1.21	14	25
18.	G 18	37.53	19	1.233	-6.010*	-0.71	0.0145	2.76	21	40
19.	G 19	38.00	16	1.042	-5.617*	-0.30	0.019	1.17	13	29
20.	G 20	36.93	25	1.063	-4.371*	0.20	0.004	0.78	11	36
21.	G 21	37.67	18	0.921	10.013**	0.19	-0.015	0.74	10	28
22.	G 22	37.07	24	0.652	-1.632	0.71	0.030	2.76	21	45
23.	G 23	36.93	25	1.167	-7.434**	-1.10	0.000	4.28	25	50
24.	G 24	41.47	2	1.274*	-1.108	0.16	0.010	0.62	8	10
25.	G 25	37.40	21	1.032	1.845	-0.50	0.040	1.95	17	38
26.	G 26	37.47	20	0.285	13.177**	0.00	0.022	0.02	2	22
27.	G 27	37.33	22	-0.012	4.788*	-0.51	0.026	1.98	18	40
28.	G 28	37.40	21	0.036	-0.144	8.00	-0.038	31.12	26	47
29.	G 29	36.73	27	0.503	3.773	-0.30	-0.015	1.17	13	40
30.	G 30	37.27	23	0.291	-3.336	0.21	0.030	0.82	12	35
31.	G 31	38.60	12	3.248**	4.582*	-0.20	0.014	0.78	11	23
32.	G 32	41.20	3	1.030	-4.407*	0.00	-0.012	0.01	1	4
33.	G 33	38.00	16	0.407*	0.509	0.01	0.029	0.05	3	19
34.	G 34	37.40	21	0.154	7.253**	-0.72	-0.052	2.80	22	43
35.	G 35	38.20	15	0.953	-4.804*	-0.11	0.066	0.43	6	21
36.	G 36	42.20	1	0.985	0.091	0.12	-0.010	0.47	7	8
37.	G 37	36.80	26	0.511	11.670**	-0.81	-0.030	3.15	24	50
38.	G 38	39.93	5	1.020	17.575**	0.09	-0.009	0.35	5	10
39.	G 39	40.67	4	1.023	8.023**	0.21	0.014	0.82	12	16
40.	G 40	41.20	3	0.672	10.173**	0.32	-0.010	1.24	15	18

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

(Table Contd...)

Sr. No.	Genotype code	Protein content (%)								
		Mean	RMi	bi	S ² di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	18.00	24	1.220	5.405**	-0.09	0.015	0.20	5	29
2.	G 2	18.93	16	-0.085	3.437*	-0.09	0.025	0.21	6	22
3.	G 3	19.07	14	-1.013	-0.759	-0.33	0.015	0.75	18	32
4.	G 4	19.67	9	0.375	-0.618	-0.41	0.059	0.93	20	29
5.	G 5	18.53	21	0.058	1.720	0.72	-0.030	1.63	30	51
6.	G 6	19.40	10	-1.201	1.129	-0.47	-0.005	1.07	23	33
7.	G 7	18.93	16	-0.487*	2.853	-0.32	-0.012	0.73	17	33
8.	G 8	18.80	18	-1.705	5.654**	0.81	0.006	1.84	31	49
9.	G 9	19.13	13	0.463	3.085*	-0.09	-0.005	0.20	5	18
10.	G 10	19.87	8	0.627	1.604	-0.31	0.038	0.70	16	24
11.	G 11	19.40	10	-0.129	0.470	-0.41	-0.005	0.93	20	30
12.	G 12	19.27	11	0.671	0.647	0.12	0.005	0.27	10	21
13.	G 13	19.13	13	0.796	-0.154	0.5	0.015	1.13	25	38
14.	G 14	18.93	16	-0.720	0.590	-0.01	-0.020	0.03	2	18
15.	G 15	18.60	20	0.560	0.156	0.12	0.038	0.27	10	30
16.	G 16	18.07	23	4.571**	1.085	-0.61	-0.020	1.38	27	50
17.	G 17	18.07	23	4.155**	-0.177	-0.49	-0.006	1.11	24	47
18.	G 18	19.27	11	1.998*	0.453	-0.47	-0.030	1.07	23	34
19.	G 19	19.40	10	4.924**	-0.971	0.00	-0.036	0.04	3	13
20.	G 20	18.87	17	4.092**	-0.766	0.10	-0.120	0.26	9	26
21.	G 21	19.40	10	0.921	-0.242*	0.42	-0.005	0.95	21	31
22.	G 22	19.20	12	0.754	0.969	-0.71	0.012	1.61	29	41
23.	G 23	19.13	13	-1.027	2.148*	0.39	0.011	0.89	19	32
24.	G 24	20.93	4	1.952*	0.342	0.21	0.039	0.48	13	17
25.	G 25	18.80	18	-0.143	-0.139	-0.51	-0.046	1.16	26	44
26.	G 26	19.20	12	0.428	-0.798	1.10	-0.005	2.50	32	44
27.	G 27	18.07	23	1.069	-0.540	0.14	0.028	0.32	11	34
28.	G 28	19.20	12	3.509**	0.667	0.25	0.018	0.57	14	26
29.	G 29	18.67	19	3.080**	2.169*	0.62	-0.025	1.41	28	47
30.	G 30	19.00	15	2.694*	-0.694	0.11	0.017	0.25	8	23
31.	G 31	18.40	22	2.041	-1.160	-0.07	0.010	0.16	4	26
32.	G 32	21.07	3	1.216	-0.665	0.45	0.035	1.02	22	25
33.	G 33	19.07	14	1.184	2.109*	-0.09	-0.012	0.20	5	19
34.	G 34	19.67	9	2.804*	2.390*	0.30	0.014	0.68	15	24
35.	G 35	20.33	7	2.831*	0.817	0.15	-0.050	0.34	12	19
36.	G 36	22.27	1	1.202	0.519	0.10	0.001	0.23	7	8
37.	G 37	18.67	19	-0.288	6.517**	-0.31	-0.020	0.70	16	35
38.	G 38	20.80	6	0.263	5.322**	0.00	-0.014	0.01	1	7
39.	G 39	20.87	5	-0.898*	-1.188	-0.09	0.025	0.21	6	11
40.	G 40	21.67	2	1.143	1.703	0.00	0.010	0.01	1	3

*Significant at 5% level of significance **Significant at 1% level of significance

RMi: Rank of Mean, bi: Regression coefficient, S²di: Deviation from Regression line, IPCA: Interaction Principal Component Analyses, ASV: AMMI stability value, RASVi: Rank of AMMI stability value, GSI: Genotype selection index

APPENDIX – XXIV

ABBREVIATIONS USED

AMMI	:	Additive Main Effect and Multiplicative Interaction
ANOVA	:	Analysis of Variance
ARS	:	Agriculture Research Station
bi	:	Regression Coefficient
CD	:	Critical Difference
cm	:	Centimeter (s)
°C	:	Degree Celsius
DF	:	Degrees of Freedom
E	:	Environment
EMS	:	Error Mean Sum of Square
<i>et. al.</i>	:	<i>et alia</i> (and others)
FYM	:	Farm yard manure
Fig.	:	Figure
g	:	Gram
GA	:	Genetic Advance
GAM	:	Genetic Advance Per Cent Mean
Ga	:	Gene Action
GEI	:	Genotype x Environment Interaction
GGE	:	Genotype and Genotype by Environment
GM	:	Grand Mean
GC	:	Genotype Code
GMS	:	Genotypic mean sum of squares
GCV	:	Genotypic coefficient of variation
GSI	:	Genotype Selection Index
GPM	:	Grand Pooled Mean
H ² b	:	Heritability
Ha	:	Hectare(s)
<i>i.e.</i>	:	<i>Id est</i> (that is)
IPCA	:	Interaction Principal Component Analyses

K ₂ O	:	Potassium
MSS	:	Mean sum of squares
MH (MS)	:	Maharashtra (state)
MT	:	Metric ton
Max.	:	Maximum
Min.	:	Minimum
N ₂ O	:	Nitrogen
No. /no.	:	Number
P ₂ O ₅	:	Phosphorus
PCV	:	Phenotypic coefficient of variation
RARS	:	Regional Agriculture Research Station
RASVi	:	Rank of AMMI Stability Value
RMi	:	Rank of Mean
σ^2_e	:	Environmental variance
σ^2_g		Genotypic variance
σ^2_p		Phenotypic variance
SS	:	Sum of squares
SE	:	Standard error
S ² di	:	Deviation from Regression line
<i>viz.,</i>	:	<i>Videlicet</i> (namely)
@	:	At the rate of
%	:	Per cent

APPENDIX-XXI

AMMI GGE Biplots of different characters for *Kharif*, 2018

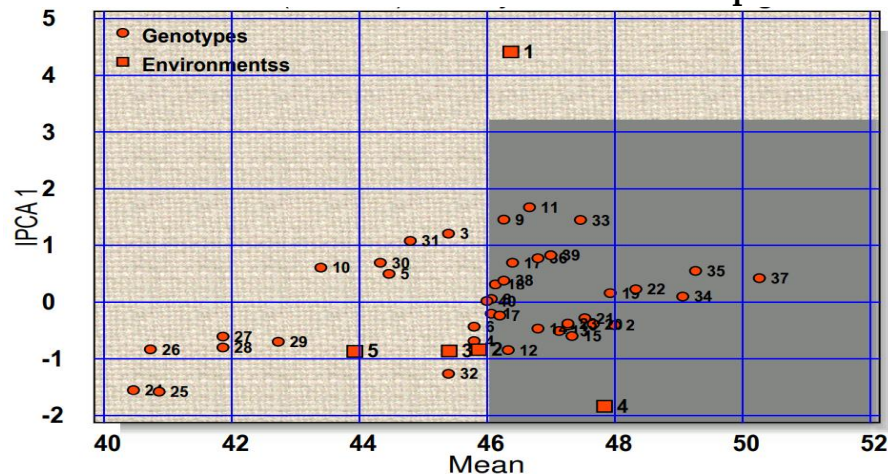


Fig. 1.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for days to 50 per cent flowering across five tested environments.

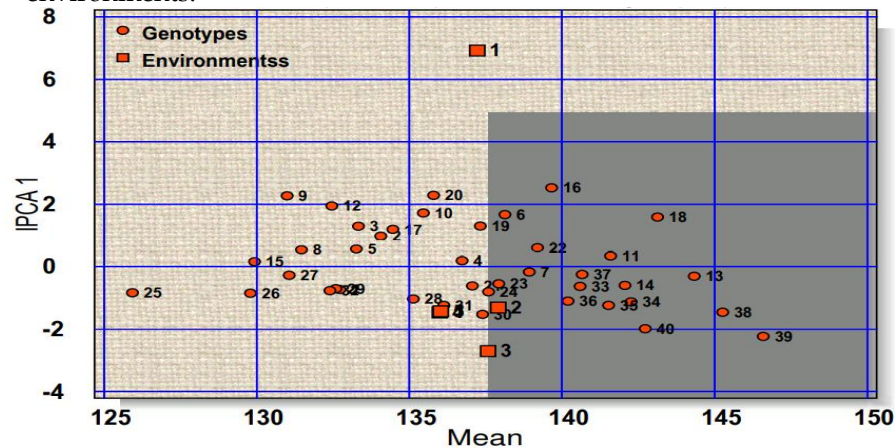


Fig. 2.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for plant height (cm) across five tested environments.

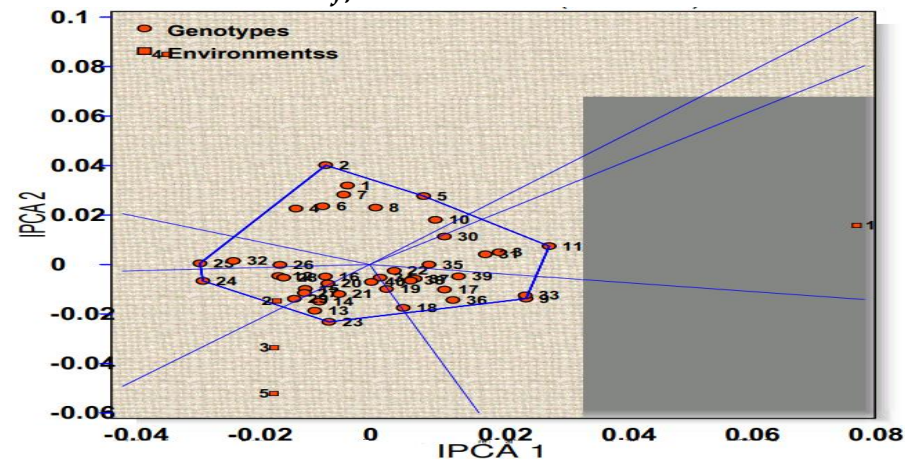


Fig. 1.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

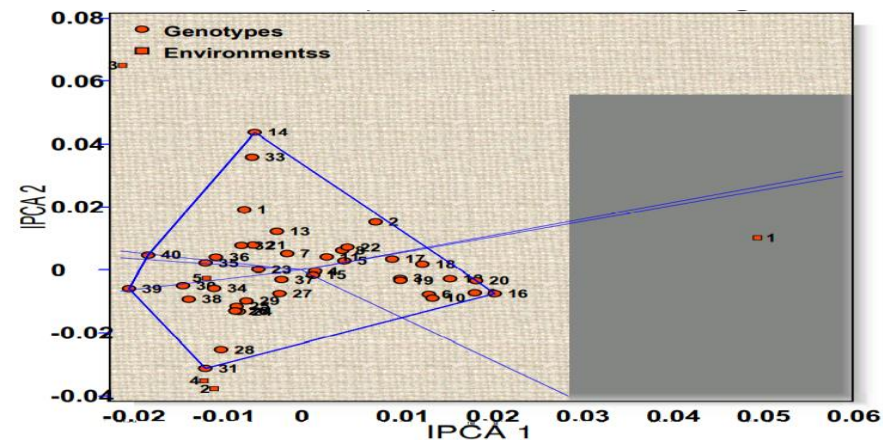


Fig. 2.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

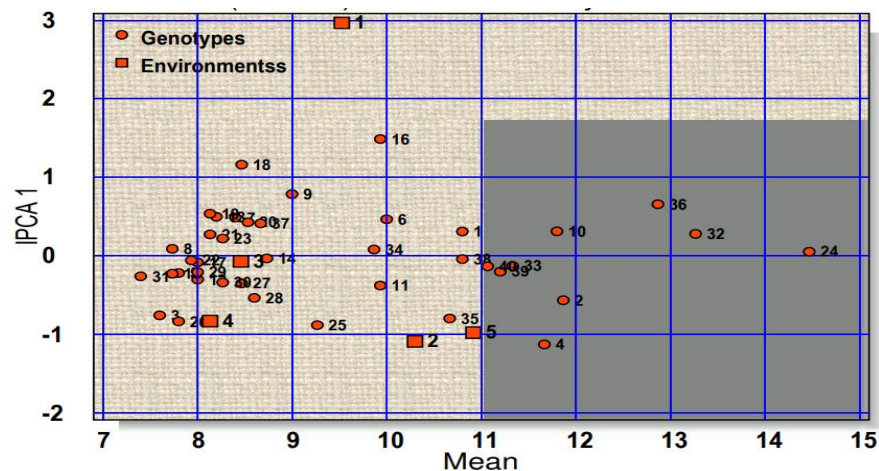


Fig. 3.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for no. of primary branches plant⁻¹ across five tested environments.

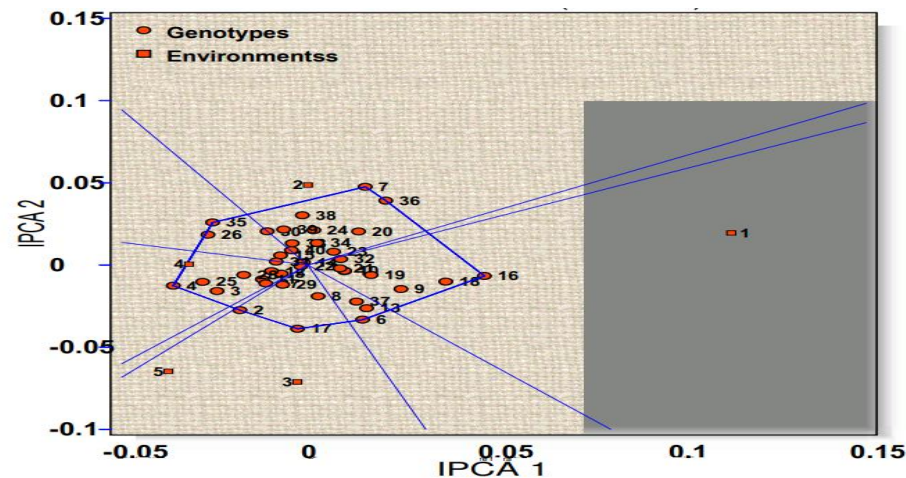


Fig. 3.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

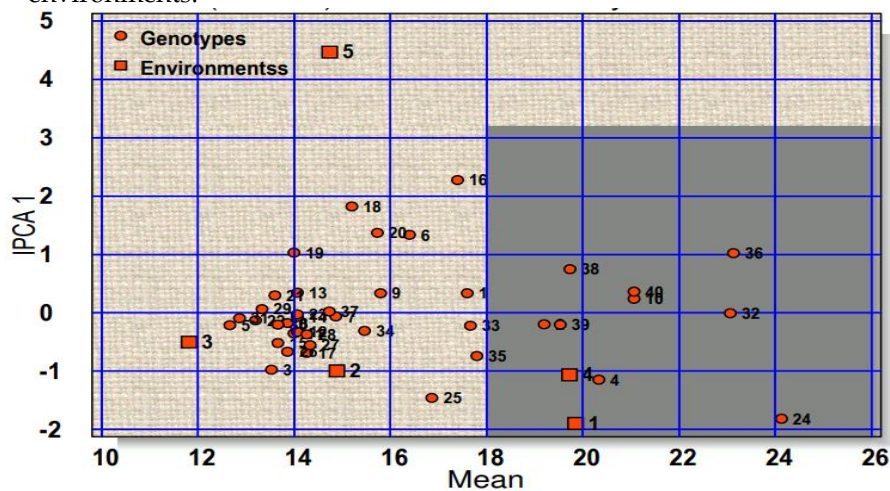


Fig. 4.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for no. of secondary branches plant⁻¹ across five tested environments.

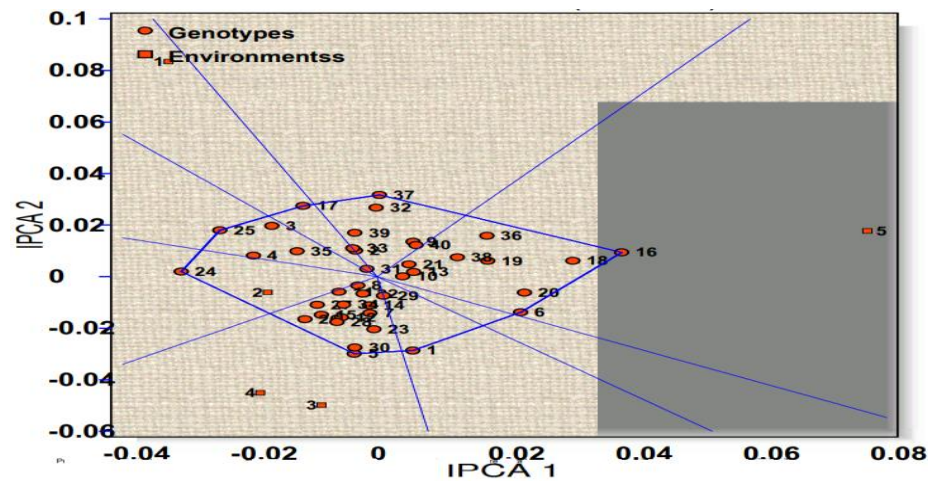


Fig. 4.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

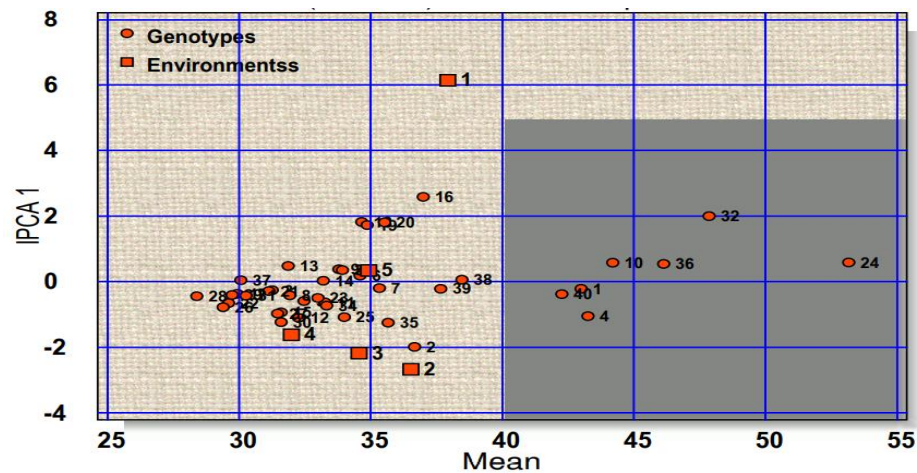


Fig. 5.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for no. of capitula plant⁻¹ across five tested environments.

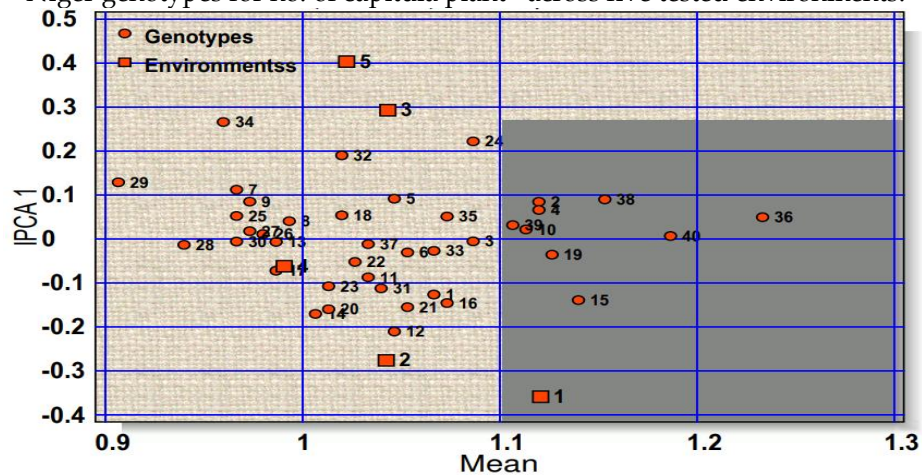


Fig. 6.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for capitulum diameter (cm) across five tested environments.

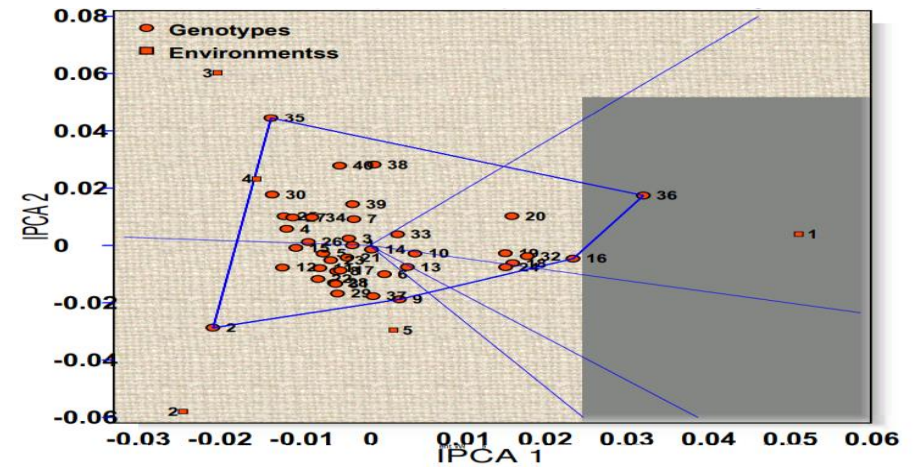


Fig. 5.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

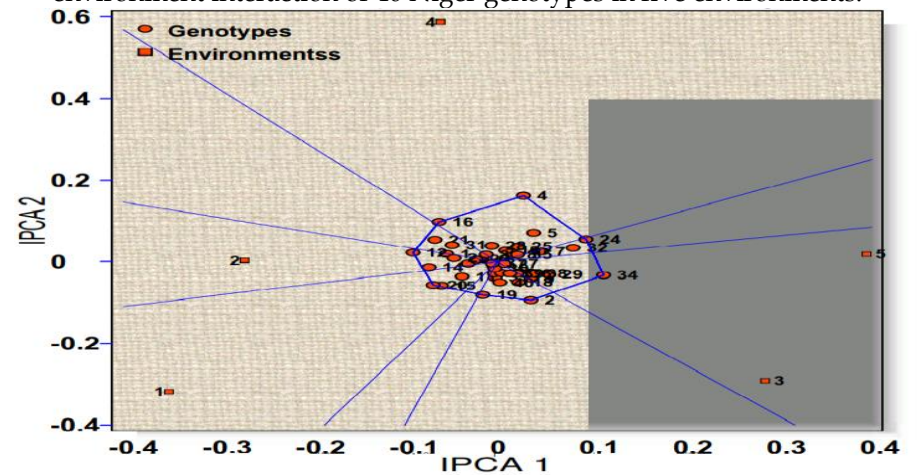


Fig. 6.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

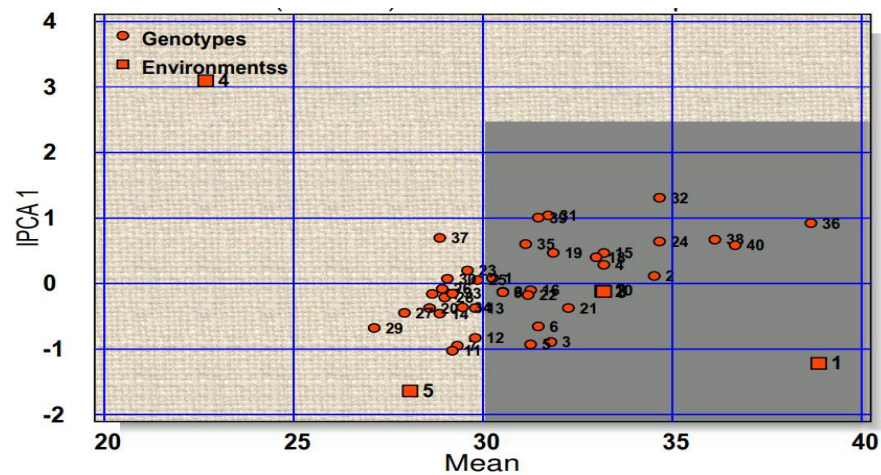


Fig. 7.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for no. of seeds capitulum⁻¹ across five tested environments.

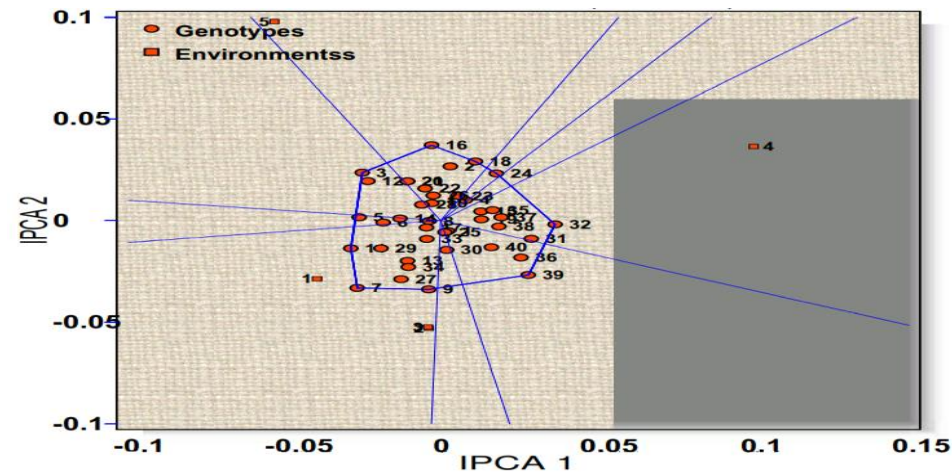


Fig. 7.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

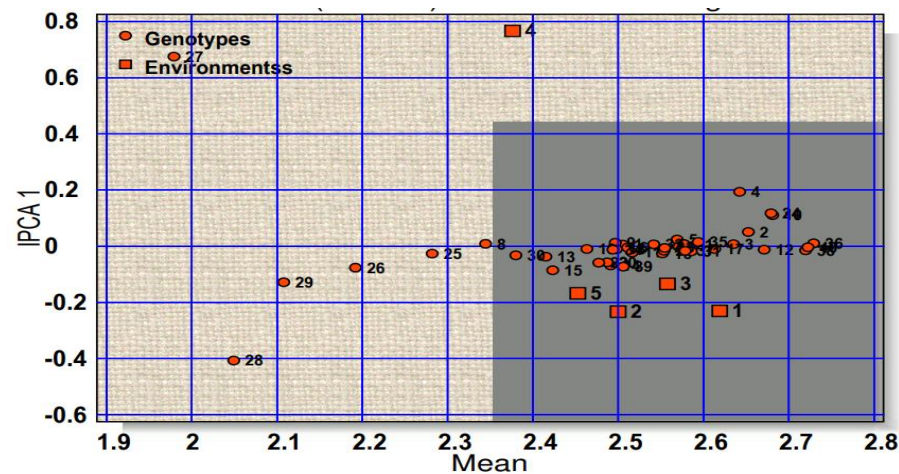


Fig. 8.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for 1000 seed weight (g) across five tested environments.

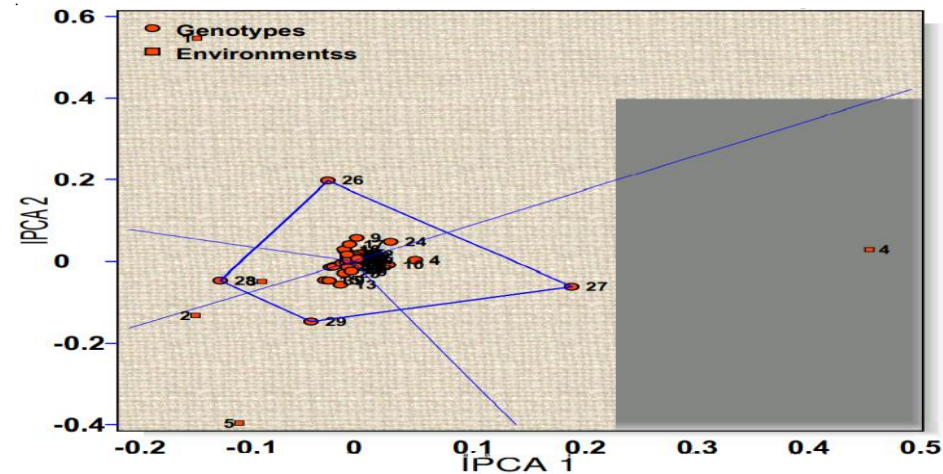


Fig. 8.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

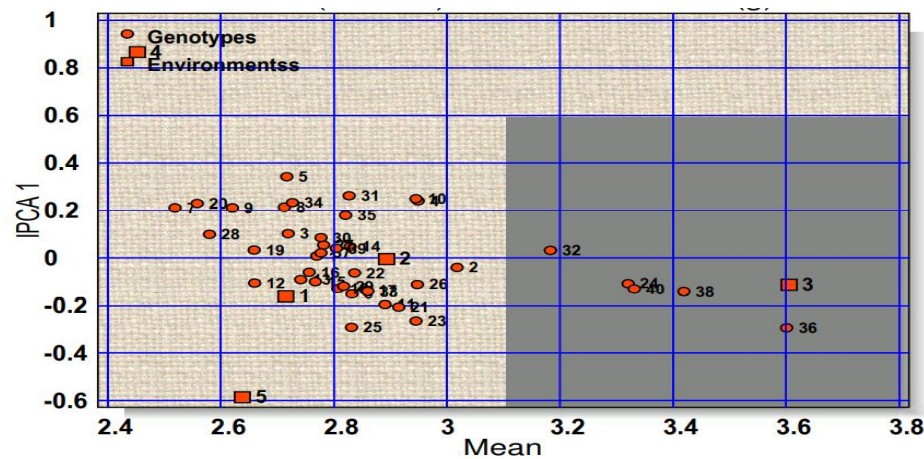


Fig. 9.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for seed yield plant⁻¹ (g) across five tested environments.

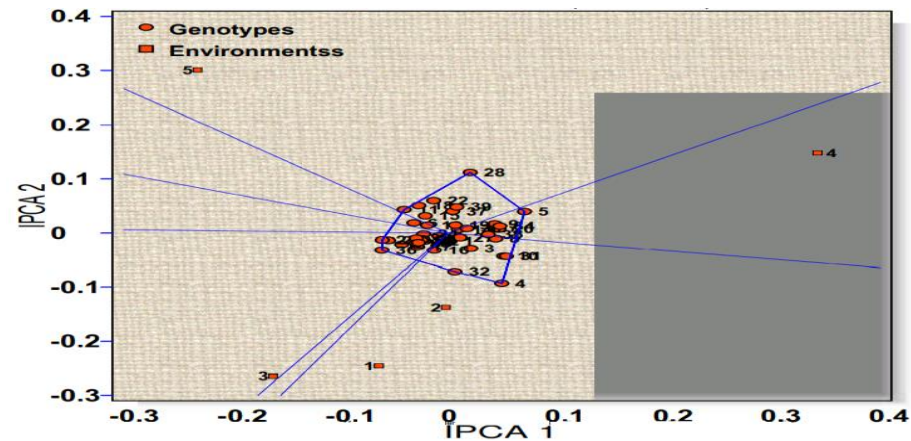


Fig. 9.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

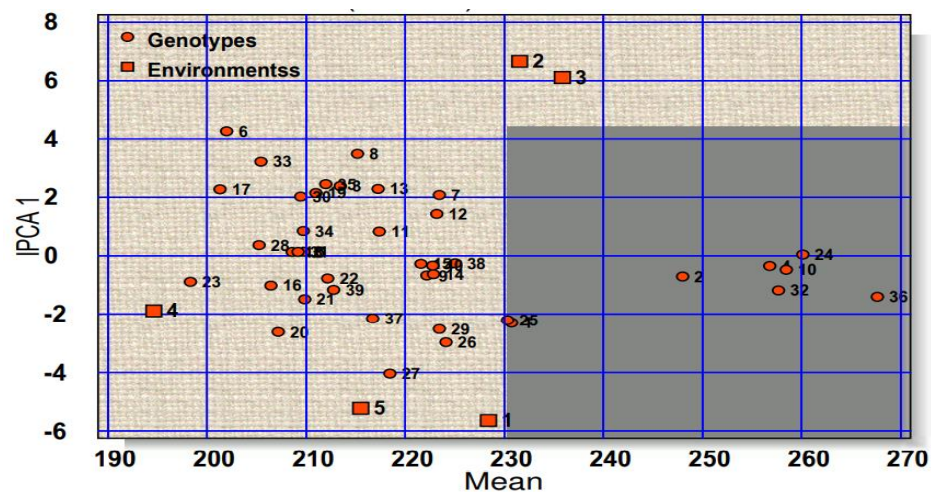


Fig. 10.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for seed yield plot⁻¹ (g) across five tested environments.

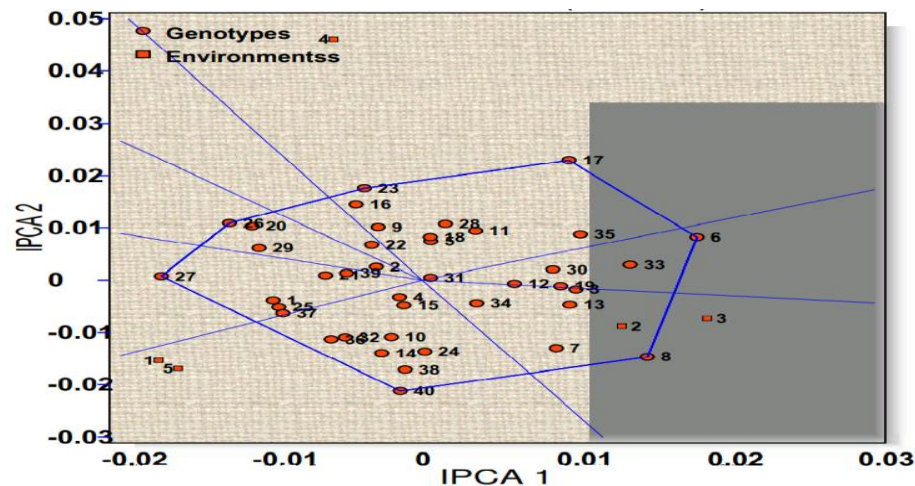


Fig. 10.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

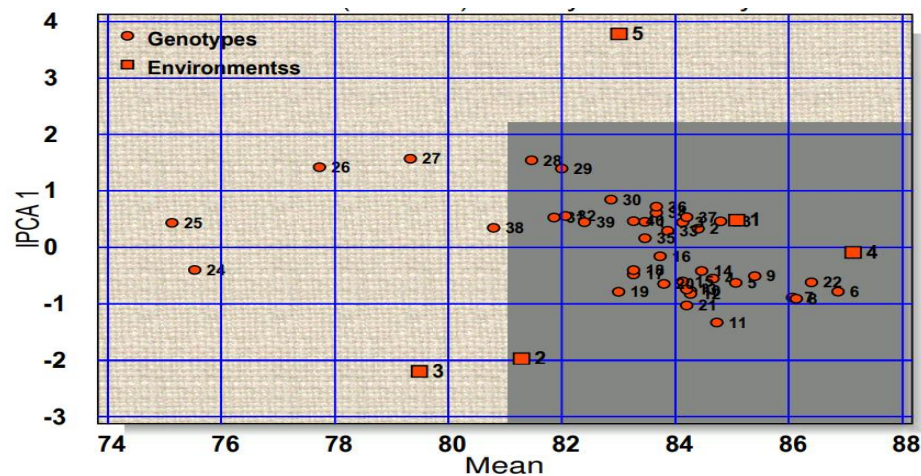


Fig. 11.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for days to maturity across five tested environments.

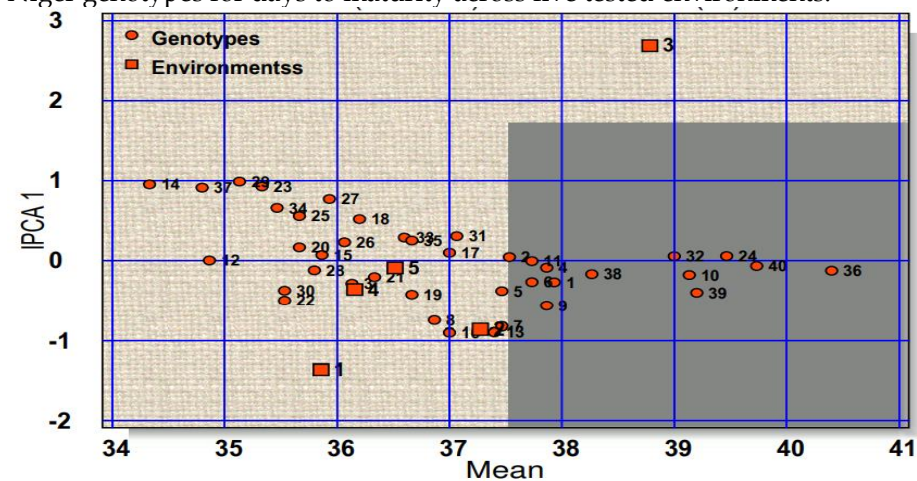


Fig. 12.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for oil content (%) across five tested environments.

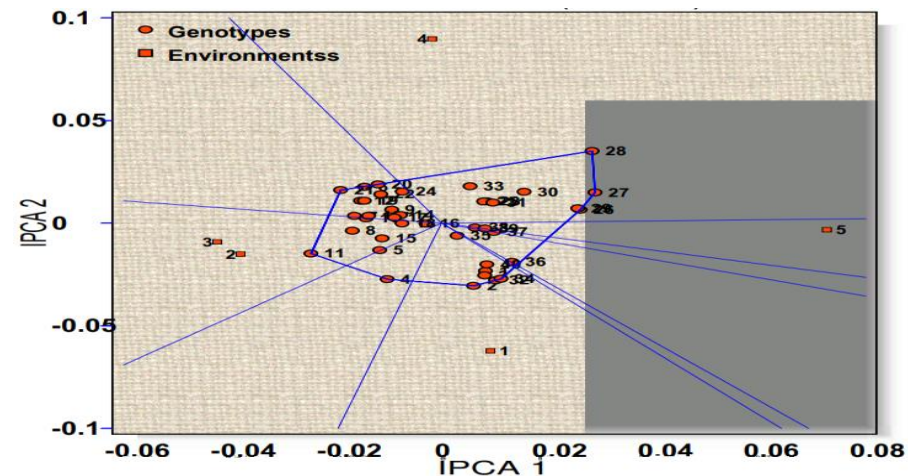


Fig. 11.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

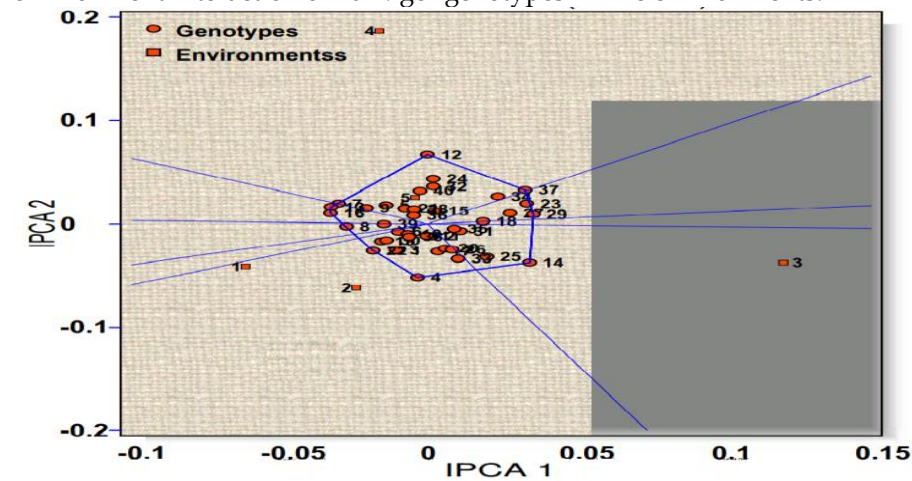


Fig. 12.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

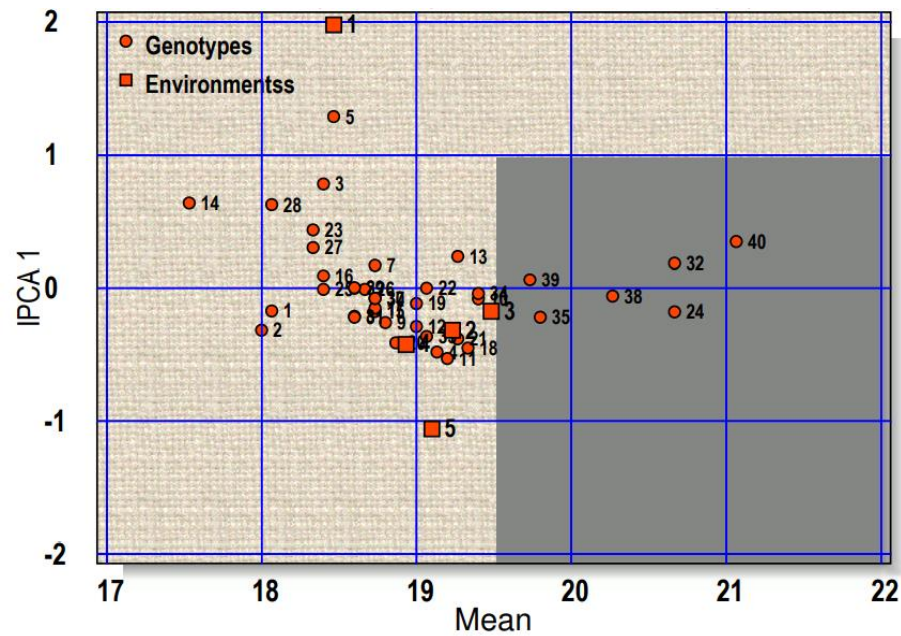


Fig. 13.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for protein content (%) across five tested environments.

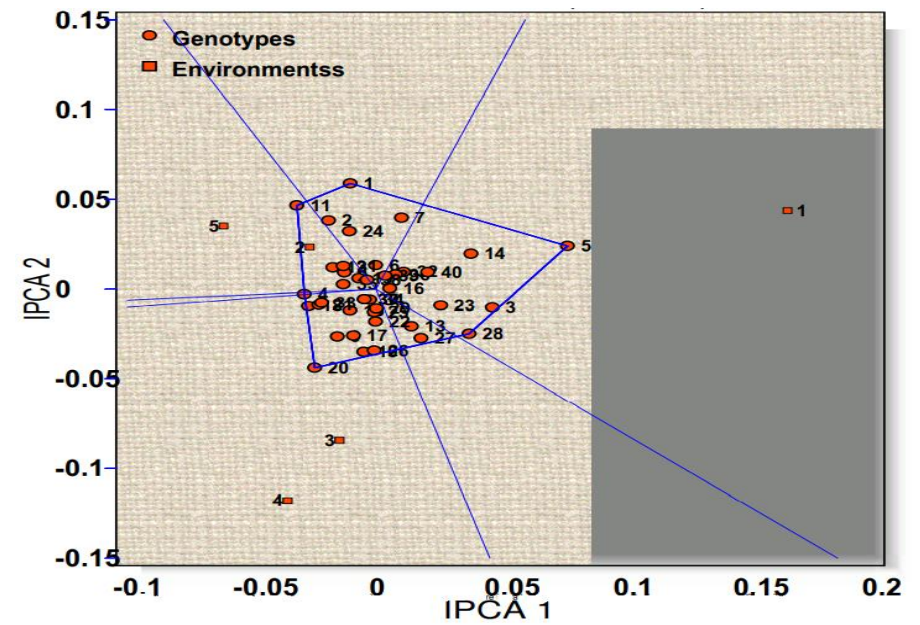


Fig. 13.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

APPENDIX-XXIII

AMMI GGE Biplots of different characters for *Kharif*, 2019

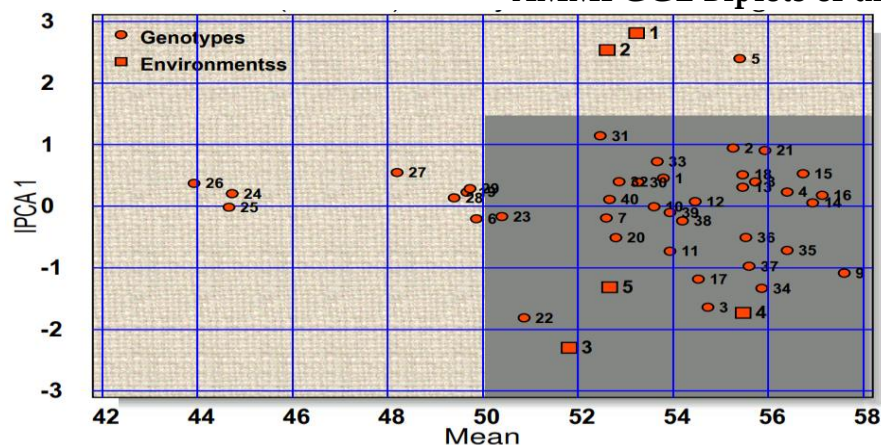


Fig. 14.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for days to 50 per cent flowering across five tested environments.

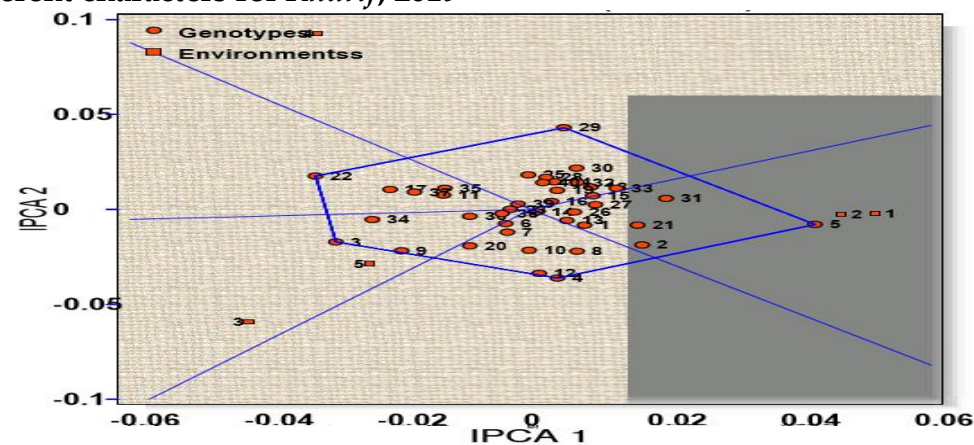


Fig. 14.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

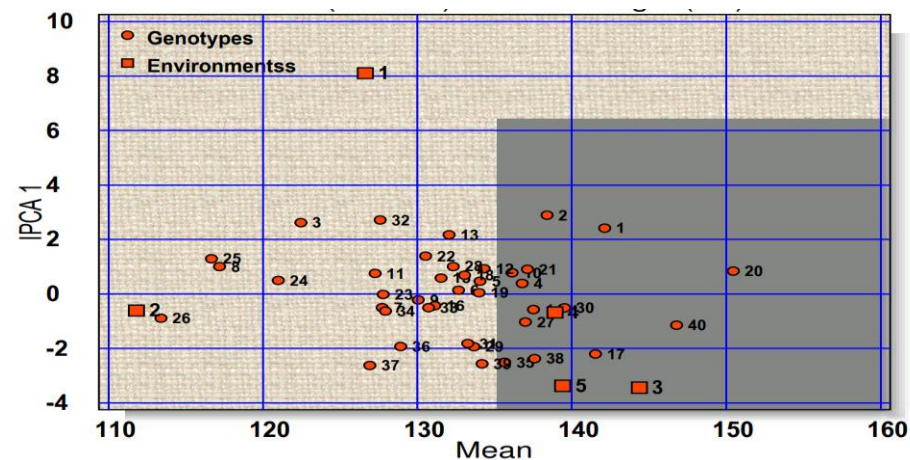


Fig. 15.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for plant height (cm) across five tested environments.

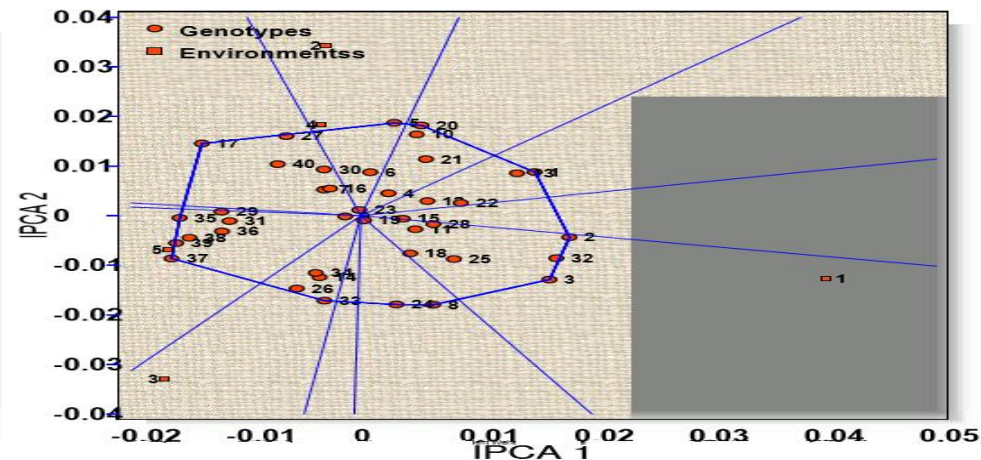


Fig. 15.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

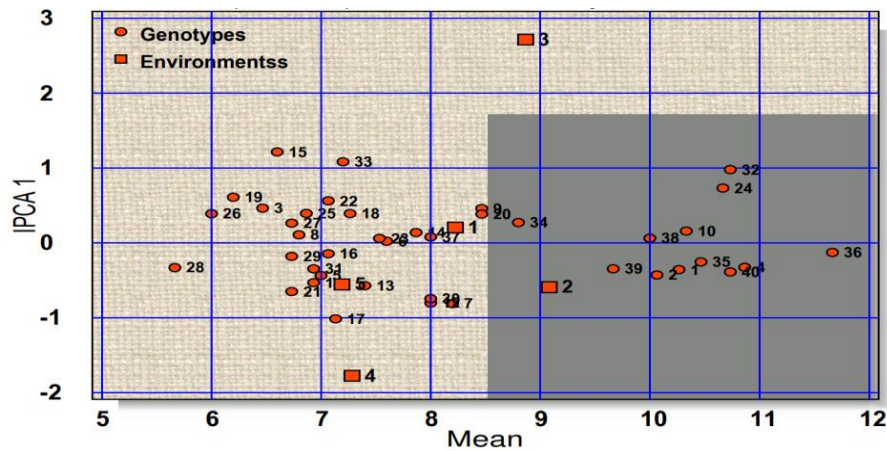


Fig. 16.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for no. of primary branches plant⁻¹ across five tested environments.

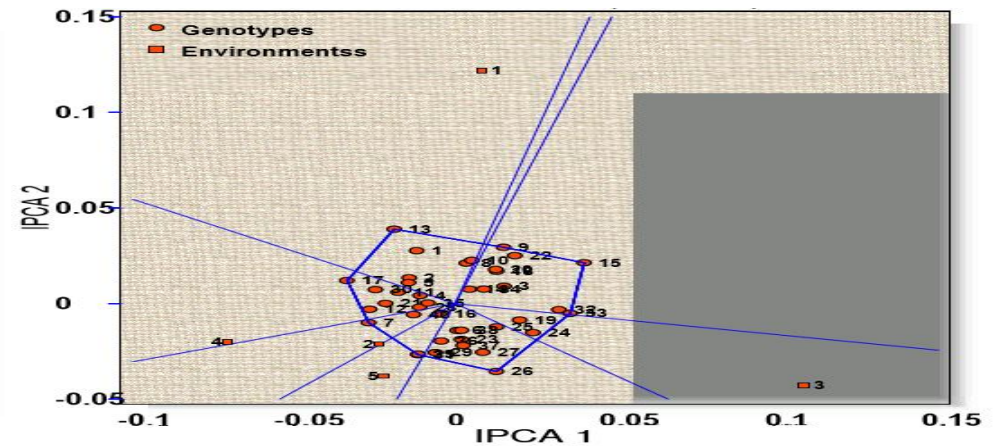


Fig. 16.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

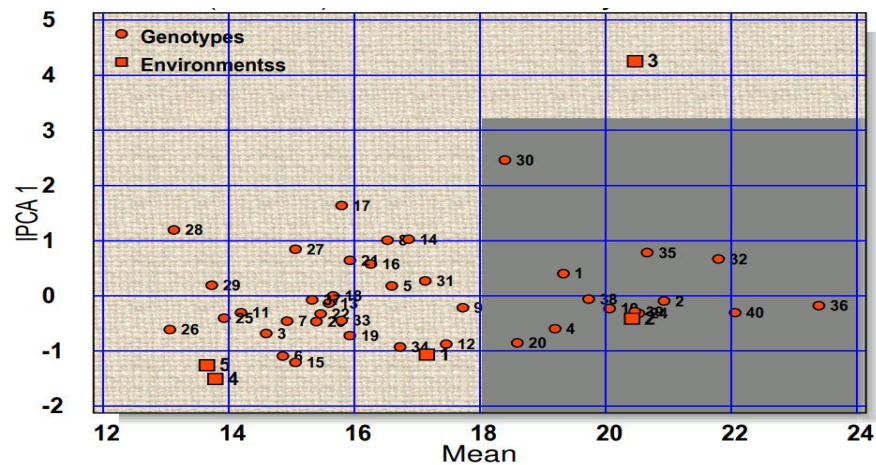


Fig. 17.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for no. of secondary branches plant⁻¹ across five tested environments.

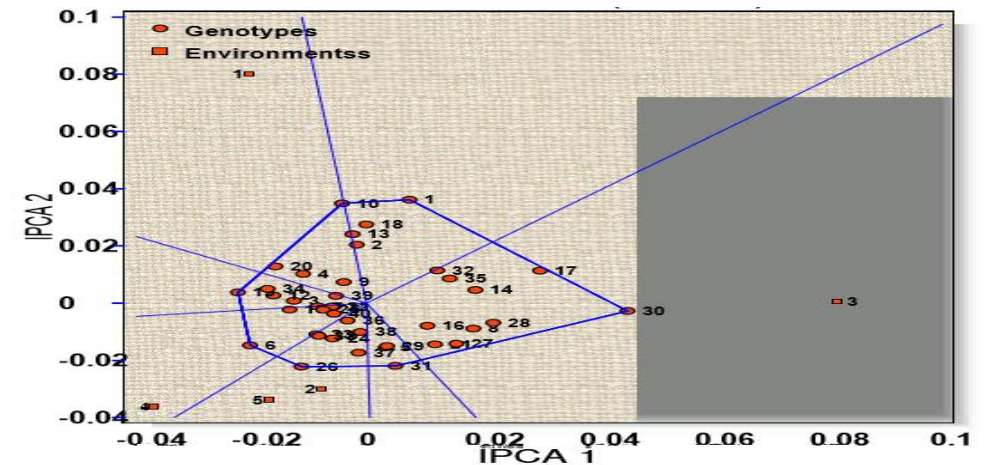


Fig. 17.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

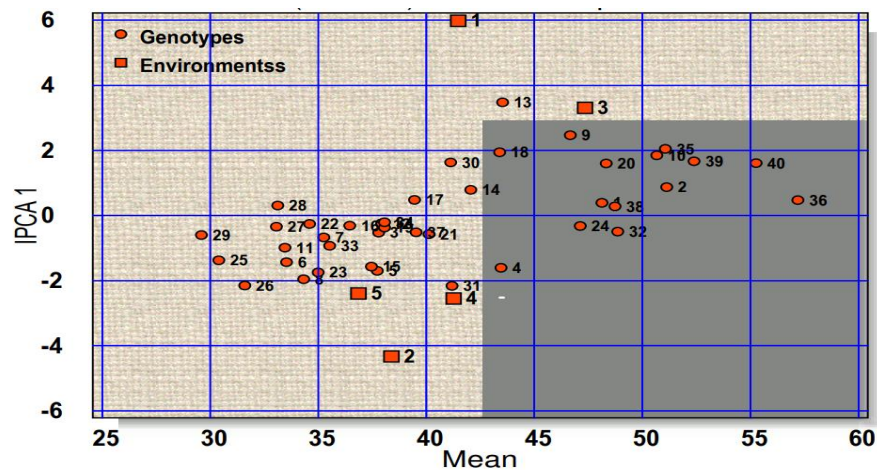


Fig. 18.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for no. of capitula plant⁻¹ across five tested environments.

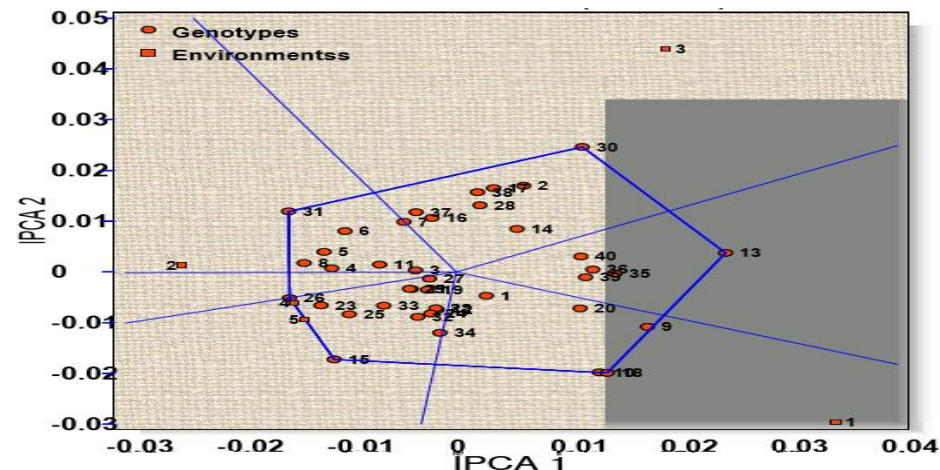


Fig. 18.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

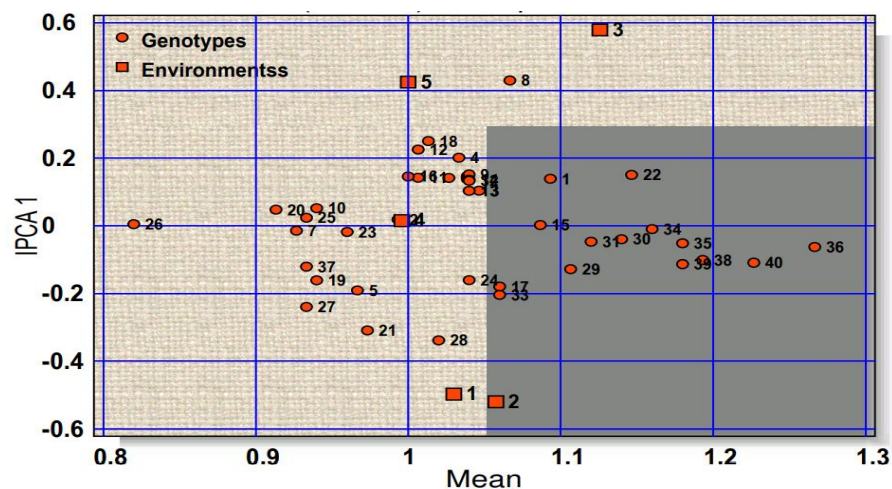


Fig. 19.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for capitulum diameter (cm) across five tested environments.

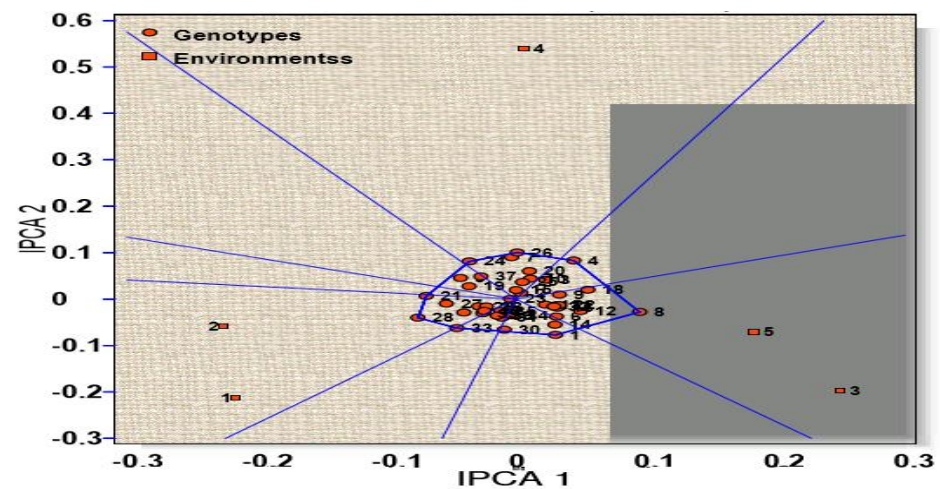


Fig. 19.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

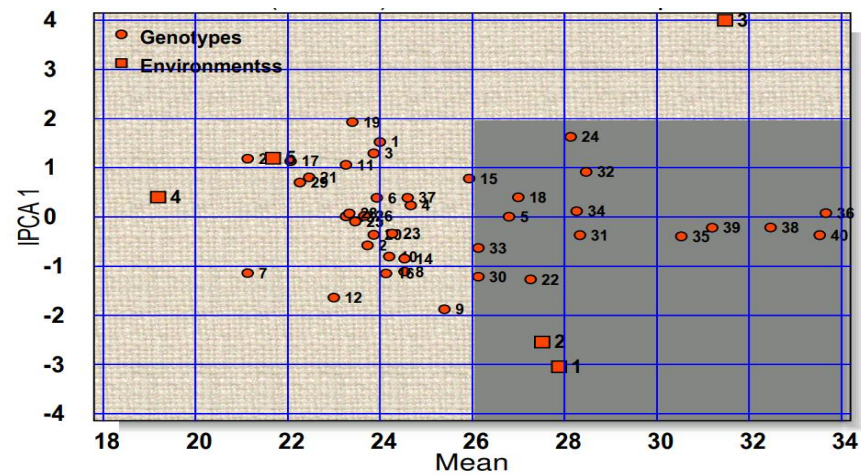


Fig. 20.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for no. of seeds capitulum⁻¹ across five tested environments.

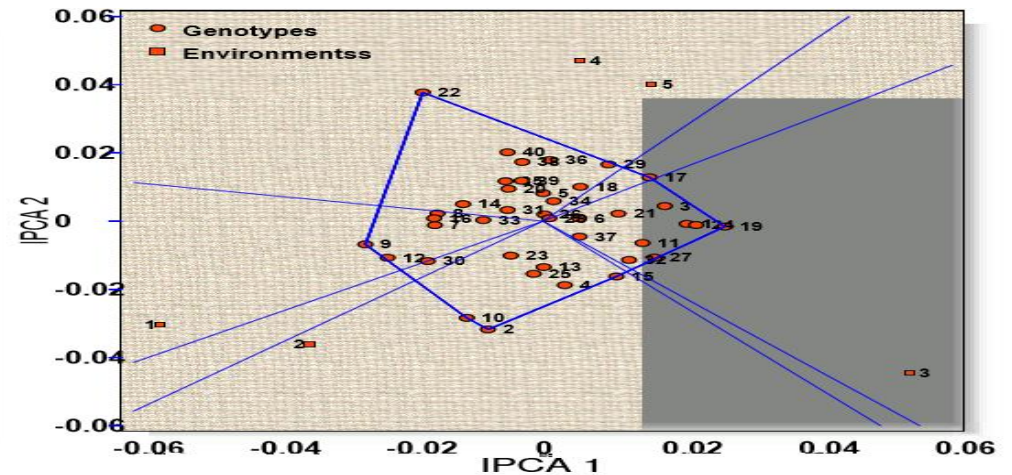


Fig. 20.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

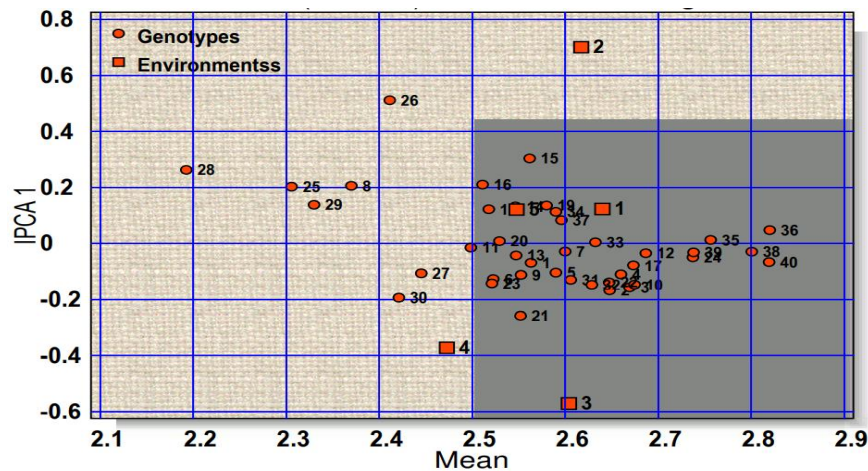


Fig. 21.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes for 1000 seed weight (g) across five tested environments.

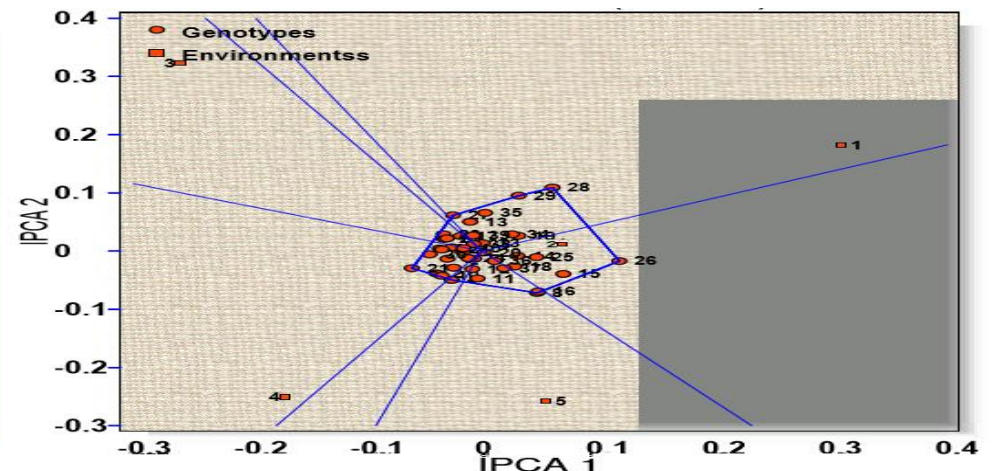


Fig. 21.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

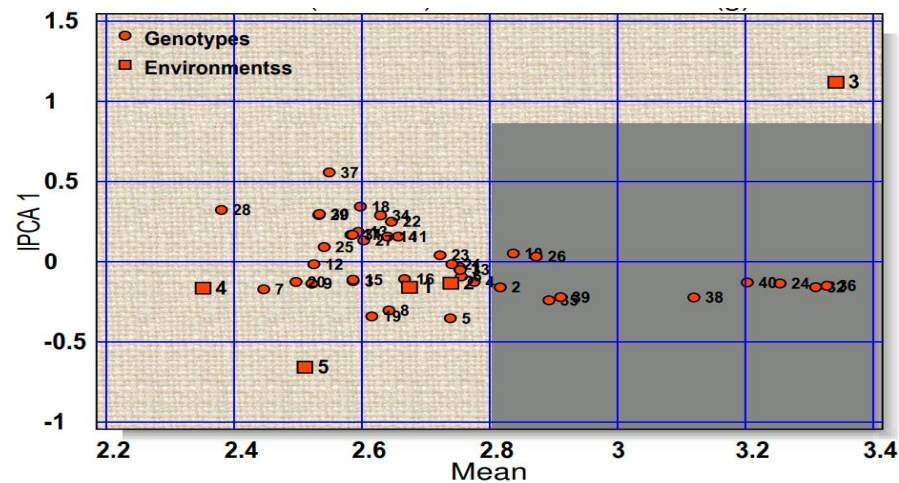


Fig. 22.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for seed yield plant⁻¹ (g) across five tested environments.

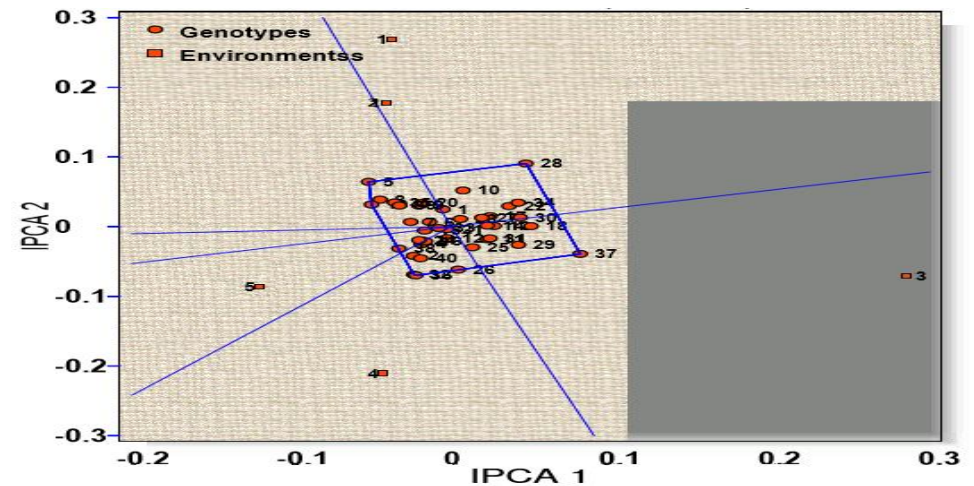


Fig. 22.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

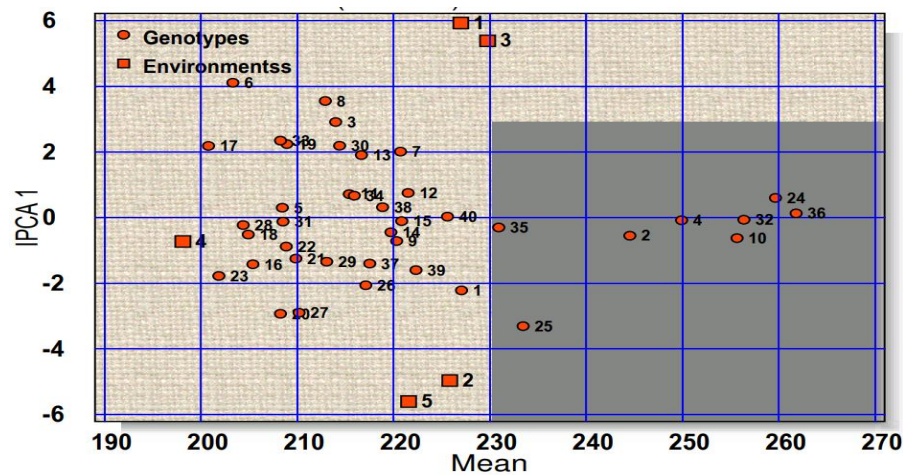


Fig. 23.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for seed yield plot⁻¹ (g) across five tested environments.

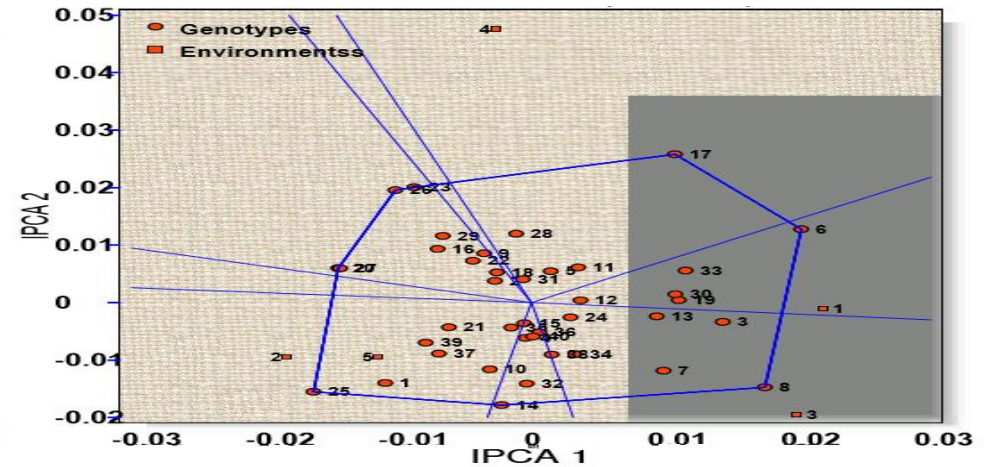


Fig. 23.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

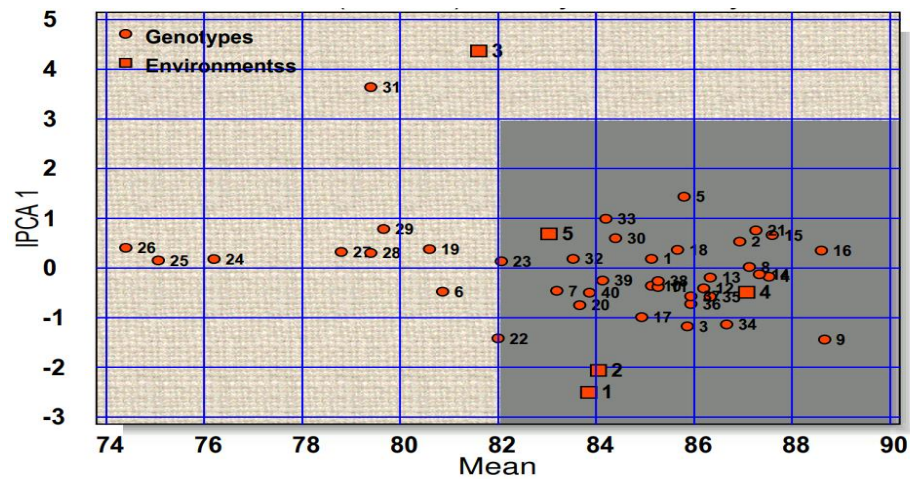


Fig. 24.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for days to maturity across five tested environments.

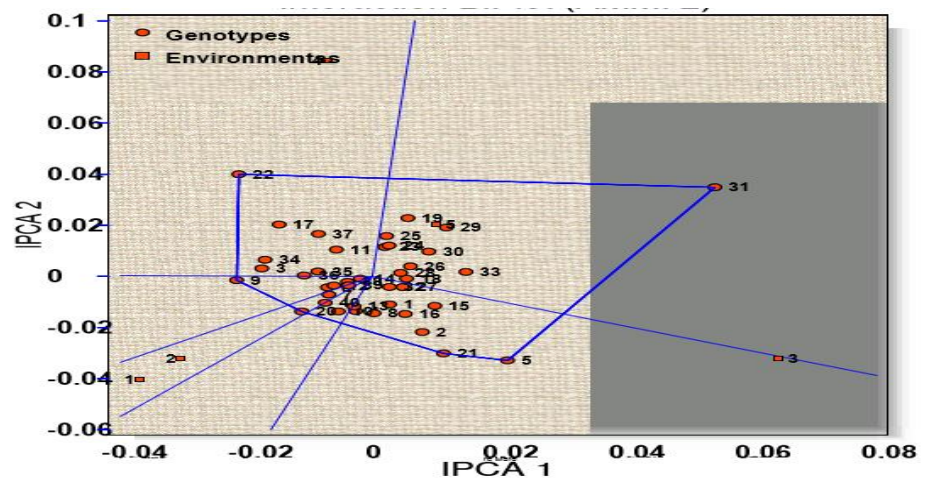


Fig. 24.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

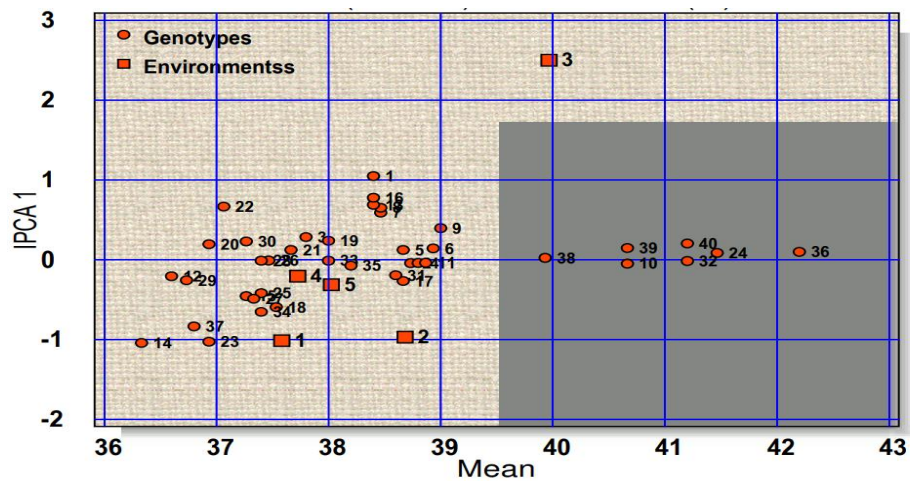


Fig. 25.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for oil content (%) across five tested environments.

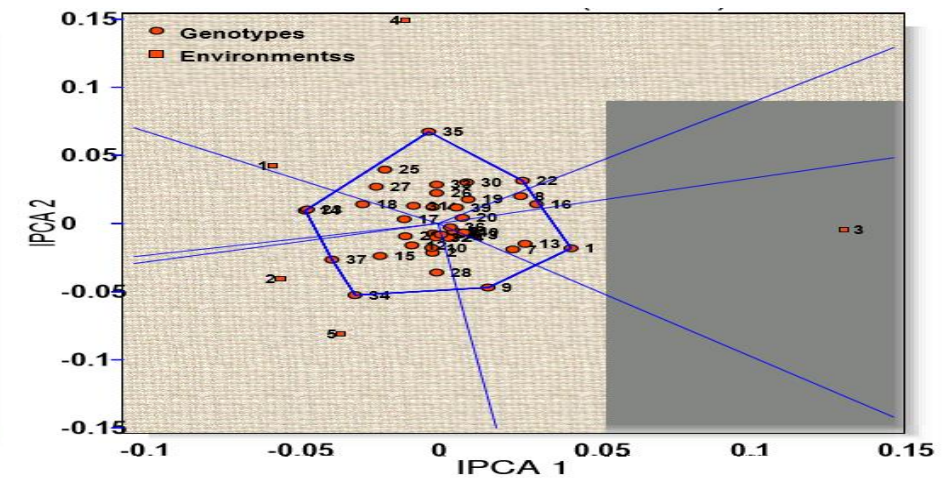


Fig. 25.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

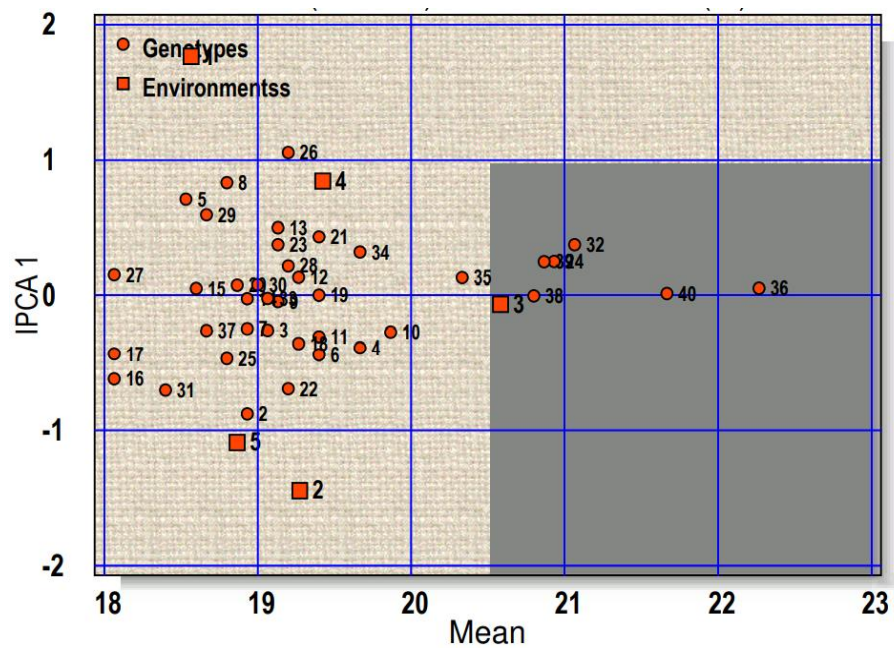


Fig. 26.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for protein content (%) across five tested environments.

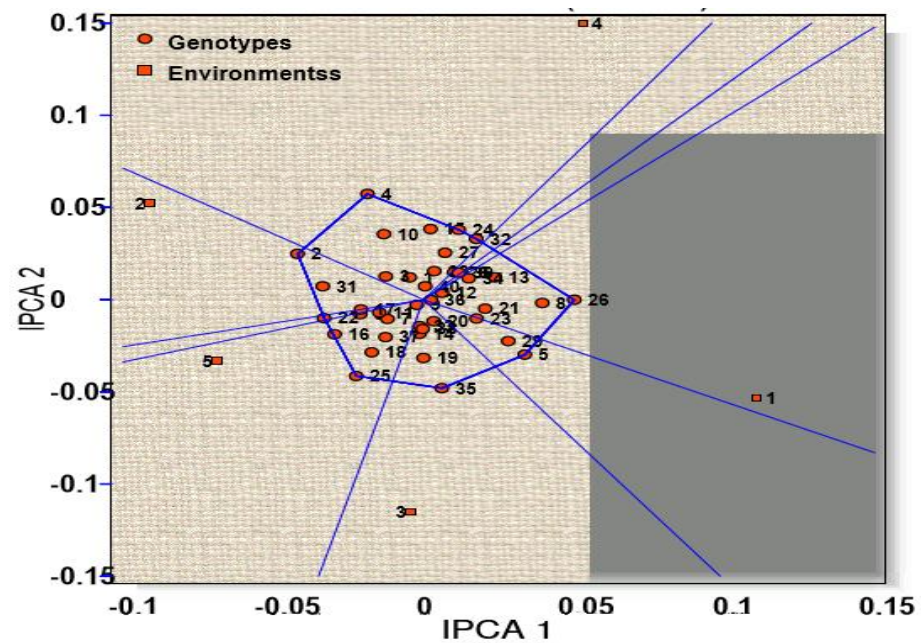


Fig. 26.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

Plate 1: Overview of the field trials on five locations



**ARS, Phondaghat
(E1)**



**ARS, Shirgaon
(E2)**



Educational and Research Farm, Dept. of Agril. Botany, Dapoli (E3)



RARS, Karjat (E4)



ARS, Palghar (E5)

Plate 2: Promising and stable Niger genotypes for yield and yield contributing traits



G36



G32



G24



G10



G4



G8



G9



G35



G25



G40

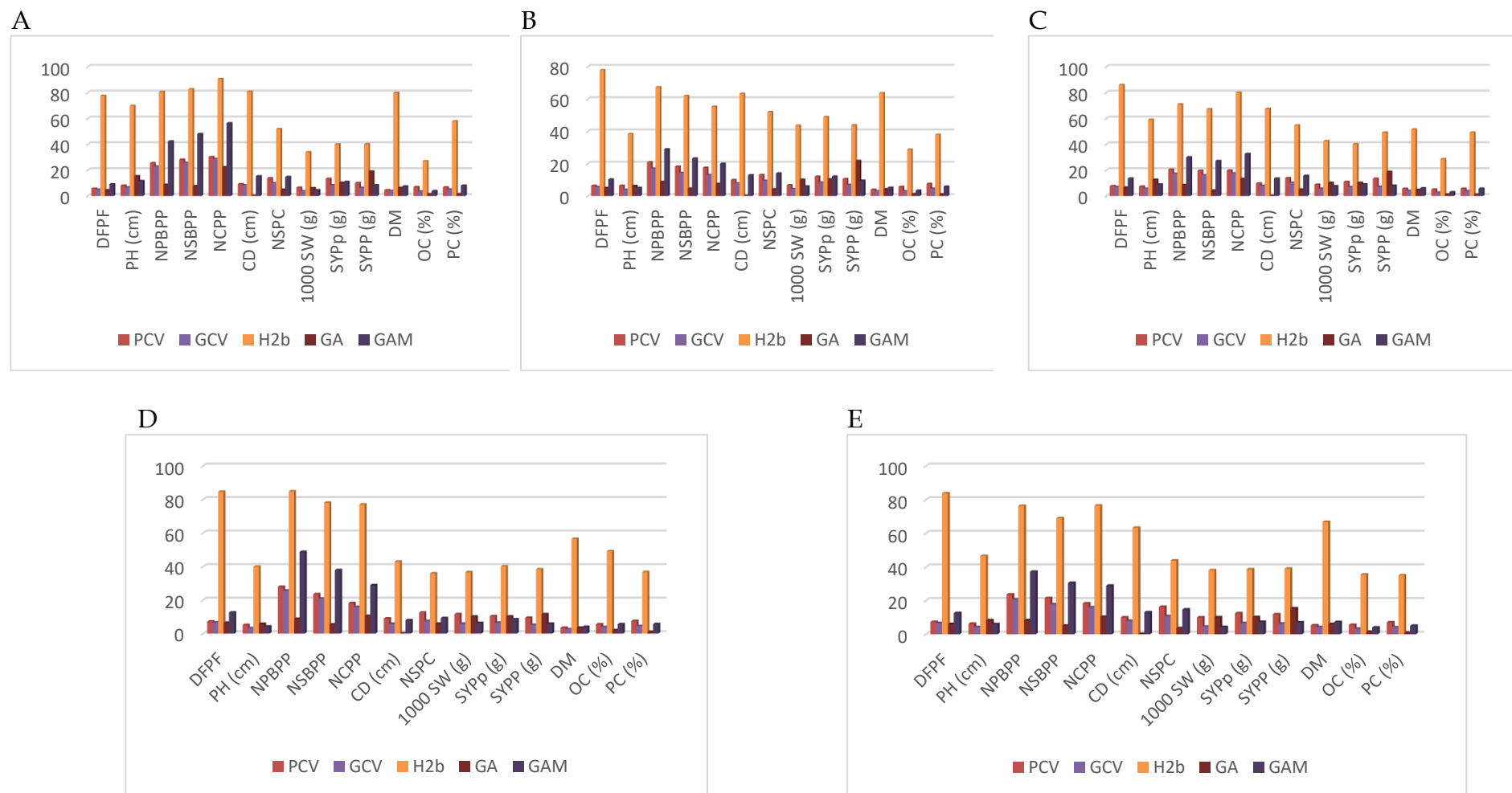


Fig. 1. Estimates of genetic parameters for quantitative and qualitative traits in niger A) ARS, Phondaghat (E1) B) ARS, Shirgaon (E2), C) Dept. of Agril. Botany, Dapoli (E3) D) RARS, Karjat (E4) and E) ARS, Palghar (E5).

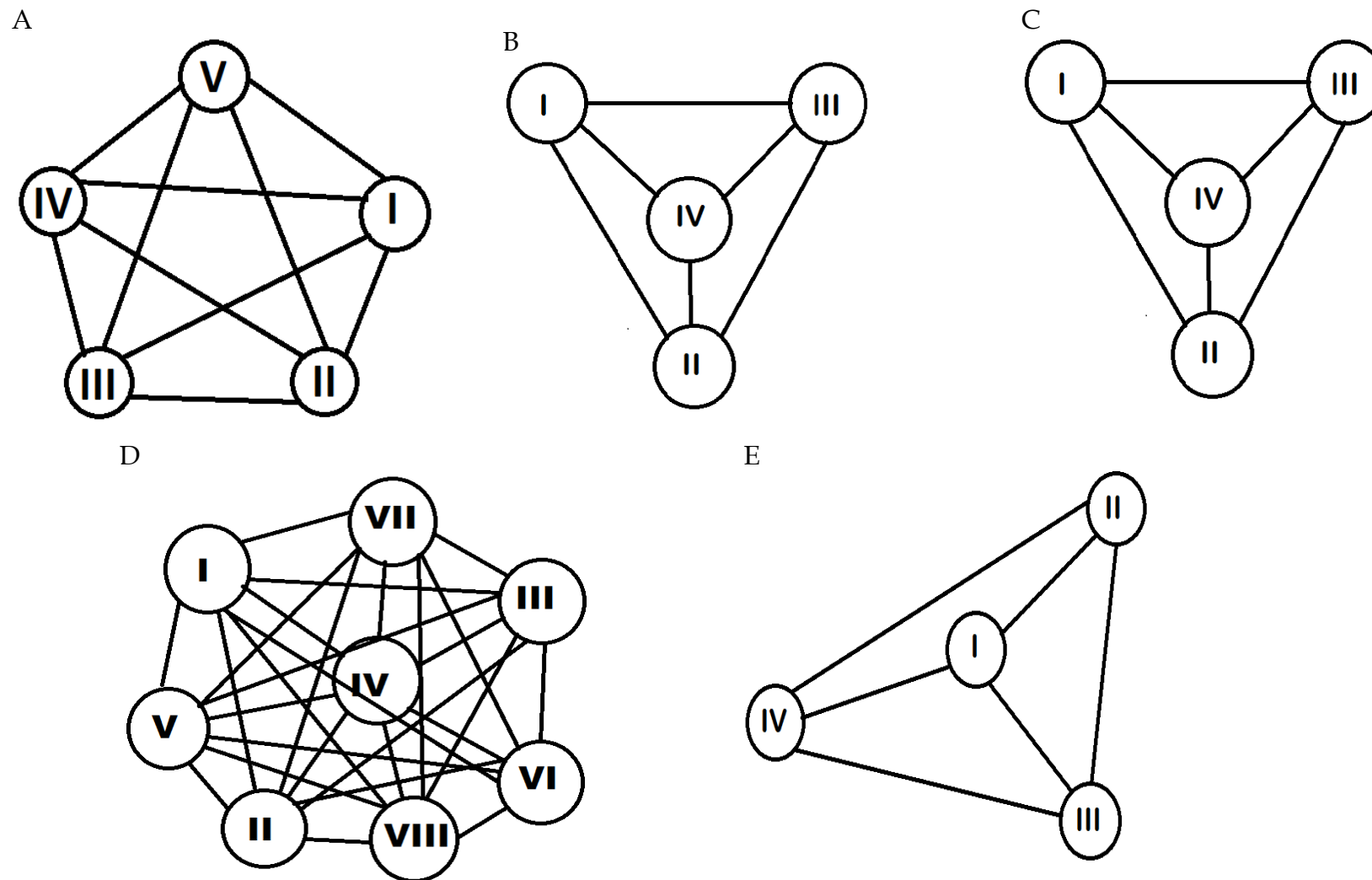


Fig. 3. Mutual relationship among the D^2 clusters in A) ARS, Phondaghat (E1) B) ARS, Shirgaon (E2), C) Dept. of Agril. Botany, Dapoli (E3), D) RARS, Karjat (E4) and E) ARS, Palghar (E5).

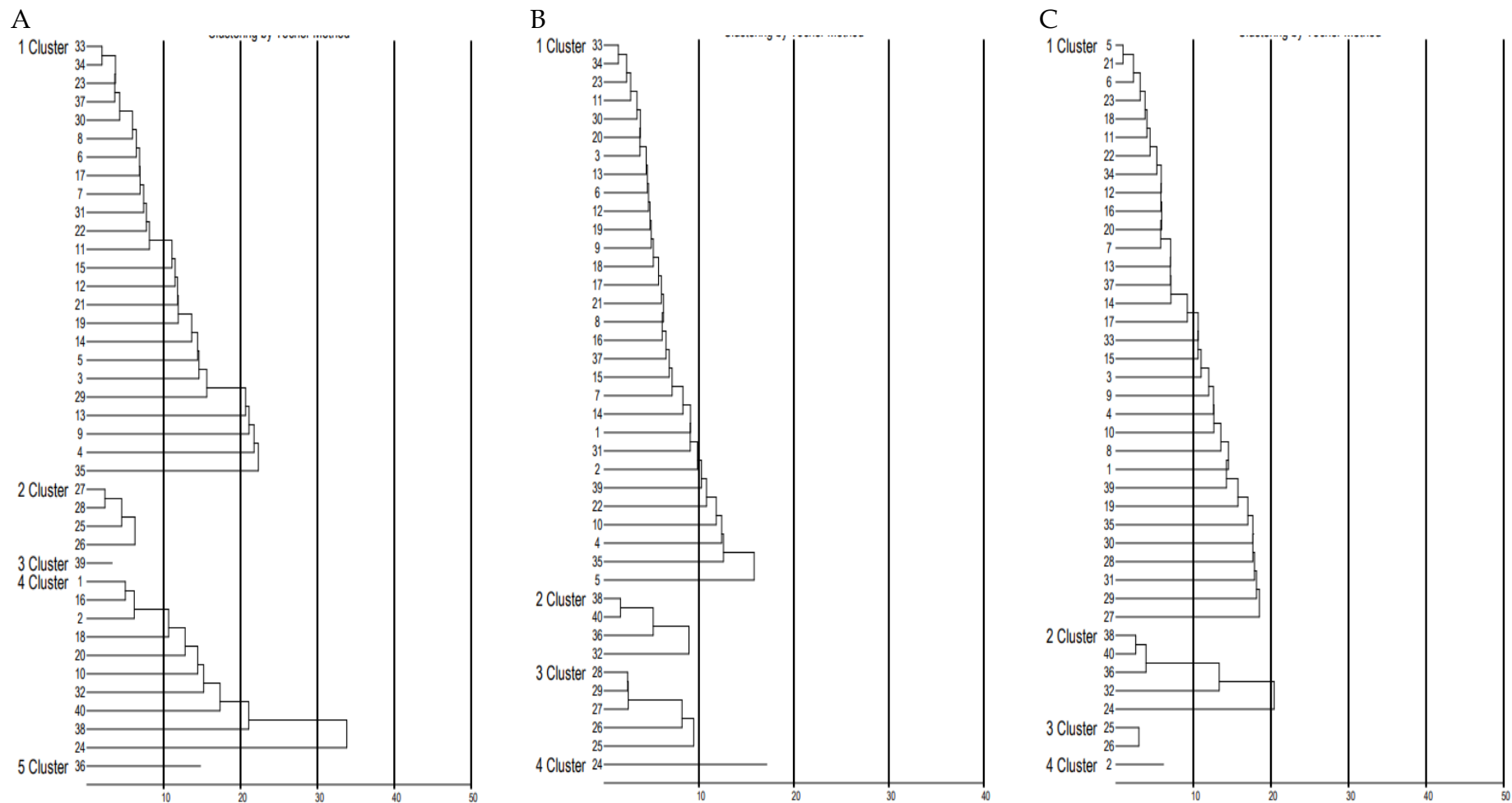


Fig. 2. Clustering pattern of 40 genotypes of niger by Tochers' Method in A) ARS, Phondaghat (E1) B) ARS, Shirgaon (E2) and C) Dept. of Agril. Botany, Dapoli (E3).

Figures Contd...

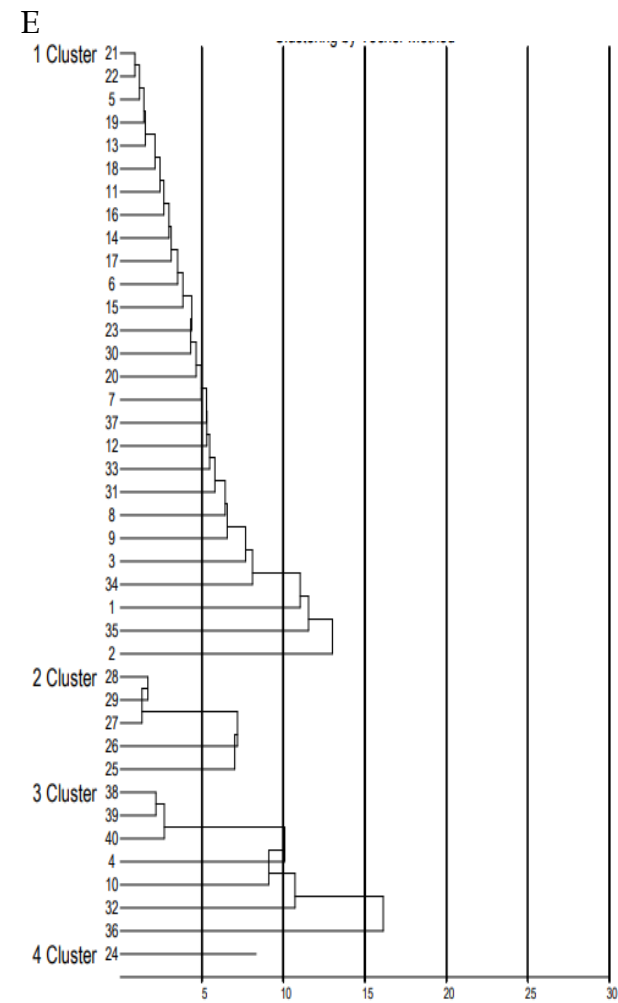
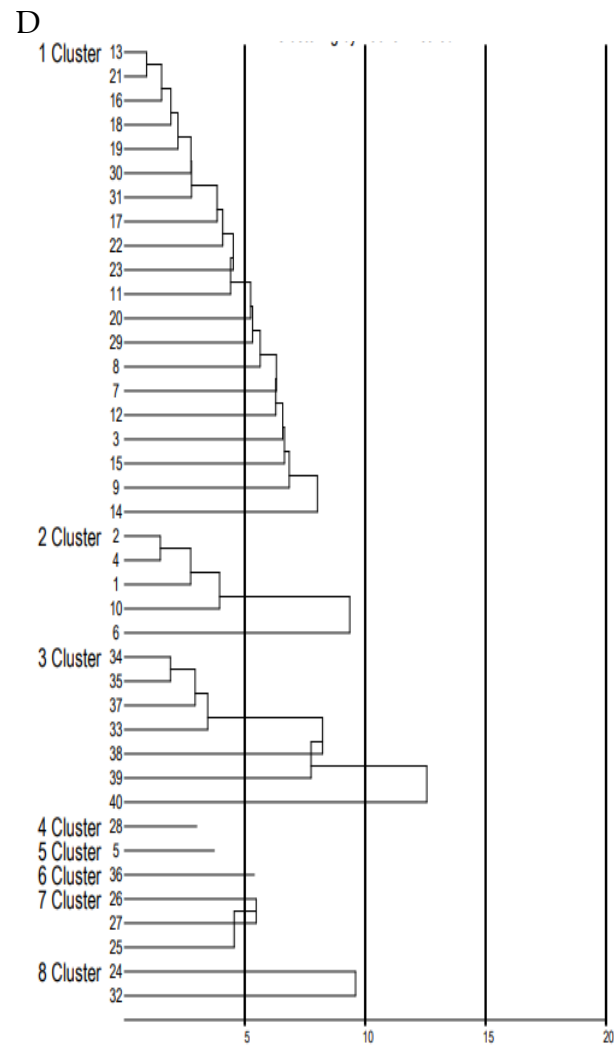


Fig. 2. Clustering pattern of 40 genotypes of niger by Tochers' Method in D) RARS, Karjat (E4) and E) ARS, Palghar (E5).

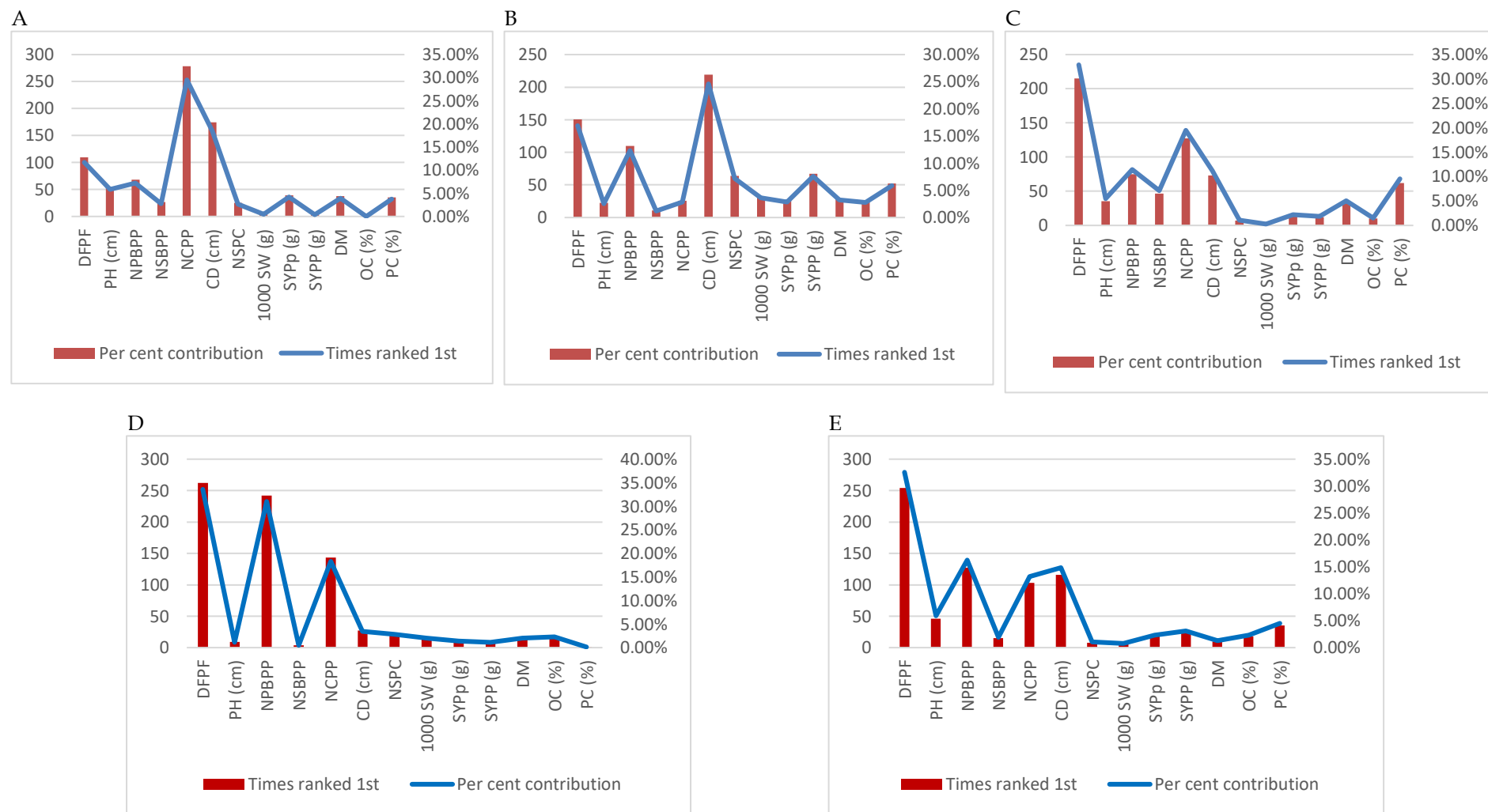


Fig. 4. Contribution of various characters towards divergence at A) ARS, Phondaghat (E1) B) ARS, Shirgaon (E2), C) Dept. of Agril. Botany, Dapoli (E3) D) RARS, Karjat (E4) and E) ARS, Palghar (E5).

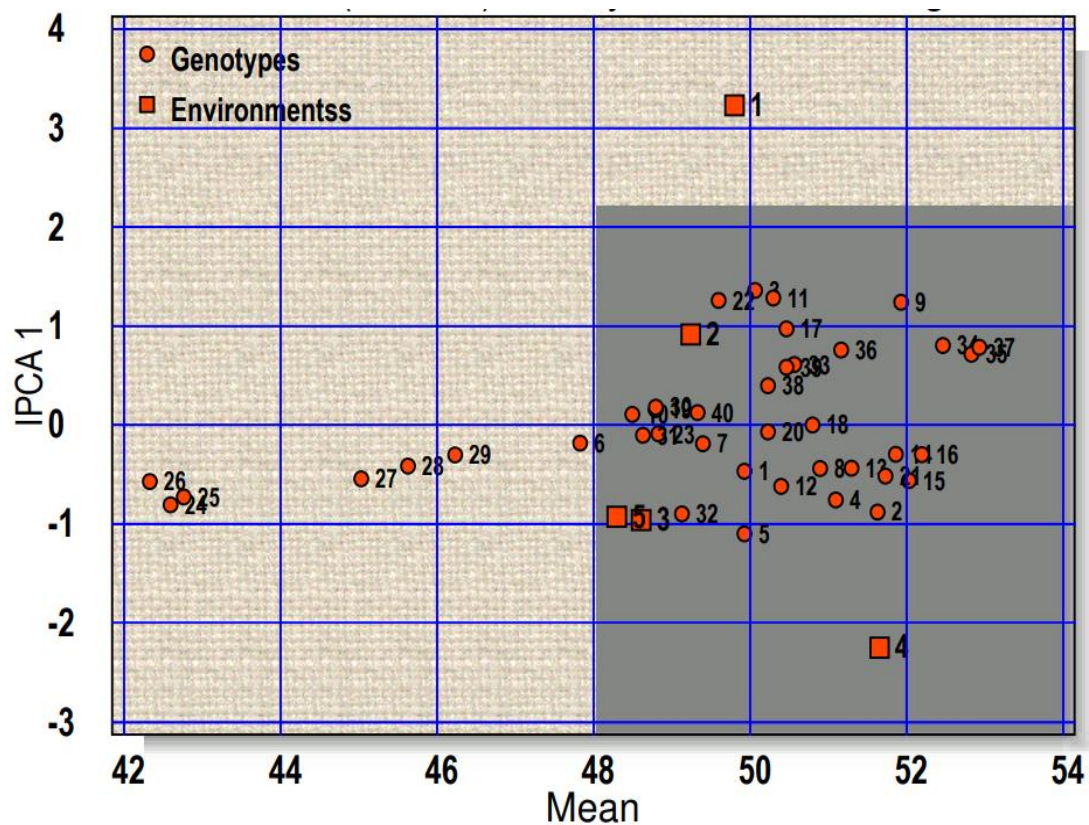


Fig. 5.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for days to 50 per cent flowering across five tested environments.

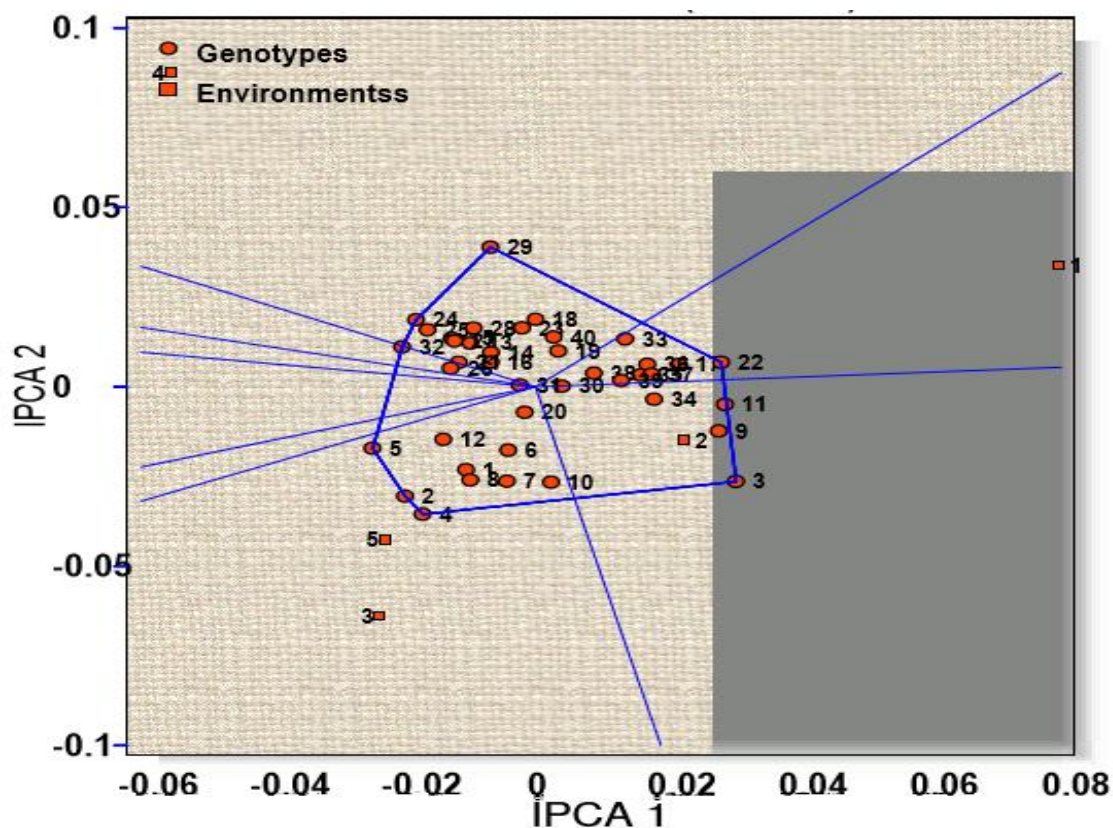


Fig. 5.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

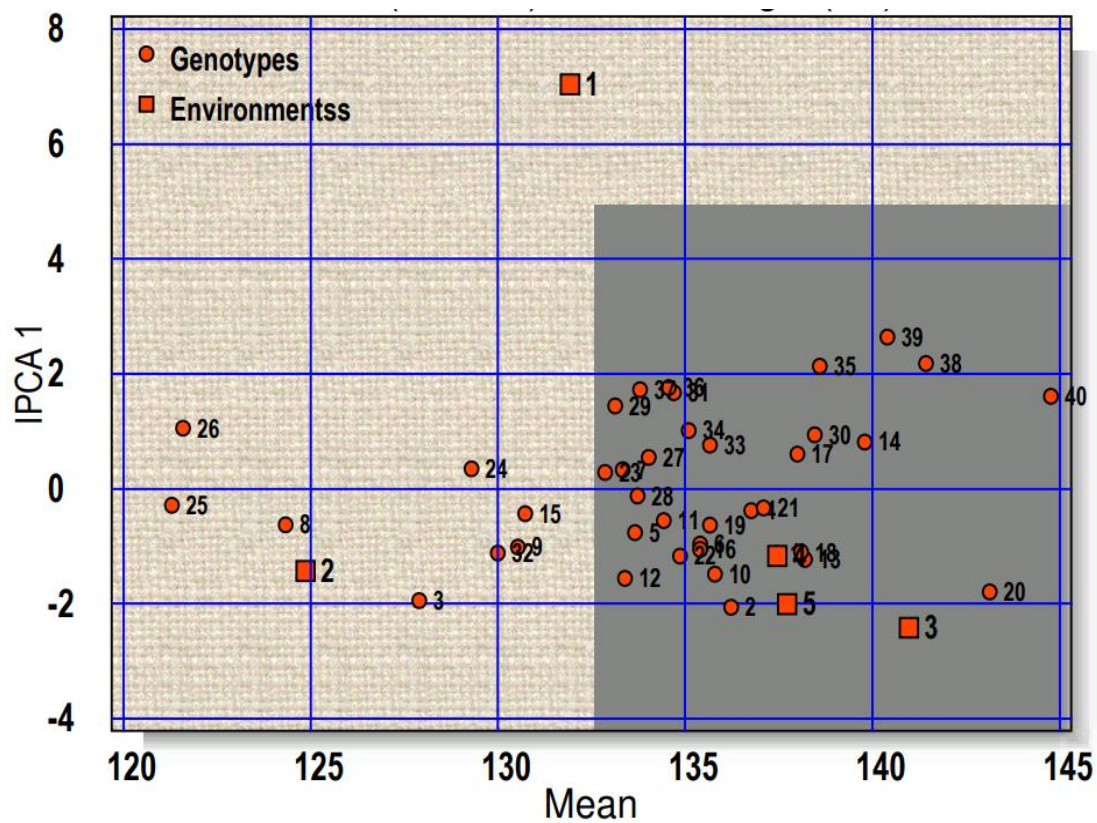


Fig. 6.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for plant height (cm) across five tested environments.

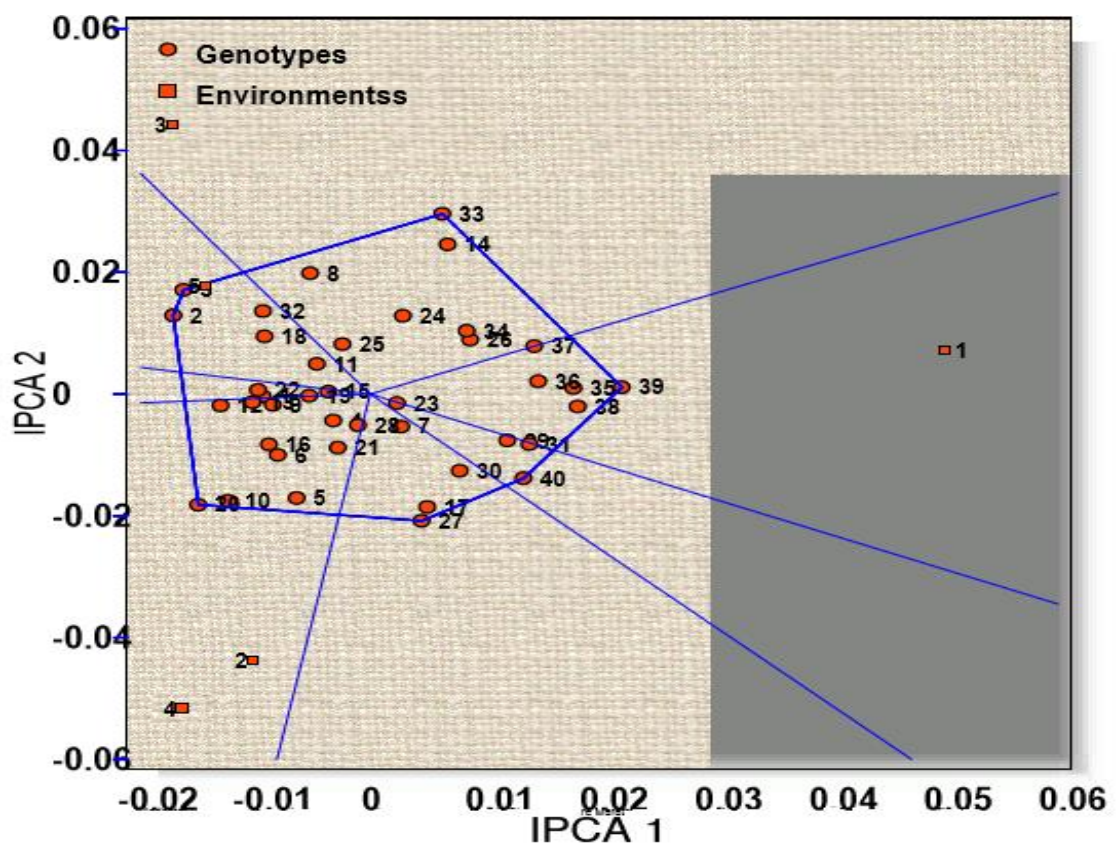


Fig. 6.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

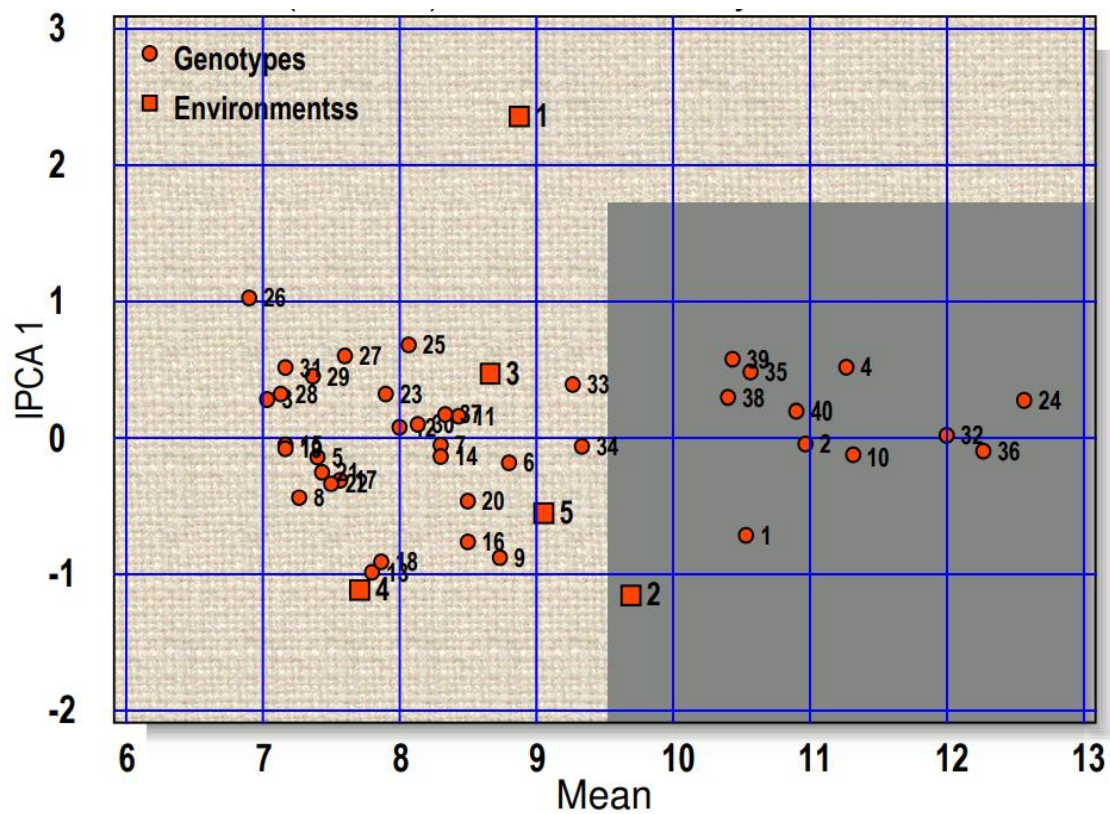


Fig. 7.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for number of primary branches plant⁻¹ across five tested environments.

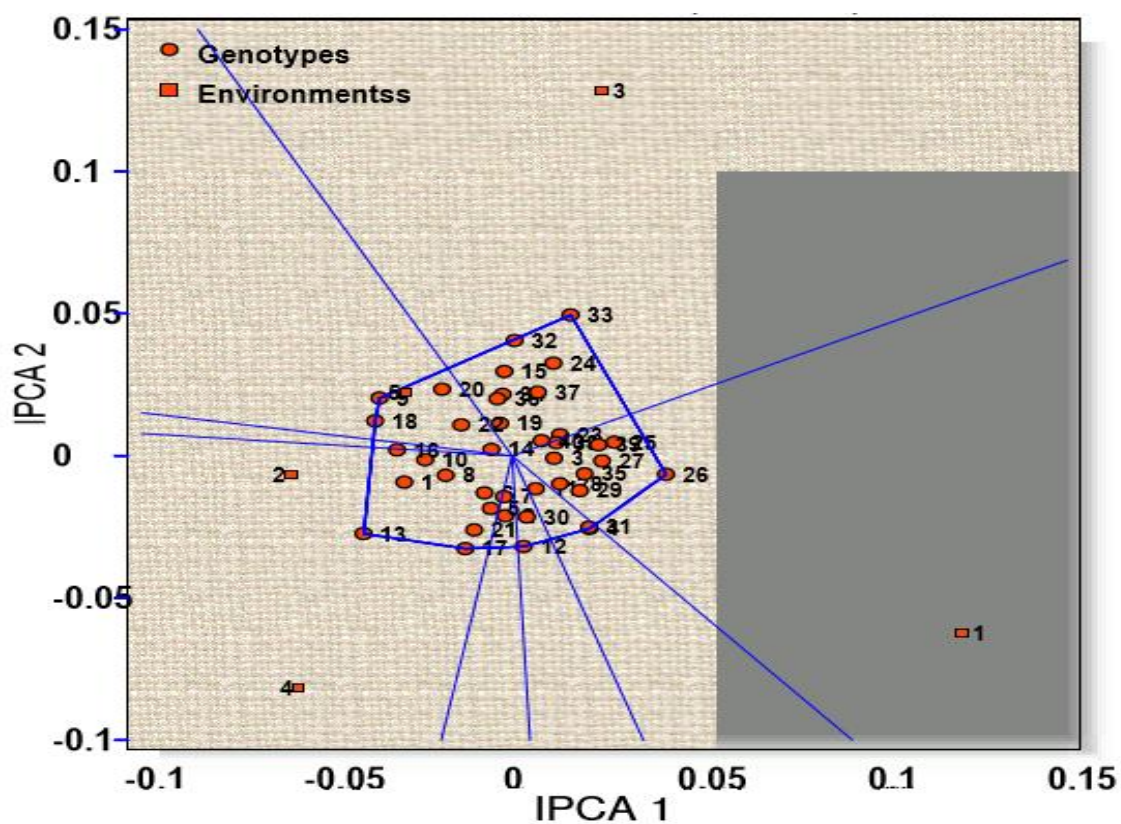


Fig. 7.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

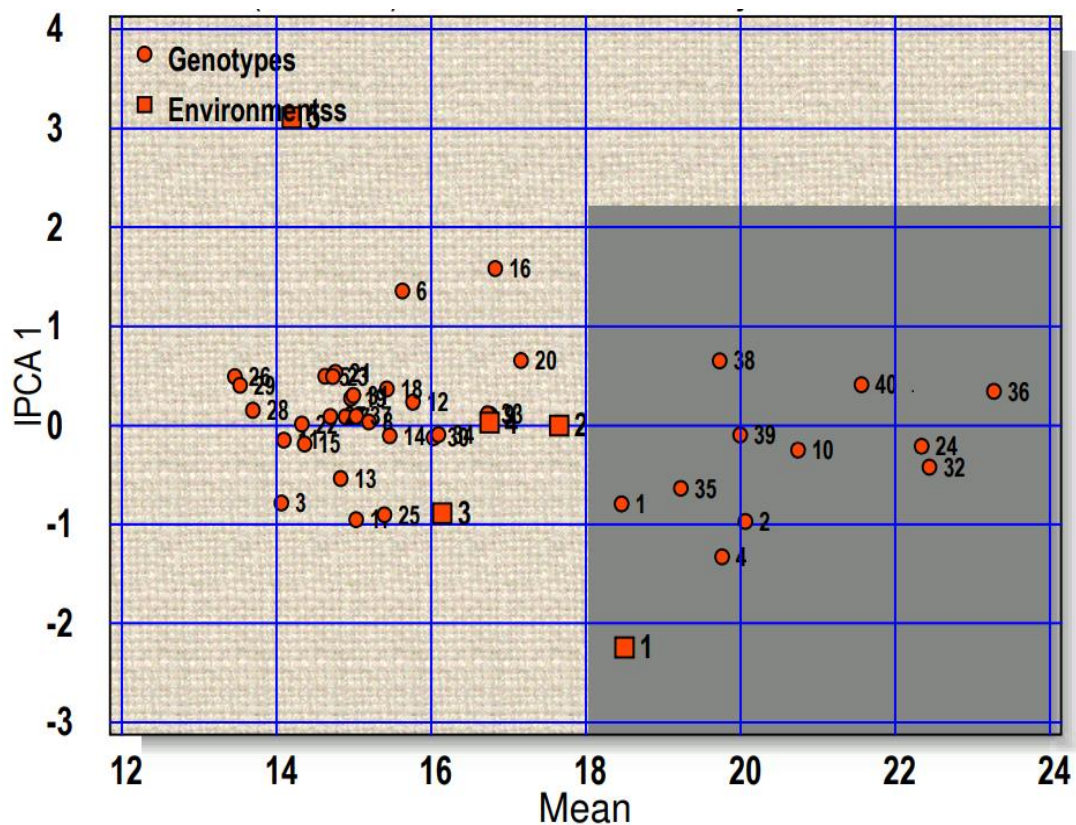


Fig. 8.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for number of secondary branches plant⁻¹ across five tested environments.

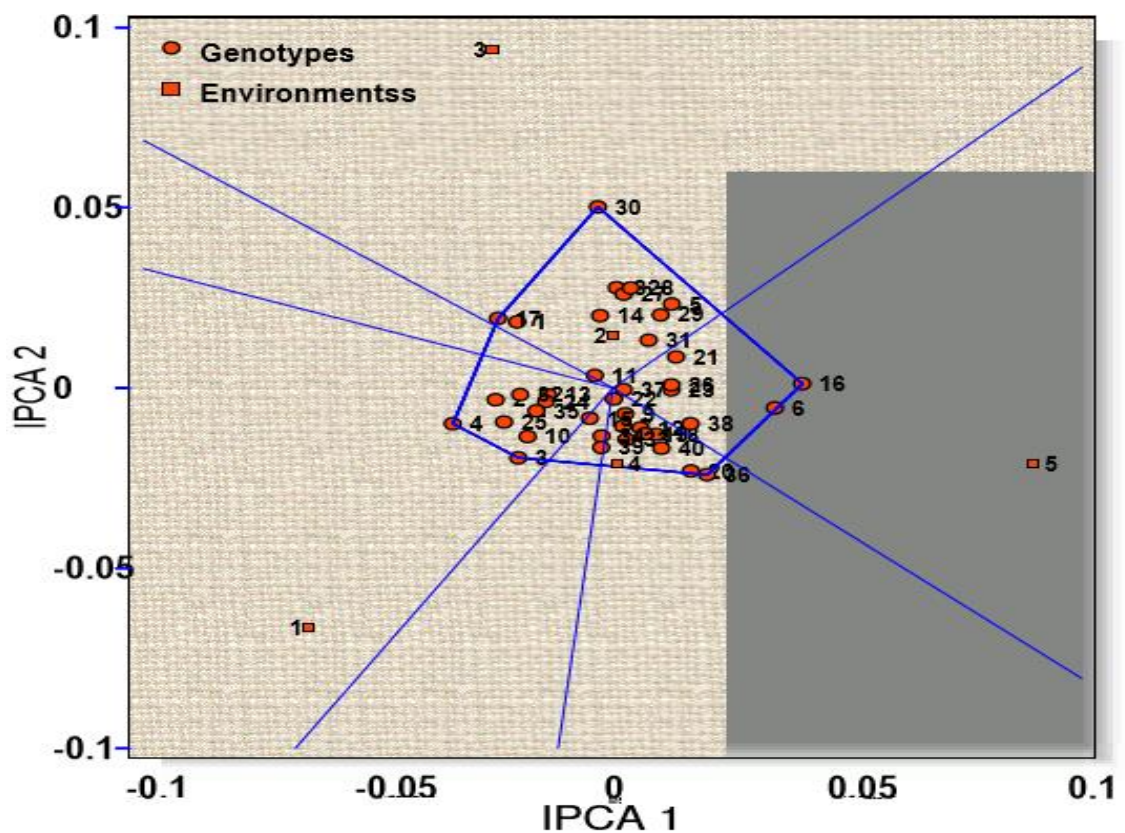


Fig. 8.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

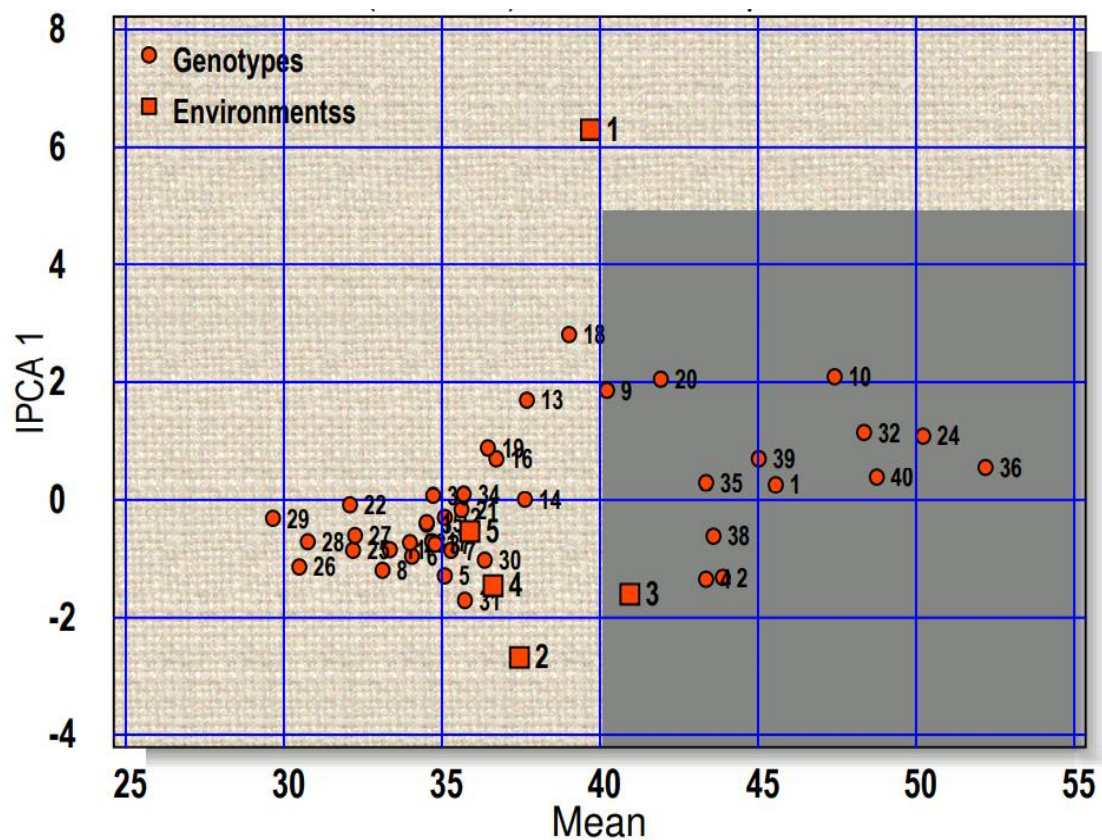


Fig. 9.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for number of capitula plant⁻¹ across five tested environments.

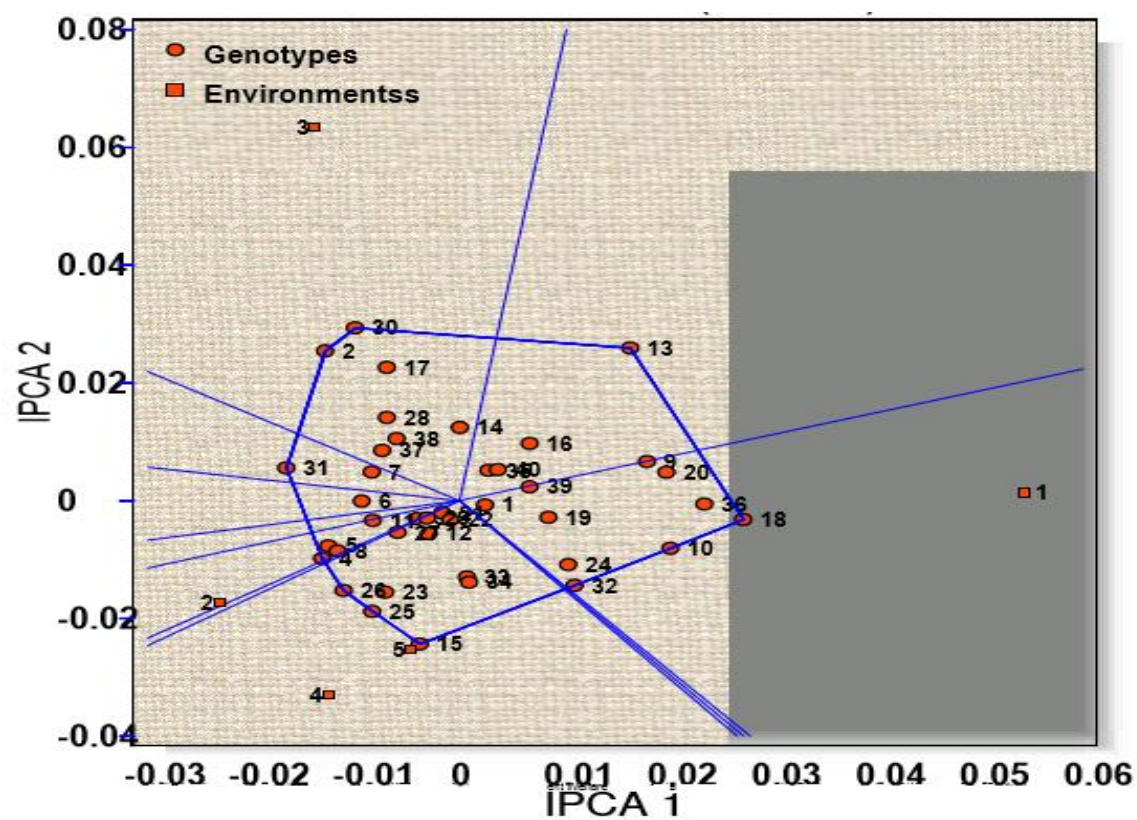


Fig. 9.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

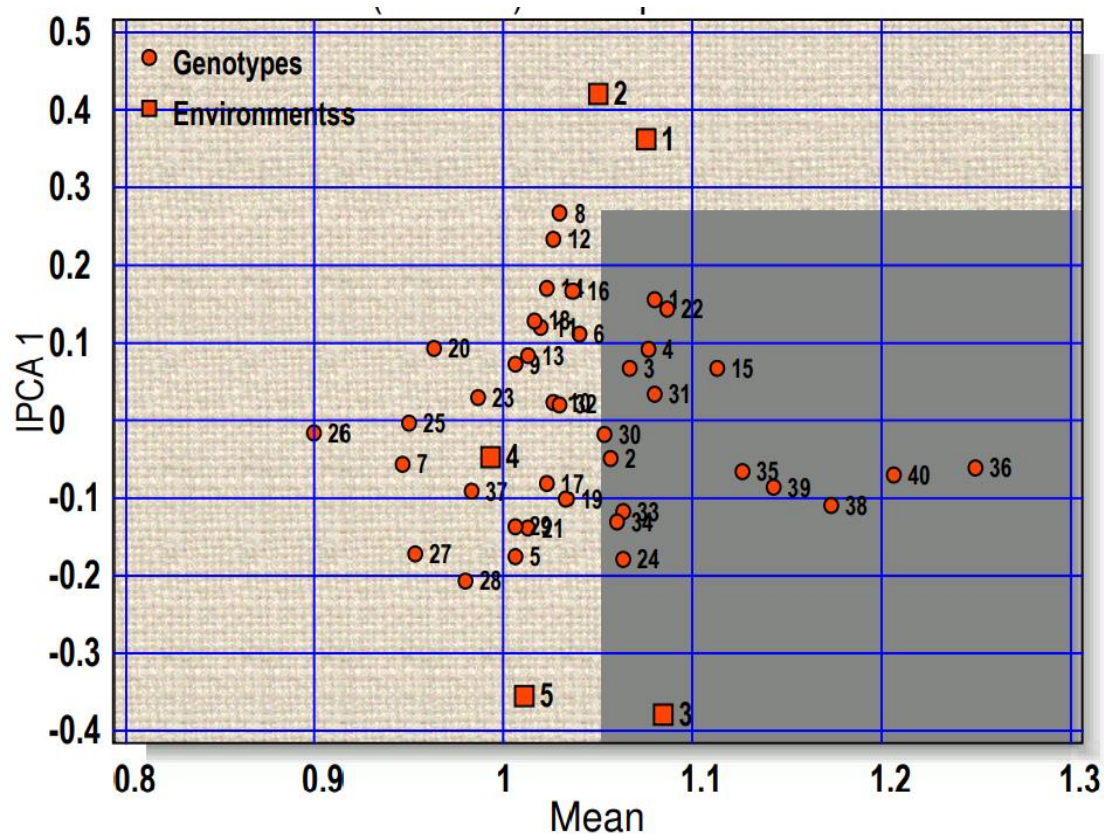


Fig. 10.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for capitulum diameter (cm) across five tested environments.

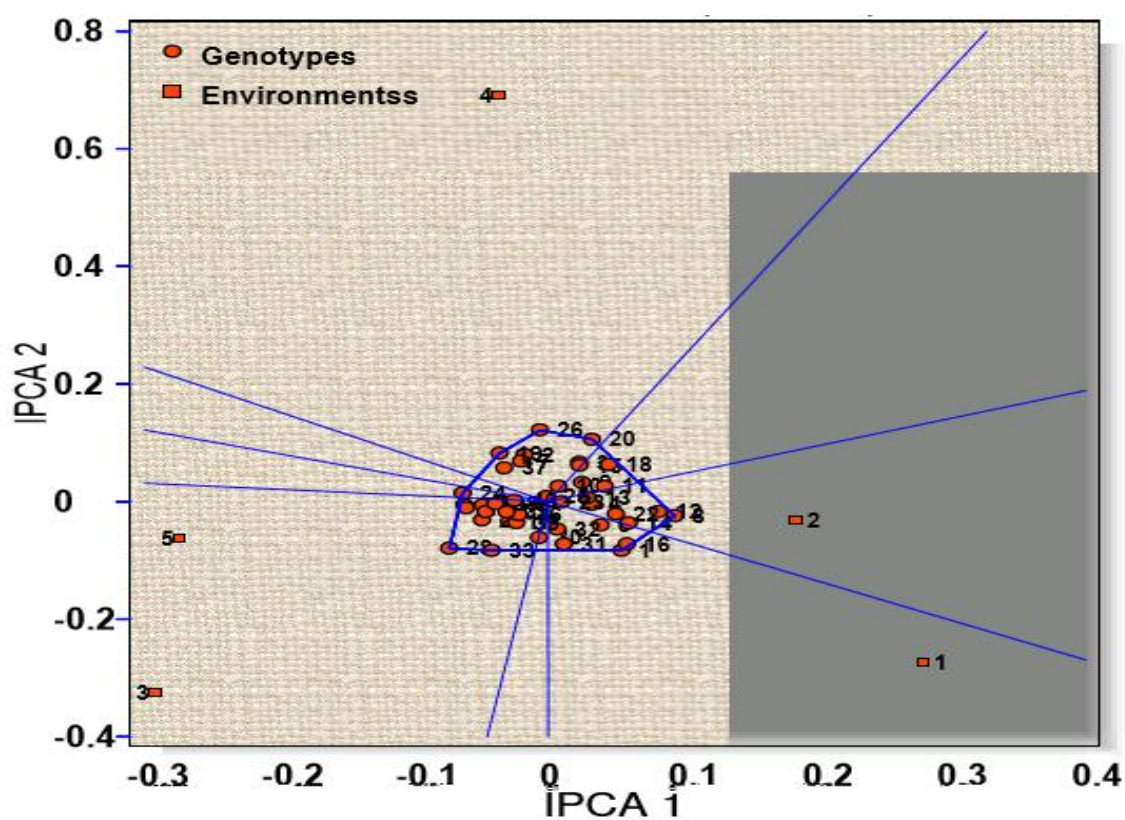


Fig. 10.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

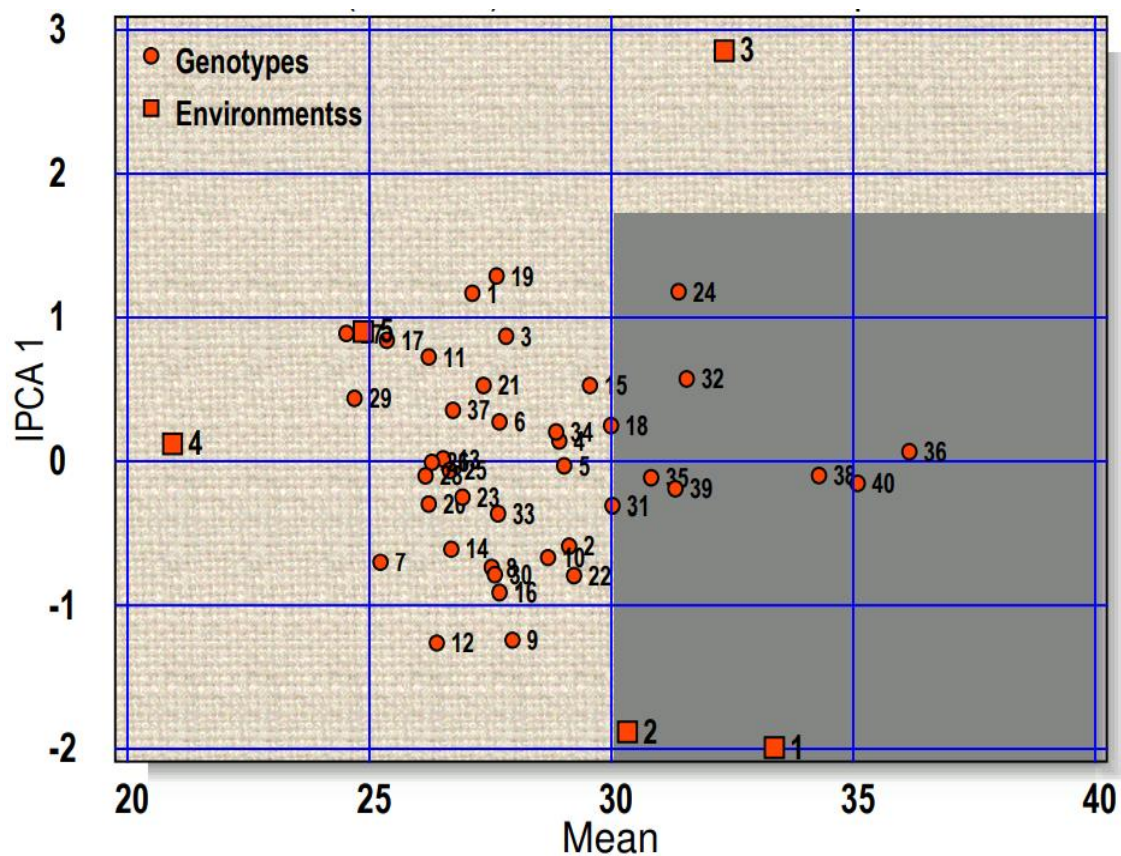


Fig. 11.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for number of seeds capitulum⁻¹ across five tested environments.

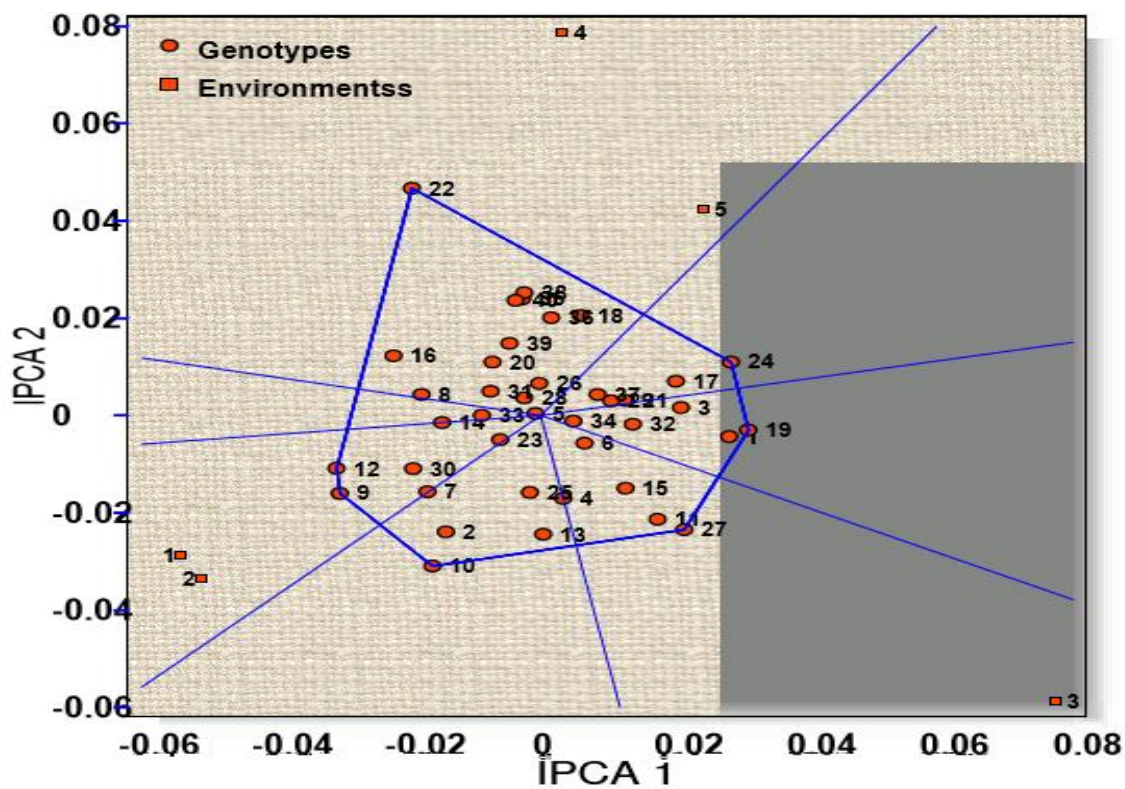


Fig. 11.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

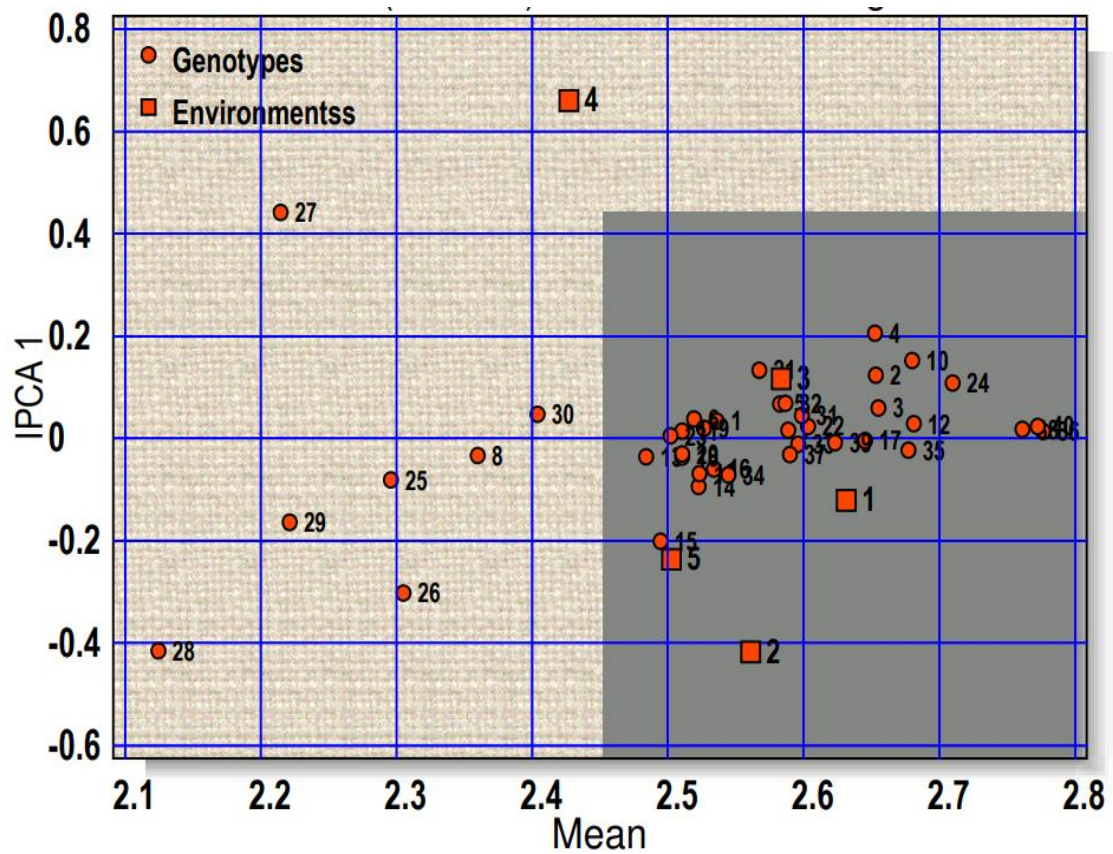


Fig. 12.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for 1000 seed weight (g) across five tested environments.

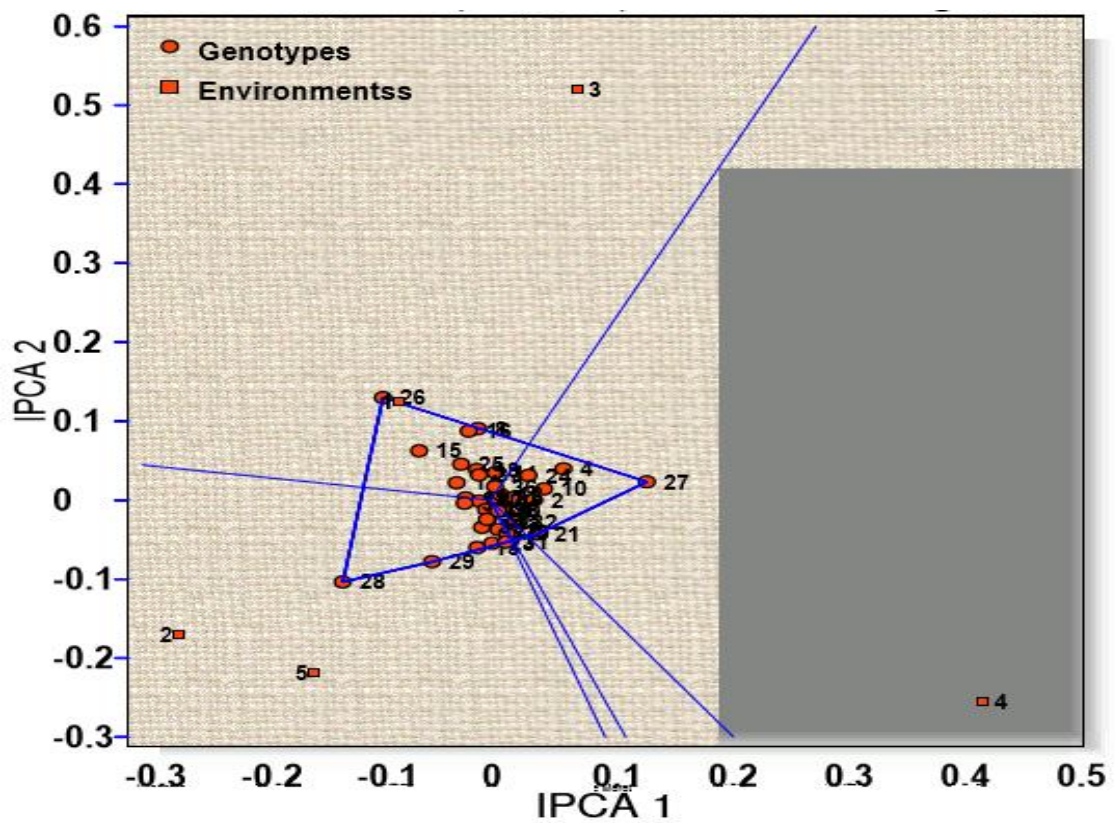


Fig. 12.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

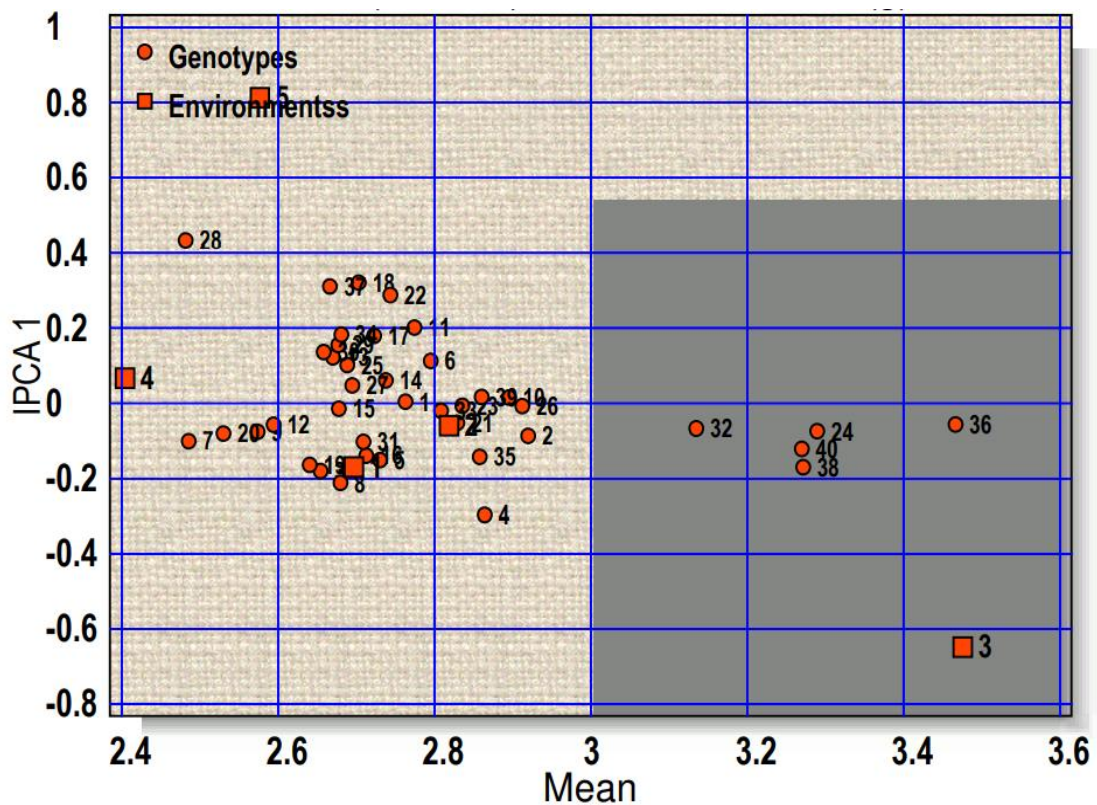


Fig. 13.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for seed yield plant⁻¹ (g) across five tested environments.

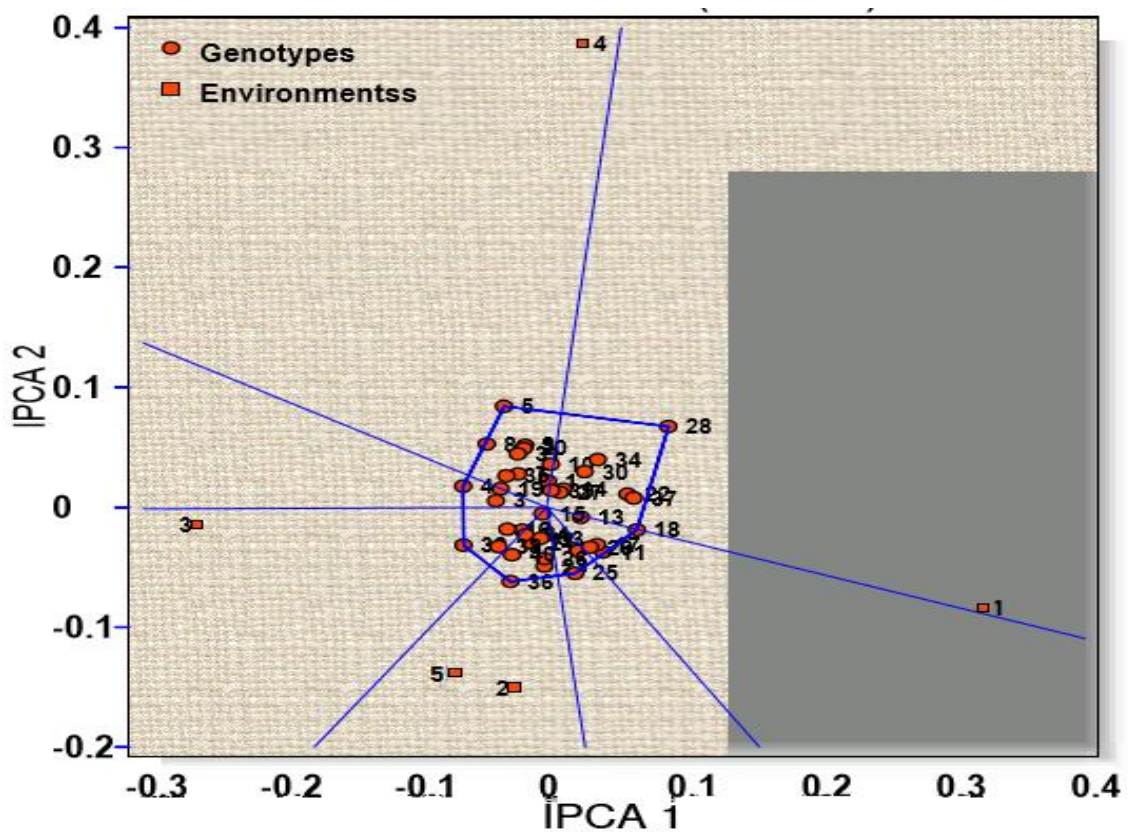


Fig. 13.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

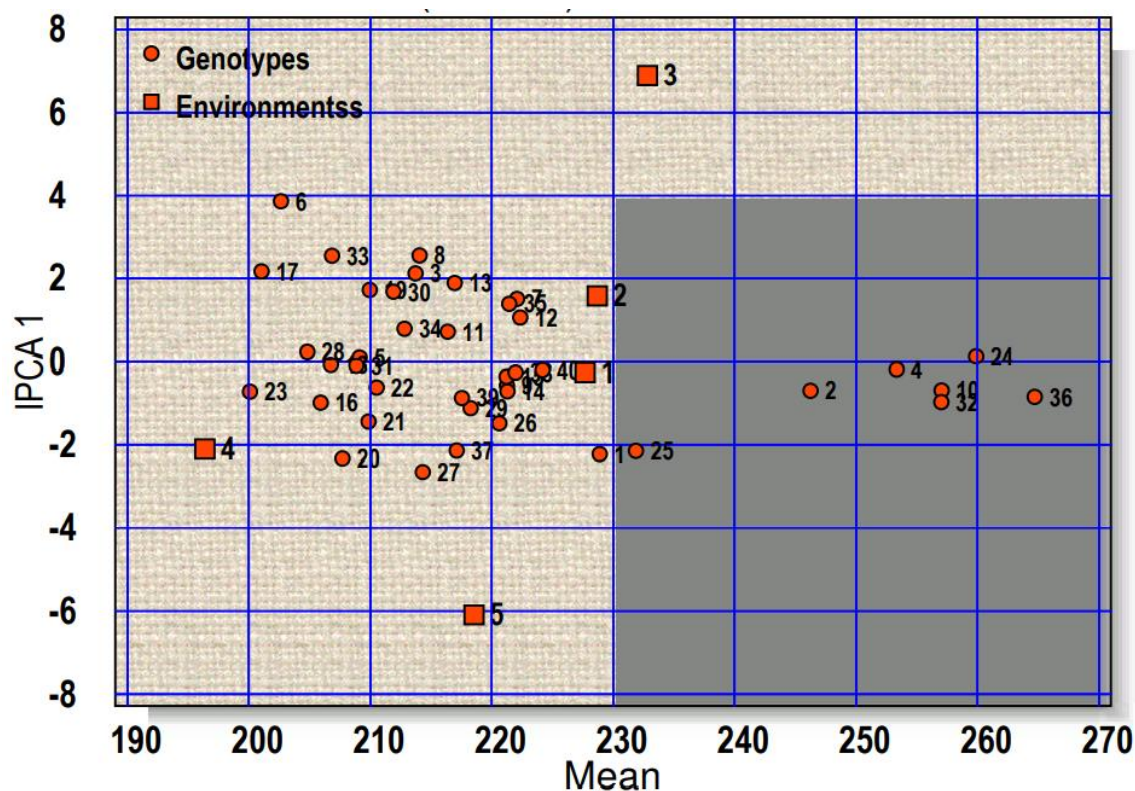


Fig. 14.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for seed yield plot⁻¹ (g) across five tested environments.

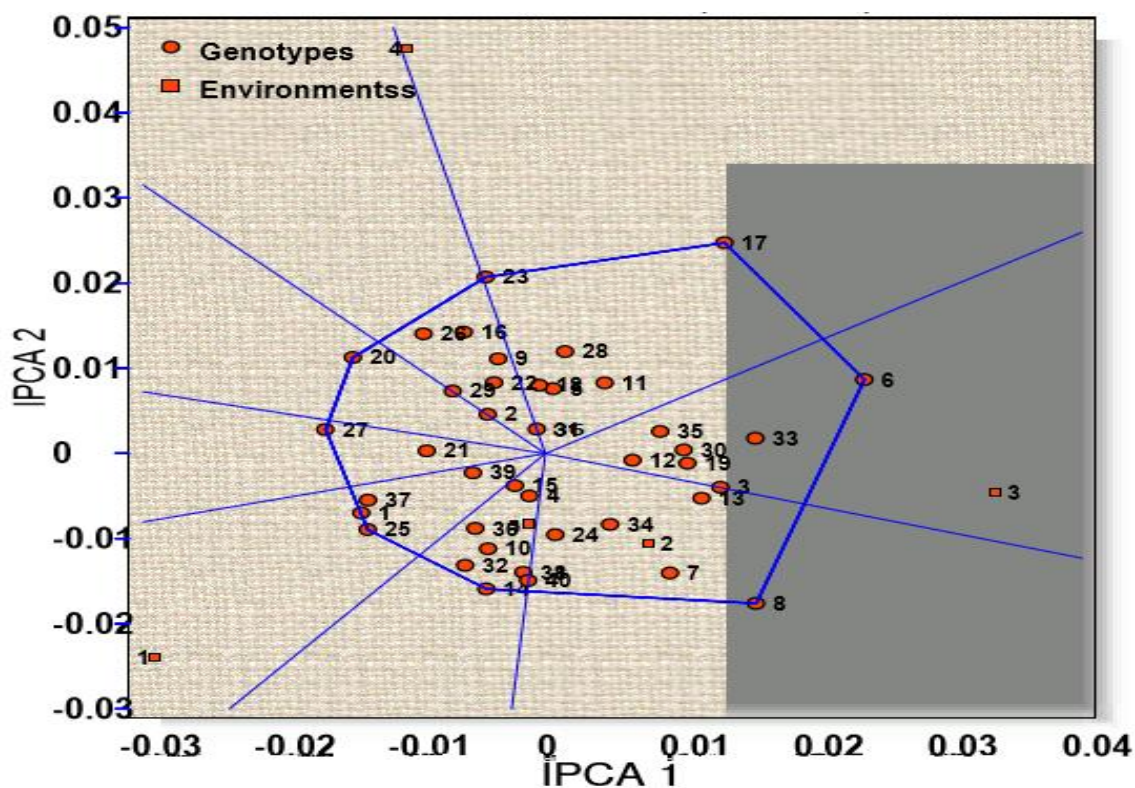


Fig. 14.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

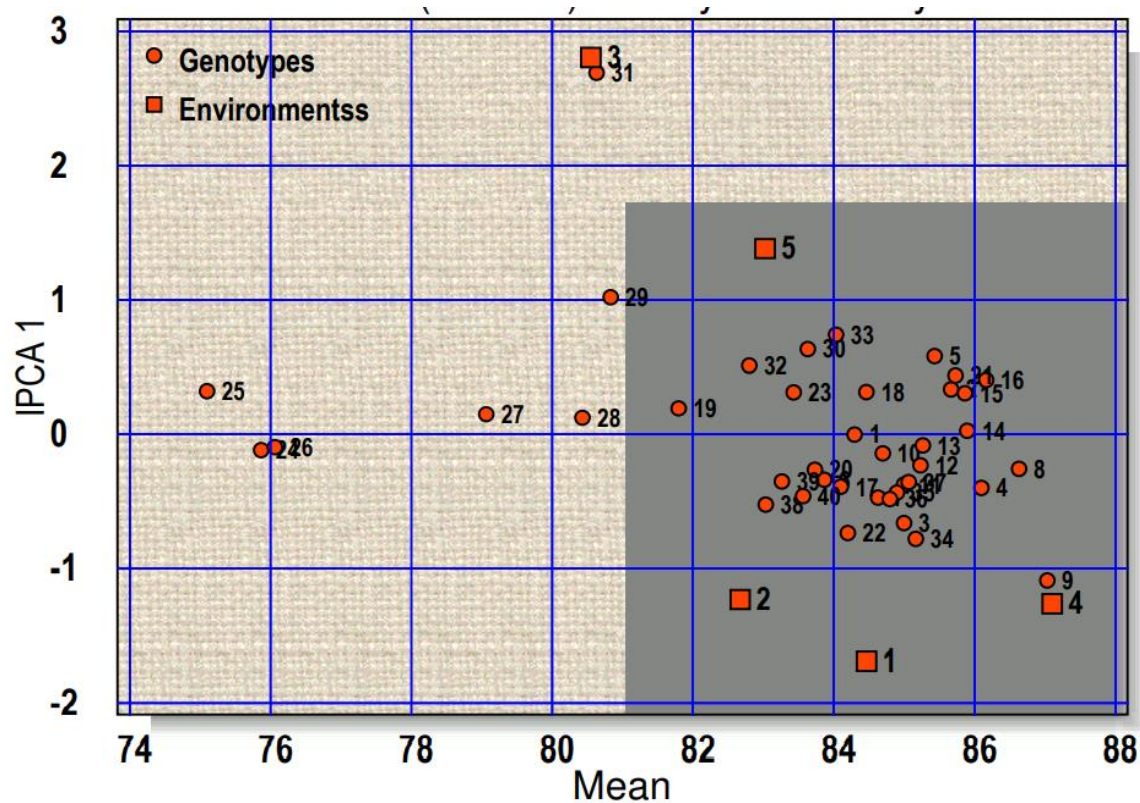


Fig. 15.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for days to maturity across five tested environments.

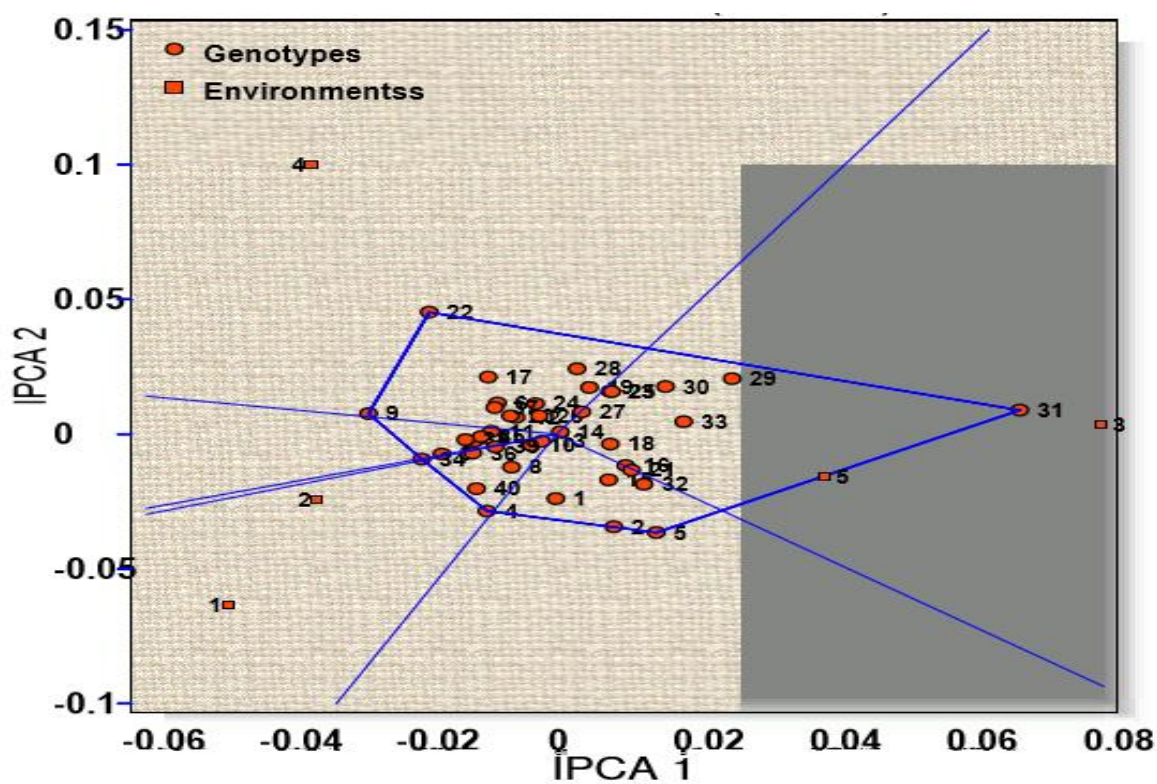


Fig. 15.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

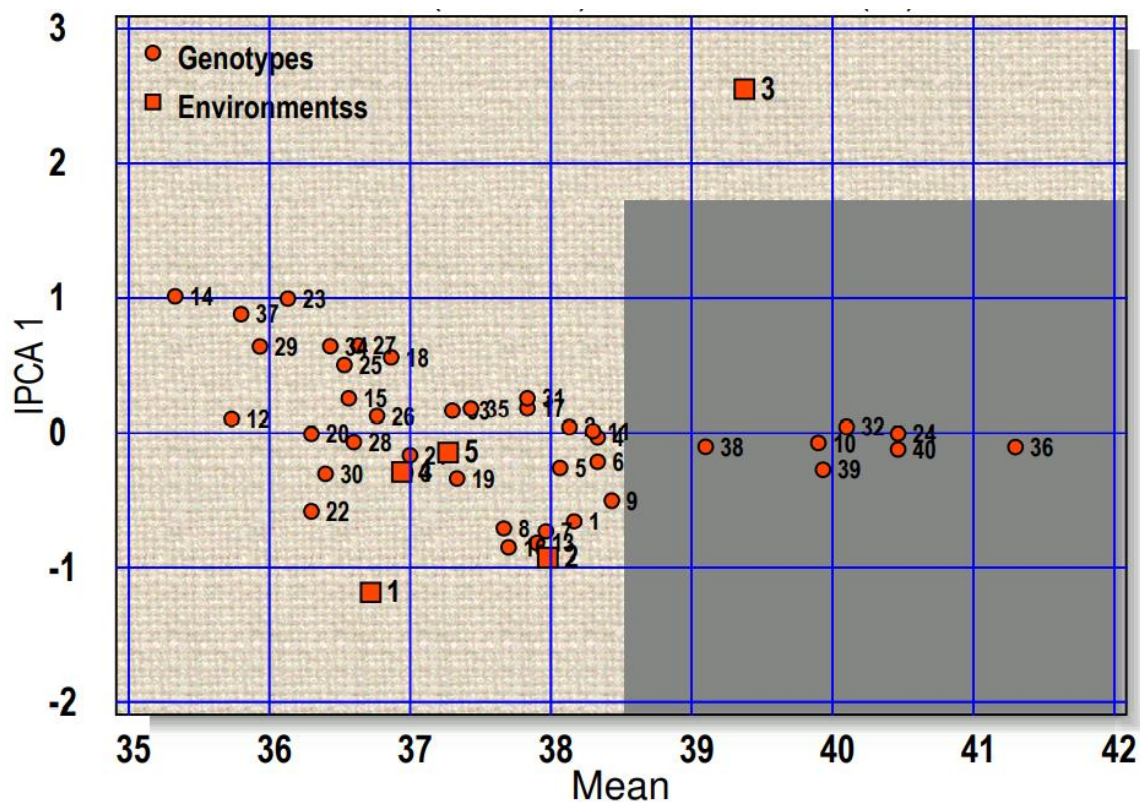


Fig. 16.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for oil content (%) across five tested environments.

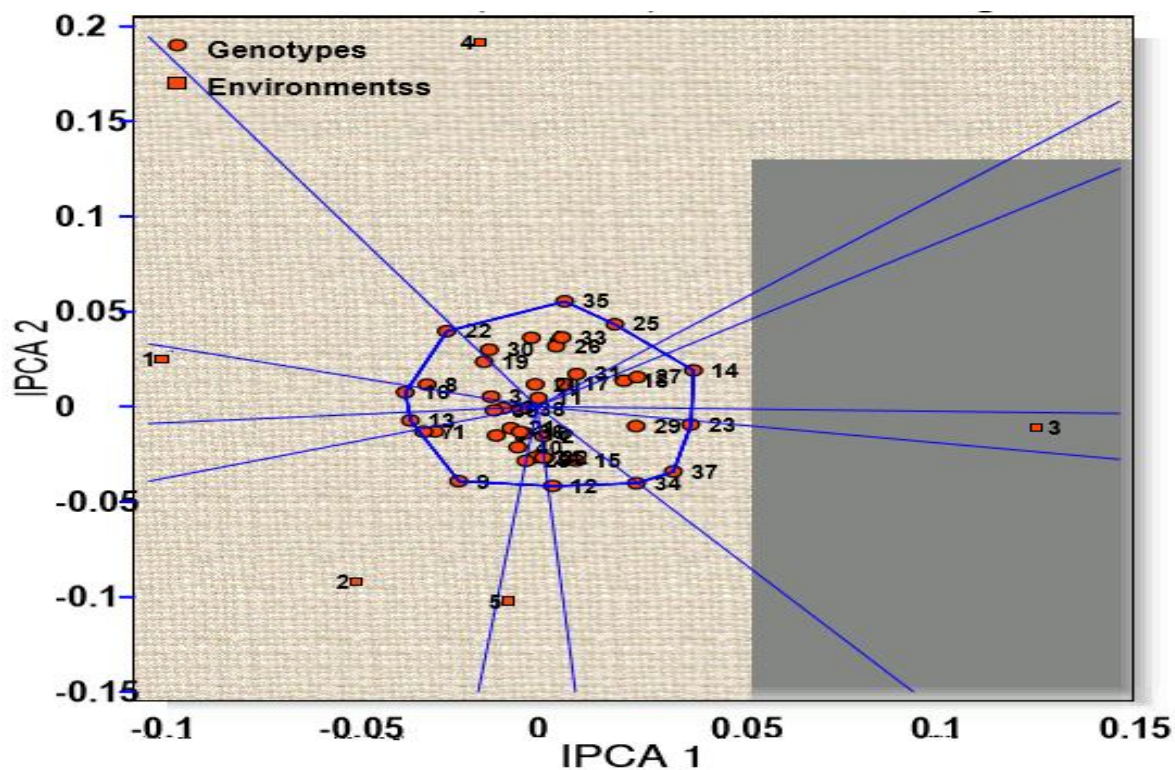


Fig. 16.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.

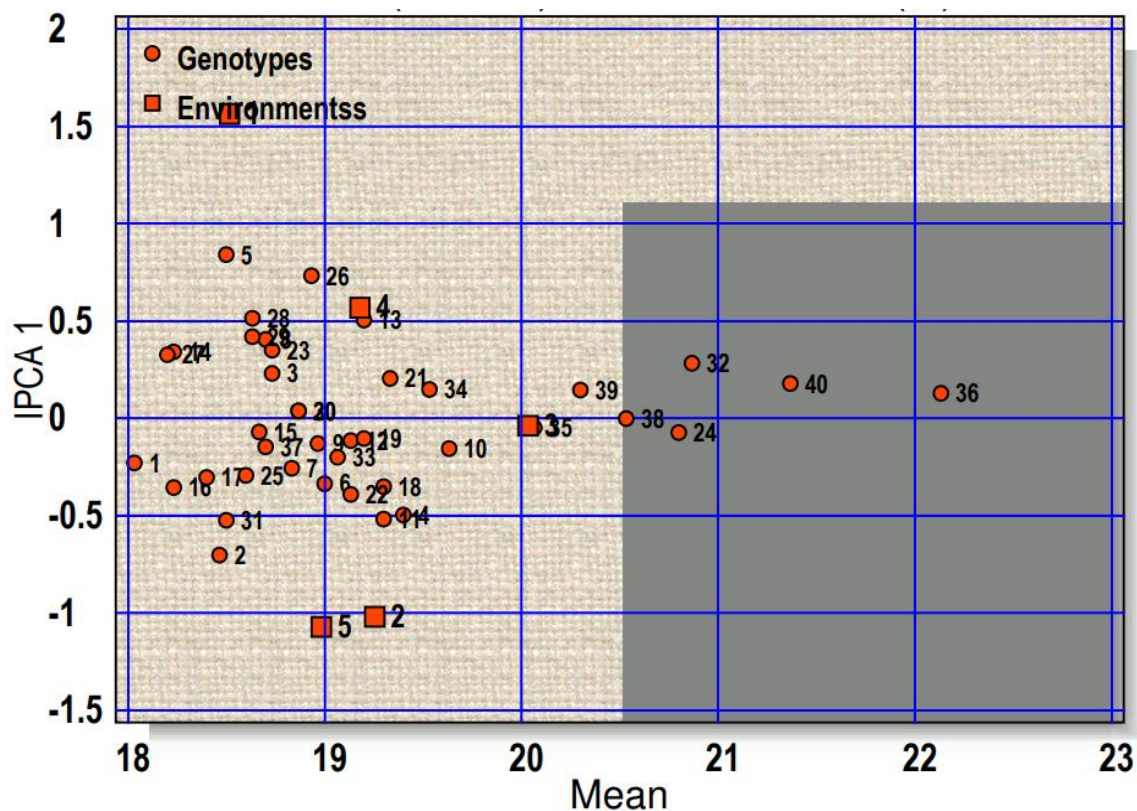


Fig. 17.1. AMMI1 biplot showing mean performance and adaptability of 40 Niger genotypes for protein content (%) across five tested environments.

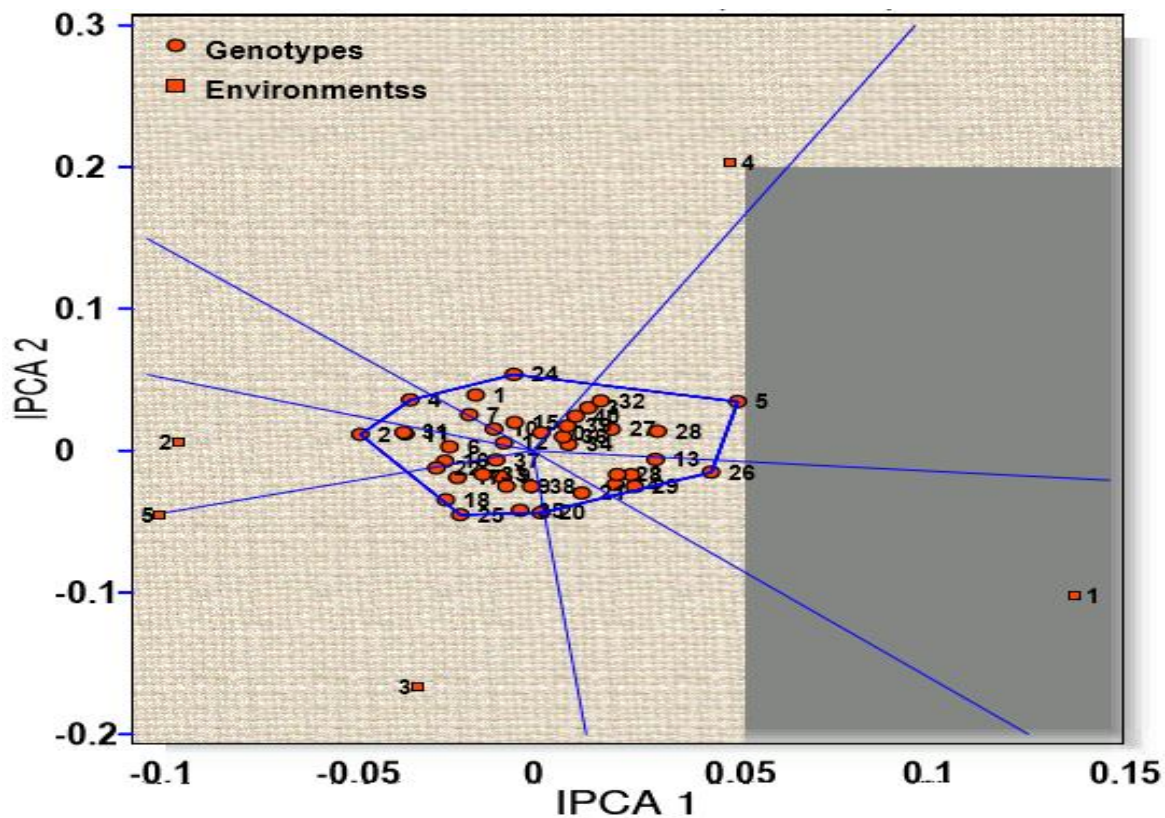


Fig. 17.2. Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 Niger genotypes in five environments.