CHARACTERIZATION AND STABILITY ANALYSIS OF TRANSPLANTED FINGER MILLET USING MORPHO-PHYSIOLOGICAL TRAITS IN SUMMER

By

ADITHYA RAJENDRAN S

MASTER OF SCIENCE

IN

GENETICS & PLANT BREEDING

DEPARTMENT OF GENETICS & PLANT BREEDING

Dr. RAJENDRA PRASAD CENTRAL AGRICULTURAL UNIVERSITY
PUSA (SAMASTIPUR), BIHAR - 848 125

2023

Reg. No. M/PBG/200/2021-22

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THESIS SUBMITTED
TO
DR. RAJENDRA PRASAD CENTRAL AGRICULTURAL UNIVERSITY PUSA (SAMASTIPUR), BIHAR-848125

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2023

Reg. No. M/PBG/200/2021-22

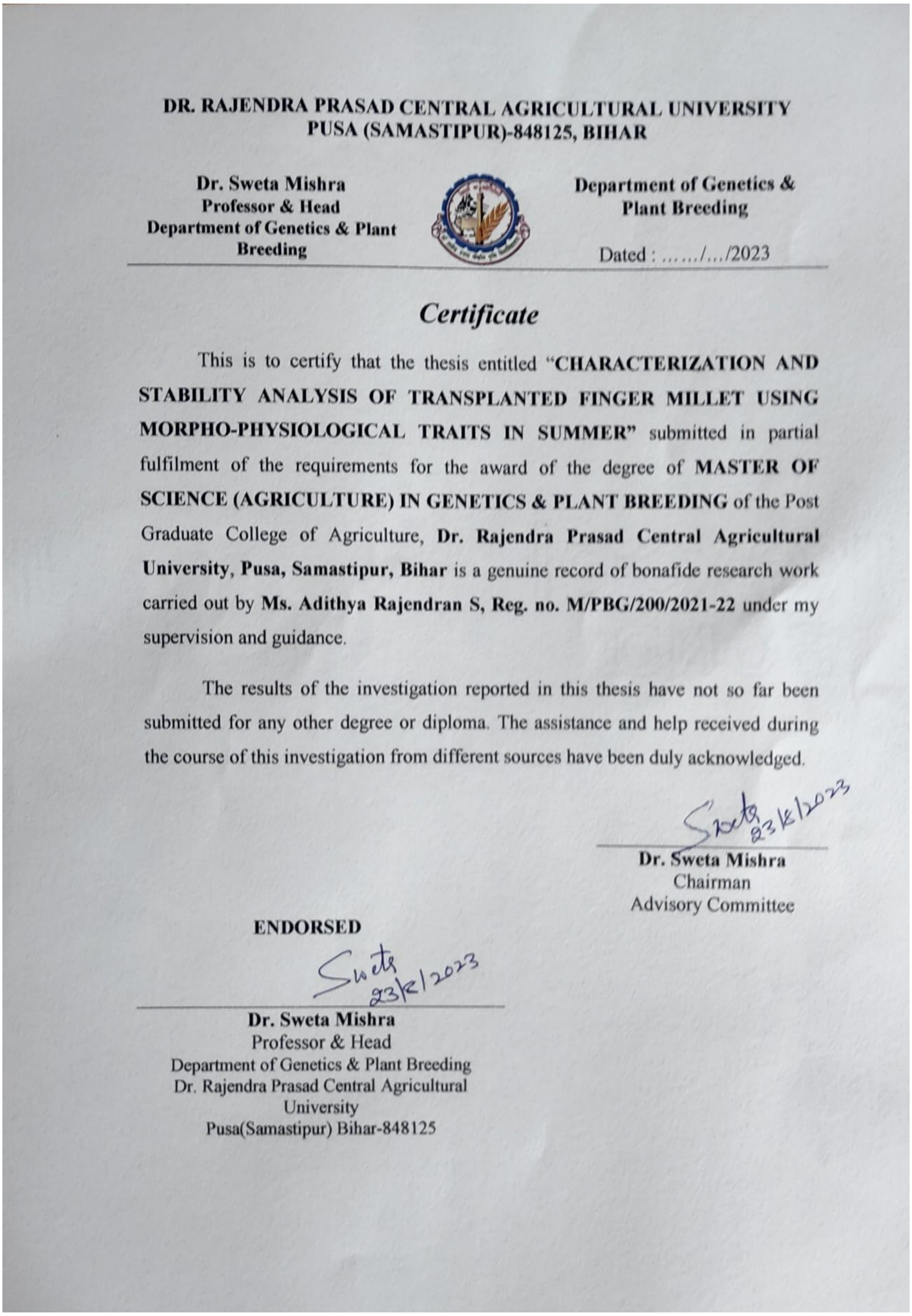
Dedicated to

My Beloved Parents

and Revered

"Who instilled in me the virtues of
perseverance and commitment and relentlessly
encouraged me to strive for excellence"

...Adithya Rajendran S



DR. RAJENDRA PRASAD CENTRAL AGRICULTURAL UNIVERSITY
PUSA (SAMASTIPUR)-848125, BIHAR

Dr. Sweta Mishra
Professor & Head
Department of Genetics & Plant Breeding

Department of Genetics & Plant Breeding

Dated : ……/…/2023

Certificate

This is to certify that the thesis entitled "**CHARACTERIZATION AND STABILITY ANALYSIS OF TRANSPLANTED FINGER MILLET USING MORPHO-PHYSIOLOGICAL TRAITS IN SUMMER"** submitted in partial fulfilment of the requirements for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE) IN GENETICS & PLANT BREEDING** of the Post Graduate College of Agriculture, **Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar** is a genuine record of bonafide research work carried out by **Ms. Adithya Rajendran S, Reg. no. M/PBG/200/2021-22** under my supervision and guidance.

The results of the investigation reported in this thesis have not so far been submitted for any other degree or diploma. The assistance and help received during the course of this investigation from different sources have been duly acknowledged.

Sweta 23/12/2023

Dr. Sweta Mishra
Chairman
Advisory Committee

ENDORSED

Sweta 23/12/2023

Dr. Sweta Mishra
Professor & Head
Department of Genetics & Plant Breeding
Dr. Rajendra Prasad Central Agricultural University
Pusa(Samastipur) Bihar-848125

Certificate

We, the undersigned, members of the Advisory Committee of **Miss ADITHYA RAJENDRAN S,** a candidate for the degree of **MASTER OF SCIENCE IN AGRICULTURE (GENETICS & PLANT BREEDING)**, have gone through the manuscript of the thesis and agree that the thesis entitled **"CHARACTERIZATION AND STABILITY ANALYSIS OF TRANSPLANTED FINGER MILLET USING MORPHO-PHYSIOLOGICAL TRAITS IN SUMMER"** may be submitted in partial fulfilment of the requirements for the award of the degree.

Sweta 23/8/2023

Dr. Sweta Mishra
Chairman
Advisory Committee

Members of the Advisory Committee

23.8.2023

Dr. D.N.Kamat
Assistant Professor
Department of Genetics & Plant Breeding

Sarita Kumari 23/08/2023

Dr. Sarita Kumari
Assistant Professor
Department of Agricultural
Biotechnology & Molecular Biology

Shailesh Kr 23/8/23

Dr. Shailesh Kumar
Assistant Professor
Department of Botany, Plant Physiology
& Biochemistry

23.8.2023

Dr. S.K.Singh
Professor and Head
Department of Plant Pathology

Certificate

This is to certify that the thesis entitled **"CHARACTERIZATION AND STABILITY ANALYSIS OF TRANSPLANTED FINGER MILLET USING MORPHO-PHYSIOLOGICAL TRAITS IN SUMMER"** submitted by **Miss Adithya Rajendran S** in partial fulfilment of the requirements for the award of the degree of **MASTER OF SCIENCE IN AGRICULTURE (GENETICS & PLANT BREEDING)** of the Post Graduate College of Agriculture, **Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar** was examined and approved on 25/09/2023.

Dr. Hariprasanna K
(External Examiner)

Sweta 25/9/23

Dr. Sweta Mishra
Chairman
Advisory Committee

Members of Advisory Committee

Dr. D. N. Kamat
Associate Professor
Department of Genetics & Plant Breeding

Sarita Kumari 25/9

Dr. Sarita Kumari
Assistant Professor
Department of Agricultural Biotechnology & Molecular Biology

Shailesh 25/9/23

Dr. Shailesh Kumar
Associate Professor
Department of Botany, Plant Physiology & Biochemistry

Dr. S.K. Singh
Professor & Head
Department of Plant Pathology
Nominee of Director of Education

Sweta 25/9/23

Dr. Sweta Mishra
Professor & Head
Department of Genetics & Plant Breeding
Dr. Rajendra Prasad Central Agricultural University, Pusa (Samastipur), Bihar-848125

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Needless to say, all errors and omissions are mine.

Date:
Place: Adithya Rajendran S

Dr. RAJENDRA PRASAD CENTRAL AGRICULTURAL UNIVERSITY PUSA (SAMASTIPUR), BIHAR – 848125

Name of the student	:	**Adithya Rajendran S**
Post Graduate degree program	:	M.Sc. (Agriculture)
Department	:	Genetics and Plant Breeding
Major Subject	:	Genetics and Plant Breeding
Minor Subject	:	Molecular Biology and Biotechnology
Registration Number	:	M/PBG/200/2021-22
Major Advisor	:	**Dr. Sweta Mishra**
Year	:	2023
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ABSTRACT

The present study was conducted to determine the effect of genotype, environment and their interaction for grain yield and to identify more stable finger millet genotypes for summer season. The experiment was laid down in Augmented block Design and 144 finer millet genotypes along with 3 checks (RAU-8, GPU-67 and VL-376) were evaluated for 2 summer seasons of 2022 (season 1) and 2023 (season 2). There were highly significant variations among genotypes for all the quantitative traits studied. The mean grain yield averaged over seasons ranged from 309.74 kg/ha to 3012.35 kg/ha in season 1 and from 429.13 kg/ha to 2931.64 kg/ha in season 2. Days to 50% flowering, days to maturity, finger length, finger width, ear length, fingers per ear, plant height, number of basal tillers, productive tillers per plant, 1000 grain weight, flag leaf blade length, flag leaf blade width and peduncle length showed significant positive correlation with grain yield in season 1 and season 2. finger length, fingers per ear, number of basal tillers, 1000 grain weight, flag leaf blade width and peduncle length showed positive direct effects with grain yield in season1 and season 2. For qualitative morphological traits most genotypes showed erect type of plant growth habit, compact ear shape, absence of finger multiple

whorls, absence of finger branching, copper brown seed colour, round shaped seeds, absence of stem culm branching, dark green coloured glume, absence of seed shattering and persistent pericarp. Some genotypes showed finger branching in thumb finger. Among the genotypes, RAU-FM-Sheohar-2009-19 (987.0) and RAU-FM-Sheohar-2009-9 (964.9) showed higher values for seed vigour index I. RAU-FM-83 (1.271), RAU-FM-Gopalganj-2009-5 (1.144) and RAU-FM-93 (0.960) showed higher values for seed vigour index II. RAU-FM-Sheohar-2009-9 (11.38cm) outperformed the check varieties in terms of seedling length. Most of the genotypes showed 100% seed germination. RAU-FM-Sheohar-2010-9 recorded higher value (18.4) for chlorophyll content. RAU-FM-82 exhibited a comparable performance with check varieties for speed of germination with a value of 3.33. RAU-FM-Sheohar-2009-9 which showed a better performance for seed vigour index I, seedling length and chlorophyll content, had high flag leaf blade length. Genotypes RAU-FM-83 and RAU-FM-Gopalganj-2009-5 which had high vigour index II also had higher values for days to 50% flowering. RAU-FM-Sheohar-2009-14 which had high seedling length and RAU-FM-82 which had high speed of germination showed higher mean performance for plant height. RAU-FM-100 also had high speed of germination as well as showed a better mean performance for days to 50% flowering and days to maturity. GGE Biplot showed that RAU-FM-Kanti-2010-1 showed stable performance for ear length; RAU-FM-Sheohar-2009-14 for fingers per ear; RAU-FM-114 for productive tillers per plant and RAU-FM-86 for 1000-grain weight, respectively. RAU-FM-86 showed better mean performance for the trait fingers per ear. As per GGE Biplot analysis, the summer season was new in Bihar where finger millet is being introduced for the first time. So, this maybe the reason that the biplot didn’t include the seasons under ideal environment. The genotypes RAU-8, GPU-67 and VL-376 were identified for stable performance in terms of yield. Though these are released varieties, they are usually grown in kharif season and were new to summer season and hence can be either evaluated for more summer seasons. The genotypes showed better performance of other traits can be selected for more summer seasons or used as a donor parent for the particular traits in pre-breeding programmes in future.

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LIST OF ABBREVIATIONS

Abbreviations for Units

%	Per cent
℃	Degree Celsius
et.al	And co workers
Temp.	Temperature
Max.	Maximum
Min.	Minimum
cm	centimetre
m	Meter
g	gram
kg	kilogram
ha	hectare
&	and
@	At the rate
Mt.	Million tonnes
Sl	serial
Viz.	Versus

Abbreviations for genetic parameters

ANOVA	Analysis of Variance
d.f	Degree of freedom
σ^2 g	Genotypic variance
σ^2 p	Phenotypic variance
C.D	Critical difference
S.E	Standard Error
C.V	Coefficient of Variation
GCV	Genotypic Coefficient of Variation
PCV	Phenotypic Coefficient of Variation
h^2	Heritability
GA	Genetic Advance
GAM	Genetic Advance as percent of Mean
X	Cross

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Abbreviations for Morphological characters

DFF	Days to 50% flowering
DM	Days to maturity
FL	Finger length
FW	Finger width
EL	Ear length
FPE	Fingers per ear
GY	Grain yield
PH	Plant height
NBT	Number of basal tillers
PTP	Productive tillers per plant
TGW	1000 grain weight
FLL	Flag leaf blade length
FLW	Flag leaf blade width
PL	Peduncle length

* * *

CHAPTER - I

INTRODUCTION

INTRODUCTION

Finger millet, a minor millet cultivated in the tropical and subtropical areas of Asia and Africa. It's mainly grown for food and can be used as fodder and medicine. The crop is highly self-pollinating and comes under the family of *Poaceae*. Eight species of diploid and tetraploid annual and perennial herbs make up the genus *Eleusine.* Since there are numerous races and subraces within the cultivated species, finger millet exhibits a broad array of diversity for the majority of key agronomic properties. It is a resilient crop that can endure environmental stress including water scarcity and temperature vagaries. Finger millet can be divided into five races based on the inflorescence morphology. With well-developed central spikes that range in number from 5 to 20, the subspecies *coracana* has some similarities with the subspecies *africana.*

Finger millet has a wide range of adaption because of its brief and adaptable growing season. The critical day length for this short-day plant is typically around 12 hours. It thrives at greater altitudes where other staple grains struggle. The typical annual rainfall requirement for finger millet is 500 mm, however it can withstand precipitation levels between 300 and 4000 mm. It can withstand high temperatures but does best in regions with an average temperature range of 11 to 28 °C. The crop thrives in tropical areas of India and Africa where the average maximum temperature is over 27 °C and the average lowest is not below 18 °C. As a result of its effective C_4 photosynthetic pathway, it can adapt to a variety of environmental and climatic conditions.

Compared to most cereal crops, the crop is considered to be drought resilient, and it has been noted that the reproductive and grain-filling stages are the most sensitive to moisture stress, greatly limiting production. Every year, stress lasts for 25 to 30 days at either stage of crop growth and significantly reduces the grain yield in finger millet. While development in yield has been substantially higher in favourable environments, it has been understood that achieving a production gain and stability under dry conditions is a difficult problem. Because of its rich nutritional content, high photosynthetic efficiency, and greater resistance to biotic and abiotic stresses than other crops, it is consequently a good crop for changing environments

Genetic diversity offers opportunities to utilise various genomic resources and technologies to manipulate desirable traits. A detailed analysis of available genetic resources and the usage of existing genetic changes may prove to be an effective method of obtaining genomic data. Through the use of advanced plant breeding techniques, a wide variety of landraces can be examined for their desirable agro-morphological characteristics. This will help to meet the rising demand for food grains and open the door for the discovery of novel and improved genotypes.

There is a tremendous amount of morphological and molecular diversity among the various *Eleusine* species. The finger millet crop's secondary centre of diversity, which is thought to be India, has grown as a result of the spread of its primary centre of diversity, which is located in the East African regions, where weedy and primitive cultivars are found. However, there has been little analysis of the genomic connections between cultivated *E. coracana* and its wild tetraploid variety.

The improvements in finger millet research might make it possible for it to be adapted to current cropping systems and evolve into an economically viable, nutritionally superior crop in the future. Along with the success of conventional plant breeding methods, current developments in genomics, transcriptomics, and proteomics technologies have made it possible to understand the genetic architecture and link between genotype and phenotype of complex features in finger millet. Furthermore, whole-genome sequencing in orphan crops like finger millet is now technically and financially possible owing to the quick advancements in DNA sequencing technology.

The annual global production of finger millet is around 4.5 million tonnes. Following peal millet and sorghum, finger millet is the third most significant millet crop in India (as per 4th advance estimate 2021-‘22). India contributes about 53.3% of the global finger millet production. In India, finger millet is cultivated in an area of 1.01 million hectares and has a production of 1.67 million tons. (Source: Final Estimates 2021-22, DES, Govt. of India). Karnataka is the leading producer of finger millet with an area of 641 thousand hectares producing 1164.06 thousand tonnes followed by Tamil Nadu with an area of 84.54 thousand hectares producing 274.50 thousand tonnes in the year 2019-‘20(Source: Millet Stats, IIMR)

The identification and characterisation of germplasm is a crucial link between the preservation and application of plant genetic resources (Umar and Kwon-Ndung, 2014). The subspecies *coracana* which is grown mainly for food is a coarse-grained mutant of domesticated form of subspecies *africana*. Cytological, morphological, and genetic data have all been used to evaluate the origins of cultivated millet.

The studies conducted on agro-morphological characterization of finger millet is limited, although it is important for identifying seed purity and characterizing seeds. The ability to detect the genetic diversity present in the germplasm by agro-morphological as well as characterization enables breeders and farmers to select superior genotypes. The characterization is important to manage and put into the use, the available landraces and germplasm collections of finger millet

The nutritional aspect of crop includes proteins, carbohydrates, dietary fibres and other minerals constituting about 5-8%, 65-75%, 15-20% and 2.5-3% respectively. Among all cereals, it contains the more than ten times higher calcium (344 mg/100 g) than any other cereal crop. Finger millet has a higher micronutrient density than rice or wheat due to its abundance in minerals like manganese, copper, magnesium, selenium, molybdenum, phosphorus, and especially calcium. The millet also contains a meagre amount of polyphenols, phylates, tannins and trypsin inhibiting factors which were once believed as “anti-nutrients” because of their metal chelating and enzyme inhibition activities. However, they are now known as nutraceuticals. A portion of the millet kernel that can be eaten is the seed coat, which has a high concentration of phytochemicals such polyphenols and dietary fibre (0.2–3.0%). Additionally, the crop residues serve as an excellent source of dry matter for livestock, particularly during dry seasons. The grains are primarily used for human consumption, while the straw of finger millet contains a significant amount of total digestible nutrients (61%), making it a valuable and nutritious fodder option for animals.

The gene bank exclusively on small millets has been established at ICAR-IIMR, Hyderabad, Telangana, India which maintains 15,861 accessions of small millet germplasm, including 8001 accessions of finger millet, 2766 of foxtail millet, 1538 in kodo millet, 939 in proso millet, 1629 in little millet and 988 in barnyard millet. The NBPGR maintains 11587 accessions of finger millet, 4244 of foxtail millet, 1005 of proso millet, 1888 of barnyard millet in the National Gene Bank; while ICRISAT maintains 7519 accessions of finger millet, 1542 of foxtail millet, 849 of proso millet, 749 of barnyard millet in its gene bank (Elangovan et al., 2022).

Finger millet grains can be stored for extended periods without being affected by storage pests, making them an ideal food commodity. *E. coracana* is tolerant to most of the diseases like root rot, smut, mottling virus, streak, mottling virus and blast which normally affect wild and African finger millet.

Grain yield is a complex characteristic influenced by multiple genes and the surrounding environment. Therefore, selecting directly based on this trait may not be effective. The effectiveness of selection depends on the traits being highly heritable. To identify the exploitable variation through selection, it is essential to partition the total phenotypic variation into heritable and non-heritable components. This knowledge helps in understanding the variability attributed to genetic factors, the actual heritable genetic variation in the progeny, and the genetic advance achievable through selection. Such a comprehensive understanding is crucial for devising successful selection procedures in the development of high yielding genotypes.

Genetic variability and diversity are crucial factors in crop improvement programs. When high diverse parents are used, they tend to produce greater heterosis in progeny, increasing the likelihood of observing transgressive segregation. Therefore, breeders must identify parents with high genetic variability to effectively combine desirable traits and develop improved crop varieties that outperform existing cultivated varieties. There is a great genetic variation among varieties and germplasm of finger millet. The availability of genetic variability in a gene pool is a prerequisite for a successful breeding program (Aditya et al., 2011) to achieve the expected genetic improvement through selection. Furthermore, the success of selection depends on the availability of heritable variances (Dabholkar, 1992). Understanding the genetic basis of yield and yield traits as well as genetic variation and relationships between accessions is vital to exploit the existing genetic variability and its potential use in breeding programs (Thormann et al., 1994). The use of physiological parameters on top of morphological traits is highly crucial and important to estimate genetic variability and its components to enhance crop improvement on the target traits.

Different genotypes show variable performance for the traits under consideration which is due to the genotype x environment interaction. High degrees of heterozygosity and/or heterogeneity make a genotype less susceptible to environmental change and more stable in terms of yield. Finger millet, on the other hand, are reportedly entirely autogamous and have low amounts of heterozygosity. This is possibly the main reason why finger millet had a high GEI (genotype x environment interaction) (Adugna et.al., 2011). These perspectives can be taken into consideration while selecting genotypes for using as a variety and parents for hybridisation programmes as well. Grain yield performance should not be the only criterion for genotype selection, as genotype with the highest grain yield may not be necessarily exhibit stability and adaptability across different locations and years. Finger millet is the most climate resilient millet and can be grown under a wide spectrum of extreme climatic conditions. Finger millet is the most climate resilient millet and can be grown under a wide spectrum of extreme climatic conditions. GGE biplot analysis presents a structural framework and distinguishes high-yielding and stable genotypes to analyze target testing locations. GGE biplot is constructed by incorporating the foremost two principal constituents (PC1 and PC2) that are obtained by decomposing the singular value of the environment-centric data. Identification and release of promising variety of finger millet is the most promising and deliverable technology for increasing productivity through its utilization in crop improvement programs.

Although finger millet varieties have been released for kharif season, in north Bihar condition there is heavy rain in this season which leads to crop loss. Besides, due to the International year of Millets-2023 the focus has shifted towards area expansion and production enhancement in finger millet. This can be achieved if new seasons are explored for the crop in this region. Encouraged by this in order to increase the effort to identify additional high yielding genotypes that can fit in to a wide range of environments this work focuses on evaluation of local germplasm for adaptation and yield potential in summer.

The present investigation entitled "**Characterization and stability analysis of transplanted finger millet using morpho-physiological traits in summer**" was proposed with the following objectives:

1. To characterize and evaluate the germplasm of Finger Millet for qualitative and quantitative traits in summer seasons
2. To evaluate the germplasm of finger millet for seed physiological traits in summer seasons
3. To study the role of Genotype x Environment interactions in the expression of various morphological characters and stability of genotypes in the summer seasons

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CHAPTER - II

REVIEW OF LITERATURE

REVIEW OF LITERATURE

Finger millet, an orphan crop, possesses immense potential in mitigating climate change and could offer threefold security in terms of food, fodder, and nutrition. It is mostly cultivated as a subsistence crop in the marginal areas of plains and hills. Considering the changes in climate inclusive of recurrent weather variations witnessed every year, it is crucial to select stable, high-yielding, area-specific, finger millet cultivars.

In the present chapter, efforts have been made to include all reviews and literatures which are relevant to the present study entitled "Characterization and Stability Analysis of Transplanted Finger Millet using Morpho-Physiological Traits in Summer".

BRIEF WORK DONE IN INDIA:

Singh *et.al.,* (2023) conducted a study on 150 finger millet accessions for evaluating the genetic diversity for agronomic traits using Augmented design. ANOVA showed that genotypes show a significant difference for agronomic traits. Traits days to 50% flowering showed highest heritability with a value of 96.67% followed by 1000 grain weight(94.43) and the least value was shown by flag leaf blade width. Genetic Advance over Mean(GAM) was highest for grain yield per plant(99.51) followed by harvest index(65.59), ear head width(59.22), productive tillers(55.54), 1000 grain weight(36.74), flag leaf blade width(25.19) and plant height(24.92). Traits such as days to maturity, days to 50% flowering, finger number on main ear, peduncle length and flag leaf blade width showed less than 20% GAM. Principle Component Analysis showed that there are 5 PCs with eigen values more than 1, holding 74.07% variability. Thus, the study showed the accessions evaluated exhibited variation for grain yield and other traits recorded, which can favour selection useful for crop improvement.

Bandyopadhyay *et.al.,* (2023) evaluated 11 finger millet genotypes for six traits using RCBD at three different locations for two seasons. ANOVA showed that genotype, environment and G X E effects exhibited a significant variation on genotypes. The variability in environmental conditions had varied impacts on different traits such that it contributed 37.3% of the variation in days to 50%

flowering, 38.6% in plant height, 58.2% in number of tillers, 65.5% in number of heads, 21.0% in number of fingers and 76.9% in grain yield. The average grain yield across different locations ranged from 16.9(E1)-38.8q/ha(E3) whereas the genotypic mean was stretched from 22.7(PF5) to 34.3q/ha(PF8) . GGE Biplot analysis showed that within the environments, certain genotypes performed well such as PF-5, PF-6 and PF-2 in E1, PF-8 in E2 and in E3, PF-10 and PF-11. Considering an ideal hypothetical genotype, PF-8 outperformed other genotypes with its high average grain yield and stable performance across the environments.

Nagaraja *et.al.*,(2023) conducted a study on 15 finger millet genotypes to assess the stable and high grain and fodder yielding genotypes by evaluating their genotype x environment interaction across twenty environments(ten locations-2 years). ANOVA showed that genotypes showed significant variation for genotype, environment and genotype x environment for grain and fodder yield. The stability analysis was done using AMMI model. The genotypes VR1101 and WN559 showed a comparable performance with checks for grain and fodder yield and broader adaptation across the environments. Environments E1 and E9 had a high discriminating ability and representativeness for seed and fodder yield respectively. These two traits showed positive correlations which was reflected in the performance too. Hence these two genotypes can be recommended for breeding purposes in future.

Bhavya *et.al*, (2022) studied finger millet genotypes for yield under drought conditions by withholding irrigation at different growth stages. Various drought tolerance indices (DTI), including geometric mean productivity, mean productivity, harmonic mean, drought resistance index, yield index, and yield stability index for each genotype, were calculated using the acquired grain yield. According to DTI, the genotype ML-365 was found to be highly resistant to drought, whereas GPU-28, KMR301, and L-5 were found to be moderately resistant, and KMR-204 and GPU-45 remained less resistant.

Elangoven *et.al.*,(2022) conducted a study on 2000 finger millet accessions to assess the polygenic traits to estimate the genotypic variability. The multi-variate analysis showed that 14 principal components contributed to variability. The grain yield contributing traits like number of tillers (80.58%) through PC 9, number of fingers on ear head (74.05%) through PC6, finger length (40.59%) through PC 2 and 100-Seed weight (25.66) through PC1 contributed to variability. Cluster analysis grouped the genotypes into four broad clusters in which 14.67% of variation was shown within the clusters and 85.33% of variation was shown between the clusters. The study identified that the accessions IC 0475183, IC 0474893, IC 0476432, IC 0475707 and IC 0476381 for early flowering, IC 0475740, IC 0475629, IC 0475059, IC 0475658 and IC 0476484 for more number of basal tillers, IC 0474962, IC 0475244, IC 0475374, IC 0475858 and IC 0475473 for number of fingers on ear head, IC 0476095, IC 0475125, IC 0474816, IC 0475407 and IC 0476587 for higher grain yield, and IC 0477419, IC 0475620, IC 0477078, IC 0475382 and IC 0475193 for more 100-seed weight were best accessions along with the traits for which they contributed.

Sharma *et.al.,* (2022) conducted a study on 31 finger millet genotypes. Thirteen yield and related traits were studied and it was observed that productive tillers, grain yield and number of heads per plot and number of fingers per head were having notable GCV of about 57.98%, 49.38%, 49.27% and 45.54% respectively. For the purpose of increasing productivity, it would be ideal to have higher GCV magnitudes, heritability combined with high genetic progress for a trait of interest.

Anuradha *et.al.,*(2022) evaluated G X E interaction by studying finger millet genotypes for six consecutive rainy seasons. An estimated collection of eleven stability parameters that were selected to determine stable genotypes showed strong positive associations. In addition, using the modified AMMI-based stability parameter (ASTAB), Non-parametric and Parametric Simultaneous Selection indices (NP-SSI and P-SSI) were computed. Entries Indaf-9, Sri Chaitanya, PR-202, and A-404, as well as VL324 and VL146 identified by the multi-year study SSI were found to be the most reliable high-yielding genotypes among the medium-to-late and early maturity genotypes.

Narasimhulu *et.al.,*(2022) conducted a study on twelve pearl millet genotypes in order to understand the significance of genotype x environment interaction during the rainy season of three years. The environment and genotype showed significant effects. AMMI model was used for the study inferring that genotypes performed differently in varied environments providing a great scope for selecting better adapting genotypes. The traits such as plant height, 1000 grain weight and fodder yield were affected by the amount of rainfall during both anthesis and grain maturation stage which indirectly influenced the grain yield. Among the different environments studied, Environment 3 was highly differentiable and the hybrid varieties such as Pratap, 86M86 and NBH- 5767 outperformed the commonly grown open pollinated varieties when grown in ideal conditions. Regarding the grain yield, both Pusa Comp.612 and Pratap showed stable performance across the various environments. Hence it is recommended to evaluate Pratap and Pusa Comp.612 in diverse locations under rainfed conditions.

Philanim *et.al.*, (2022) conducted a study on stability analysis using thirty genotypes of rice bean in hilly region of Eastern India. the genotypes showed significant differences for the traits studied. The first two principal components (IPCA1,90.4% and IPCA2,9.6%) could explain100% of the total of the interaction variation. Correlation study revealed a strong association($p<0.01$) between stability parameters. Stability index was considered to determine the multi-trait stability and identify the promising genotypes and evaluating the strength and weakness of each genotype. The results showed that genotype BSKB 28 exhibited higher productivity in terms of number of pods and seed yield per plant whereas genotype Ukhrul 15 showed higher productivity in terms of number of seeds per pod. The study assessed seven genotypes as promising ones which were Bete 6, IC002567, Ukhrul 6, Ukhrul 14, Ukhrul 15, Bete 4 and BSKB 3.

Naik *et.al.*, (2021) evaluated twenty finger millet genotypes for seven agronomic traits to assess the genetic variability, character association and diversity among them. Traits such as s number of productive tillers per plant (29.04% and 24.33%), test weight (24.54% and 21.21), no. of fingers per head and finger length (22.11 and 21.21) showed high phenotypic and genotypic coefficient of variation. All characters showed high broad sense heritability except peduncle length. Four characters showed high heritability , genetic advance, PCV and GCV which were test weight (97.34% and 49.20%), finger length (92.01% and 41.91%, number of productive tillers per plant (70.15% and 41.97%) and number of fingers per head. The plant height showed positive correlation with peduncle length followed by test weight and finger width. Through Kclustering approach , the genotypes were grouped into two clusters in which cluster I consists of 14 members and cluster II consists of 6 members.

Ladumor *et.al*(2021) conducted an experiment on thirty-five finger millet genotypes for eighteen characters including yield and yield attributing traits and quality traits. Principal component analysis indicates that two principal components PC-1 and PC-2 contributed 74.89% and 24.26% respectively of the total variation. The genotypes viz., VL-314, Dapoli-1, Dapoli-2, KOPN-235, KOPN-942, Phule Nachni, VR-708, VR-847, PR-202, KMR-204 and GNN-7 were accumulated on positive side of PC1 axis which accounted for days to 50% flowering, days to maturity, plant height, main ear head length, finger length and harvest index contributed maximum towards divergence. On other axis, only two genotypes OEB-532 and Indira Ragi-1 are accumulated on positive side of PC-2 which accounted for chlorophyll content was important traits contributed maximum towards divergence. PC-1 and PC-2 was providing maximum genetic variation. The positive signifying genotypes could be useful in finger millet breeding in future.

Chavan *et.al.*,(2020) conducted a study on 13 finger millet genotypes using 2 checks to derive the correlation coefficient and direct and indirect effects of morphological characters such as plant height, days 50% flowering, number of tillers per plant, number of fingers per ear, length of finger, test weight, straw yield per plant, harvest index and days to maturity on grain yield. The study revealed that plant height, days 50% flowering, number of tillers per plant, number of fingers per ear, length of finger, test weight, straw yield per plant and harvest index showed positive effects with grain yield at both genotypic and phenotypic effects whereas days to maturity showed positive effects with grain yield only at phenotypic levels. The major component which contributed to grain yield as harvest index (%) followed by straw yield per plant (g), number of fingers per ear, number of tillers per plant, plant height concluded through path coefficient analysis had highest direct effects on grain yield per plant at both genotypic and phenotypic level.

Madhavilatha *et.al.*, (2020) evaluated finger millet genotypes at different locations to identify stable and high yielding ones as most of them failed to show a stable performance. For the number of productive tillers and grain yield ha^{-1}, the linear component of the genotype x environment (G x E) reaction was significant, showing the different responses of genotypes evaluated for these traits in various environments. PPR 1041, one of the tested genotypes, showed average stability for the number of productive tillers per plant, showing the broad adoptability of this genotype. The genotype VR 990 was discovered to have average grain yield stability, demonstrating the genotype's extensive local adaptability.

Singh *et.al.*,(2020) conducted a study on 38 cowpea accessions to estimate the stability by growing them in five different seasons for nine quantitative traits. Except peduncle length and plant height, other characters were significant for GXE interaction variance showing that the yield was not stable across the environments. The study showed that the genotype C-863 performed well comparing to the check and also exhibited non-significant deviation from regression line and regression coefficient less than unity which is suitable for favourable environment for characters like seed yield per plant and number of clusters per plant. The genotypes C-863, C-1085, C-956 for seed yield per plant, C-1013 and C-1126 for number of pods per plant, C-1133 for number of clusters per plant and C-863 and C-1089 for number of peduncles per plant may be effectively used for future cowpea breeding programmes.

Aralikatti *et.al.*, (2020) studied forty-two finger millet genotypes to analyse the heritability, genetic advance of yield and eleven component traits. ANOVA showed that the traits showed highly significant variations for genotype. The characters such as finger length and ear head length showed high phenotypic and genotypic coefficient of variation. Finger length and ear head length showed high estimate for genetic advance and heritability indicating that selection of these characters can accumulate more addictive genes which can be used for the improvement of characters and thereby selecting for breeding programmes in future.

Suman *et.al.*, (2019) conducted a study on investigated 55 genotypes of finger millet using multivariate analysis, a significant statistical approach that makes it simple to evaluate significant polygenic traits that are crucial to a plant breeding program. The components with larger Eigen values more than 1.33 contributed to overall variability according to PCA. The first four major components contributed 33.61, 12.91, 12.14, and 7.87% of the total variance, respectively. Grain yield and productive tillers per plant, 1000 grain weight, days to flowering as well as maturity are the important traits which contributed to overall variability. This study suggested that the above listed characters should be given importance for finger millet programmes in future.

Dubey *et.al.*,(2019) conducted a study on three different finger millet crosses of various maturity groups to analyse their response in terms of genetic potential transferred from F_4 to F_5 generations. The heritability was found to be significant for traits such as plant height and finger length. Narrow sense heritability was low for all traits considered(<30%). Correlation studies showed that grain yield was notably associated with ear weight, total tillers, productive tillers and fingers per ear within the F_4 and F_5 generations. Path analysis revealed that ear weight has maximum direct effect on grain yield. The study helps to dissect the traits which can still be selected in the F4 generation when most of the traits have become fixed.

Negi *et.al.*, (2019) studied 35 different genotypes of finger millet, including three checks, PRM-1, PRM-2, and VL-149, for seed quality traits. Data on 14 quantitative traits such as first count, standard germination, length of root, shoot and seedling, fresh weight as well as dry weight of seedling, relative growth index, vigour index-I & II were collected. ANOVA demonstrated that all of the traits were important. The relation between seed vigour and other seed quality parameters were proved using correlation test. A strong positive correlation is established between seedling vigour II and other parameters like fresh weight and dry weight of seedling along with vigour index I.

Jawale *et.al.*,(2017) conducted stability analysis on forty finger millet genotypes by studying yield and its related traits in four environments. Genotypes L48 and MR 34 showed wide adaptability as they showed average stability in the number of fingers in all environments. genotypes such as DPI 20114, DPI 20132, L 48, MR 34, DM 4, DM 7, GPU 58 and VR 847 showed better performance for length of fingers under favourable environments. General stability for grain yield per plant was found in the genotypes DPI 20132, L 48, L112, DM 4, GPU 58, and VR 849. The study helped to conclude that these genotypes, which showed better and more stable performance in different environments, can be used for breeding programs

Patel *et.al.*, (2015) conducted a study to characterize 15 genotypes of Ocimum species using Principal Component Analysis for 11 quantitative traits and estimated the stability using Eberhart and Russel model across three different environments. Traits such as leaf length, oil content and 1000 seed weight were accounting for 46.6% of variability. Hierarchical cluster analysis produced two different clusters namely *Sanctum* and *Basilicum* which included OCS-I to OCS-6, OCG-13 and OCB-7 to OCB-11, OCA-12, OCK-15 respectively. OCS-2 and OCB-9 had higher values for S^2d_i and high oil content performed well under favourable environments whereas OCS-1 produced below average oil content. It was concluded that OCB-9, OCB-8, OCB-7, OCB-11 and OC-A12 were identified to be stable and better performing genotypes as they were able to adapt to wide range of environments.

Kumar *et.al.*, (2014) did a study on quantitative characters using 140 finger millet germplasms. ANOVA showed a significant difference among genotypes indicating a high degree of variability. PCA showed that biological yield, harvest index, the number of fingers per ear, and productive tillers/plant have favourable effects on grain yield. An appropriate criterion can be followed for developing superior varieties using these characteristics which contributes to grain yield also.

Batth *et.al.*,(2013) conducted a study on 25 garlic genotypes and performed a multi-trait selection using GGE Biplot analysis. The trait association study showed that traits such as plant height, bulb length and number of cloves per bulb as the main determinants of bulb weight and seven genotypes were identified to have desirable morphological variation. Genotype PG-18 exhibited stable performance across different environments with high yield potential. Other genotypes such as PG-1, PG-19, PG-17, NRCWG-2, PG-32, JGL-96-198, PG-30 and NRCRG-1 were also identified as stable genotypes. This will help breeders to select desirable genotypes from existing variability to develop better varieties.

Karad *et.al.*,(2013) characterized finger millet accessions using RAPD markers and molecular analysis was done. This revealed that there were moderate to high variations in the finger millet accessions taken. These genotypes were organized into three mega-clusters by the UPGMA based clustering study. It demonstrates that cluster I's highest 28 genotypes were divided into five subclusters, whereas clusters II and III each comprised only two genotypes. The genotypes VL 149, KOPN 338, KOPN 929, and KOPN 161 showed the highest genetic diversity in this RAPD analysis; these genotypes can be considered parents of interest and crossed with elite material to create new breeding populations or to simultaneously transfer multiple traits/genes for crop improvement of finger millet.

Misra *et.al.*, (2009) conducted a study involving the multi-location trials on late duration finger millet genotypes in different planting conditions in two locations over a period of three years during the kharif season. AMMI model was used to study the G X E interaction of grain yield. Genotypes OEB-56, OEB-71 and VR-822 showed high mean and positive interactions so that they can be selected for early direct sown and early transplantation conditions whereas genotype PES-110 showed better results in early and late transplantation conditions but not in direct sown conditions. Other genotypes exhibited adaptation to single environment only such as genotype Chilika performed best under late transplanting conditions.

Das *et.al.,*(2007) evaluated the genetic relationships of finger millet genotypes using RAPD markers with which amplification of 124 DNA fragments were done and the genetic similarity was based on the presence or absence of bands. Using Cluster analysis, two major clusters of 30 genotypes were made in which first major cluster comprised of only one genotype Dibyasinha and the other 29 genotypes were included in the second major cluster which was gain divided into two minor clusters. A first minor cluster has only three varieties, i. e. Neelachal, OEB-56 and Chilika and second sub-minor cluster has 26 genotypes. The genotypes Neelachal and OEB-56 exhibit a 86% similarity with each other and 80% similarity with Chilika. The genotypes collected from southern part of india exhibited high similarity index comparing to those from northern India. Finger millet genotypes from various agroclimatic areas of India contribute to a wide genetic base and this is helpful for crop improvement programmes in future.

BRIEF WORK DONE IN ABROAD:

Tesfaye *et.al.,* (2023) studied G X E interaction by conducting seven multi-environmental trials in RCBD. The findings indicated that the spatial and factor analytic (FA) models were effective methods of data analysis for this research under the linear mixed model, and this was supported by evidence of heritability measure. Two clusters of correlated environments were discovered, and by ranking average Best Linear Unbiased Predictors (BLUPs) within clusters, it was possible to choose better and stable varieties. The first cluster was selected because it had a larger proportion of highly heritable environments. Based on this cluster, the best four varieties with relatively high yield performance across correlated environments were Bako-09, 203439, 203325, and 203347.

Yenasew *et.al.,* (2022) conducted study on elite finger millet genotypes for determining the effect of germination period on physico-chemical properties of the crop. The results indicated that the shoot length, germination percentage, germination loss, and total titratable acidity increased as the germination period increased whereas the pH value, ash, and fat content decreased from 6.43 to 5.97, 2.41 to 1.67 mg/100 g, and 2.41 to 1.67 mg/100 g, respectively, and the protein content increased. All varieties of germinated flour showed a significant rise in colour L (P 0.05), whereas colours a and b (redness) decreased. The results showed that germination enhanced the physicochemical characteristics of superior finger millet flour.

Mwangoe *et.al.,* (2022) conducted a study on finger millet genotypes for evaluating the morpho-physiological and agronomic traits of crop for drought conditions. The results showed that genotype had an impact on plant height, number of productive tillers, number of digits, harvest index, and finger length as well as seedling vigour. The plant stand, peduncle length, number of fingers, finger length, and days to 50% flowering were all influenced by location. For the number of fingers, yield, and harvest index, there was a significant interaction effect between genotype and location. The best genotypes for drought tolerance were determined to be lines ICFX 1420314-2-1-1-1, P8-1-1-1-1, and ICFX 1420415-3-1-1-2 based on their superior morpho-physiological traits that can tolerate soil water deficit with higher grain yield. To increase production in semi-arid areas, these selected genotypes can be suggested to farmers and included in crop improvement programmes.

Yalaukani *et.al.,* (2022) conducted a study on 40 fingermillet germplasm to identify genetic diversity and agro-morphological traits that help in the identification of superior seeds for crop improvement programmes. using Kompetitive Allele Specific PCR (KASP) SNP markers. Alpha lattice was used to organize the experiment. Agro-morphological phenotypic data was gathered, and multivariate analysis was performed. AMOVA was performed on genotypic data using the R statistical software. AMOVA found that a variation of 48% and 52% is seen within and among germplasm respectively with other three major components contributing to 42% of phenotypic variation.

Kandel *et.al.,* (2022) evaluated the stability in grain yield in sixteen finger millet genotypes in different environment conditions and thereby analyzing the G x E interaction. Environmental sensitivity is found in the genotypes GE-0382, KLE-216, NE94, and KLE-559, which produce greater grain yield in all environments. Moreover, GGE biplot analysis demonstrates that the genotypes GE-0382 (3.46 t/ha) and KLE-559 (2.74 t/ha) are more reliable and adaptable for the environment under study. Therefore, it is likely that these genotypes are utilized for developing suitable finger millet varieties for widespread cultivation throughout Nepal's mid-hill climate.

Asungre *et.al.*,(2022) evaluated twenty-four pearl millet single cross hybrids at four different environments during two cropping seasons to estimate genetic variability, heritability and stability of grain yield and components as well as grain micronutrients across the different environments. AMMI model is used for studying the G X E interaction. The interaction between IPCA 1 and IPCA 2 contributed significantly to the observed variation in the studied traits, ranging from 75.95% for downy mildew incidence to 91.28% for grain Zn content. IPCA 1 was responsible for 50.7%, 63.2% and 64.1% of grain yield, grain Fe and grain Zn content respectively whereas IPCA 2 accounted for 30.8%, 26.3% and 27.1% of grain yield, grain Fe and grain Zn content respectively. Hybrids such as ICMH IS 16013, ICMH 177023 and ICMH 16075 exhibited both high yield and stability. On the other hand, hybrids such as ICMH 177023, ICMH IS 166044, ICMH IS 16076 and ICMH IS 16214 showed high levels of Fe and Zn content. The traits showed moderate to high broad-sense heritability particularly in grain yield and grain micronutrient content, increasing the potential for significant trait improvement through recurrent selection.

Mulualem *et.al.*,(2022) conducted a study on eleven finger millet genotypes to assess the variation and variance components such as genetic advance for different agronomic characters. The analysis showed that mean squares of tested genotypes were highly significant for agronomic characters indicating the heterogeneity among the genotypes. Heritability estimations ranged from 12.18 % for tillers per plant to 97.35 % for days to maturity. The results showed a significant level of character variability between genotypes which can be used for breeding programs in future.

Karuinawan *et.al.*,(2021) conducted a study on orange fleshed sweet potato with 50 genotypes and 7 checks using Augmented design to assess the yield stability of crop grown under three different ecosystems. The genotypes were selected based on traits such as yield and its components and tuber quality across the environments. The yield stability of selected genotypes were analysed using the parametric, non-parametric, Additive Main effects and Multiplicative Interaction (AMMI), AMMI Stability Value (ASV), and Genotype and Genotype by Environment (GGE) biplot models. Ten genotypes were found to better performing through different analysis models. Genotypes F1-069, F1-077, F1-226, F1-038 and F1-128 were found to be stable based on parametric and non-parametric stability models. AMMI analysis identified F1-128,F1-135, F1-038 and F1-069 as stable genotypes. F1-38, F1-69 and F1-128 were found to be stable in ASV analysis. GGE Biplot also identified F1-38 and F1-69 as stable genotypes. Thus, it was concluded that F1-38 and F1-69 as most stable genotypes through various stability analysis models and were recommended as superior varieties.

Greveniotis *et.al.,* (2021) conducted a study aiming at the forage stability of common vetch crop using six genotypes grown across six different environments. The cultivation was done using strip plot by growing the genotypes randomized with low-input cultivation systems. The varieties such as Alexandros and Tempi showed stability for days to 50% flowering whereas Pigasos and Zefyros varieties showed stability for fresh forage yield. The stability analysis models such as AMMI and GGE Biplot were used for demonstrating the stability performance. Zefyros was the most stable variety, when dry and fresh fodder yield is considered. Correlation analysis showed appositive correlation between fresh forage yield and days to 50% flowering which can be used for indirect breeding purpose in future.

Getahun *et.al.,* (2021) conducted a study to estimate the heritability and gene numbers for yield and yield components in parent, filial and back cross generations in finger millet crop at two different locations using six basic and four reciprocal cross. The result showed the number of genes estimated in both locations ranged from -0.23 to 88.78, indicating that the presence of many genes with small cumulative effect and epistasis gene effect will bias an estimate of the number of genes. Medium to high narrow sense heritability value coupled with high genetic advance showed the influence of additive variance and ease of improvement for biomass yield and number of ears in this population. While low, medium and high narrow sense heritability observed together with the low genetic gain in most traits; which showed the presence of small additive variance in most traits with the influence of epistasis; hence intensive selection is required to exploit the characters. In most traits, the number of genes estimated to be negative and/or very small indicates that epistasis was significant and the existence of environmental effect in both locations. The results indicate the presence of genetic variability for developing improved varieties through crossing and selection.

Wang *et.al.,* (2021) evaluated finger millet accessions from two different locations (South Asia and Africa) using EST-SSR markers for assessing the genetic diversity. 116 alleles were produced using 40 primers ranging in size from 135 to 457bp with a PIC value of 0.18225. 40 primers showed polymorphism and the PIC value of 13 primers were >0.3. Based on the combined data of both markers, the finger millet accessions were grouped with the help of principal coordinate and phylogenetic analyses. The genotypes are grouped as those from South Asia and other from Africa and the SSR markers developed through this study can be used for genetic analyses of finger millet in future

Belete *et.al.,* (2020) conducted a study on ten finger millet genotypes for evaluating grain yield across different environments. The combined ANOVA for grain yield demonstrated changes among genotypes, environments, and GEI that were highly significant (p 0.01) in terms of grain yield. Environment, genotype and GEI contributed 78.7%, 1.5% and 9.8% respectively of the total variation. Several univariate and AMMI model were used to identify high yielding and stable varieties. The most stable finger millet varieties according to the eco-valence method were G10, G3,G7 and G8. According to the stability variance, the most stable varieties were G2, G4, G1 and G10. Gudetu was identified as a stable and high yielding cultivar by AMMI analysis. BD19 and OM19, which are regarded as relatively high yielding and stable environments, were closer to to the origin and made less of an effect on the GEI. In conclusion, it can be said that varieties G7 and G4 are more stable, yield more than others, and contribute less to GEI. Therefore, these varieties were recommended for commercial use at different locations of Southwestern Ethiopia.

Mukami *et.al.,* (2019) investigated physiological and biochemical responses to finger millet germplasm due to mannitol induced drought stress. Comparative analysis of relative water content, chlorophyll, proline and malondialdehyde (MDA) content were done to determine the physiological and biochemical response to drought. The decrease in germination and early seedling growth was observed but the root growth was increased. The stress has also led a triggered decrease in relative water content and chlorophyll content. Parameters that indicate oxidative damage, like proline concentration and MDA level, increased. In contrast to the other varieties, varieties GBK043137 and GBK043094 were less impacted by drought, as evidenced by significant variations in their physiological parameters. The research reveals the variations between finger millet's physiological and biochemical responses to drought, which is important for breeding and identifying drought-tolerant finger millet varieties.

Anteneh *et.al.,* (2019) evaluated 225 finger millet genotypes for studying the genetic diversity by analysing 16 morpho-physiological traits for two dry seasons of 2016 and 2017. ANOVA showed that the genotypes showed highly significant variation for all traits except days to emergence and number of fingers per earhead. Number of earhead per plant highest genotypic(27.11%) and phenotypic(25.03%) coefficient of variation whereas broad sense heritability was highest for culm diameter(95.35%) and lowest for number of ear heads per plant (3.04%). The genetic advance ranged from 18.4% for grain yield/plot to 51.46% for ear-heads/plant. Cluster analysis based on the 16 morpho-agronomic traits revealed five distinct clusters comprising 13 to 64 accessions. Culm diameter, numbers of ear-heads/plant, ear-head width, and grain yield/plant could be used as selection criteria due to high GCV, heritability and genetic advance. The study helped to conclude that genetic diversity present in the finger millet genotypes can be used for breeding programs in future.

Woyann *et.al.,* (2019) conducted a study on wheat genotypes to evaluate the adaptability and stability using 140 wheat genotypes grown in three different locations under Augmented Design. The genetic parameters were estimated using different models and selection was based on Harmonic Mean of the Relative Performance of the Genetic Values(HMRPGV) using individual and joint analysis. In joint analysis, 33 genotypes were identified to be performing well in terms of productivity, stability and adaptability and can be used for future use.

Dhami *et.al.,* (2019) conducted a study with a goal of identifying high yielding finger millet genotypes. He used five genotypes with one local variety kept as a check which were studied under different locations. The experiment was laid in a RBD and the analysis showed that grain yield exhibited a significant genotype x environment interaction. According to the study, the genotypes KLE236 (2.35 t/ha) and KLE-158 (2.22 t/ha) provided the highest grain production on average across locations and years, followed by DR-2 (1.91 t/ha) and GE-0116 (1.72 t/ha). The pooled ANOVA for grain yield indicated that genotypic variation was very significant for environments, but G X E interaction was not. Genotypes which are adapted to high yielding conditions have regression coefficients higher than 1.0 and therefore more susceptible to environmental changes and for those with regression coefficient less than 1 are resistant to environmental changes and therefore more adaptable to low yielding conditions. A genotype with a low G x E interaction is more likely to be stable over a wide range of situations.

Damtie *et.al.*, (2019) conducted a study on twenty-four finger millet genotypes to evaluate high yielding genotypes tolerant to head blast and to estimate comparative influence for entire variability and cluster them based on genetic distance. ANOVA showed that the traits under study showed significant variation. High genotypic and phenotypic coefficients of variations were recorded for logging, plant aspect, head blast, grain yield and finger length. High heritability estimate were resulted from plant aspect, finger length, maturity date, logging and flowering date. Traits like logging score, plant aspect, head blast score, grain yield and finger length verified comparatively high genetic advance as percentage of the mean estimates while low for phenological traits such as flowering and maturity date. The principal component analysis illustrated the first three principal components explained most of the variability observed in the data set. Traits like days to flowering, days to maturity, blast score, plant aspect and grain yield found to be more important in contributing the observed variability. Four phenotypically divergent clusters which showed highly significant intercluster distance were observed from cluster analysis. Resistance to stress and high yielder genotypes were found under cluster two which could be utilized as a parent to develop superior and adaptable finger millet varieties to the area.

Kebede *et.al.*, (2018) evaluated ten finger millet genotypes along with one standard check under different environmental conditions. The genotype, environment and G X E interactions showed variations which were significant in AMMI model analysis. Genotypes 214995 and BKFM0063 were high yielding and along with genotype BKFM0052 showed stability in yield in Eberhart and Russell Model analysis. In GGE Biplot analysis, the stability of genotype 214995 was more evident and thus it was concluded that this genotype is recommended for the climatic conditions of Northern Ethiopia

Kumari *et.al.*, (2018) studied 14 quantitative traits of 139 finger millet germplasm of two seasons. Characters such as grain yield, panicle exertion, weight of 20 mature ears, number of productive tillers and length of the longest finger showed high variability comparing to others. Correlation analysis is used to established the relation between grain yield and other characters. Principal component analysis for analysing the variability of different characters which help to prove that finger millet germplasm of Sri Lanka followed the similar trend as the global ones in terms of variability.

Morsy *et.al.*, (2016) evaluated 52 soybean genotypes grown across two different seasons under Augmented Design to study the similarity and dissimilarity parameters using cluster analysis. The results showed that the tested genotypes and checks showed a significant difference and genotypes Hobbit, Weber, DR 101, F5H8L151, Hartwing, L86-k-96, Forrest and Eigen-87 outperformed the checks. The smallest coefficient of similarity obtained by cluster analysis between two groups was 0.193. The groups contained node 48 and node 50 and 4, 21, 37, 38, 5, 8, 12, 25, 26, 31, 33, 7, 24, 29, 6, 13, 23, 27, 19, 20, 22, 34, 35, 41, 43, 28, 30, 4, 50, 42, 36, 39, 44, 45, 49, 51, 46, 52, 48 and 47 came under node 50. Cluster analysis suggests that the crossing of two genotypes with maximum distance levels or dissimilarity produce good offspring. And also, cluster analysis helps in the dividing the genotypes into groups based on similarity and dissimilarity thereby helping the breeder in effective breeding program.

Eric *et.al.*, (2016) conducted a study on 340 finger millet germplasm for analysing the association and heritability of 19 quantitative traits. Correlation coefficient analysis showed that the traits such as finger width, grains per spikelet, threshing percent, peduncle length and panicle exertion showed a positive correlation with grain yield and hence these traits can be considered for yield selection. According to Path Coefficient Analysis, productive tillers per plant, 1000 grain weight, grains per spikelet and threshing percent showed positive direct effects with grain yield. This information can be used for improving the grain yield. Heritability estimates showed that fingers per panicle, flag leaf blade length, 1000 grain weight, productive tillers per plant, finger length, peduncle length and panicle exertion exhibited higher values for heritability which demonstrated the potential for improvement through selection.

Dasanayaka *et.al.*, (2016) conducted a quantitative study on randomly selected finger millet genotypes. Weight of grain per ear and weight of sun-dried ear showed the highest positive and significant coefficient of variation. Phenotypic correlation between weight of grain per ear was highly significant and positively associated with days to flowering, flag leaf width, flag leaf length, plant height, culm thickness, finger length, finger width, days to maturity and weight of sun-dried ears, flag leaf width, flag leaf length, plant height, culm thickness, finger length, finger width, days to maturity arid weight of sun-dried ears. These genotypes were grouped into different clusters in cluster analysis on the basis of which the genotypes are used for different breeding programmes.

Malambane *et.al.*, (2015) studied genetic variations in finger millet genotypes in 2 different seasons which showed high variations in most of the traits studied. Grain yield per plant showed highest variation ranging from 15g-144g whereas lowest variation was shown by fingers per panicle ranging from 5-11 fingers per panicle. Dendrogram revealed that the qualitative traits recorded between landraces and cultivated ones showed high variation which helps in distinguishing the varieties. The study of genetic variation in morphological traits helped in the selection of superior genotypes

Umar *et.al.*,(2014) conducted characterization studies in finger millet accessions grown in northern Nigeria in different cropping seasons. According to the standard finger millet descriptors, field data on morphological traits like plant height, leaf length, leaf diameter, finger length, finger width, and number of fingers were documented. Additionally, 1000 seed weight was also recorded. The findings demonstrated that Ex-Kwi's plant height was significantly different from all other nine accessions, while Ex-Riyom's maximum leaf length was only significantly different from Ex-Dantse. The genotypes showed significantly more genetic diversity for the traits such as plant height, 1000 seed weight, leaf length, and number of tillers than all other traits when phenotypic and genotypic characteristics of the various accessions were evaluated. These findings tend to imply that selected morphological traits exhibit significant levels of variability. In particular, the ANOVA model described 87% of the variations, leaving only 13% undetermined for. Six main distinct groups were discovered by the cluster analysis based on morphological characteristics, and one landrace formed an independent cluster for the pooled analysis for three years.

Fentie *et.al.*, (2013) evaluated nine genotypes of finger millet under various environmental conditions in order to conduct a study on the effect of genotype, environment, and their interaction on grain yield. The combined ANOVA for yield demonstrated that genotypes performed differently in various environments and was significant for genotype, environment, and their interactions. Adet and Delgi were considered to be favourable environments in the AMMI analysis, whereas Sanja and Chilga were regarded as unfavorable and Finoteselam and Merawi were considered average environments. Wama, Tadesse, Gute, and ACC#203572 exhibit higher average mean yields within genotypes. The most responsive genotypes in the AMMI 2 biplot are Degu, ACC#203572, Tadesse, Gute, and BRC-029-1, while the most discriminating environments are Delgi and Finoteselam. hence different genotypes were assigned for environmental conditions in such a way that genotype Gute was fit for Delgi and Sanja and best suitable genotype for Adet and Chilga were Degu and Wama

Adugna *et.al.*, (2011) conducted a study on 44 indigenous accessions for determining the adaptation range and superiority of genotypes based on the yield potential. White and coloured accessions as a check were used . Data on grain yield, flowering time, and plant height were obtained. The results revealed that genotype, environment, and G X E interaction results. Distribution of cultivars to increase production of finger millet by using the white seed accession from the mixed set and three more accessions from the colourful set since they were the most stable and had above average mean grain yield in all environments was suggested.

Wolie *et.al.*,(2006) evaluated 88 finger millet genotypes using Augmented Block Design. The path coefficients as well as the genotypic and phenotypic correlations of traits were estimated. It was determined that grain yield showed a significant correlation with characters such as plant height(r_g=0.574 and r_p=0.446), number of ears per plant($r_{g=}$ 0.443 and r_p= 0.364), number of fingers per ear(r_g=0.532 and r_p=0.329), finger length(r_g=0.426 and r_p=0.361), biomass yield(r_g and r_p=0.839), harvest index(r_g=0.476 and r_p=0.336) and thousand kernel weight(r_g=0.267 and r_p=0.225). Traits such as biomass yield, finger length, number of fingers per ear and number of ears per plant having positive effects on grain yield whereas plant height, days to heading and days to maturity having negative effect were shown by phenotypic path analysis. The positive effects of biomass yield, number of tillers per plant and finger length on grain yield were shown by genotypic path analysis. Thus, through correlation analysis, it was shown all these characters contributed to yield and hence for improving the yield potential of the given genotypes.

Bezaweletaw *et.al.*,(2006) conducted a study on 66 finger millet genotypes of which 64 were landraces and 2 being the standard varieties using agro-morphological characters for the assessment of variability and association of characters. The mean squares of characters were highly significant in which days to maturity and grain yield per plant showed the highest and lowest values respectively. The phenotypic and genotypic coefficient of variation ranged between 6.52-24.21% in both cases for days to maturity and grain yield per plant whereas it was 8.05-31.23% for other characters. Heritability estimates ranged from 20% for grain-filling duration to 84% for days to heading. Values of expected genetic advance varied from 6.67-44.14% for grain-filling duration and finger width, respectively. Finger width and length exhibited high heritability coupled with high genetic advance. Grain yield per plant showed positive correlation with productive tillers, 1,000-grain weight, the number of grains per spikelet and finger number and negative correlation with characters such days to heading and maturity. The genotypic correlation and path-coefficient analysis showed 1,000-grain weight, finger number and productive tillers influenced grain yield per plant and hence showed that finger millet landraces also showed variability in characters. This can be helpful for the selection of parents for hybridization programmes.

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CHAPTER - III

MATERIALS AND METHODS

MATERIALS AND METHODS

The present investigation entitled “Characterization and stability analysis of transplanted finger millet using morpho-physiological traits in summer” was carried out during the two seasons of summer of 2022 and 2023 in Augmented Block Design with 144 finger millet genotypes and 3 checks at Small Millets Research Farm at Tirhut College of Agriculture, Dholi.

The details of the experiments are given below:

3.1 EXPERIMENTAL SITE

The field had a uniform topography, productive soil and optimum climatic conditions for the growth and development of finger millet crop. The particulars of materials used and experimental techniques followed during the course of investigation are presented in this section.

3.2 EXPERIMENTAL DESIGN AND EXPERIMENTAL MATERIAL

The present experiment was conducted during the 2 summer seasons. The nursery was planted on 3rd February, 2022 and 2nd February, 2023 in season 1 and season 2, respectively. The crop was transplanted on 3rd March 2022 and 2nd March 2023 in both the seasons, in that order. The layout followed was Augmented Block Design. There were 144 finger millet genotypes planted in 8 blocks with 18 genotypes in each block and 3 checks randomised in each block with spacing of 22.5cm x 10cm. The weather data was recorded in both the seasons and the data has been mentioned in Appendix 1.

3.3 FIELD PREPARATION

Summer deep ploughing is advocated to expose the weed seeds, hibernating insects and disease causal organisms to high temperatures. Land preparation ensured adequate tilth as well as incorporation of all crop residues, crop volunteers and weeds. Initial ploughing was carried out once at optimum. Before sowing secondary tillage with cultivator and multiple tooth hoe to prepare smooth seed bed was done. Fully decomposed FYM was incorporated in soil@ 10t/ha at final ploughing, which helped in better root growth. Transplanting was done on semi-puddled soil.

3.4 PLOT SIZE AND SPACING

For germplasm evaluation trials, the plots comprised of 5 rows of 3m length spaced at 22.5cm between the rows with recommended spacing of 10cm between the plants.

3.5 SEED TREATMENT

Seeds of all the entries including checks pertaining to varietal evaluation trials were treated with Carbendazim @ 2g/kg of seed for the control of blast.

3.6 FERTILIZER RECOMMENDATION

Fertilizer dose of 20kg N, 20kg P and 20kg K/ha was applied as basal dose. The remaining 20kg N was applied 30-40 days after transplanting around panicle initiation phase.

3.7 IRRIGATION

Irrigation was provided at critical stages *viz*. 30-45 days (seedling elongation stage), 65- 70 days (reproductive or heading stage), 75-80 days (panicle emergence) and 90-95 days (grain development stage).

3.8 HARVEST

1) Grain yield: Test entries with different maturity durations were harvested at different times as per the maturity groups (early, mid and late), within 10 days of attaining the physiological maturity. The grains were dried to10-12% moisture for recording grain yield and other observations.

2) Fodder yield: For recording dry fodder yield, after removing the earheads the straw was harvested by cutting at the base and sun-dried properly for a week to obtain the dry matter. Straw was turned twice for uniform and complete drying. Straw yield was recorded using a platform balance.

3.9 PARAMETERS CONSIDERED FOR STUDY AND THEIR OBSERVATIONAL PROCEDURES

Five random plants from each row representing a genotype were selected. The observations of parameters to be studied were recorded. The traits analysed and the protocols followed are briefed below:

3.9.1 Quantitative morphological traits

- **Days to 50% flowering**

  Number of days after sowing to the date on which 50% plants in the plot start flowering i.e.; opening of flowers as characterized by exserted anthers outside the spikelet.

- **Days to maturity**

  Number of days after sowing to the date on which seed of most of the plants in a plot become hard; it happened about a week after physiological maturity.

- **Finger length (cm)**

  It was measured from the base of the longest finger on the main ear to the tip.

- **Finger width (cm)**

  It was measured at the widest point of Finger.

- **Ear length (cm)**

  Measured from the base of thumb finger to tip of earhead in 10 randomly selected plants. The measurement was taken during dough stage.

- **Number of Fingers per ear**

  The average number of fingers per earhead was recorded in 10 randomly selected plants during dough stage of crop.

- **Fodder yield (kg/ha)**

  All the plants in a plot were harvested and sun dried thoroughly in the field to reduce moisture content in straw to about 20% before weighing.

- **Grain yield (kg/ha)**

  All the earheads in the plot was harvested, dried and threshed. The grains of all the genotypes were thoroughly sun dried to get uniform moisture before weighing.

- **Plant height (cm)**

  The average height from the base level to the tip of the earhead of the main tiller was recorded at the time of harvest in 10 randomly selected plants.

- **No. of basal tillers**

  It is determined by the total number of tillers which a plant bears, this data was recorded in 10 randomly selected plants per plot.

- **Productive tillers per plant**

  Total number of tillers including the main shoot bearing the earheads was recorded in 10 randomly selected plants. The observations are taken when the crop was fully matured.

- **1000 grain weight (g):**

  A composite sample of 20g from each plot was drawn and 1000 seeds was counted manually after the crop has been harvested. The weight of 1000 seeds was expressed in g .

- **Flag leaf blade length (cm):**

  Flag leaf blade length is measured from ligule to flag leaf blade tip.

- **Flag leaf blade width (cm):**

  Flag leaf blade width is measured at the widest point of the flag leaf.

- **Peduncle length (cm):**

  Peduncle length is measured from earhead base to the topmost node of main tiller.

3.9.2 Qualitative morphological traits

- **Plant growth habit**

  It was determined at 2-4 leaf stage after sowing. It was classified into erect, decumbent or prostrate.

- **Ear shape**

  The observations were noted at dough stage. It was classified into droopy, open, semi-compact, compact or fist like

- **Finger multiple whorl**

  It is defined as the arrangement of spikes in different whorls. It was classified into either present or absent. It was determined at dough stage of crop.

- **Finger branching**

  It was recorded at dough stage. It was determined as either present or absent.

- **Position of finger branching**

  It was determined either as in thumb finger or in all the fingers

- **Seed colour**

  It was classified into either white, light brown, copper brown or dark brown

- **Seed shape**

  It was determined by either round, reniform or ovoid.

- **Glume colour**

  It was either white, light green, dark green, light purple or dark purple. It was determined during flowering stage.

- **Stem culm branching**

  It was determined as either absent or present

- **Seed shattering**

  Seed shattering was determined by the development of the abscission layer, which was located at the junction of the seed base and the pedicel. It was determined as either absent or present.

- **Pericarp persistence after threshing:**

  It was either non persistent or persistent. It was determined after the harvest of the crop.

3.9.3 Seed physiological traits:

Two replications each of 10 finger millet seeds were sown in germination trays and readings were taken for 10 days from the date of sowing.

- **Seed vigour index :**

  Seed vigour is defined as the sum total of those properties of the seed which determine the level of activity and performance of the seed or seed lot during germination and seedling emergence. Two types of seed vigour index i.e., seed vigour index 1 and 2 were considered.

i. **Seed vigour index 1 :**

Calculation of seed vigour index 1 requires seedling length. It was measured using ruler. It was calculated using the formula:

Seed vigour index 1= germination % x seedling length

ii. **Seed vigour index 2 :**

Calculation of seed vigour index 2 requires seedling dry weight.Four seedlings of each genotype were dried in hot air oven at a temperature of 70℃ for 72 hours by wrapping them in an aluminium foil. The total weight was taken on the fourth day. The individual seedling weight was then taken by dividing the total weight with number of seedlings taken. It was calculated by the formula:

Seed Vigour Index 2 = germination% x seedling dry weight

- **Seed germination percentage:**

  Total number of seeds germinated on each day were counted and recorded.

  It was determined by the formula,

$$\text{Germination \%} = \frac{\text{number of germinated seeds}}{\text{total number of seeds}} \times 100$$

- **Seedling length:**
  It was measured using a ruler. Measurement was taken from the base of the root to the tip of shoot. Three seedlings were uprooted and the mean of the readings were recorded.
- **Chlorophyll content:**
  It is measured by using SPAD meter (Soil Plant Analysis Development). The chlorophyll content of intact leaf samples was measured and displayed when the sample was held upon the camera of the instrument.
- **Speed of germination:**
  It was calculated by the formula,
  Speed of germination= $\sum(Gt/Dt)$

Where,

Gt=number of germinated seed

Dt=time corresponding to Gt in days

3.10 EXPERIMENTAL MATERIAL USED IN THE STUDY

The 144 local germplasm and 3 checks used in this study were obtained from the Small Millets scheme, TCA, Dholi, RPCAU:

Table 3.1 : List of 144 Genotypes used for study

Genotype Number	Name of entry	Parentage
G1.	RAU-FM-Sheohar-2009-1	Collected from Sheohar in the year 2009
G2.	RAU-FM-Sheohar-2009-2	
G3.	RAU-FM-Sheohar-2009-3	
G4.	RAU-FM-Sheohar-2009-4	
G5.	RAU-FM-Sheohar-2009-5	
G6.	RAU-FM-Sheohar-2009-6	
G7.	RAU-FM-Sheohar-2009-7	
G8.	RAU-FM-Sheohar-2009-8	
G9.	RAU-FM-Sheohar-2009-9	
G10.	RAU-FM-Sheohar-2009-10	
G11.	RAU-FM-Sheohar-2009-11	
G12.	RAU-FM-Sheohar-2009-12	
G13.	RAU-FM-Sheohar-2009-13	
G14.	RAU-FM-Sheohar-2009-14	
G15.	RAU-FM-Sheohar-2009-15	
G16.	RAU-FM-Sheohar-2009-16	
G17.	RAU-FM-Sheohar-2009-17	
G18.	RAU-FM-Sheohar-2009-18	
G19.	RAU-FM-Sheohar-2009-19	
G20.	RAU-FM-Sheohar-2009-20	
G21.	RAU-FM-Madhubhani-2009-1	Collected from Madhubhani in the year 2009
G22.	RAU-FM-Madhubhani-2009-2	
G23.	RAU-FM-Madhubhani-2009-3	
G24.	RAU-FM-Madhubhani-2009-4	
G25.	RAU-FM-Madhubhani-2009-5	
G26.	RAU-FM-Madhubhani-2009-6	
G27.	RAU-FM-Madhubhani-2009-7	

Cont…

G28.	RAU-FM-Madhubhani-2009-8	
G29.	RAU-FM-Madhubhani-2009-9	
G30.	RAU-FM-Madhubhani-2009-10	
G31.	RAU-FM-Madhubhani-2009-11	
G32.	RAU-FM-Madhubhani-2009-12	
G33.	RAU-FM-Madhubhani-2009-13	
G34.	RAU-FM-Madhubhani-2009-14	
G35.	RAU-FM-Madhubhani-2009-15	
G36.	RAU-FM-Madhubhani-2009-16	
G37.	RAU-FM-Madhubhani-2009-17	
G38.	RAU-FM-Madhubhani-2009-18	
G39.	RAU-FM-Madhubhani-2009-19	
G40.	RAU-FM-Madhubhani-2009-20	
G41.	RAU-FM-Madhubhani-2009-21	
G42.	RAU-FM-Madhubhani-2009-22	
G43.	RAU-FM-Madhubhani-2009-23	
G44.	RAU-FM-Madhubhani-2009-24	
G45.	RAU-FM-Madhubhani-2009-25	
G46.	RAU-FM-Madhubhani-2009-26	
G47.	RAU-FM-Madhubhani-2009-27	
G48.	RAU-FM-Madhubhani-2009-28	
G49.	RAU-FM-Madhubhani-2009-29	
G50.	RAU-FM-Madhubhani-2009-30	
G51.	RAU-FM-Sheohar-2010-1	Collected from Sheohar in the year 2010
G52.	RAU-FM-Sheohar-2010-2	
G53.	RAU-FM-Sheohar-2010-3	
G54.	RAU-FM-Sheohar-2010-4	
G55.	RAU-FM-Sheohar-2010-5	
G56.	RAU-FM-Sheohar-2010-6	
G57.	RAU-FM-Sheohar-2010-7	
G58.	RAU-FM-Sheohar-2010-8	
G59.	RAU-FM-Sheohar-2010-9	
G60.	RAU-FM-Sheohar-2010-10	

Cont…

G61.	RAU-FM-Madhubhani-2010-1	Collected from Madhubhani in the year 2010
G62.	RAU-FM-Madhubhani-2010-2	
G63.	RAU-FM-Madhubhani-2010-3	
G64.	RAU-FM-Madhubhani-2010-4	
G65.	RAU-FM-Madhubhani-2010-5	
G66.	RAU-FM-Madhubhani-2010-6	
G67.	RAU-FM-Madhubhani-2010-7	
G68.	RAU-FM-Madhubhani-2010-8	
G69.	RAU-FM-Madhubhani-2010-9	
G70.	RAU-FM-Madhubhani-2010-10	
G71.	RAU-FM-Gopalganj-2009-1	Collected from Gopalganj in the year 2009
G72.	RAU-FM- Gopalganj-2009-2	
G73.	RAU-FM- Gopalganj-2009-3	
G74.	RAU-FM- Gopalganj-2009-4	
G75.	RAU-FM- Gopalganj-2009-5	
G76.	RAU-FM-Kanti-2010-1	Collected from Kanti, Muzzafarpur in the year 2010
G77.	RAU-FM-Kanti-2010-2	
G78.	RAU-FM-Kanti-2010-3	
G79.	RAU-FM-Kanti-2010-4	
G80.	RAU-FM-80	RAU 8 x RAU 3
G81.	RAU-FM-81	RAU 8 x RAU 3
G82.	RAU-FM-82	RAU 8 x RAU 3
G83.	RAU-FM-83	RAU 8 x BR 407
G84.	RAU-FM-84	RAU 3 x BR 407
G85.	RAU-FM-85	RAU 8 x PR 202
G86.	RAU-FM-86	RAU 8 x PR 202
G87.	RAU-FM-87	RAU 3 x PR 202
G88.	RAU-FM-88	RAU 8 X GPU 28
G89.	RAU-FM-89	RAU 3 X GPU 28
G90.	RAU-FM-90	RAU 8 X IE 4425
G91.	RAU-FM-91	source/parentage not known
G92.	RAU-FM-92	
G93.	RAU-FM-93	

Cont…

G94.	RAU-FM-94	
G95.	RAU-FM-95	
G96.	RAU-FM-96	
G97.	RAU-FM-97	
G98.	RAU-FM-98	
G99.	RAU-FM-99	
G100.	RAU-FM-100	
G101.	RAU-FM-101	
G102.	RAU-FM-102	
G103.	RAU-FM-103	
G104.	RAU-FM-104	
G105.	RAU-FM-105	
G106.	RAU-FM-106	
G107.	RAU-FM-107	
G108.	RAU-FM-108	
G109.	RAU-FM-109	
G110.	RAU-FM-110	
G111.	RAU-FM-111	
G112.	RAU-FM-112	
G113.	RAU-FM-113	
G114.	RAU-FM-114	
G115.	RAU-FM-115	
G116.	RAU-FM-116	
G117.	RAU-FM-117	
G118.	RAU-FM-118	
G119.	RAU-FM-119	
G120.	RAU-FM-120	
G121.	RAU-FM-121	
G122.	RAU-FM-122	
G123.	RAU-FM-123	
G124.	RAU-FM-124	
G125.	RAU-FM-125	
G126.	RAU-FM-126	

Cont…

G127.	RAU-FM-127	
G128.	RAU-FM-128	
G129.	RAU-FM-129	
G130.	RAU-FM-130	
G131.	RAU-FM-131	
G132.	RAU-FM-132	
G133.	RAU-FM-133	
G134.	RAU-FM-134	
G135.	RAU-FM-135	
G136.	RAU-FM-136	
G137.	RAU-FM-137	
G138.	RAU-FM-138	
G139.	RAU-FM-139	
G140.	RAU-FM-140	
G141.	RAU-FM-141	
G142.	RAU-FM-142	
G143.	RAU-FM-143	
G144.	RAU-FM-144	
Check 1	RAU-8(local check)	
Check 2	GPU-67(national check)	
Check 3	VL-376(national check)	

3.11 STATISTICAL EVALUATION

3.11.1 ANALYSIS OF VARIANCE

For analysis of variance, the method given by Federer (1956) and Federer and Raghavarao (1975) was used. The total variance that could be assigned to different sources was partitioned in the following manner:

Table 3.2: Analysis of Variance for Augmented Block Design

S.No	Source of Variation	d.f	S.S	M.S.S	F Value
1	Block	b-1	bSS	bMS	bMS/EMS
2	Test	t-1	tSS	tMS	tMS/EMS
3	Check	c-1	cSS	cMS	cMS/EMS
4	Genotype	v-1	vSS	vMS	vMS/EMS
5	Check vs Test	1	cvSS	cvMS	cvMS/EMS
6	Error	(c-1) (b-1)	ESS	EMS	

Where,

b = number of blocks

v = number of genotypes

c = number of checks

3.11.2 ESTIMATION OF VARIABILITY

Different variability parameters such as mean, range and percent of variance for various traits were calculated for all new selections.

Mean

The individual genotype's mean was computed as the arithmetic mean of the values of each character:

$$X = \frac{1}{n}\sum_{i=1}^{n} X_i$$

Where,

X = Mean

$\sum X_i$ = total sum of observations for the trait

n = Number of observations

Range

This denotes the maximum and the minimum value of the character in the material

$$\text{Range} = X_n - X_i$$

Where,

X_n = highest mean value of each character

X_i = lowest mean value of each character

3.11.3 Components of Variance

Genotypic Variance

Variance regarding genotypes present in the population is known as genotypic variance (VG or σ^2_g). Formula used to calculate genotypic variance:

$$\text{Genotypic variance}(\sigma^2_g) = \frac{\text{GMS-EMS}}{\text{number of replications(r)}}$$

Environmental or Error Variance

The environmental variance (VE or σ^2_e) is the variance due to environmental deviation.

$$\sigma^2_e = EMS$$

Phenotypic Variance

The overall variance contained in a population for a specific trait is denoted by phenotypic variance (Vp or σ^2_p), which is computed using the formula.

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

Where,

σ^2_g = genotypic variance

σ^2_e = error variance

3.11.4 Standard Error of Mean

The formula used for calculating standard error of mean is given as under:

$$SEm = \sqrt{\frac{2EMS}{r}}$$

Where,

r= no. of replications.

3.11.5 Critical Difference

The formula used to calculate critical difference is given as

$$CD = \sqrt{\frac{2EMS}{r}} \times t_{value\ at}\ 5\%$$

Where,

r = number of replications

t_{value}= table value of error difference at 5% level of significance

EMS = error mean sum of squares

The presence of substantial “F” value suggests that the treatments differ significantly. However, when comparing two different treatments, CD value is used.

3.11.6 Genotypic and Phenotypic Co-efficient of Variability

It is an evolved measure of variability. In statistics, a coefficient of variation refers to the ratio between a sample's standard deviation and the sample mean.

$$\text{CV} = \frac{\text{standard deviation}}{\text{mean}} \text{ x } 100$$

This study computed three types of coefficients of variation: (PCV), genotypic coefficient of variation (GCV), and error/environmental coefficient of variation (ECV). **Burton and De vane(1953)** provided the formulas for calculating PCV, GCV, and ECV.

$$\text{PCV}(\%) = \frac{\text{phenotypic standard deviation}}{\text{mean}} \text{ X } 100$$

$$= \frac{\sqrt{\sigma^2 p}}{\bar{X}} \text{x } 100$$

$$\text{GCV}(\%) = \frac{\text{genotypic standard deviation}}{\text{mean}} \text{ X } 100$$

$$= \frac{\sqrt{\sigma^2 g}}{\bar{X}} \text{ x } 100$$

$$\text{ECV}(\%) = \frac{\text{Error standard deviation}}{\text{mean}} \text{ X } 100$$

Where,

$\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance

$\sigma^2 e$ = error variance

$\bar{X}$ =mean of character

3.11.7 Genetic Advance

Genetic advance is defined as an increase in the mean genotypic value of selected plants over the parental population. The formula to measure genetic advance was developed by Lush (1949), Johnson et al. (1955), and Allard (1955).

$$\textbf{GA= K. } \boldsymbol{\sigma_p}\textbf{.h}^2$$

$$= \text{K.}\sigma_p.\frac{\sigma^2 g}{\sigma^2 p}$$

Where,

K=selection differential at 5% level intensity, i.e.,2.06 which is constant

σ_p=phenotypic standard deviation

h^2=heritability in broadsense

Genetic advance as percent of mean (GA%)

$$\textbf{GA (\%) = } \frac{\textbf{GA}}{\bar{\textbf{X}}} \textbf{ x 100}$$

3.11.8 Heritability (Broad sense)

The ratio of genotypic to phenotypic variance was used to calculate heritability, and expressed as a percentage. Formula proposed by Johnson et al,(1955) was used to calculate heritability as follows:

$$h^2 \text{ (broad sense)} = \frac{\sigma^2_g}{\sigma^2_p} x\ 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

h^2 = Heritability (broad sense)

3.11.9 Analysis of Correlation coefficients:

Correlation coefficient shows the mutual relationship between variables but do not imply any relationship between cause and effect. Al-Jibouri et.al., (1958) and Panse and Sukhatme (1967) provided the formula to find the Simple correlation coefficients between two characters.

Genotypic correlation coefficient:

Genotypic correlation between traits x and y is given by

$$\mathbf{r_{xy(g)}} = \frac{\sigma^2 g(xy)}{\sqrt{\sigma^2 g(xy).\ \sigma^2(y)}}$$

Where,

$\sigma^2_g(xy)$= genotypic covariance between traits x and y

$\sigma^2_g(x)$ = genotypic variance for x

$\sigma^2_g(y)$ = genotypic variance for y

Phenotypic correlation coefficient:

Phenotypic correlation coefficient between traits x and y is given by

$$\mathbf{r_{xy(p)}} = \frac{\sigma^2 p(xy)}{\sqrt{\sigma^2 p(xy).\ \sigma^2(y)}}$$

Where,

$\sigma^2_p(xy)$= phenotypic covariance between traits x and y

$\sigma^2_p(x)$ = phenotypic variance for x

$\sigma^2_p(y)$ = phenotypic variance for y

3.11.10 Test of significance

Comparison was made on the estimated values with the table value of the correlation coefficient recommended by Fisher and Yates, 1938 at (n-2) treatment degree of freedom at five percent and one percent level of significance in order to assess the significance of the correlation coefficient. It is regarded as significant if the calculated value or correlation coefficient is higher than the tabular value.

3.11.11 Path Coefficient Analysis

The Dewey and Lu method (1959) was used to calculate the path coefficients for the component traits associated with grain yield in this study. Based on the simultaneous solution of the following equations, the direct and indirect effects of the experiment were calculated

Py_1 +	$Py_2\, r_{12}$ +	$Py_3\, r_{13}$ + ………… +	$Py_1\, r_{1n} = ry_1$
$Py_2\, r_{12}$ +	Py_2 +	$Py_3\, r_{23}$ + ………….+	$Py_n\, r_{2n} = ry_2$
-	-	- -	- -
-	-	- -	- -
-	-	- -	- -
$Py_1\, r_{1n}$ +	$Py_2\, r_{2n}$ +	$Py_3\, r_{3n}$ +…………..+	$Py_n = ry_n$

Py1, Py2, Py3…………………..Pyn are the direct path effects of 1, 2,3………..…, n variables on dependent variable 'y' and r12, r13, r19……………….. r (r - 1)n are the genotypic coefficient of correlation between various independent variables ry1, ry2…………………………ryn are the genotypic correlation coefficients of independent variables with dependent variable `y' Py1r12, Py3r23………… Pynr2n are the indirect effects. It was assumed that the variation in the independent variable, which remained undetermined after including all the variables, was primarily due to the variable(s) that were not considered as part of this investigation. Using the formula below, the degree of determination (P2yx) of such variable(s) on the dependent variable was calculated.

P2yx = 1 - (P2y1 + 2Py1r12 + 2Py1 Py3r13…………..+ P2y2 + 2Py2 2Py3r23 + P2y3 + 2Py4r34………………..+ P2yn) and residual effect (R2) = P2yx.

3.12 STABILITY ANALYSIS

3.12.1 GGE Biplot Method

The term ‘‘GGE biplot’’ first used by Yan *et al*., (2000) refers to a biplot that shows the genotype (G) and interaction of genotype and environment (G×E) components in a XY graph. The GGE biplot technique recently has been found to be more useful as it is more effective in G × E interaction studies and it eliminates the noise caused by the environment (E) and focuses on the genotype (G) and interaction of genotype and environment (G×E) components (Blanche *et al*., 2006). GGE biplot can also be useful to graphically show the “which own where” pattern of the studied data which helps to recognize high yielding and stable genotypes and representative and discriminating nature of test environment.

In GGE Biplot for environment, the most stable environment is placed close to the dot of ideal and average environment and in the concentric area of ideal environment dot. In case of GGE Biplot for varieties, the desirable varieties are placed near to ideal variety and in the concentric variety of ideal variety dot.

Here, given two-way data of genotypes evaluated in X environments, the main performance (Y) of i^{th} genotype in the j^{th} environment can be explained as follows:

$Yij = \mu + \acute{\alpha}_i + \beta_j + \Phi_{ij} + \sum_{ij}$ …………………… (1)

Where,

μ= grand mean

$\acute{\alpha}_i$ = genotype row main effect

β_j = environment main effect

Φ_{ij} = individual G X E interaction

$\sum_{ij}$ = error

This two-way data model cannot be adequately approximated into graphical representation without decomposing the n^{th} genotype and the X^{th} environment two way table (P). This table decomposition is achieved via singular value decomposition (SVD).

Where,

P is decomposed into

$Pij = \sum_{i=1}^{r} 2ij \ \lambda \ \eta ij$……………………… (2)

Here,

r = number of principal components representing the two-way table (P)

2ij = genotype vector

λ = environmental vector

η = singular value

Where, data centering focus on assessment of genotypes (G) in multi environment trial (MET) data. The two-way table prepared in above equation number 2 merges with the mean performance of Y equation number 1, thereby equations number 1 and 2 eventually turns into-

$$P_{ij} = Y_{ij} - \boldsymbol{\mu} - \beta_j$$

$$= \alpha_i + \phi_{ij} \text{ ……. } (3)$$

This equation comprises both the genotype main effects and interaction of genotype and environment (G×E) and it called GGE biplot (Yan *et al.*, 2000).

All centering methods including genotype (G), environment (E) and interaction of genotype and environment (G×E) centered method were constructed in biplot of GGE, where standardization (data scaling) and transformation option were inclusive, thus GGE biplot is lastly written as

$$\phi_{ij} = Y_{ij} - \boldsymbol{\mu} - \beta_j / S_j$$

$$= (\alpha_i + \phi_{ij} / S_j) \text{ …………… } (4)$$

Where S_j is a scaling factor and can be equal to 1, whereas the other variables are defined in earlier equations. Standardization was done such that all columns were given equal weightage (Yan, 2005).

A number of researchers have demonstrated the effectiveness and convenience of GGE biplot as graphically addressing problem related to genotype (G) evaluation in multi environment trial (Yan and Kang 2003, Yan and Tinker 2005).

3.12.2 Models for interaction of genotype and environment (G×E) biplot

Based on research emphasis, GGE biplot can be of different models. Out of many models, this model takes into account a genotype (G) centered data set along with environment (E) centered data set with following equations-

$$P_{ij} = (Y_{ij} - \boldsymbol{\mu} - \alpha_i) = \beta_j + \phi_{ij} \text{ Genotype centred……..(5)}$$

$$P_{ij} = (Y_{ij} - \boldsymbol{\mu} - \beta_j) = \alpha_i + \phi_{ij} \text{ Environment centred……..(6)}$$

All the variables are as per with the defined equation in the previous equation.

All the variables in this study focus on environment centered data model and the data subjected to singular value partitioning (SVP). The resultant Principal components 1 and 2 from the singular value partitioning were used to construct GGE biplot, other smaller principal component analysis (PCA) was regarded as residual and not explained.

Fig 1:Experimental Field

✠✠✠

CHAPTER - IV

EXPERIMENTAL RESULTS

EXPERIMENTAL FINDINGS

The present investigation entitled "Characterization and stability analysis of transplanted finger millet using morpho-physiological traits in summer" was carried out with the following three objectives:

1. To characterize and evaluate germplasm of finger millet for quantitative and qualitative traits in summer seasons
2. To evaluate germplasm of finger millet for seed physiological traits in summer seasons
3. To study the role of genotype x environment interactions in the expression of various morphological characters and stability of genotypes in summer seasons

The results obtained for the parameters studied under these mentioned objectives are presented in this chapter. In season 1 and season 2, twenty genotypes failed to perform due to various reasons such as absence of germination, non-flowering etc. as the finger millet crop was being tested in the new environment.

CHARACTERIZATION AND EVALUATION OF FINGER MILLET GENOTYPES FOR QUANTITATIVE AND QUALITATIVE TRAITS IN SUMMER SEASONS

4.1 Variability for morphological traits

Significant variation for the morphological traits in 144 finger millet genotypes and 3 check varieties has been summarized in Table 1 and Table 2. Present investigation showed a wide range of variation in the morphological traits which are said to affect the yield.

Days to 50% flowering

There are highly significant differences ($P<0.05$) among the genotypes for days to 50% flowering (Table 4). The days to 50% flowering ranged from 59.0 (G2) to 93.0 (G122) in season 1 with a mean of 77.56; from 62.0 (G2) to 92.0 (G75) with a mean of 78.36. While on pooled basis, it ranged from 60.5 to 91.5 with a mean of 77.96.

Days to maturity

Highly significant differences were observed for days to maturity in finger millet genotypes. The days to maturity ranged from 92.0 (G2) to 122.0 (GPU-67) in season 1 with a mean of 113.78; from 89.0 (G2) to 123.0 (G34) in season 2 with a mean of 114.12. While on pooled basis, it ranged from90.5 to 121.5 with a mean of 113.94. Based on days to maturity the genotypes were classified into early (< 100 days), medium (100 – 120 days) and late (> 120 days) maturing genotypes. Based on the pooled data for both the seasons, one genotype (G2)had been grouped as early maturing, 105 genotypes as medium maturing and 14 genotypes as late maturing genotypes. Among the check varieties, RAU-8 and VL-376 were medium maturing and GPU-67 was late maturing.

Finger length(cm)

The finger length ranged from 4.2cm (G96) to 7.3cm (G5) in season 1 with a mean of 5.57; from 4.2cm (G128) to 8.2cm (G19) in season 2 with a mean of 5.85. While on pooled basis, it ranged from4.25 to 7.7 with a mean of 5.71. According to the pooled data, 14 genotypes out-performed the checks in finger length.

Finger width(cm)

The finger width ranged from 0.5cm (G128) to 0.92cm (GPU-67) in season 1 with a mean of 0.68; from 0.46cm (G100) to 0.96cm (G17) in season 2 with a mean of 0.69. While on pooled basis, it ranged from 0.49 to 0.90 with a mean of 0.68. Based on pooled data, no genotype had higher finger width than the check varieties.

Ear length(cm)

The ear length ranged from 6.3cm (G116) to 11.7cm (G112) in season 1 with a mean of 9.26; from 5.8cm (G116) to 11.8cm (G76) in season 2 with a mean of 9.20. While on pooled basis, it ranged from 6.05 to 11.45 with a mean of 9.23. Based on pooled data, 53 genotypes had higher ear length over the check varieties.

Fingers per ear

The fingers per ear ranged from 4.28 (G63) to 9.23 (RAU-8) in season 1 with a mean of 6.86; from 4.78 (G67) to 9.14 (RAU-8) in season 2 with a mean of 6.83. While on pooled basis, it ranged from 4.87 to 9.18 with a mean of 6.84

Fodder Yield(kg/ha)

The fodder yield ranged from 534.39 kg/ha(G59) to 5506.17 kg/ha(GPU-67) in season 1 with a mean of 1691.48; from 643.28 kg/ha(G139) to 4856.23 kg/ha(GPU-67) in season 2 with a mean of 1708. While on pooled basis, it ranged from 680.51 kg/ha to 4929.28 kg/ha with a mean of 1700.28

Grain yield(kg/ha)

The grain yield ranged from 309.74 kg/ha(G126) to 3012.35 kg/ha(RAU-8) in season 1 with a mean of 1172.78; from 429.13 kg/ha(G87) to 2931.64 kg/ha(VL-376) in season 2 with a mean of 1203.78. While on pooled basis, it ranged from 373.94 to 2935.38 with a mean value of 1177.57. Based on pooled data, no genotype had higher grain yield than the check varieties.

Plant height(cm)

The plant height ranged from 65.4cm (G117) to 115.5cm (G95) in season 1 with a mean of 89.89; from 24.6cm (G111) to 114.7cm (G95) in season 2 with a mean of 90.93. While on pooled basis, it ranged from 52.4 to 115.1 with a mean of 90.4. Based on pooled data the plant height greater than the check varieties were not observed in any genotypes.

Number of basal tillers

The number of basal tillers ranged from 2.45 (G141) to 8.43 (RAU-8) in season 1 with a mean of 5.51; from 2.95 (G129) to 8.62 (RAU-8) in season 2 with a mean of 5.78. While on pooled basis, it ranged from 2.87 to 8.52 with a mean of 5.64. Based on pooled data , no genotypes showed greater number of basal tillers than the check varieties.

Number of Productive tillers per plant

The number of productive tillers per plant ranged from 1.02 (G58) to 2.83 (GPU-67) in season 1 with a mean of 2.01; from 1.13 (G58) to 2.78 (G126) in season 2 with a mean of 1.98. While on pooled basis, it ranged from 1.22 to 2.75 with a mean of 1.99. Based on pooled data, 15 genotypes showed higher number of productive tillers than the check varieties.

1000 grain weight(g)

The 1000 grain weight ranged from 1.34g (G121) to 3.16g (G99) in season 1 with a mean of 2.43; from 1.34g (G100) to 3.12g (G86) in season 2 with a mean of 2.31. While on pooled basis, it ranged from 1.35 to 3.11 with a mean of 2.37 . Based on pooled data, 12 genotypes had higher 1000 grain weight as compared to the check varieties.

Flag leaf blade length(cm)

The flag leaf blade length ranged from 17.9cm (G83) to 44.6cm (GPU-67) in season 1 with a mean of 33.05; from 22.3cm (G90) to 45.2cm (G14) in season 2 with a mean of 34.07. While on pooled basis, it ranged from 20.4 to 43.7 with a mean of 33.5. Based on pooled data, nine genotypes had higher leaf blade length than the check varieties.

Flag leaf blade width(cm)

The flag leaf blade width ranged from 0.8cm (G102, G112, G121 and G139) to 2.6cm (G17, RAU-8 and VL-376) in season 1 with a mean of 1.88; from 1.1cm (G83) to 2.6cm (RAU-8) in season 2 with a mean of 1.85. While on pooled basis, it ranged from 0.95 to 2.5 with a mean of 1.86. Based on pooled data, no genotype has higher flag leaf blade width than the check varieties.

Peduncle length(cm)

Peduncle length ranged from 9.1cm (G36) to 24.6cm (G14 and G28) in season 1 with a mean of 15.46; from 9.2cm (G56) to 25.5cm (G24) in season 2 with a mean of 15.47. While on pooled basis, it ranged from 9.6 to 22.9 with a mean of 15.4. Based on pooled data, nine genotypes had higher peduncle length than the check varieties.

Table 4.1: Mean, Range and Coefficient of Variation for season 1

S.No.	Characters	Mean ± S.E.	Range		C.V.
			Min.	Max.	
1.	Days to 50% flowering	77.56±0.60	59.0	93.0	9.60
2.	Days to maturity	113.78±0.50	92.0	122.0	5.28
3.	Finger length(cm)	5.57±0.07	4.0	7.3	14.47
4.	Finger width(cm)	0.68±0.01	0.5	0.92	17.51
5.	Ear length(cm)	9.26±0.11	6.3	11.7	14.23
6.	Fingers per ear	6.86±0.09	4.28	9.23	15.56
7.	Fodder yield(kg/ha)	1691.48±100.29	534.39	5506.17	71.89
8.	Grain yield(kg/ha)	1172.78±65.70	309.74	3012.35	67.92
9.	Plant height(cm)	89.89±1.10	65.4	115.5	14.88
10.	Number of basal tillers	5.51±0.11	2.45	8.43	23.21
11.	Productive tillers per plant	2.01±0.03	1.02	2.83	20.14
12.	1000 grain weight(g)	2.43±0.04	1.34	3.16	21.43
13.	Flag leaf blade length(cm)	33.05±0.57	17.9	44.6	20.84
14.	Flag leaf blade width(cm)	1.88±0.03	0.8	2.6	22.30
15.	Peduncle length(cm)	15.46±0.28	9.1	24.6	21.78

Table 4.2: Mean, Range and Coefficient of Variation for season 2

S.No.	Characters	Mean ± S.E	Range		C.V
			Min.	Max.	
1.	Days to 50% flowering	78.36±0.62	62.0	92.0	9.55
2.	Days to maturity	114.12±0.51	89.0	123.0	5.42
3.	Finger length(cm)	5.85±0.06	4.2	8.2	13.06
4.	Finger width(cm)	0.69±0.01	0.46	0.96	15.67
5.	Ear length(cm)	9.20±0.11	5.8	11.8	14.12
6.	Fingers per ear	6.83±0.08	4.78	9.14	13.96
7.	Fodder yield(kg/ha)	1708±92.74	643.28	4856.23	65.80
8.	Grain yield(kg/ha)	1203.78±60.77	429.13	2931.64	61.20
9.	Plant height(cm)	90.93±1.10	24.6	114.7	14.73
10.	Number of basal tillers	5.78±0.09	2.95	8.62	18.91
11.	Productive tillers per plant	1.98±0.03	1.13	2.78	16.32
12.	1000 grain weight(g)	2.31±0.04	1.34	3.12	22.05
13.	Flag leaf blade length(cm)	34.07±0.48	22.3	45.2	16.92
14.	Flag leaf blade width(cm)	1.85±0.03	1.1	2.6	17.08
15.	Peduncle length(cm)	15.47±0.22	9.2	25.5	17.16

Table 4.3:Mean, Range and Coefficient of Variation in pooled environment

S.No.	Characters	Mean ±S.E	Range		C.V
			Min.	Max.	
1.	Days to 50% flowering	77.96±0.54	60.5	91.5	8.40
2.	Days to maturity	113.94±0.45	90.5	121.5	4.80
3.	Finger length(cm)	5.71±0.05	4.25	7.70	0.05
4.	Finger width(cm)	0.68±0.01	0.49	0.90	14.9
5.	Ear length(cm)	9.23±0.09	6.05	11.45	12.6
6.	Fingers per ear	6.84±0.07	4.87	9.18	12.7
7.	Fodder yield(kg/ha)	1700.21±92.13	680.51	4929.28	0.66
8.	Grain yield(kg/ha)	1177.57±59.77	373.94	2935.38	61.54
9.	Plant height(cm)	90.41±0.98	52.45	115.1	13.20
10.	Number of basal tillers	5.64±0.08	2.8	8.5	19.20
11.	Productive tillers per plant	1.99±0.02	1.22	2.75	15.40
12.	1000 grain weight(g)	2.37±0.03	1.35	3.11	18.90
13.	Flag leaf blade length(cm)	33.55±0.46	20.4	43.7	16.80
14.	Flag leaf blade width(cm)	1.86±0.02	0.95	2.5	18.10
15.	Peduncle length(cm)	15.46±0.20	9.65	22.9	16.30

4.2 Analysis of Variance

The analysis of variance was done for fifteen characters in each of the two environments independently as well as across the environments. Tables 4 to 6 provide the pooled analysis of variance for fifteen traits of 120 finger millet genotypes. The 144 finger millet genotypes' pooled analysis of variance revealed highly significant variation for each trait. For each character, the variation caused by the environment was determined to be significant. It was determined that the genotype by environment (G x E) interaction was significant for all the sources of variation for days to 50% flowering, days to maturity, finger length, finger width, ear length, fingers per ear, grain yield, plant height, number of basal tillers, productive tillers per plant, 1000 grain weight, flag leaf blade length, flag leaf blade width and peduncle length.

Table 4.4: Pooled Analysis of Variance for Days to 50% flowering, Days to Maturity, Finger Length, Finger Width, Ear Length and Fingers per Ear

Source of Variation	Degree of Freedom	Mean sum of squares					
		Days to 50%flowering	Days to maturity	Finger length	Finger width	Ear length	Fingers per ear
Genotype	122	47.81**	33.62**	0.51**	0.01**	1.58**	0.84**
Check	2	379.12**	210.01**	0.80**	0.02**	5.54**	0.88
Test	119	42.63	30.22**	0.49**	0.01**	1.41**	0.69**
Test vs Check	1	1.29	85.08**	2.07**	0.63**	13.52**	17.95**
Block	7	8.98	4.26	0.10	0.00	0.08	0.37
Residual	14	21.60	13.44	0.06	0.00	0.07	0.27

****significant at α=0.01**

Table 4.5: Pooled Analysis of Variance for Grain Yield, Plant Height, No.of Basal Tillers and Productive Tillers per Plant

Source of Variation	Degree of Freedom	Mean sum of squares			
		Grain Yield	Plant height	No. of basal tillers	Productive tillers per plant
Genotype	122	601769.65**	163.67**	1.33**	0.11**
Check	2	245654.72	74.65	7.25**	0.71**
Test	119	100834.94	132.56	0.93**	0.09**
Test vs Check	1	60925229.16**	4043.55**	37.50**	1.44**
Block	7	91798.31	24.78	0.58**	0.01
Residual	14	102675.69	24.77	0.18	0.02

****significant at α=0.01**

Table 4.6: Pooled Analysis of Variance for 1000 Grain Weight, Flag Leaf Blade Length, Flag Leaf Blade Width and Peduncle Length

Source of Variation	Degree of Freedom	Mean Sum of Square			
		1000 Grain Weight	Flag Leaf Blade Length	Flag Leaf Blade Width	Peduncle Length
Genotype	122	0.23**	36.77**	0.13**	7.16**
Check	2	0.08**	51.65**	0.00	1.30
Test	119	0.17**	27.52**	0.08**	7.28**
Test vs Check	1	7.40**	1108.19**	6.88**	5.26
Block	7	0.03	3.86	0.01	2.85
Residual	14	0.02	3.89	0.01	1.77

****significant at $\alpha=0.01$**

4.3 Variance components and Coefficient of variation

The phenotypic, genotypic and environmental components of variances and their respective coefficients of Variations were estimated for different characters and are presented in Table 7.

Days to 50% flowering

In season 1 the environmental, genotypic and phenotypic variances were observed as 2.92, 36.97 and 39.90, respectively and the environmental coefficient of variation was observed as 2.22 while the genotypic and phenotypic coefficients of variation were observed to be 7.90 and 8.20, respectively. In season 2, the environmental, genotypic and phenotypic variances were observed as 6.47, 37.62 and 44.09, respectively and the environmental coefficient of variation was observed as 3.27 while the genotypic and phenotypic coefficients of variation were observed to be 7.90 and 8.55, respectively.

Days to maturity

In season 1, the environmental, genotypic and phenotypic variances were observed as 1.06, 27.07 and 28.14, respectively and the environmental coefficient of variation was observed as 0.91 while the genotypic and phenotypic coefficients of variation were observed to be 4.59 and 4.68, respectively. In season 2, the environmental, genotypic and phenotypic variances were observed as 0.92, 31.03 and

31.96, respectively and the environmental coefficient of variation was observed as 0.84 while the genotypic and phenotypic coefficients of variation were observed to be 4.90 and 4.97, respectively.

Finger length

In season 1, the environmental, genotypic and phenotypic variances were observed to be 0.04, 0.50 and 0.54, respectively and the environmental, genotypic and phenotypic coefficients of variation were observed to be 3.66, 12.77 and 13.29, respectively. In season 2, the environmental, genotypic and phenotypic variances were 0.04, 0.48 and 0.53, respectively and the environmental, genotypic and phenotypic coefficients of variation were 3.61, 11.83 and 12.37, respectively.

Finger width

In season 1, the environmental, genotypic and phenotypic variances were 0.02, 0.01 and 0.08, respectively and the environmental, genotypic and phenotypic coefficients of variation were 2.13, 13.42 and 13.59, respectively. In season 2, the environmental, genotypic and phenotypic variances were 0.02, 0.05 and 0.07, respectively and the environmental, genotypic and phenotypic coefficients of variation were 6.74, 11.33 and 13.18, respectively.

Ear length

In season 1, the environmental, genotypic and phenotypic variances were 0.06, 1.50 and 1.56, respectively and the environmental, genotypic and phenotypic coefficients of variation were 2.79, 13.31 and 13.60, respectively. In season 2, the environmental, genotypic and phenotypic variances 0.01, 1.36 and 1.46, respectively and the environmental, genotypic and phenotypic coefficients of variation were 3.41, 12.75 and 13.19, respectively.

Fingers per ear

In season 1, the environmental, genotypic and phenotypic variances were 0.08, 0.77 and 0.85, respectively and the environmental, genotypic and phenotypic coefficients of variation were 4.31, 13.03 and 13.72, respectively. In season 2, the environmental, genotypic and phenotypic variances were 0.17, 0.50 and 0.67, respectively and the environmental, genotypic and phenotypic coefficients of variation were 6.09, 10.59 and 12.21, respectively.

Grain yield

Under season 1, the environmental, genotypic and phenotypic variances were 10100.71, 83115.47 and 93216.19 respectively and the environmental, genotypic and phenotypic coefficients of variation were 11.77, 33.76 and 35.75 respectively. Under season 2, the environmental, genotypic and phenotypic variances were 9647.63, 61856.30 and 71503.94 respectively and the environmental, genotypic and phenotypic coefficients of variation were 10.99, 27.84 and 29.93 respectively.

Plant height

Under season 1, the environmental, genotypic and phenotypic variances were 4.39, 118.52 and 122.91 respectively and the environmental, genotypic and phenotypic coefficients of variation were 2.39, 12.45 and 12.68 respectively. Under season 2, the environmental, genotypic and phenotypic variances were 4.62, 122.98 and 127.61 respectively and the environmental, genotypic and phenotypic coefficients of variation were 2.43, 12.55 and 12.78 respectively.

Number of basal tillers

Under season 1, the environmental, genotypic and phenotypic variances were 0.35, 0.78 and 1.14 respectively and the environmental, genotypic and phenotypic coefficients of variation were 11.48, 17.08 and 20.57 respectively. Under season 2, the environmental, genotypic and phenotypic variances were 0.08, 0.63 and 0.72 respectively and the environmental, genotypic and phenotypic coefficients of variation were 5.21, 14.45 and 15.36 respectively.

Productive tillers per plant

Under season 1, the environmental, genotypic and phenotypic variances were 0.02, 0.11 and 0.12 respectively and the environmental, genotypic and phenotypic coefficients of variation were 2.49, 17.45 and 17.63 respectively. Under season 2, the environmental, genotypic and phenotypic variances were 0.02, 0.06 and 0.08 respectively and the environmental, genotypic and phenotypic coefficients of variation were 7.62, 12.91 and 14.99 respectively.

1000 grain weight

Under season 1, the environmental, genotypic and phenotypic variances were 0.0036, 0.1904 and 0.1940 respectively and the environmental, genotypic and phenotypic coefficients of variation were 2.560, 18.650 and 18.825 respectively. Under season 2, the environmental, genotypic and phenotypic variances were 0.04, 0.13 and 0.18 respectively and the environmental, genotypic and phenotypic coefficients of variation were 9.32, 16.73 and 19.14 respectively.

Flag leaf blade length

Under season 1, the environmental, genotypic and phenotypic variances were 3.20, 28.04 and 31.25 respectively and the environmental, genotypic and phenotypic coefficients of variation were 5.62, 16.64 and 17.56 respectively. Under season 2, the environmental, genotypic and phenotypic variances were 4.33, 19.62 and 23.95 respectively and the environmental, genotypic and phenotypic coefficients of variation were 6.24, 13.30 and 14.69 respectively.

Flag leaf blade width

Under season 1, the environmental, genotypic and phenotypic variances were 0.02, 0.09 and 0.10 respectively and the environmental, genotypic and phenotypic coefficients of variation were 7.10, 16.77 and 18.21 respectively. Under season 2, the environmental, genotypic and phenotypic variances were 0.02, 0.03 and 0.05 respectively and the environmental, genotypic and phenotypic coefficients of variation were 7.90, 9.92 and 12.68 respectively.

Peduncle length

Under season 1, the environmental, genotypic and phenotypic variances were 1.82, 8.43 and 10.26 respectively and the environmental, genotypic and phenotypic coefficients of variation were 8.66, 18.63 and 20.55 respectively. Under season 2, the environmental, genotypic and phenotypic variances were 1.61, 4.98 and 6.60 respectively and the environmental, genotypic and phenotypic coefficients of variation were 8.09, 14.21 and 16.35 respectively.

The results showed that the magnitude of phenotypic components of variance were higher than the genotypic components of variance for all the characters. Further, the genotypic components of variance were higher than the environmental components of variance. The genotypic and phenotypic components of variances were close to each other for finger length, finger width ear length, productive tillers per plant, 1000 grain weight in season 1 and days to maturity and finger width in season 2. Lower values of the environmental variance were evinced for days to 50% flowering and days to maturity in season 1 and season 2. High GCV was obtained for grain yield while it was low for days to maturity. Similarly, high PCV was obtained for grain yield while it was low for days to maturity.

Table 4.7: Genotypic (GV), Phenotypic (PV) and Environmental (EV) Variance and Genotypic (GCV), Phenotypic (PCV) and Environmental (ECV) Coefficient of Variation for season 1

S.No.	Characters	GV	PV	EV	GCV	PCV	ECV
1.	Days to 50% flowering	36.97	39.90	2.92	7.90	8.20	2.22
2.	Days to maturity	27.07	28.14	1.06	4.59	4.68	0.91
3.	Finger length (cm)	0.50	0.54	0.04	12.77	13.29	3.66
4.	Finger width (cm)	0.01	0.08	0.02	13.42	13.59	2.13
5.	Ear length (cm)	1.50	1.56	0.06	13.31	13.60	2.79
6.	Fingers per ear	0.77	0.85	0.08	13.03	13.72	4.31
7.	Grain yield(tonnes/ha)	83115.47	93216.19	10100.71	33.76	35.75	11.77
8.	Plant height (cm)	118.52	122.91	4.39	12.45	12.68	2.39
9.	Number of basal tillers	0.78	1.14	0.35	17.08	20.57	11.48
10.	Productive tillers per plant	0.11	0.12	0.02	17.45	17.63	2.49
11.	1000 grain weight (g)	0.19	0.19	0.03	18.65	18.82	2.56
12.	Flag leaf blade length (cm)	28.04	31.25	3.20	16.64	17.56	5.62
13.	Flag leaf blade width(cm)	0.09	0.10	0.02	16.77	18.21	7.10
14.	Peduncle length(cm)	8.43	10.26	1.82	18.63	20.55	8.66

Table 4.8: Genotypic (GV), Phenotypic (PV) and Environmental (EV) Variance and Genotypic (GCV), Phenotypic (PCV) and Environmental (ECV) Coefficient of Variation for season 2

S.No.	Characters	GV	PV	EV	GCV	PCV	ECV
1.	Days to 50% flowering	37.62	44.09	6.47	7.90	8.55	3.27
2.	Days to maturity	31.03	31.96	0.92	4.90	4.97	0.84
3.	Finger length (cm)	0.48	0.53	0.04	11.83	12.37	3.61
4.	Finger width (cm)	0.05	0.07	0.02	11.33	13.18	6.74
5.	Ear length (cm)	1.36	1.46	0.01	12.75	13.19	3.41
6.	Fingers per ear	0.50	0.67	0.17	10.59	12.21	6.09
7.	Grain yield (tonnes/ha)	61856.30	71503.94	9647.63	27.84	29.93	10.99
8.	Plant height(cm)	122.98	127.61	4.62	12.55	12.78	2.43
9.	Number of basal tillers	0.63	0.72	0.08	14.45	15.36	5.21
10.	Productive tillers per plant	0.06	0.08	0.02	12.91	14.99	7.62
11.	1000 grain weight (g)	0.13	0.18	0.04	16.73	19.14	9.32
12.	Flag leaf blade length(cm)	19.62	23.95	4.33	13.30	14.69	6.24
13.	Flag leaf blade width (cm)	0.03	0.05	0.02	9.92	12.68	7.90
14.	Peduncle length (cm)	4.98	6.60	1.61	14.21	16.35	8.09

4.4 Estimation of heritability, genetic advance and genetic advance expressed as percentage of mean

The heritability in broad sense (h^2), Genetic advance (GA), along with the Genetic Advance expressed as percent of mean (GAM) for each trait under investigation has been presented in tables and experimental findings for each trait is presented below:

Days to 50% flowering

The heritability (h^2) was calculated as 92.68%, genetic advance was 12.05 and GAM was 15.67 for season 1. The heritability was calculated as 85.32%, genetic advance was 11.67 and GAM was 15.03 for season 2.

Days to maturity

The heritability (h^2) was calculated as 96.20%, genetic advance was 10.51 and GAM was 9.27 for season 1. The heritability was calculated as 97.10%, genetic advance was 11.30 and GAM was 9.95 for season 2.

Finger length

The heritability (h^2) was calculated as 92.38%, genetic advance was 1.40 and GAM was 25.29 for season 1. The heritability was calculated as 91.48%, genetic advance was 1.37 and GAM was 23.31 for season 2.

Finger width

The heritability (h^2) was calculated as 97.54%, genetic advance was 0.17 and GAM was 27.31 for season 1. The heritability was calculated as 73.80%, genetic advance was 0.13 and GAM was 20.04 for season 2

Ear length

The heritability (h^2) was calculated as 95.79%, genetic advance was 2.47 and GAM was 26.84 for season 1. The heritability was calculated as 93.32%, genetic advance was 2.32 and GAM was 25.36 for season 2.

Fingers per ear

The heritability (h^2) was calculated as 90.13%, genetic advance was 1.71 and GAM was 25.48 for season 1. The heritability was calculated as 75.10%, genetic advance was 1.27 and GAM was 18.89 for season 2.

Grain yield

The heritability (h^2) was calculated as 89.16%, genetic advance was 560.79 and GAM was 65.68 for season 1. The heritability was calculated as 86.51%, genetic advance was 476.52 and GAM was 53.34 for season 2.

Plant height

The heritability (h^2) was calculated as 96.43%, genetic advance was 22.022 and GAM was 25.20 for season 1. The heritability was calculated as 96.38%, genetic advance was 22.42 and GAM was 25.38 for season 2

No.of basal tillers

The heritability (h^2) was calculated as 68.89%, genetic advance was 1.51 and GAM was 29.20 for season 1. The heritability was calculated as 88.46%, genetic advance was 1.54 and GAM was 28.00 for season 2

Productive tillers per plant

The heritability (h^2) was calculated as 98.01%, genetic advance was 0.69 and GAM was 35.59 for season 1. The heritability was calculated as 74.12%, genetic advance was 0.43 and GAM was 22.89 for season 2

1000 grain weight

The heritability (h^2) was calculated as 98.15%, genetic advance was 0.89 and GAM was 38.06 for season 1. The heritability was calculated as 76.28%, genetic advance was 0.66 and GAM was 30.09 for season 2

Flag leaf blade length

The heritability (h^2) was calculated as 89.74%, genetic advance was 10.33 and GAM was 32.48 for season 1. The heritability was calculated as 81.92%, genetic advance was 8.25 and GAM was 24.78 for season 2.

Flag leaf blade width

The heritability (h^2) was calculated as 84.78%, genetic advance was 0.57 and GAM was 31.81 for season 1. The heritability was calculated as 61.17%, genetic advance was 0.28 and GAM was 15.98 for season 2.

Peduncle length

The heritability (h^2) was calculated as 82.21%, genetic advance was 5.42 and GAM was 34.80 for season 1. The heritability was calculated as 75.48%, genetic advance was 3.99 and GAM was 25.43 for season 2.

Table 4.9: Heritability (h^2), Genetic Advance (GA) and Genetic Advance as per cent of mean for season 1

S.No.	Characters	Heritability (%)	Genetic Advance	GA as % of Mean
1.	Days to 50% flowering	92.68	12.05	15.67
2.	Days to maturity	96.2	10.51	9.27
3.	Finger length(cm)	92.38	1.40	25.29
4.	Finger width(cm)	97.54	0.17	27.31
5.	Ear length(cm)	95.79	2.47	26.84
6.	Fingers per ear	90.13	1.71	25.48
7.	Grain yield(kg/ha)	89.16	560.79	65.68
8.	Plant height(cm)	96.43	22.02	25.20
9.	Number of basal tillers	68.89	1.51	29.20
10.	Productive tillers per plant	98.01	0.69	35.59
11.	1000 grain weight(g)	98.15	0.89	38.06
12.	Flag leaf blade length(cm)	89.74	10.33	32.48
13.	Flag leaf blade width(cm)	84.78	0.57	31.81
14.	Peduncle length(cm)	82.21	5.42	34.80

Table 4.10: Heritability (h^2), Genetic Advance (GA) and Genetic Advance as per cent of mean for season 2

S.No.	Characters	Heritability (h^2)	Genetic Advance	GA as % of Mean
1.	Days to 50% flowering	85.32	11.67	15.03
2.	Days to maturity	97.10	11.30	9.95
3.	Finger length(cm)	91.48	1.37	23.31
4.	Finger width(cm)	73.80	0.13	20.04
5.	Ear length(cm)	93.32	2.32	25.36
6.	Fingers per ear	75.10	1.27	18.89
8.	Grain yield(kg/ha)	86.51	476.52	53.34
9.	Plant height(cm)	96.38	22.42	25.38
10.	Number of basal tillers	88.46	1.54	28.00
11.	Productive tillers per plant	74.12	0.43	22.89
12.	1000 grain weight(g)	76.28	0.66	30.09
13.	Flag leaf blade length(cm)	81.92	8.25	24.78
14.	Flag leaf blade width(cm)	61.17	0.28	15.98
15.	Peduncle length(cm)	75.48	3.99	25.43

4.5 Correlation Analysis

Phenotypic Correlation Analysis

The different values of phenotypic correlation coefficient obtained for different traits have been categorized as per Searle (1965).

4.5.1 The estimates of genotypic correlation analysis for season 1 are given below

Days to 50% flowering

The trait days to 50% flowering showed strong positive correlation with days to maturity (0.9879), finger length (0.9052), finger width (0.8926), ear length (0.9157), fingers per ear (0.8918), plant height (0.9147), number of basal tillers (0.8346), productive tillers per plant (0.8764), 1000 grain weight (0.8396), flag leaf blade length (0.8376), flag leaf blade width (0.8354), peduncle length (0.8228) and grain yield (0.5637)

Days to maturity

The trait days to maturity showed strong positive correlation with finger length (0.9256), finger width (0.9090), ear length (0.9345), fingers per ear (9165), plant height (0.9281), number of basal tillers (0.8314), productive tillers per plant (0.8814), 1000 grain weight (0.8593), flag leaf blade length (0.8670), flag leaf blade width (0.8628), peduncle length (0.8387) and grain yield (0.5761)

Finger length

The trait finger length showed strong positive correlation with finger width (0.8993), ear length (0.8705), fingers per ear (0.8790), plant height (0.8677), number of basal tillers (0.7983), productive tillers per plant (0.8204), 1000 grain weight (0.8151), flag leaf blade length (0.8464), flag leaf blade width (0.8354), peduncle length (0.7936) and grain yield (0.5855)

Finger width

The trait finger width showed strong positive correlation with ear length (0.8672), fingers per ear (0.8619), plant height (0.8568), number of basal tillers (0.7742), productive tillers per plant (0.8239), 1000 grain weight (0.7949), flag leaf blade length (0.8234), flag leaf blade width (0.8106), peduncle length (0.7751) and grain yield (0.5919)

Ear length

The trait ear length showed strong positive correlation with fingers per ear (0.8727), plant height (0.8601), number of basal tillers (0.8015), productive tillers per plant (0.8319), 1000 grain weight (0.7835), flag leaf blade length (0.7792), flag leaf blade width (0.7659), peduncle length (0.7726) and grain yield (0.5126)

Fingers per ear

The trait fingers per ear showed strong positive correlation with plant height (0.8698), number of basal tillers (0.7986), productive tillers per plant (0.8157), 1000 grain weight (0.8401), flag leaf blade length (0.8522), flag leaf blade width (0.8335), peduncle length (0.8403) and grain yield (0.6036)

Plant height

The trait plant height showed strong positive correlation with number of basal tillers (0.8050), productive tillers per plant (0.8140), 1000 grain weight (0.8331), flag leaf blade length (0.8292), flag leaf blade width (0.8656), peduncle length (0.8060) and grain yield (0.5858).

Number of basal tillers

The trait number of basal tillers showed strong positive correlation with productive tillers per plant (0.8277), 1000 grain weight (0.7160), flag leaf blade length (0.7336), flag leaf blade width (0.6927),peduncle length (0.7314) and grain yield (0.5579).

Productive tillers per plant

The trait productive tillers per plant showed strong positive correlation with 1000 grain weight (0.7603), flag leaf blade length (0.7720), flag leaf blade width (0.7688), peduncle length (0.7656) and grain yield (0.5655)

1000 grain weight

The trait 1000 grain weight showed strong positive correlation with flag leaf blade length (0.9450), flag leaf blade width (0.8532), peduncle length (0.8451) and grain yield (0.7643)

Flag leaf blade length

The trait flag leaf blade length showed strong positive correlation with flag leaf blade width (0.8895), peduncle length (0.8486) and grain yield (0.7690)

Flag leaf blade width

The trait flag leaf blade width showed strong positive correlation with peduncle length (0.7783) and grain yield (0.6678)

Peduncle length

The trait peduncle length showed strong positive correlation with grain yield (0.7151).

4.5.2 The estimates of phenotypic correlation coefficient for season 2 are given below

Days to 50% flowering

The trait days to 50% flowering showed strong positive correlation with days to maturity (0.998), finger length (1.00), finger width (0.999), ear length (0.994), fingers per ear (0.977), plant height (0.998), number of basal tillers (0.947), productive tillers per plant (0.975), 1000 grain weight (0.996), flag leaf blade length (0.989), flag leaf blade width (0.964), peduncle length (0.992) and grain yield (0.899)

Days to maturity

The trait days to maturity showed strong positive correlation with finger length (0.999), finger width (0.998), ear length (0.997), fingers per ear (0.979), plant height (0.995), number of basal tillers (0.955), productive tillers per plant (0.978), 1000 grain weight (0.990), flag leaf blade length (0.984), flag leaf blade width (0.965), peduncle length (0.992) and grain yield (0.883).

Finger length

The trait finger length showed strong positive correlation with finger width (0.996), ear length (0.991), fingers per ear (0.969), plant height (0.986), number of basal tillers (0.933), productive tillers per plant (0.979),1000 grain weight (1.00), flag leaf blade length (1.00), flag leaf blade width (0.969), peduncle length (0.993) and grain yield (0.912).

Finger width

The trait finger width showed strong positive correlation with ear length (0.982), fingers per ear (1.00), plant height (1.00), number of basal tillers (0.942), productive tillers per plant (0.979), 1000 grain weight (0.989), flag leaf blade length (0.993), flag leaf blade width (0.986), peduncle length (0.981) and grain yield (0.954)

Ear length

The trait ear length showed strong positive correlation with fingers per ear (0.978), plant height (0.989), number of basal tillers (0.962), productive tillers per plant (0.981), 1000 grain weight (0.986), flag leaf blade length (0.964), flag leaf blade width (0.950), peduncle length (0.995) and grain yield (0.855)

Fingers per ear

The trait fingers per ear showed strong positive correlation with plant height (0.999), number of basal tillers (0.962), productive tillers per plant (0.969), 1000 grain weight (0.946), flag leaf blade length (0.954), flag leaf blade width (0.959), peduncle length (0.995) and grain yield (0.889)

Plant height

The trait plant height showed strong positive correlation with number of basal tillers (0.964), productive tillers per plant (0.979), 1000 grain weight (0.973), flag leaf blade length (0.983), flag leaf blade width (0.971), peduncle length (0.971) and grain yield (0.917).

Number of basal tillers

The trait number of basal tillers showed strong positive correlation with productive tillers per plant (0.983), 1000 grain weight (0.925), flag leaf blade length (0.924), flag leaf blade width (0.918),peduncle length (0.969) and grain yield (0.821).

Productive tillers per plant

The trait productive tillers per plant showed strong positive correlation with 1000 grain weight (0.978), flag leaf blade length (0.967), flag leaf blade width (0.926), peduncle length (0.982) and grain yield (0.904)

1000 grain weight

The trait 1000 grain weight showed strong positive correlation with flag leaf blade length (0.993), flag leaf blade width (0.946), peduncle length (0.982) and grain yield (0.897)

Flag leaf blade length

The trait flag leaf blade length showed strong positive correlation with flag leaf blade width (0.976), peduncle length (0.960) and grain yield (0.922)

Flag leaf blade width

The trait flag leaf blade width showed strong positive correlation with peduncle length (0.918) and grain yield (0.892)

Peduncle length

The trait peduncle length showed strong positive correlation with grain yield (0.843).

Table 4.11: Phenotypic Correlation Coefficient among different quantitative traits for season 1

Traits	DFE	DM	FL	FW	EL	FPE	PH	NBT	PTP	TGW	FLL	FLW	PL	GY
DFE		0.9879**	0.9052**	0.8926**	0.9157**	0.8918**	0.9147**	0.8346**	0.8764**	0.8396**	0.8376**	0.8354**	0.8228**	0.5637**
DM			0.9256**	0.9090**	0.9345**	0.9165**	0.9281**	0.8314**	0.8814**	0.8593**	0.8670**	0.8628**	0.8387**	0.5761**
FL				0.8993**	0.8705**	0.8790	0.8677**	0.7983**	0.8204**	0.8151**	0.8464**	0.8354**	0.7936**	0.5855**
FW					0.8672**	0.8619**	0.8568**	0.7742**	0.8239**	0.7949**	0.8234**	0.8106**	0.7751**	0.5919**
EL						0.8727**	0.8601**	0.8015**	0.8319**	0.7835**	0.7792**	0.7659**	0.7726**	0.5126**
FPE							0.8698**	0.7986**	0.8157**	0.8401**	0.8522**	0.8335**	0.8403**	0.6036**
PH								0.8050**	0.8140**	0.8331**	0.8292**	0.8656**	0.8060**	0.5858**
NBT									0.8277**	0.7160**	0.7336**	0.6927**	0.7314**	0.5579**
PTP										0.7603**	0.7720**	0.7688**	0.7656**	0.5655**
TGW											0.9450**	0.8532**	0.8451**	0.7643**
FLL												0.8895**	0.8486**	0.7690**
FLW													0.7783**	0.6678**
PL														0.7151**

**significant at α=0.01

Table 4.12: Phenotypic Correlation Coefficient among different quantitative traits for season 2

Traits	**DFE**	**DM**	**FL**	**FW**	**EL**	**FPE**	**PH**	**NBT**	**PTP**	**TGW**	**FLL**	**FLW**	**PL**	**GY**
DFE		0.9879**	0.9052**	0.8926**	0.9157**	0.8917**	0.9117**	0.8603**	0.9005**	0.8421**	0.8931**	0.8827**	0.8805**	0.6370**
DM			0.9256**	0.9090**	0.9345**	0.9164**	0.9301**	0.8833**	0.9115**	0.8501**	0.9034**	0.9039**	0.8913**	0.6397**
FL				0.8993**	0.8705**	0.8790**	0.8660**	0.8320**	0.8435**	0.8180**	0.8660**	0.8705**	0.8683**	0.6263**
FW					0.8672**	0.8619**	0.8664**	0.8236**	0.8440**	0.8231**	0.8643**	0.8581**	0.8316**	0.6621**
EL						0.8726**	0.8792**	0.8299**	0.8662**	0.7677**	0.8024**	0.8220**	0.8382**	0.5682**
FPE							0.8857**	0.8473**	0.8511**	0.8029**	0.8594**	0.8778**	0.8308**	0.6430**
PH								0.8439**	0.8597**	0.8148**	0.8537**	0.8710**	0.8454**	0.6401**
NBT									0.8531**	0.7647**	0.8002**	0.7942**	0.7989**	0.6113**
PTP										0.7985**	0.8380**	0.8397**	0.8294**	0.6337**
TGW											0.9192**	0.8388**	0.8404**	0.7816**
FLL												0.9085**	0.8437**	0.7489**
FLW													0.8080**	0.6992**
PL														0.6568**

**significant at α=0.01

4.6 Path Coefficient Analysis

The direct and indirect effects of quantitative characters on grain yield estimated by path coefficient analysis using simple correlations are given. The values of path coefficients have been categorized as per Lenka and Mishra (1973).

4.6.1 The results of path analysis for season 1 have been described as follows

Days to 50% flowering

The trait days to 50% flowering exerted a negative direct effect on grain yield (-6.5889) and the trait showed no positive indirect effects on grain yield.

Days to maturity

The trait days to maturity exerted a direct effect on grain yield (4.4968) and the trait exerted positive indirect effect through days to 50% flowering (4.4804) finger length (4.4862), finger width(4.4862), ear length (4.4954), fingers per ear (4.4805), plant height (4.4461), no. of basal tillers (4.2587), productive tillers per plant (4.4483), 1000 grain weight (4.4815),flag leaf blade length (4.3369), flag leaf blade width (4.3537) and peduncle length (4.4899).

Finger length

The trait finger length exerted a direct effect on grain yield(0.8628) and the trait exerted positive indirect effect through days to 50% flowering (0.8522), days to maturity (0.8608), finger width (0.8599),fingers per ear (0.8589), ear length (0.8558), plant height (0.8433), no .of basal tillers (0.7881), productive tillers per plant (0.8539), 1000 grain weight (0.8594), flag leaf blade length (0.8483), flag leaf blade width (0.8534) and peduncle length (0.8671) .

Finger width

The trait finger width exerted a negative direct effect on grain yield (-0.4167) and the traits showed no positive indirect effects on grain yield.

Ear length

The trait ear length exerted a negative direct effect on grain yield (-1.7524) and the traits showed no positive indirect effects on grain yield

Fingers per ear

The trait fingers per ear exerted a positive direct effect on grain yield (1.4416) and the trait exerted positive indirect effect through days to 50% flowering (1.4301), days to maturity (1.4418), finger length (1.4351), finger width (1.4561), ear length

(1.423), plant height (1.4465), no. of basal tillers (1.3642), productive tillers per plant (1.4323), 1000 grain weight (1.4624), flag leaf blade length (1.4115), flag leaf blade width (1.4304) and peduncle length (1.4318).

Plant height

The trait plant height exerted a negative direct effect on grain yield (-2.6068) and the traits showed no positive indirect effects on grain yield.

Number of basal tillers

The trait number of basal tillers exerted a positive direct effect on grain yield (1.6766) and the trait exerted positive indirect effect through days to 50% flowering (1.6176), days to maturity (1.5879), finger length (1.5314), finger width (1.5480), ear length (1.5303), plant height (1.6166), productive tillers per plant (1.6455), 1000 grain weight (1.5494), flag leaf blade length (1.5045), flag leaf blade width (1.5135) and peduncle length (1.6668)

Productive tillers per plant

The trait productive tillers per plant exerted a positive direct effect on grain yield (0.3265) and the trait exerted positive indirect effect through days to 50% flowering (0.3232), days to maturity (0.3230), finger length (0.3232), finger width (0.3252), ear length (0.3196), fingers per ear (0.3244), plant height (0.3210), no. of basal tillers (0.3205), 1000 grain weight (0.3236), flag leaf blade length (0.3166), flag leaf blade width (0.3123) and peduncle length (0.3339).

1000 grain weight

The trait 1000 grain weight exerted a positive direct effect on grain yield (1.1591) and the trait exerted a positive indirect effect through days to 50% flowering (1.1401), days to maturity (1.1552), finger length (1.1545), finger width (1.1851), ear length (1.1412), fingers per ear (1.1758), plant height (1.1470), no. of basal tillers (1.0711), productive tillers per plant (1.1487), flag leaf blade length (1.1311), flag leaf blade width (1.1212) and peduncle length (1.1311)

Flag leaf blade length

The trait flag leaf blade length exerted a negative direct effect on grain yield (-1.8351) and the traits showed no positive indirect effects on grain yield.

Flag leaf blade width

The trait flag leaf blade width exerted a positive direct effect on grain yield (2.8054) and the trait exerted a positive indirect effect through days to 50% flowering (2.6866), days to maturity (2.7162), finger length (2.7748), finger width (2.7863), ear length (2.7075), fingers per ear (2.7835), plant height (2.7357), no .of basal tillers (2.5325), productive tillers per plant (2.6833), 1000 grain weight (2.7137), flag leaf blade length (2.7293) and peduncle length (2.7004)

Peduncle length

The trait peduncle length exerted a positive direct effect on grain yield (1.4694) and the traits exerted a positive indirect effect through days to 50% flowering (1.4623), days to maturity (1.4671), finger length (1.4766), finger width (1.4677), ear length (1.4466), fingers per ear (1.4593), plant height (1.4559), no .of basal tillers (1.4608), productive tillers per plant (1.5025), 1000 grain weight (1.4338), flag leaf blade length (1.4359) and flag leaf blade width (1.4143).

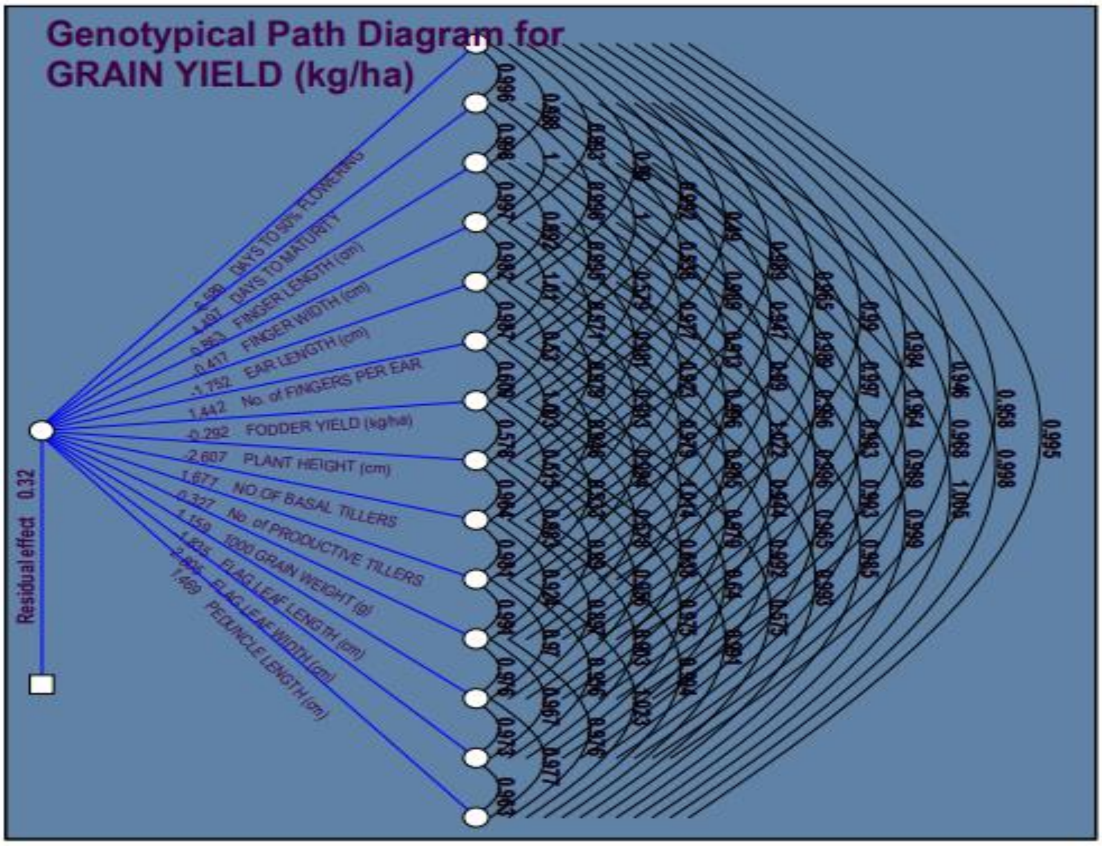

Fig 2: Genotypic Path Diagram for Season 1

4.6.2 The results of path analysis for season 2 have been described as follows

Days to 50% flowering

The trait days to 50% flowering exerted a positive direct effect on grain yield (3.7192) and the trait showed positive indirect effect through days to maturity (3.7149), finger length (3.7378),finger width (3.7161), ear length (3.6993), fingers per ear (3.6360), plant height (3.7124), no . of basal tillers (3.5239), productive tillers per plant (3.6290), 1000 grain weight (3.7046), flag leaf blade length (3.6812), flag leaf blade width (3.5881) and peduncle length (3.6923).

Days to maturity

The trait days to maturity exerted a negative direct effect on grain yield (-14.9880) and the trait showed no positive indirect effect on grain yield.

Finger length

The trait finger length exerted a direct effect on grain yield (4.0999) and the trait exerted positive indirect effect through days to 50% flowering (4.1204), days to maturity (4.0978), finger width (4.0867), fingers per ear (3.9726), ear length (4.0669), plant height (4.0446), no. of basal tillers (3.8259), productive tillers per plant (4.0162), 1000 grain weight (4.1619), flag leaf blade length (4.1041), flag leaf blade width (3.9765) and peduncle length (4.0710) .

Finger width

The trait finger width exerted a positive direct effect on grain yield (3.5809) and the traits showed positive indirect effect through days to 50% flowering (3.5779), days to maturity (3.5745), finger length (3.5694), ear length (3.5257), fingers per ear (3.5879), plant height (3.5927), no. of basal tillers (3.3731), productive tillers per plant (3.5027), 1000 grain weight (3.5437), flag leaf blade length (3.5592), flag leaf blade width (3.5317) and peduncle length (3.5157)

Ear length

The trait ear length exerted a negative direct effect on grain yield (-1.5169) and the traits showed no positive indirect effects on grain yield

Fingers per ear

The trait fingers per ear exerted a positive direct effect on grain yield (5.3785) and the trait exerted positive indirect effect through days to 50% flowering (5.2581), days to maturity (5.2682), finger length (5.2115), finger width (5.3890), ear length (5.2611), plant height (5.3780), no. of basal tillers (5.1762), productive tillers per plant (5.2127), 1000 grain weight (5.0890), flag leaf blade length (5.1362), flag leaf blade width (5.1598) and peduncle length (5.1536).

Plant height

The trait plant height exerted a negative direct effect on grain yield (-8.6003) and the traits showed no positive indirect effects on grain yield.

Number of basal tillers

The trait number of basal tillers exerted a positive direct effect on grain yield (1.6706) and the trait exerted positive indirect effect through days to 50% flowering (1.5828), days to maturity (1.5962), finger length (1.5589), finger width (1.5736), ear length (1.6083), fingers per ear (1.6078), plant height (1.6107), productive tillers per plant (1.6427), 1000 grain weight (1.5462), flag leaf blade length (1.5448), flag leaf blade width (1.5344) and peduncle length (1.6199)

Productive tillers per plant

The trait productive tillers per plant exerted a negative indirect effect on grain yield (-0.9592) and the traits showed no positive indirect effect on grain yield.

1000 grain weight

The trait 1000 grain weight exerted a positive direct effect on grain yield (1.2391) and the trait exerted a positive indirect effect through days to 50% flowering (1.2342), days to maturity (1.2272), finger length (1.2578), finger width (1.2262), ear length (1.2218), fingers per ear (1.1724), plant height (1.2066), no. of basal tillers (1.1468), productive tillers per plant (1.2130), flag leaf blade length (1.2304), flag leaf blade width (1.1731) and peduncle length (1.2178)

Flag leaf blade length

The trait flag leaf blade length exerted a negative direct effect on grain yield (-2.2432) and the traits showed no positive indirect effects on grain yield.

Flag leaf blade width

The trait flag leaf blade width exerted a positive direct effect on grain yield (6.6428) and the trait exerted a positive indirect effect through days to 50% flowering (6.4086), days to maturity (6.4119), finger length (6.4430), finger width (6.5516), ear length (6.3137), fingers per ear (6.3728), plant height (6.4543), no .of basal tillers (6.1015), productive tillers per plant (6.1518), 1000 grain weight (6.2891), flag leaf blade length (6.4884) and peduncle length (6.1041)

Peduncle length

The trait peduncle length exerted a positive direct effect on grain yield (4.4675) and the traits exerted a positive indirect effect through days to 50% flowering (4.4351), days to maturity (4.4345), finger length (4.4360), finger width (4.3861), ear length (4.4466), fingers per ear (4.2806), plant height (4.3420), no .of basal tillers (4.3320), productive tillers per plant (4.3890), 1000 grain weight (4.3909), flag leaf blade length (4.2893) and flag leaf blade width (4.1052).

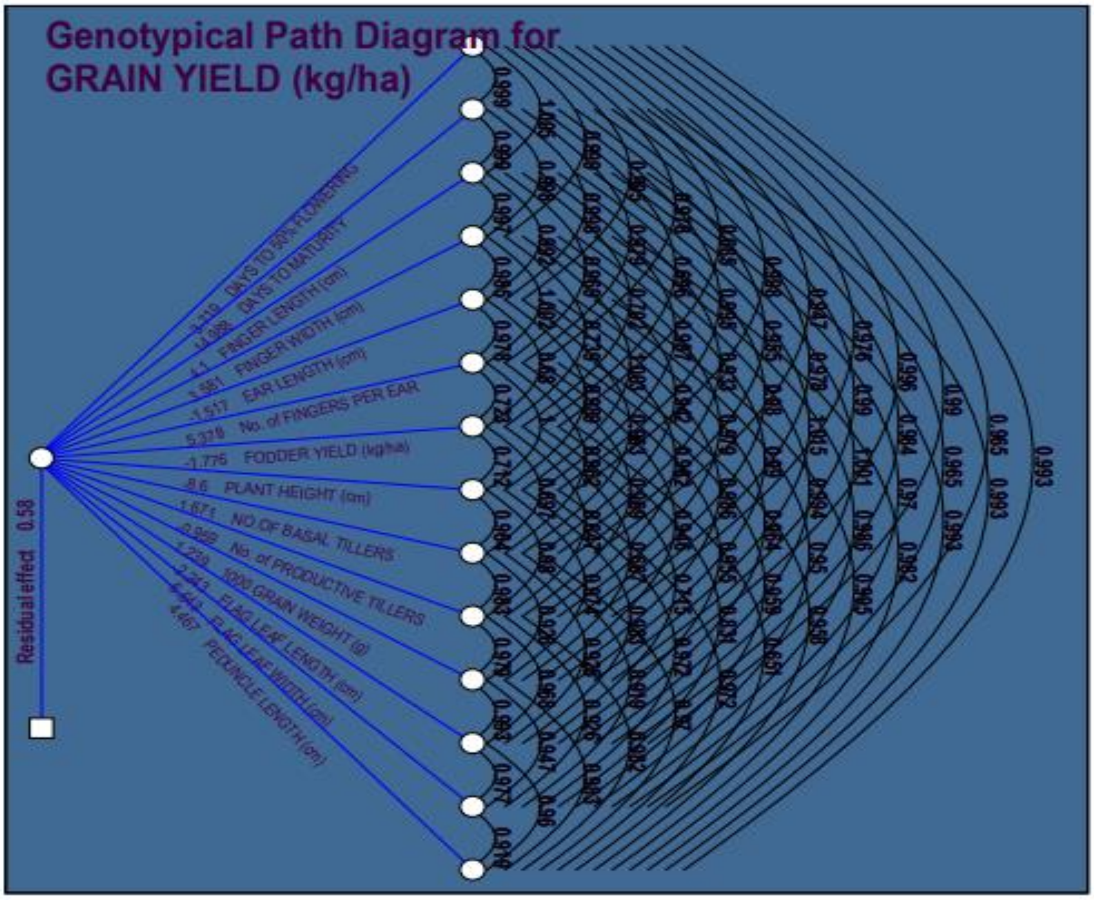

Fig.3 : Genotypic Path Diagram for Season 2

4.7 Mean Performance of finger millet genotypes in two seasons

Mean performance of finger millet genotypes for traits such as ear length, fingers per ear, grain yield, productive tillers per plant and 1000 grain weight has been depicted on Appendix I for season 1 and Appendix II for season 2.

Ear length

Genotypes G94, G112, G46, G58 and G93 in season 1 and G101, G132, G139 and G118 in season 2 showed a higher value for ear length and outperformed the check varieties.

Fingers per ear

Genotypes G10, G21, G24, G108 and G114 in season 1 and G86, G108, G107, G49 and G29 in season 2 outperformed the check varieties with higher value for fingers per ear.

Grain yield

In both season 1 and season 2, no genotypes have outperformed the check varieties for grain yield.

Productive tillers per plant

In season 1, no genotypes outperformed the check varieties but G108, G19, G82 and G98 showed comparable values for the trait. In season 2, G126, G77, G76 and G106 outperformed the check varieties.

1000 grain weight

In season 1, G34, G129, G11 and G86 and in season 2, G129, G87, G78, G74 and G130 showed a better performance comparing to check varieties.

4.8 Qualitative Traits

The data recorded for the qualitative traits of finger millet has been depicted on Appendix III

Plant growth habit

The check varieties namely RAU-8 and GPU-67 showed erect form of plant growth habit whereas decumbent type was shown by GPU-67. Among the germplasm, erect type of growth habit is shown by 120 genotypes whereas decumbent type of growth habit is shown by nine genotypes and one genotype(RAU-FM-Sheohar-2010-4) showed prostrate type of growth habit.

Ear shape

In the field, fist type of ear head is shown by 13 genotypes. 45 genotypes showed compact ear shape. Semi-compact type of ear shape is shown by 34 genotypes whereas 28 genotypes showed open ear shape. The check varieties RAU-8, GPU-67 and VL-376 showed semi-compact type of ear shape.

Finger Multiple Whorl

Finger multiple whorl is observed to be absent for all check varieties whereas among germplasm, multiple whorls of fingers are present in 21 genotypes and it is absent in 99 genotypes.

Finger Branching

In the field, the trait is found to be absent in check varieties. Only 11 genotypes showed finger branching whereas it is absent for 109 genotypes.

Position of Finger Branching

In the field, 11 genotypes showed presence of finger branching in thumb fingers whereas other genotypes including checks showed no finger branching.

Seed Colour

Among the checks, RAU-8 seeds dark brown in colour and seeds of GPU-67 and VL-376 are copper brown in colour. White seeds are produced by 5 genotypes, 14 genotypes produced light brown seeds, 52 genotypes produced copper brown coloured seeds and dark brown coloured seeds are produced by 49 genotypes.

Seed Shape

All the genotypes including checks produced round shaped seeds.

Glume Colour

In the field, white coloured glume colour is seen in 3 finger millet genotypes whereas 16 genotypes showed light green, 93 genotypes showed dark green and 8 genotypes showed light purple glume colour. All the check varieties RAU-8, GPU-67 and VL-376 showed dark green glume colour.

Stem Culm Branching

Stem culm branching is found to be absent in check variety RAU-8 whereas it is present in both the other two check varieties GPU-67 and VL-376. Stem culm branching is present in 40 genotypes in the field and the trait is absent in 80 genotypes.

Seed Shattering

Seed shattering is present in check variety GPU-67 whereas the trait is absent in other check varieties RAU-8 and VL-376. Among the germplasm, 111 genotypes showed no seed shattering and the trait is present in 9 genotypes.

Pericarp Persistence after Threshing

Pericarp is persistent in 82 genotypes and it is absent in 38 genotypes after threshing. Among the check varieties, pericarp is persistent in RAU-8 and GPU-67 whereas it is absent for VL-376.

EVALUATION OF FINGER MILLET GERMPLASM FOR SEED PHYSIOLOGICAL TRAITS IN SUMMER SEASONS

For analysing seed physiological traits, seeds of 144 genotypes were sown and G144 failed to germinate.

Seed Vigour Index I

Seed Vigour Index I of given genotypes were computed using parameters such as seed germination percentage and seedling length. Significant differences were noted among the genotypes. The values of seed vigour index ranged from 50.5(RAU-FM-139) to 987.0(RAU-FM-Sheohar-2009-19). The check varieties such as RAU-8, GPU-67 and VL-376 showed seed vigour index of 840.0, 945.5 and 895.0 respectively. Genotypes such as RAU-FM-Sheohar-2009-19, RAU-FM-Madhubhani-2009-4, RAU-FM-Sheohar-2009-9and RAU-FM-Sheohar-2010-3 outperformed the check varieties and recorded the values of 987.0,977.5,964.9 and 954.0 respectively. Genotype RAU-FM-139 (50.5) recorded the lowest value for seed vigour index 1 followed by RAU-FM-Madhubhani-2009-5(100.1) and RAU-FM-Madhubhani-2010-

1(107.8). Based on the values, the genotypes were grouped under low, medium and high seed vigour indices. Low seed vigour index ranged from 50.0 to 400.0 and eleven genotypes came under this category. Seventy genotypes are grouped under medium seed vigour index which ranged from 401.0 to 700.0 and sixty-two genotypes under the category of high seed vigour index which ranged from 701.0 to 987.0.

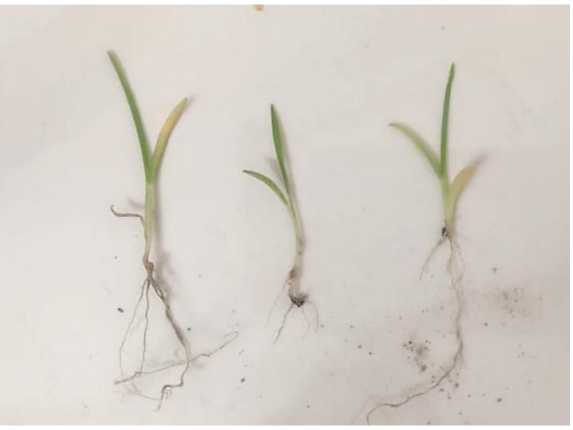

Fig 4: Genotypes showing higher seed vigour index I

Seed Vigour Index II

Seed Vigour Index II was calculated using the parameters such as seed germination percentage and seedling dry weight. Genotypes showed a wide range of values for seed vigour index II. The values ranged from 0.046 (RAU-FM-139) to 1.271 (RAU-FM-83). The check varieties such as RAU-8, GPU-67 and VL-376 showed values of 0.938, 0.945 and 0.866 respectively. Genotypes such as RAU-FM-83, RAU-FM- Gopalganj-2009-5,RAU-FM-126, RAU-FM-Kanti-2010-4, RAU-FM-93 and RAU-FM-98 showed better performance compared to check varieties with values of 1.271, 1.144, 1.004, 0.977, 0.960 and 0.949 respectively. The lowest value of seed vigour index II was shown by genotype RAU-FM-139(0.046) followed by RAU-FM-Madhubhani-2010-1(0.186), RAU-FM-Madhubhani-2009-5(0.204) and RAU-FM-135(0.210) respectively. The genotypes are grouped into three categories based on the values such as low, medium and high seed vigour indices. Low seed vigour index II category ranged from 0.046 to 0.400 in which twelve genotypes were recorded. Seventy-two genotypes came under medium seed vigour index which ranged from 0.401 to 0.700 and high seed vigour index ranged from 0.700 to 1.271 under which fifty-nine genotypes were present.

Seed Germination Percentage

Seed germination percentage indicates the number of viable seeds present in a seed lot. All the three check varieties (RAU-8, GPU-376 and VL-376) showed 100% germination percentage. Thirty-five genotypes also showed 100% germination. The least seed germination percentage was 15% which was shown by two genotypes, RAU-FM-Madhubhani-2010-1 and RAU-FM-139. Based on the values, genotypes were grouped as those with low (15-45%), medium(46-80%) and high(81-100%) seed germination percentage. Nine genotypes showed low seed germination percentage whereas twenty-six genotypes and ninety-seven genotypes were grouped under medium and high seed germination percentage respectively.

Seedling Length

Genotypes showed significant variation in their mean seedling length. The check varieties RAU-8 showed a seedling length of 8.40 cm whereas a length of 9.45 cm and 8.95 cm were recorded for GPU-67 and VL-376, respectively. Genotype RAU-FM-139 (3.27 cm) recorded the lowest value followed by genotype RAU-FM-Madhubhani-2009-5 (4.00 cm). Genotypes which outperformed the check varieties included RAU-FM-Sheohar-2009-11 (11.95 cm), RAU-FM-Sheohar-2009-9 (11.38 cm), RAU-FM-Sheohar-2009-14 (11.04 cm), RAU-FM-Sheohar-2009-19 (10.96 cm), RAU-FM-Sheohar-2009-10 (9.94 cm), RAU-FM-Sheohar-2010-4 (9.93 cm), RAU-FM-119 (9.91 cm), RAU-FM-Madhubhani-2009-4 (9.77 cm), RAU-FM-Madhubhani-2010-7 (9.72 cm), RAU-FM-Sheohar-2009-8 (9.70 cm), RAU-FM-Sheohar-2009-15 (9.64 cm), RAU-FM-Madhubhani-2009-19 (9.59 cm), RAU-FM-Madhubhani-2009-20 (9.58 cm), RAU-FM-Madhubhani-2009-21 (9.57 cm), RAU-FM-Sheohar-2010-3 (9.54 cm) and RAU-FM-Sheohar-2009-13 (9.49 cm). The recorded values of mean seedling length for genotypes ranged from 3.27 cm (RAU-FM-139) to 11.95 cm (RAU-FM-Sheohar-2009-11) which when grouped as low (3.00-6.00 cm), medium (6.01-9.00 cm) and high (9.01-12.00 cm) included eleven, one hundred two and thirty genotypes in each group respectively.

Chlorophyll Content (SPAD value)

Soil Plant Analysis Development (SPAD) value provides the greenness or relative chlorophyll content of the leaves. The values recorded for chlorophyll content varied from 1.6 to 19.1 shown by genotypes RAU-FM-Sheohar-2009-3 and RAU-

FM-Sheohar-2009-7 respectively. The check varieties RAU-8, GPU-67 and VL-376 showed values of 12.8, 9.9 and 9.8 respectively. The varieties which outperformed the check varieties are RAU-FM-Sheohar-2009-7 (19.1), RAU-FM-Sheohar-2010-9 (18.4), RAU-FM-Gopalganj-2009-1 (16.4), RAU-FM-Sheohar-2010-4 (15.9), RAU-FM-130 (15.7), RAU-FM-126 (15.2), RAU-FM-128 (15.2), RAU-FM-Madhubhani-2009-24 (15.1), RAU-FM-Sheohar-2009-9(14.7), RAU-FM-109 (14.2), RAU-FM-136 (14.2), RAU-FM-Sheohar-2009-15 (14.1), RAU-FM-Madhubhani-2009-4 (14.1), RAU-FM-106 (13.4), RAU-FM-Madhubhani-2010-5 (13.4), RAU-FM-142 (13.3) and RAU-FM-131 (13.1). Some varieties such as RAU-FM-Sheohar-2009-3 (1.6) and RAU-FM-111 (3.0) showed low SPAD value. The genotypes can be grouped based on values as low (1.0-9.5), medium (9.6-15.5) and high (15.6-20.0) SPAD value. Eighty-four genotypes were grouped under low SPAD value category whereas fifty four and five genotypes showed medium and high SPAD values respectively.

Speed of Germination

Speed of germination expresses the rate of germination in terms of the total number of seeds that germinate in a given interval of time. Higher values indicate greater and faster germination. The values recorded for each genotypes showed a nominal variation. The check varieties RAU-8, GPU-67 and VL-376 recorded values of 3.20, 3.20 and 3.33, respectively. Among the genotypes, the values varied from 0.41 to 3.33. The varieties that exhibited a comparable performance to check varieties with recorded mean speed of germination value of 3.33 included RAU-FM-82, RAU-FM-100, RAU-FM-104 and RAU-FM-118. Genotype RAU-FM-Madhubhani-2010-1 showed least value of 0.41 for mean speed of germination followed by RAU-FM-139 (0.45) and RAU-FM-Madhubhani-2009-5 (0.55). Based on the values obtained, genotypes are grouped for low (0.10-1.50), medium (1.51-2.50) and high (2.51-3.50) mean speed of germination. Fourteen genotypes were grouped under low speed of germination whereas fifty-four genotypes and seventy five genotypes were grouped under medium and high speed of germination.

Table 4.13 : Variability for seed physiological traits

S.No	Characters	Mean± S.E.	Range		C.V
			Min.	Max.	
1.	Seed Vigour Index I	659.08±15.0	50.5	987	27.18
2.	Seed Vigour Index II	0.66±0.02	0.046	1.271	30.40
3.	Seed Germination %	84.01±1.6	15	100	22.25
4.	Seedling Length	7.83±0.12	3.27	11.95	17.70
5.	Chlorophyll Content	9.0±0.3	1.6	19.1	33.68
6.	Speed of Germination	2.43±1.6	0.41	3.33	27.36

4.9 Correlation Analysis

The estimate of correlation coefficient among different characters has been given in table 1

Significant positive correlation was shown by seed vigour index I with seed vigour index II (0.271) and seed germination percent (0.806); seed vigour index II with speed of germination (0.202); seedling length with chlorophyll content (0.642) and speed of germination (0.966); chlorophyll content with speed of germination (0.558).

Non-significant correlation was shown by seed vigour index I with seedling length (-0.079), chlorophyll content (-0.046) and speed of germination (-0.055); seed vigour index II with seed germination percent (0.059), seedling length (0.067) and chlorophyll content (0.047); seed germination percent with seedling length (0.102). chlorophyll content (-0.07) and speed of germination (0.116).

Table 4.14: Correlation coefficient among seed physiological traits

Characters	Seed vigour index I	Seed vigour index II	Seed germination %	Seedling length	Chlorophyll content	Speed of germination
Seed vigour index I		0.271***	0.806***	-0.079	-0.046	-0.055
Seed vigour index II			0.059	0.067	0.047	0.202***
Seed germination %				0.102	-0.07	0.116
Seedling length					0.642***	0.966***
Chlorophyll content						0.558***

*****significant at 0.001 level**

ROLE OF GENOTYPE X ENVIRONMENT INTERACTIONS IN THE EXPRESSION OF VARIOUS MORPHOLOGICAL CHARACTERS AND STABILITY OF GENOTYPES IN SUMMER SEASONS

4.10 GGE Biplot

The GGE-biplot graphically represents the relationship between genotypes, environments, GxE interactions and used for identification of stable genotypes in this study. The effects of Genotype and Genotype x Environment and Environment components on yield and yield contributing traits were studied to determine the best performing genotypes for the selected environment. The performance of genotypes in two different seasons with regard to yield and yield contributing traits were analysed using GGE Biplot model in which the genotypes' behaviour with respect to environment were divided into the IPCA1 and IPCA2 axes.

4.11.1 Ear length

What -won – where pattern of GGE biplot

Polygon view of GGE Biplot evaluated the performance of 144 genotypes in two different seasons. In fig. 3A, the genotypes were grouped into 8 sectors;(I, II, III, IV, V, VI, VII and VII). Season 1 was located in sector VI and season 2 was located in sector V. The genotypes located in the vertices of polygon performed better compared to others with respect to that particular environment belonging to the sector. In the study, G21, G48, G72, G76, G96, G112 and G116 genotypes were located on the vertices of the polygon. Among them, G76 won in season 2 and in season 1, G112 was the best performer. There were outstanding performers in other sectors such as G21 in sector I, G48 in sector IV, G72in sector VII but no environment was included in these groups. Some genotypes fell into these groups but these genotypes could not be recommended for any of the seasons taken into consideration. The generated biplot in the study revealed 100% (PC1= 88.44%, PC2=11.56%) of the total GGE variation, which significantly explained environment centred data and increased the model's ability for predicting the stability of finger millet genotypes across the environments.

Stability of finger millet genotypes based on GGE biplot

The best performing genotype is shown(fig. 3B) in the concentric circle and the graph showed G132 with maximum value for ear length and have G76, G139, G140, G61 and other genotypes located in a circular pattern away from the centre. The ranking of genotypes can be done as G132>G76>G139>G140>G61 in terms of ear length. As G76 performed well in season 1 and 2, this genotype can be selected for ear length in breeding programmes.

Evaluation of environment based on biplot

The evaluation for environment for ear length clearly depicts the ideal test environment as the centre of the concentric circles on the graph(fig. 3C) and as a point on the Average Environment coordinate Axis (AEA) facing upwards with a distance from the GGE biplot origin equal to the longest vector of all environments. According to the graph, season 1 and season 2 are located at a significant distance from the concentric point indicating that they are distant from features of an ideal environment.

4.11.2 Fingers per ear

What -won – where pattern of GGE biplot

Polygon view of GGE Biplot evaluated the performance of 144 genotypes in two different seasons. In fig. 4A, the genotypes were grouped into 6 sectors;(I, II, III, IV, V and VI). Season 1 was located in sector III and Season 2 was located in sector IV. The genotypes located in the vertices of polygon performed better compared to others with respect to that particular environment belonging to the sector. In the study, G10, G14, G19, G63, G67 and G113 genotypes were located on the vertices of the polygon. Among them, G14 won season 1 and G10 in season 2. There were outstanding performers in other sectors such as G63 in sector I and G19 in sector II but no environment was included in these groups. Some genotypes fell into these groups but these genotypes could not be recommended for any of the seasons taken into consideration. The generated biplot in the study revealed 100% (PC1= 84.64%, PC2=15.36%) of the total GGE variation, which significantly explained environment centred data and increased the model’s ability for predicting the stability of finger millet genotypes across the environments.

Stability of finger millet genotypes based on GGE biplot

The best genotype present inside the circle(fig.4B) is G14 having maximum value for fingers per ear followed by other genotypes such as G48, G107, G24, G71 and G114 which are closer to G14 comparing to other genotypes. So, the ranking can be made as G14>G48>G107>G24>G71>G114 in terms of stability to fingers per ear. G14 can be selected for fingers per ear for breeding programmes as it performed well in season 1 and season 2.

Evaluation of environment based on biplot

The evaluation for environment for fingers per ear clearly depicts the ideal test environment as the center of the concentric circles on the graph(fig.4C) and as a point on the Average Environment coordinate Axis (AEA) facing upwards with a distance from the GGE biplot origin equal to the longest vector of all environments. According to the graph, season 1 and season 2 are equi-distant from the concentric point showing that they are not in proximity to an optimal environment

4.11.3 Grain yield

What -won – where pattern of GGE biplot

Polygon view of GGE Biplot evaluated the performance of 144 genotypes in two different seasons. In fig. 5A, the genotypes were grouped into 5 sectors;(I, II, III, IV and V). Season 1 was located in sector I and season 2 was located in sector II. The genotypes located in the vertices of polygon performed better compared to others with respect to that particular environment belonging to the sector. In the study, check1, check2, check 3, G26, G27 and G117 genotypes were located on the vertices of the polygon. Among them, check1, 2 and 3 won season 1 and in season 2, no genotype was included. There were outstanding performers in other sectors such as G117 in sector IV and G27 in sector V but no environment was included in these groups. Some genotypes fell into these groups but these genotypes could not be recommended for any of the seasons taken into consideration. The generated biplot in the study revealed 100% (PC1= 97.04%, PC2=2.96%) of the total GGE variation, which significantly explained environment centred data and increased the model's ability for predicting the stability of finger millet genotypes across the environments.

Stability of finger millet genotypes based on GGE biplot

The best performing genotypes present inside the concentric circles(fig.5B) were check-1(RAU-8), check-2(GPU-67) and check-3(VL-376) and other genotypes are far from them. This depicts that the check varieties showed stable performance as well as highest value for grain yield. The ranking can be made as check-1=check-

3>check-2>G67>G34 in terms of stability to grain yield. Though no genotype outperformed the check varieties, G67 exhibited a comparable performance to check varieties and hence this genotype can be evaluated for more summer seasons.

Evaluation of environment based on biplot

The evaluation for environment for grain yield clearly depicts the ideal test environment as the center of the concentric circles on the graph(fig.5C) and as a point on the Average Environment coordinate Axis (AEA) facing upwards with a distance from the GGE biplot origin equal to the longest vector of all environments. According to the graph, season 1 and season 2 are located at a significant distance from the concentric point indicating that they are distant from features of an ideal environment.

4.11.4 Productive tillers per plant

What -won – where pattern of GGE biplot

Polygon view of GGE Biplot evaluated the performance of 144 genotypes in two different seasons. In fig. 6A, the genotypes were grouped into 8 sectors;(I, II, III, IV, V, VI, VII and VII). Season 2 was located in sector III and season 1 was located in sector V. The genotypes located in the vertices of polygon performed better compared to others with respect to that particular environment belonging to the sector. In the study, G8, G15, G20, G67, G108, G114 and G126 genotypes were located on the vertices of the polygon. Among them, G126 won season 2 and in season 1, G114 was the best performer. There were outstanding performers in other sectors such as G20 in sector II, G8 and G108 in sector VI but no environment was included in these groups. Some genotypes fell into these groups but these genotypes could not be recommended for any of the seasons taken into consideration. The generated biplot in the study revealed 100% (PC1= 79.54%, PC2=20.46%) of the total GGE variation, which significantly explained environment centred data and increased the model's ability for predicting the stability of finger millet genotypes across the environments.

Stability of finger millet genotypes based on GGE biplot

The best performing genotype was G114 with maximum number of productive tillers per plant (fig.6B). Other genotypes which showed a comparable performance to G114 was presented in the concentric circles. In terms of stability to productive tillers per plant, the ranking of genotypes can be made as G114>G93>G67>G70>check-2.

In both seasons, G114 outperformed the check varieties and hence this genotype can be used for breeding programmes in future.

Evaluation of environment based on biplot

The evaluation for environment for productive tillers per plant clearly depicts the ideal test environment as the center of the concentric circles on the graph(fig.6C) and as a point on the Average Environment coordinate Axis (AEA) facing upwards with a distance from the GGE biplot origin equal to the longest vector of all environments. According to the graph, the positions of season 1 and season 2 exhibit a considerable distance from concentric point, suggesting that they are far from characteristics of an ideal environment.

4.11.5 1000 grain weight

What -won – where pattern of GGE biplot

Polygon view of GGE Biplot evaluated the performance of 144 genotypes in two different seasons. In fig. 7A, the genotypes were grouped into 11 sectors;(I, II, III, IV, V, VI, VII, VII, VII, IX, X and XI). Season 1 was located in sector II and season 2 was located in sector XI. The genotypes located in the vertices of polygon performed better compared to others with respect to that particular environment belonging to the sector. In the study, G17, G50, G86, G92, G99, G100, G129 and G140 genotypes were located on the vertices of the polygon. Among them, G99 won season 1 and in season 2, G50 and G86 were the best performers. There were outstanding performers in other sectors such as G100 in sector V, G17 in sector VII but no environment was included in these groups. Some genotypes fell into these groups but these genotypes could not be recommended for any of the seasons taken into consideration. The generated biplot in the study revealed 100% (PC1= 90.29%, PC2=9.71%) of the total GGE variation, which significantly explained environment centred data and increased the model’s ability for predicting the stability of finger millet genotypes across the environments.

Stability of finger millet genotypes based on GGE biplot

The best performing genotype with highest value for 1000 grain weight was G34 (fig. 7B). Other genotypes G129, G86, G89, G77, G66 and G99 were present in concentric rings. The ranking of genotypes can be done as G34 > G89 > G129 > G86

> G77 > G66 in terms of stability to 1000 grain weight. G86 showed stable performance for 1000 grain weight in both seasons and hence this genotype can be used for selection for 1000 grain weight.

Evaluation of environment based on biplot

The evaluation for environment for 1000 grain weight clearly depicts the ideal test environment as the center of the concentric circles on the graph(fig.7C) and as a point on the Average Environment coordinate Axis (AEA) facing upwards with a distance from the GGE biplot origin equal to the longest vector of all environments. According to the graph, season 1 and season 2 are located at a significant distance from the concentric point indicating that they are distant from features of an ideal environment.

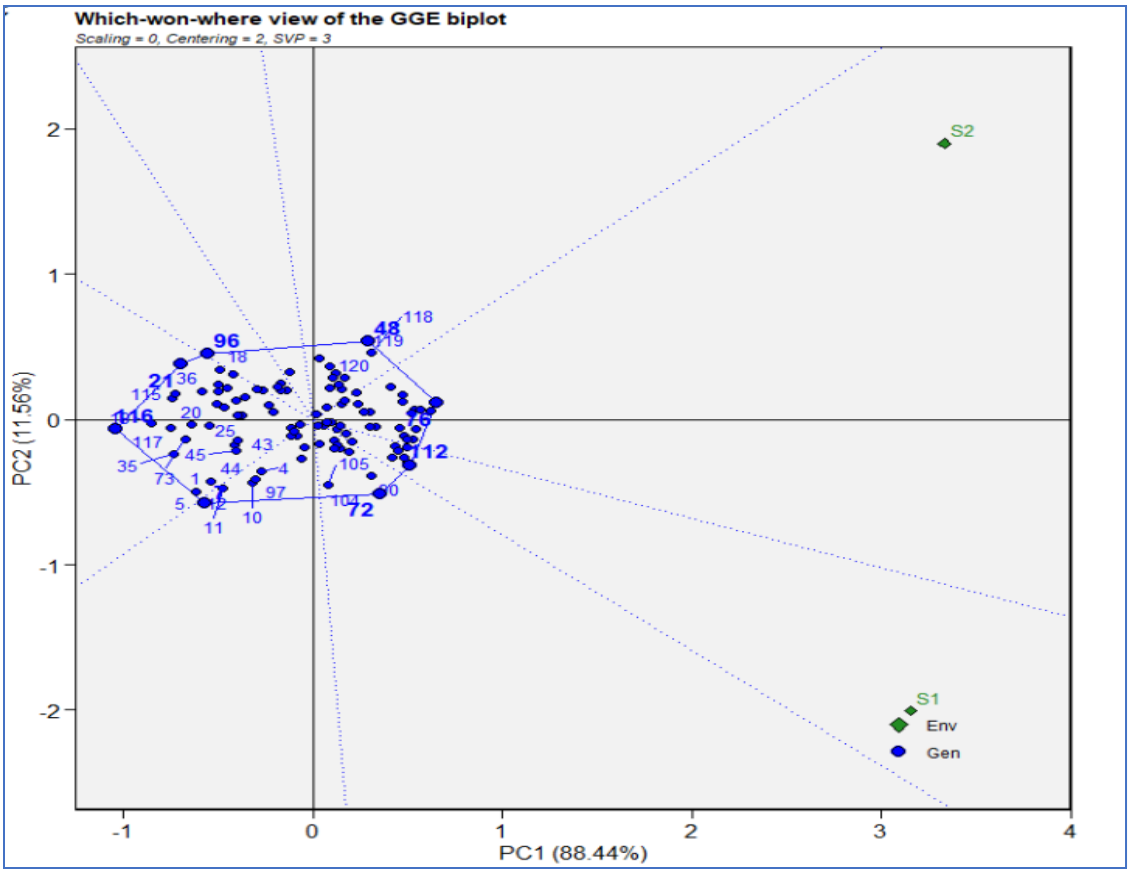

Fig 5A: Diagrammatic Representation of GGE Biplot showing best performing genotype in environment for Ear Length

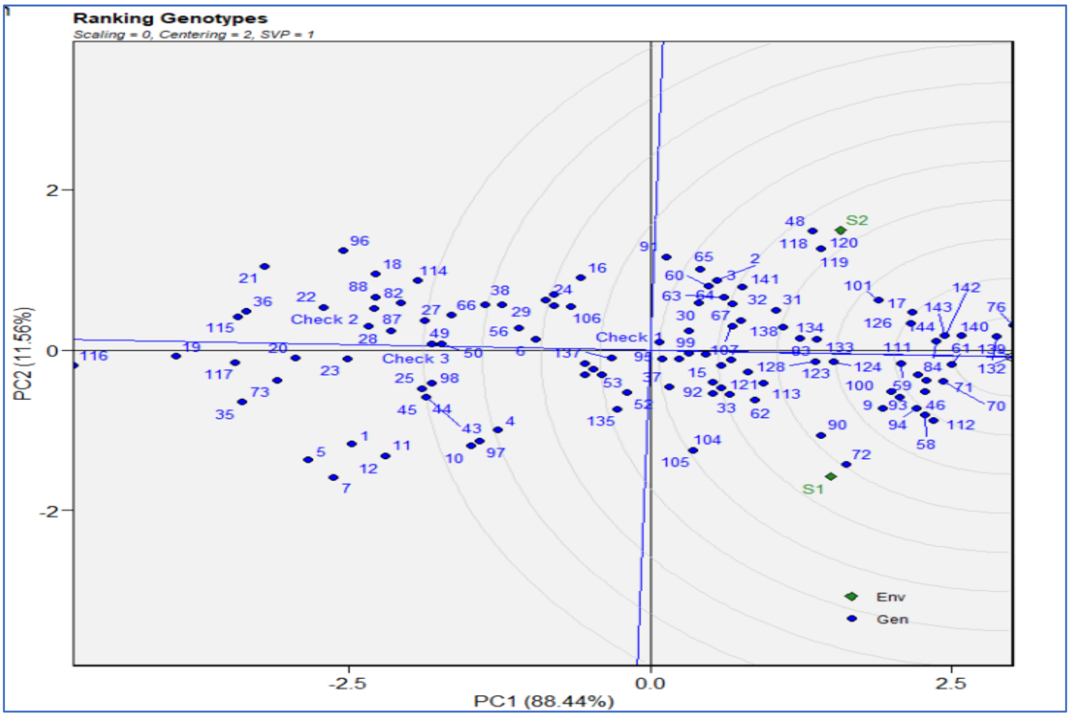

Fig.5B: Comparing genotypes with best genotypes for Ear Length

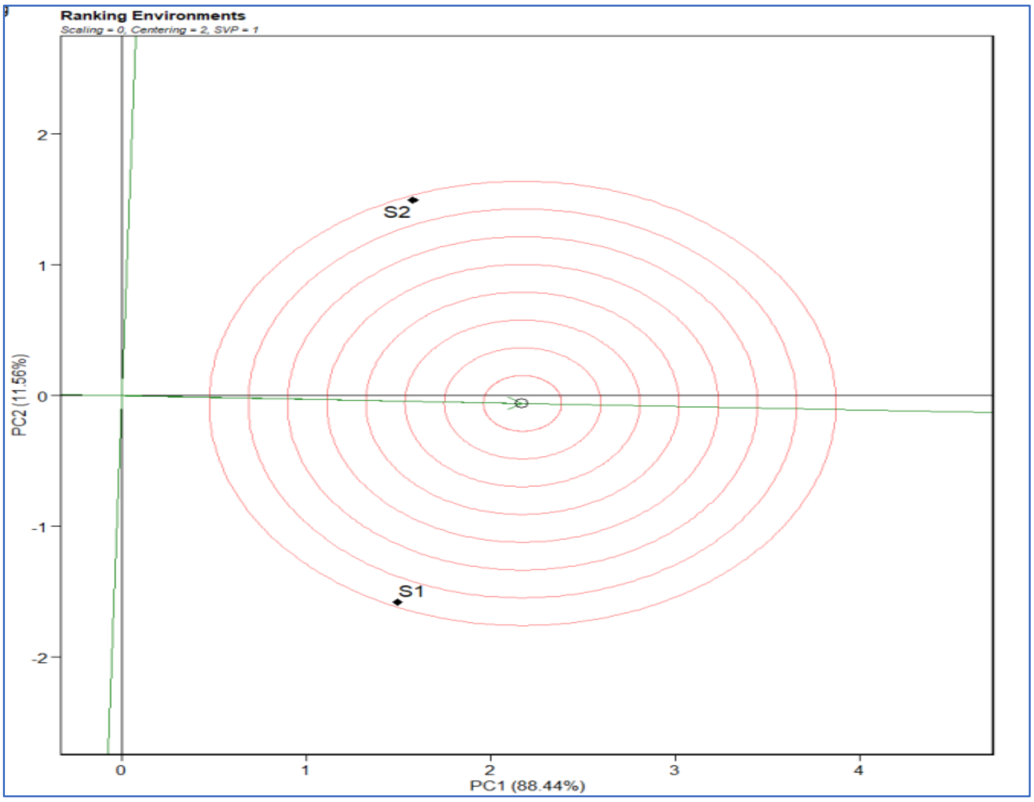

Fig.5C: Comparing environments with ideal environment for Ear Length

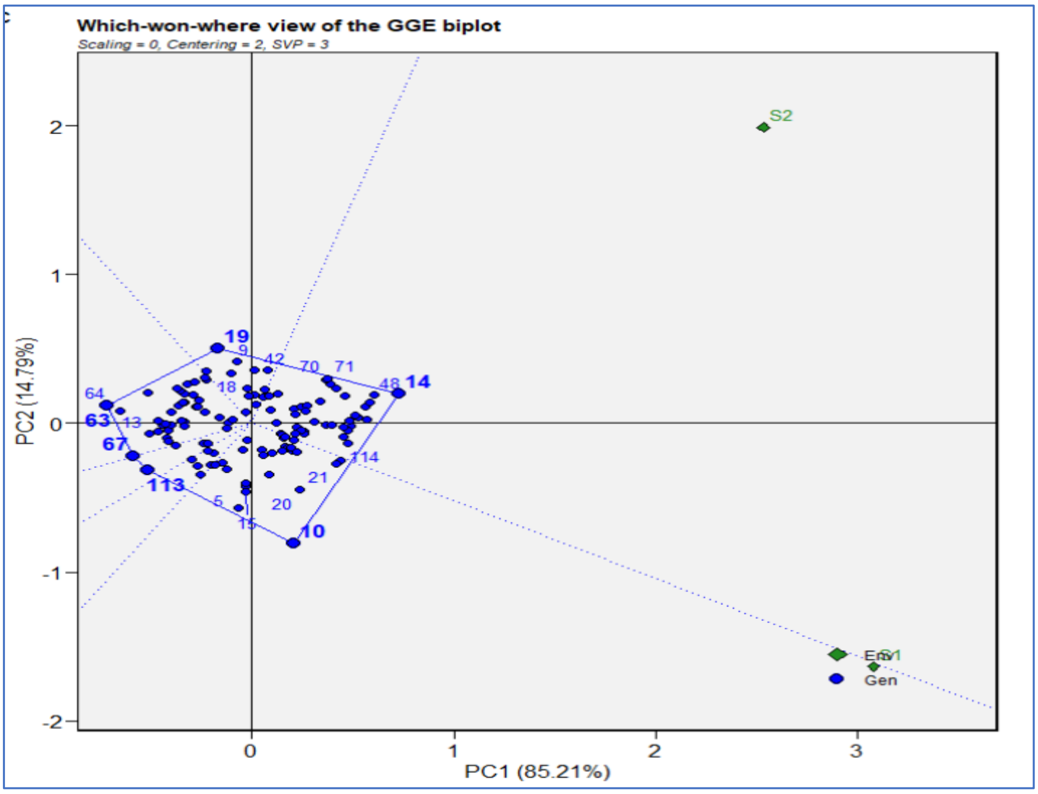

Fig 6A: Diagrammatic Representation of GGE Biplot showing best performing genotype in environment for Fingers per Ear

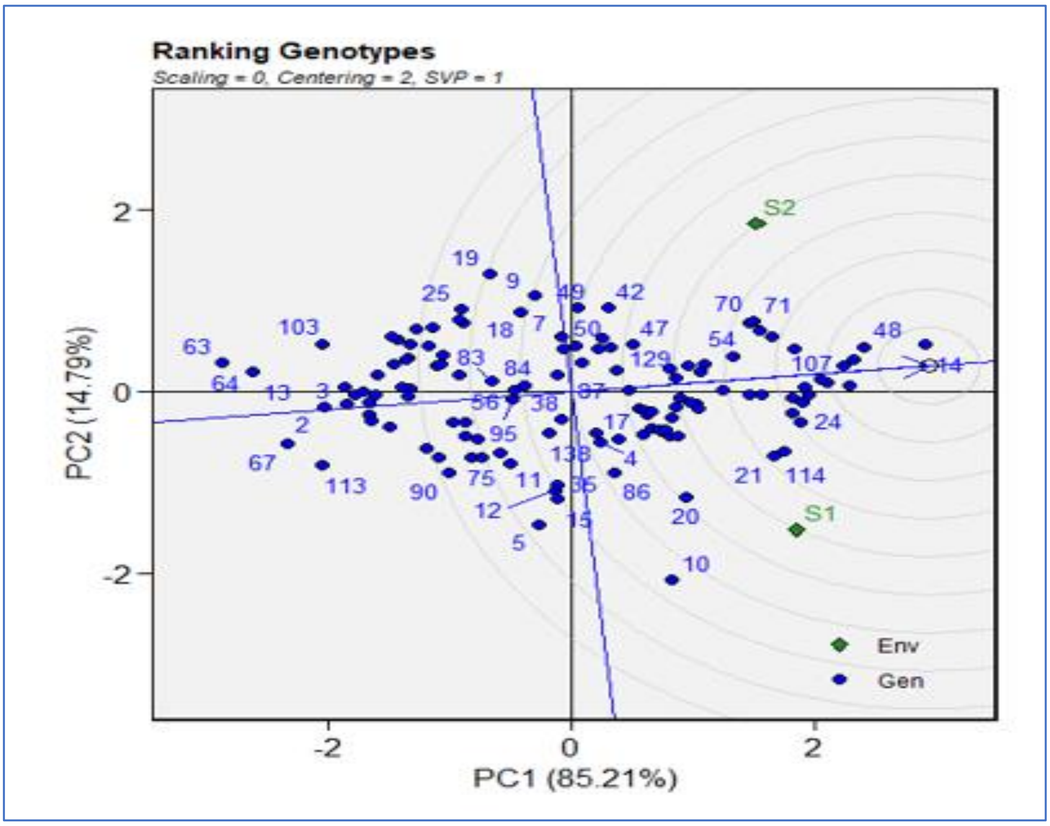

Fig.6B: Comparing genotypes with best genotypes for Fingers per Ear

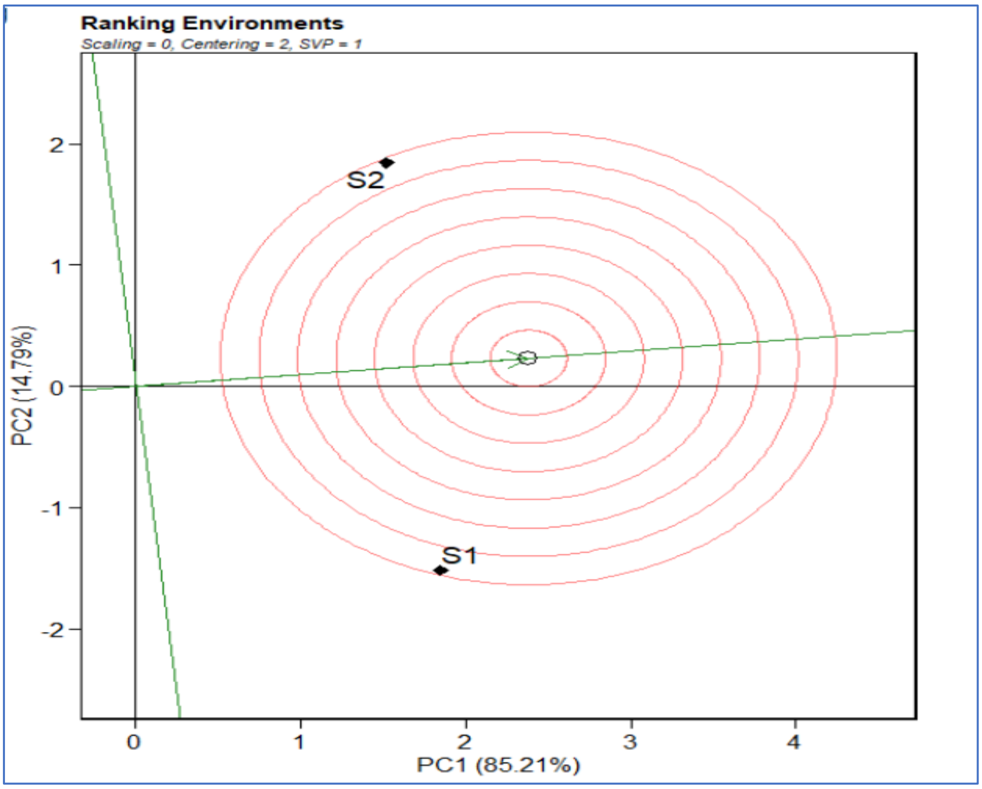

Fig.6C: Comparing environments with ideal environment for Fingers per Ear

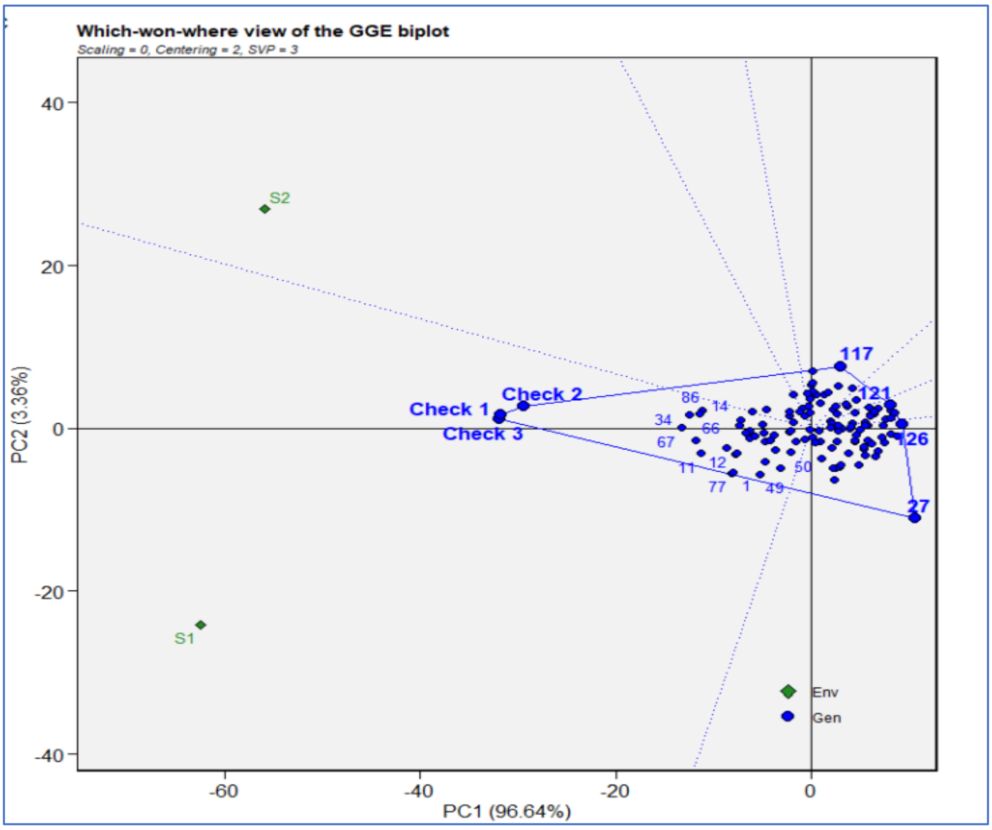

Fig 7A: Diagrammatic Representation of GGE Biplot showing best performing genotype in environment for Grain Yield

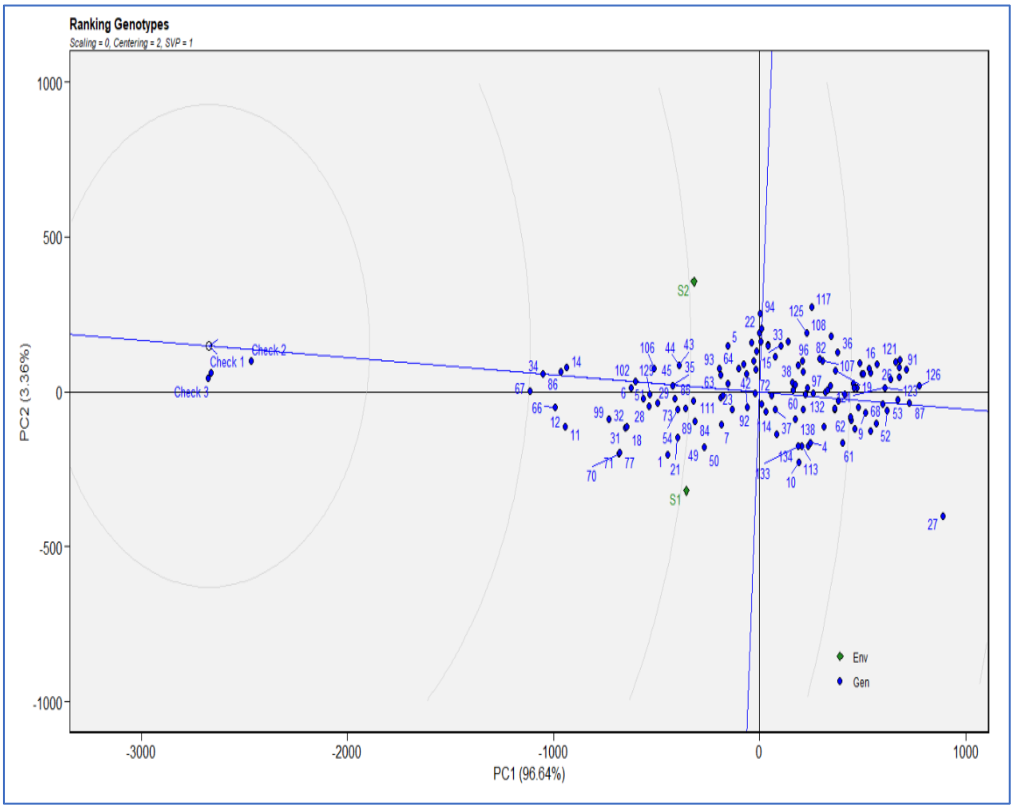

Fig.7B: Comparing genotypes with best genotypes for Grain Yield

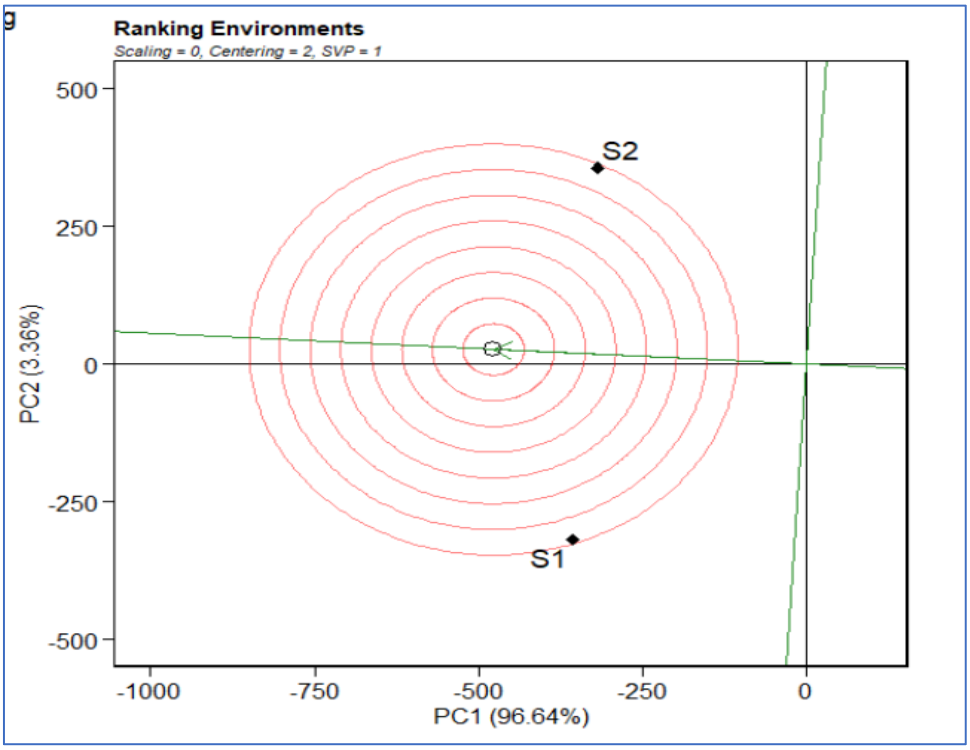

Fig.7C: Comparing environments with ideal environment for Grain Yield

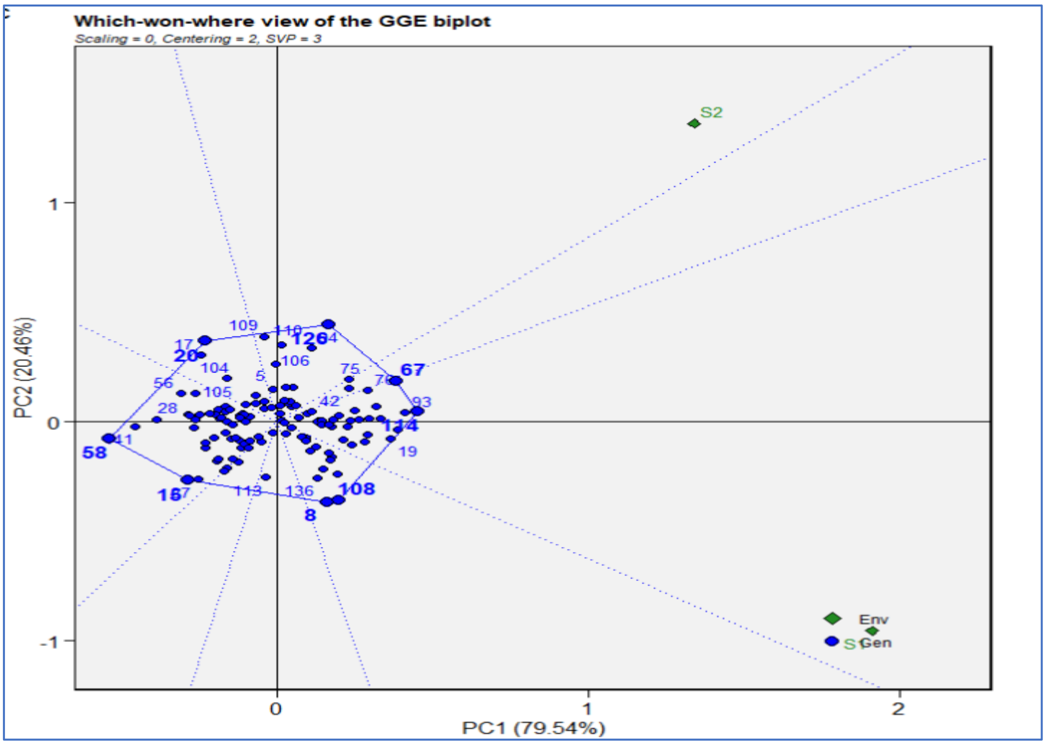

Fig.8A: Diagrammatic Representation of GGE Biplot showing best performing genotype in environment for Productive Tillers per Plant

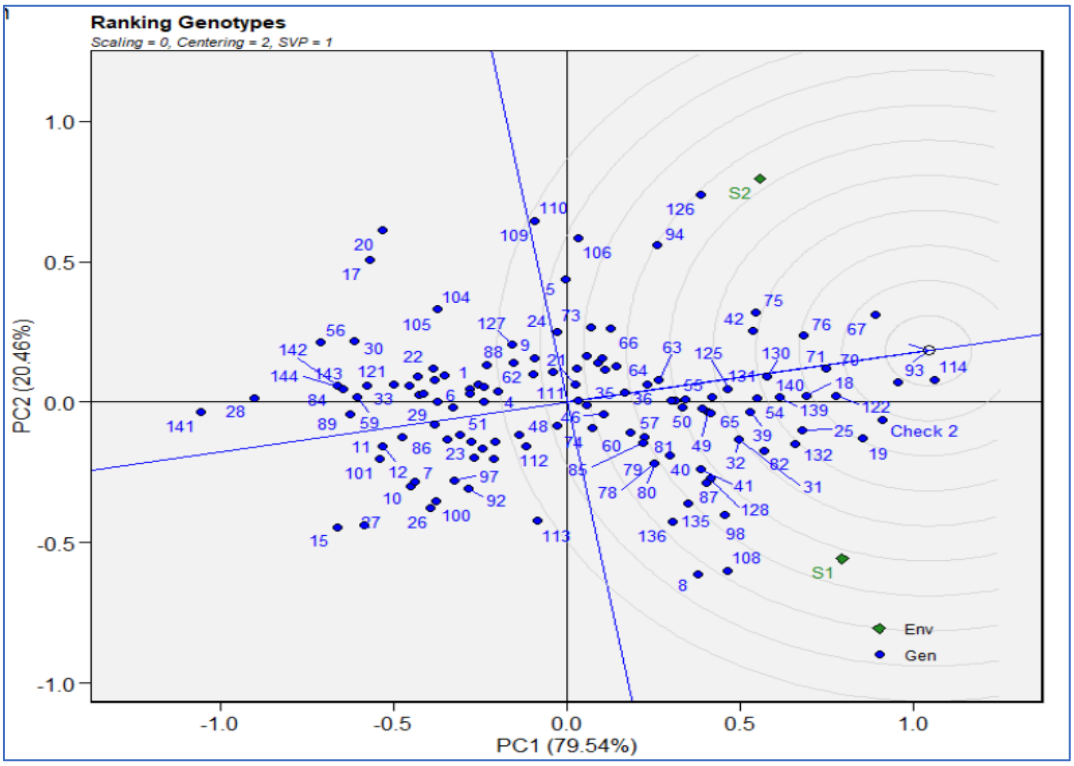

Fig.8B: Comparing genotypes with best genotypes for Productive Tillers per Plant

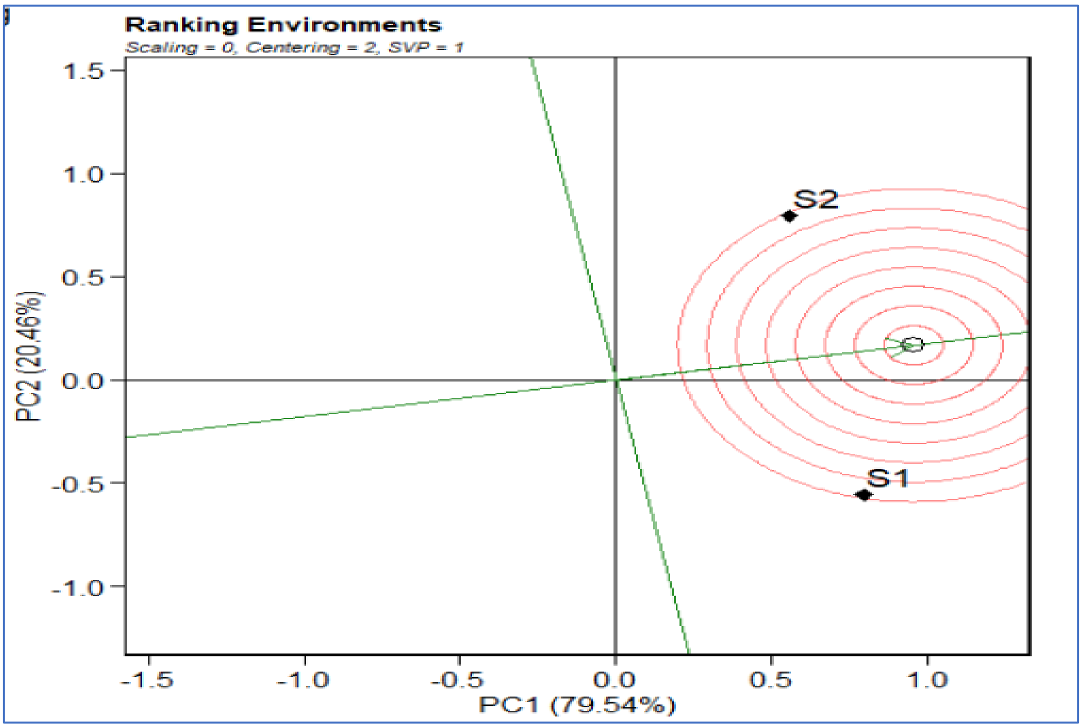

Fig.8C: Comparing environments with ideal environment for Productive Tillers per Plant

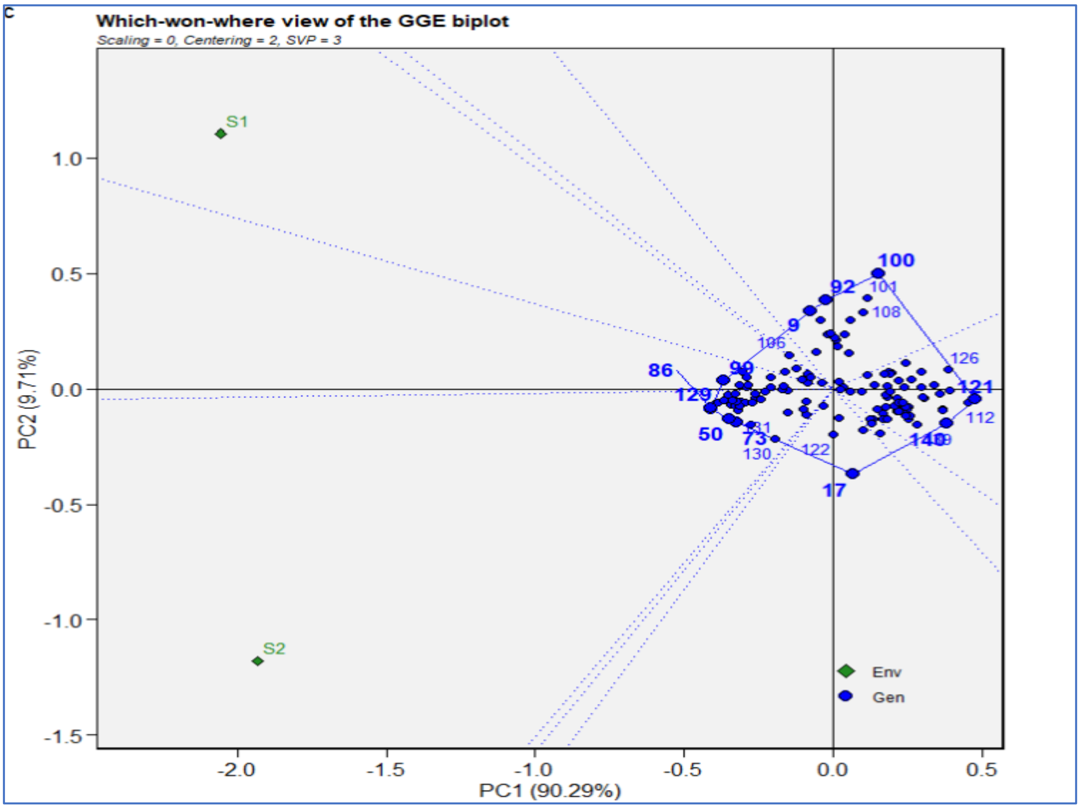

Fig 9A: Diagrammatic Representation of GGE Biplot showing best performing genotype in environment for 1000 Grain Weight

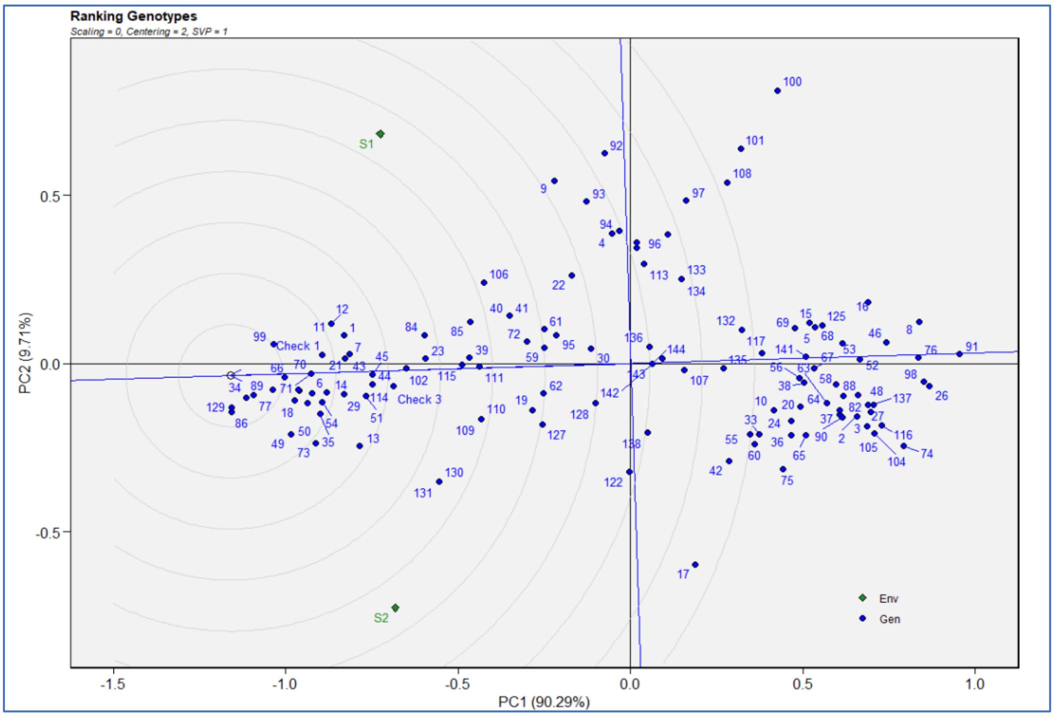

Fig.9B: Comparing genotypes with best genotypes for 1000 Grain Weight

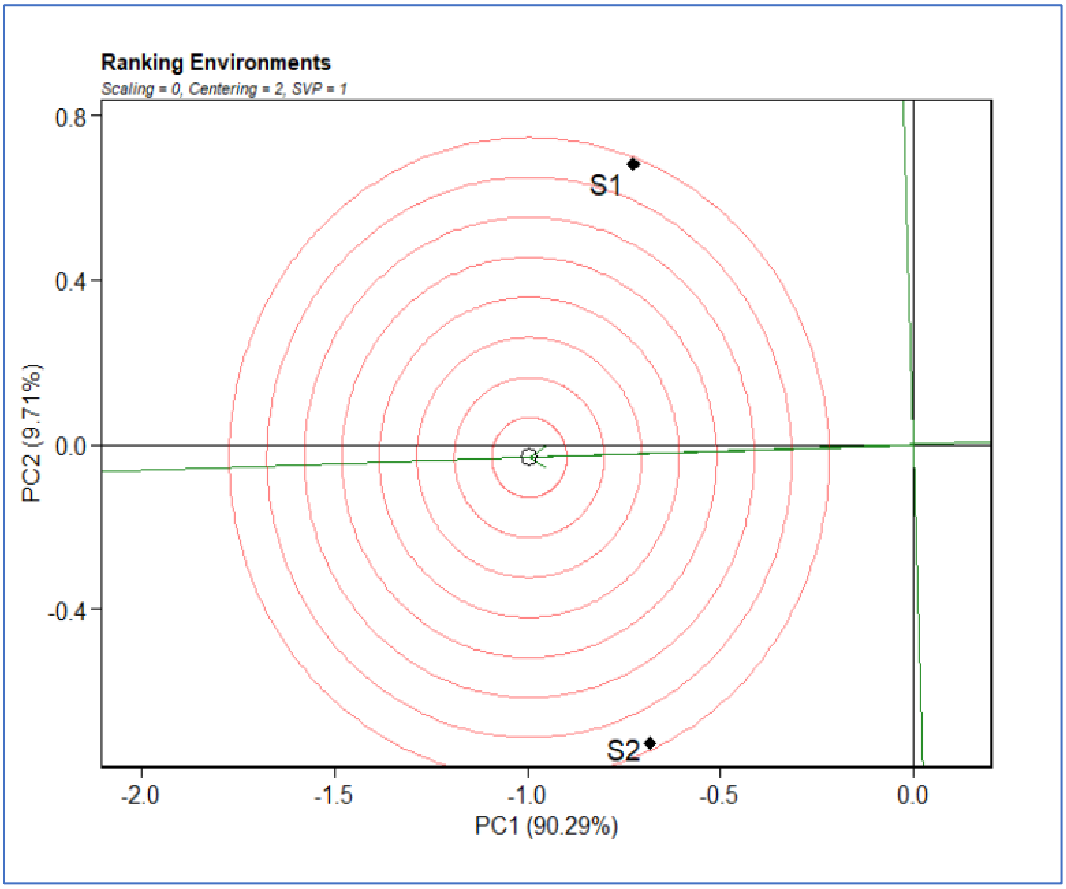

Fig.9C: Comparing environments with ideal environment for 1000 Grain Weight

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CHAPTER - V

DISCUSSION

DISCUSSION

As a part of current investigation, 144 finger millet genotypes along with 3 checks were evaluated for two summer seasons of 2022 and 2023. As a result of the research, efforts have been made to derive information on different genetic parameters viz., Mean performance, Genotypic Coefficient of Variation, Phenotypic Coefficient of Variation, Heritability and Genetic Advance as percent of Mean, Path Coefficient Analysis and GGE Biplot Analysis. The inferences that can be drawn from the results obtained for these parameters for various traits under the present study are being discussed in detail as follows:

Genotypes G94 and G101 outperformed the check varieties for ear length; G10 and G86 for fingers per ear; G34 and G129 for 1000 seed weight, in season 1 and season 2, respectively, as per the mean performance. However, for grain yield, the checks were better than the germplasm entries, this can be explained as finger millet is a kharif season crop and the adaptability of this crop has been checked in a new season (summer) in this study; besides, the genotypes tested were Germplasm entries that were collected from all across the state of Bihar and there has been no selection in these entries, while the checks used were released varieties. Therefore, this may be the reason that none of the genotypes outperformed the check varieties.

There was significant variation among genotypes for all traits considered under study. For all the traits studied, the mean sum of squares for genotypes were significant, indicating that there is enormous amount of variability present among them, whereas that of Test, Check, Test Vs Check and Block were not significant for traits such as fingers per ear, flag leaf blade length, number of basal tillers and peduncle length. Similar results were found in the work done by Singh *et.al.* (2023). In season 1, extensive range of variability was shown by traits like days to 50% flowering, grain yield, fodder yield, flag leaf length and peduncle length whereas in season 2, it was seen in days to maturity, grain yield and fodder yield.

GCV, PCV and ECV as well as variations between them, reveal the degree to which the environment is involved in controlling the traits. It was observed that the values of PCV were higher than GCV for all the traits taken under study. This indicates the presence of variation not only among genotypes but also due to the influence of environment. Traits like days to 50% flowering and days to maturity exhibited low values for GCV and PCV which is less than 10 % whereas traits such as plant height, fingers per ear, finger length, finger width, ear length and productive tillers per plant showed moderate values for GCV as well as for PCV (10-20%). Higher magnitude (>20%) for GCV and PCV was shown by grain yield and similar result was observed in the study conducted by Sharma et.al. (2022)

Heritability and genetic advance are the two important parameters which helps the process of selection. Heritability (broad sense) represents the amount of total phenotypic variance that contributes to genotypic variance. Genetic advance measures the genetic gain under selection. In general context, heritability (b.s) is a measure of how much of variation is heritable and is an evaluative estimate based on plant population. However, heritability as a measure of values cannot be used to draw any conclusions, since heritability in general sense, includes both additive and non-additive gene behaviour and the reaction to selection is primarily determined by the degree of heritable variance present in relation to phenotypic variation. As a result, it is more tempting to divide observed heterogeneity into heritable and non-heritable components. Since heritability and genetic advance are complementary terms, heritability predictions along with GA are used to forecast genetic advancement due to selection.

In the current experiment, higher value for heritability was observed for traits such as days to 50% flowering, finger length, ear length, grain yield, days to maturity, productive tillers per plant and 1000 grain weight. Similar results were observed in the study conducted by Singh *et.al*. (2023), Naik *et.al*. (2021), Aralikatti *et.al*. (2020), Asungre *et.al*. (2022). But the observation done by Singh et.al. (2023) for heritability of flag leaf width was in disagreement with that of our study, which exhibited high value for heritability.

High value for genetic advance was shown by plant height and grain yield by Singh *et.al* (2023), Anteneh *et.al*. (2019). Lower value of heritability was shown by days to maturity and days to 50% flowering which was similar to the results found by Damtie *et.al*. (2019). Other traits such as finger length, finger width, ear length, fingers per ear, number of basal tillers, 1000 grain weight, productive tillers per plant, flag leaf length, flag leaf width and peduncle length showed lower values for genetic advance.

A crop's potential capacity is primarily measured in terms of its yield potential or yield per unit area. Since yield is a polygenic trait controlled by multiple genes and significantly affected by environment and its component traits, it has a high level of complexity. An understanding of association between contributing traits and their relative contribution to yield is essential to bring a rational improvement in the desired traits. As a result, it is necessary to investigate the relationship between different characters and yield as well as within themselves. The degree and orientation of association is interpreted to understand how a character's transition will affect other characters at the same time. A high-level positive correlation coefficient at the genotypic and phenotypic level between the component traits and yield is necessary for selection based on yield.

It was shown that number of fingers per ear, number of basal tillers and productive tillers per plant were positively correlated with grain yield. These results are in agreement with the findings of Dubey *et.al.* (2019). Days to 50% flowering, days to maturity, flag leaf length, flag leaf width, plant height, finger length and fingers per ear showed positive correlation with grain yield which were similar to the results shown in the work of Dasanayaka *et.al*. (2016). The results obtained from our study were in agreement with the work of Wolie *et.al*. (2006), except for the negative correlation shown by them between plant height and grain yield. The results of Bezaweletaw *et.al*. (2006). were also in disagreement showing a negative correlation shown between days to maturity and grain yield while it was positive in the present investigation.

Path analysis divide the correlation coefficient into assessments of direct and indirect effects of independent factors of a dependent variable using the standardised partial regression coefficient. Path analysis reveals whether the association of independent characters on dependent character (yield) is due to their direct effects or is a consequence of their indirect effects via other components. In season 1 and season 2, traits such as fingers per ear and productive tillers per plant showed positive direct effects with grain yield. Similar results were observed in the work done by Kumar *et.al*. (2004) and Eric *et.al*. (2016). Other traits such as finger length, number of basal tillers, 1000 grain weight, flag leaf width and peduncle length also showed positive direct effects with grain yield in both seasons.

For the seed vigour index I, the genotypes, RAU-FM-Sheohar-2009-19, RAU-FM-Madhubhani-2009-4, RAU-FM-Sheohar-2009-9 and RAU-FM-Sheohar-2010-3 outperformed the check varieties. RAU-FM-Sheohar-2009-19 showed a high mean performance for finger length in season 2. RAU-FM-83, RAU-FM-Gopalganj-2009-5, RAU-FM-126, RAU-FM-Kanti-2010-4, RAU-FM-93 and RAU-FM-98 outperformed the check varieties RAU-8, GPU-67 and VL-376 which showed seed vigour index II values of 0.938, 0.945 and 0.866, respectively. The seedling lengths for the genotypes RAU-FM-Sheohar-2009-11, RAU-FM-Sheohar-2009-9 and RAU-FM-Sheohar-2009-14 outperformed the checks. For chlorophyll content, the genotypes RAU-FM-Sheohar-2009-7, RAU-FM-Sheohar-2010-9 and RAU-FM-Gopalganj-2009-1 showed higher values than check varieties. The genotypes which outperformed the check varieties for the speed of germination were RAU-FM-82, RAU-FM-100, RAU-FM-104 and RAU-FM-118.

Correlation analysis for seed physiological traits showed that seed vigour index I is positively correlated with seed vigour index II which is similar to the results presented by Negi *et.al*. (2019) Other traits such as seed vigour index II with speed of germination and seedling length with chlorophyll content were not in agreement with this finding though they showed positive correlation with each other.

RAU-FM-Sheohar-2009-9 which showed a better performance for seed vigour index I, seedling length and chlorophyll content, had high flag leaf blade length. Genotypes RAU-FM-83 and RAU-FM-Gopalganj-2009-5 which had high vigour index II also had higher values for days to 50% flowering. RAU-FM-Sheohar-2009-14 which had high seedling length and RAU-FM-82 which had high speed of germination showed higher mean performance for plant height. RAU-FM-100 also had high speed of germination as well as showed a better mean performance for days to 50% flowering and days to maturity.

GGE Biplot model studies the genotype, environment and genotype x environment interactions and helps in the identification of superior genotypes for high yield and stability across diverse environmental conditions. For ear length, G21, G48, G72, G76, G96, G112 and G116 genotypes were the most responsive genotypes; G10, G14, G19, G63, G67 and G113 for fingers per ear ; G8, G15, G20, G67, G108, G114 and G126 for productive tillers per plant; G17, G50, G86, G92, G99, G100, G129 and G140 for 1000 grain weight, respectively. Genotypes exhibiting stable as well as better performance for ear length (G76), fingers per ear (G14), productive tillers per plant (G114) and 1000 grain weight (G86) were identified. Though no genotypes outperformed the checks, G67 exhibited a comparable performance with check for grain yield. Hence this genotype can be tested for more summer seasons. The seasons were analysed which showed that both the season 1 and season 2 were having characteristics distinct from the ideal environment and hence they were plotted away from the concentric point representing the ideal environment. Similar studies of stability analysis using GGE Biplot was done by Kandel *et.al*. (2022), Kebede *et.al*. (2018) and Bandyopadhyay *et.al*. (2023) in finger millet.

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CHAPTER - VI

SUMMARY AND CONCLUSION

SUMMARY AND CONCLUSION

The present investigation “**Characterization and Stability Analysis of Transplanted Finger Millet using Morpho-Physiological Traits in Summer”** was conducted with the aim of selecting the genotypes for donor traits to be utilized in the development of finger millet varieties specifically adapted for summer season. A comprehensive survey of literature was done to have an outlook on previous works done on these aspects and to assess the research gap.

The study was carried out at Small Millets Research Farm at Tirhut College of Agriculture, Dholi using 144 finger millet germplasm and 3 checks involving quantitative traits such as days to 50% flowering, days to maturity, finger length, finger width, ear length, fingers per ear, fodder yield, grain yield, plant height, number of basal tillers, productive tillers per plant, 1000 grain weight, flag leaf blade length, flag leaf blade width and peduncle length. The mean data recorded were recorded for these traits and analyzed for accomplishing the following objectives:

- To characterize and evaluate the germplasm of finger millet for qualitative and quantitative traits in summer seasons
- To evaluate the germplasm of finger millet for seed physiological traits in summer seasons
- To study the role of genotype x environment interactions in the expression of various morphological characters and stability of genotypes in the summer seasons

The important findings of the work are briefly mentioned in the following

- Analysis of Variance revealed highly significant variation among all characters between checks as well as germplasm
- High values for GCV and PCV were observed for grain yield in season 1 and season 2. For all traits, the values of PCV is higher than that of GCV indicating that the variation is contributed not only by genotype but by environment also.
- The highest value of heritability was for 1000 grain weight and productive tillers per plant followed by finger width in season 1. In season 2, days to

maturity showed higher value for heritability followed by plant height. Grain yield showed higher values for heritability and genetic advance in both seasons. In season 1 and 2, grain yield showed higher values for Genetic Advance as percent of Mean (GAM)

- In season 1 and season 2, all the quantitative traits showed strong positive correlation among each other including each other indicating that a simultaneous improvement of traits can be performed. Plant height normally shows a negative correlation to grain yield. In this study, plant height is showing positive correlation with grain yield. This can be explained as, since finger millet is a C4 crop, it can fix photosynthetic products more efficiently comparing to C3 plants so more the biomass, more will be the C-fixation that can be efficiently partitioned to the sink.
- Path coefficient analysis showed that the traits such as fingers per ear, productive tillers per plant and 1000 grain weight had positive direct effects on grain yield whereas ear length exerted negative direct effects in season 1 and in season 2, fingers per ear and 1000 grain weight had positive direct effects whereas ear length and productive tillers per plant exerted negative direct effects on grain yield.
- As per the mean performance, G94 and G101 outperformed the check varieties for ear length; G10 and G86 for fingers per ear; G34 and G129 for 1000 seed weight, in season 1 and season 2 respectively. For productive tillers per plant, in season 1, no genotypes outperformed the check varieties and G126 showed a better performance in season 2. The genotypes couldn't show a better mean performance than check varieties for grain yield in both season 1 and 2. This can be explained as finger millet is a kharif season crop and the adaptability of this crop has been checked in a new season (summer) in this study; besides, the genotypes tested were Germplasm entries that were collected from all across the state of Bihar and there has been no selection in these entries, while the checks used are released varieties. Therefore, this may be the reason that none of the genotypes outperformed the check varieties.
- Considering qualitative traits, most genotypes showed erect type of plant growth habit, compact ear shape, absence of finger multiple whorls, absence

of finger branching, copper brown seed colour, round shaped seeds, absence of stem culm branching, dark green coloured glume, absence of seed shattering and persistent pericarp. Some genotypes showed finger branching in thumb finger.

- RAU-FM-Sheohar-2009-19 and RAU-FM-139 for seed vigour index I; RAU-FM-83 and RAU-FM-139 for seed vigour index II; RAU-FM-Sheohar-2009-11 and RAU-FM-139 for seedling length; RAU-FM-Sheohar-2009-7 and RAU-FM-Sheohar-2009-3 for chlorophyll content, showed higher and lower values respectively. Hundred genotypes showed 100% seed germination other than check varieties. The genotypes showed a comparable performance with check varieties for speed of germination with RAU-FM-82, RAU-FM-100, RAU-FM-104 and RAU-FM-118 showing the higher value.
- Seed vigour index II is considered to be more important than seed vigour index I as the former involves seedling dry weight and it showed significant positive correlation with speed of germination; seed vigour index I with seed vigour index II and seed germination %; seedling length with chlorophyll content and speed of germination and chlorophyll content with speed of germination, showed significant positive correlation.
- Stability analysis was done using GGE Biplot model, according to which, G76 showed a better performance for ear length in both seasons indicating that this genotype can be selected for trait ear length for breeding programmes. G14 showed better performance for fingers per ear for both seasons indicating that this genotype can be used for selection of fingers per ear. For the selection for trait productive tillers per plant, G114 can be used as it was an outperforming variety. Similarly, G86 showed a better performance for 1000 seed weight. As 1000 seed weight stands for seed size which affects the seed processing, better performing genotype G86 can be used for selection for this trait. The analysis showed that no genotype outperformed the check varieties for grain yield as was evinced by the mean performance. But G67 exhibited a comparable performance with check varieties and hence this genotype can be evaluated for more summer seasons for grain yield or can be used as a parent.

- The stability analysis showed that the seasons taken for evaluation are not close to ideal environment. This can be explained as; summer season is being tested for first time for introduction of finger millet as a new crop in this season, as it is being grown as a kharif crop which till now is considered as the ideal environment, however genotypes can be selected for donor traits and can be utilized in the breeding programmes for developing varieties specifically adapted for summer season.

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APPENDICES

APPENDIX I

Mean Performance of finger millet genotypes for Grain Yield and 1000-Grain Weight for Season 1

Genotype No.	1000 Seed Weight		Grain Yield	
	Season 1	Season 2	Season 1	Season 2
G1	3.06	2.61	1318.39	774.85
G2	1.81	1.77	721.58	714.73
G4	2.70	1.86	777.28	343.93
G5	2.08	1.66	867.54	844.77
G6	3.01	2.80	1306.64	1053.85
G7	3.01	2.64	1059.04	674.66
G8	1.87	1.44	737.64	745.61
G9	2.93	1.86	513.91	238.36
G10	2.00	1.92	862.06	332.50
G11	3.11	2.61	1630.15	1175.32
G13	2.80	2.82	862.33	714.76
G14	2.98	2.77	1497.45	1310.95
G15	1.66	1.89	675.50	672.58
G16	1.50	1.77	367.54	314.70
G17	1.85	2.41	719.39	714.69
G18	3.03	2.85	1413.91	977.04
G19	2.50	2.38	569.71	562.40
G20	1.94	1.84	566.69	398.16
G21	3.00	2.64	1284.66	911.24
G22	2.69	2.01	745.98	899.07
G23	2.83	2.48	1029.38	864.40
G24	1.93	1.89	987.41	878.16
G25	1.53	1.48	618.41	540.40
G26	1.71	1.54	331.30	387.11
G27	1.78	1.71	493.58	455.38
G28	3.03	2.80	1318.00	1079.12
G29	2.93	2.72	1208.12	1013.44

G30	2.50	2.13	696.60	578.22
G31	2.99	2.81	1445.01	1102.26
G33	1.97	1.98	677.67	783.30
G34	3.13	2.92	1632.54	1499.33
G35	2.94	2.81	1191.38	1052.40
G36	1.90	1.92	522.80	600.13
G37	1.75	1.73	987.70	1197.73
G38	1.89	1.73	811.15	1230.39
G39	2.65	2.34	1025.97	1224.08
G42	1.89	2.17	1082.76	1299.92
G43	2.82	2.05	1239.59	1294.10
G46	1.80	2.57	806.22	1613.71
G47	1.49	1.48	596.00	1199.53
G48	1.71	1.29	743.25	1003.75
G49	2.87	1.65	1325.97	894.57
G51	2.79	2.86	1442.02	1338.16
G52	1.82	2.63	587.08	1650.98
G54	2.87	1.58	1342.02	834.04
G55	1.93	2.78	640.17	1245.82
G56	1.94	2.17	434.00	938.13
G57	1.79	1.95	625.36	910.22
G58	1.85	1.94	573.51	1006.61
G59	2.54	1.89	841.41	941.08
G60	1.90	2.39	717.95	1286.61
G61	2.58	2.18	685.85	1067.43
G62	2.45	2.35	604.37	830.00
G63	1.83	2.49	980.30	856.49
G65	1.81	1.95	903.14	1387.04
G66	3.03	2.06	1650.05	1344.39
G67	1.93	2.97	1705.61	1844.52
G68	1.92	1.90	458.69	1966.08
G69	2.05	1.79	612.40	794.27
G70	2.98	1.85	1519.19	945.99
G72	2.59	2.91	838.94	1527.02

G73	2.87	2.84	1302.12	1377.00
G74	1.62	3.23	787.37	1687.72
G75	1.83	2.07	635.31	1279.87
G76	1.77	2.36	560.88	1029.88
G77	3.10	1.85	1546.71	1087.54
G78	2.60	3.25	864.73	1692.71
G82	1.85	2.16	623.63	1477.82
G83	1.61	2.08	355.39	1269.52
G84	2.86	1.77	1208.60	992.59
G85	2.79	2.78	1168.86	1523.55
G86	3.11	2.66	1586.52	1577.83
G87	1.74	3.33	393.71	2018.00
G88	1.82	2.10	375.27	2066.00
G89	3.07	2.05	1213.66	968.62
G90	1.81	3.20	496.49	1582.64
G91	1.73	2.64	169.47	2381.94
G92	2.89	1.51	885.35	246.45
G93	2.83	1.78	845.46	715.84
G94	1.92	2.70	575.66	856.53
G95	2.62	2.27	673.38	813.47
G96	2.59	1.83	528.01	604.77
G97	2.62	1.72	567.97	525.48
G98	1.75	1.64	302.01	373.33
G99	3.20	2.85	1351.11	1092.39
G100	2.65	1.30	395.55	215.54
G101	2.61	1.50	264.19	204.46
G102	2.87	2.64	1174.81	1098.46
G103	1.56	1.58	248.64	277.03
G104	1.75	1.85	674.07	777.18
G106	2.88	2.30	1078.76	1066.49
G107	2.28	2.09	453.33	539.56
G108	2.57	1.60	369.87	570.49
G109	2.57	2.57	616.65	289.77
G111	2.68	2.46	1086.03	855.94

G112	1.37	1.35	697.64	528.10
G113	2.54	1.91	899.61	475.98
G114	2.87	2.71	962.08	586.07
G115	2.72	2.49	806.28	886.22
G116	1.71	1.79	508.50	488.76
G117	2.11	1.87	563.81	779.81
G118	2.59	1.89	699.36	457.81
G121	1.34	1.29	358.38	366.01
G122	2.15	2.39	571.96	438.35
G123	2.31	2.08	470.97	347.84
G125	2.04	1.69	638.28	732.09
G126	1.67	1.31	344.66	241.68
G127	2.44	2.85	843.00	854.00
G128	2.37	2.70	837.52	738.89
G129	3.13	3.43	1377.71	1169.58
G130	2.54	3.18	818.59	530.40
G132	2.21	2.25	855.76	638.01
G133	2.44	2.26	952.74	566.19
G135	2.17	2.37	832.03	723.83
G136	2.37	2.47	915.43	534.22
G137	1.78	2.15	973.46	937.98
G138	2.20	2.66	904.46	640.59
G139	1.43	1.99	617.35	538.89
G141	2.02	2.18	704.05	464.94
G142	2.33	2.50	994.17	787.12
RAU-8(check-1)	3.04	2.59	2841.86	2070.75
GPU-67(Check-2)	3.01	2.97	2671.03	2652.58
VL-376(Check-3)	2.84	2.83	2864.78	2745.05

APPENDIX II

Mean Performance of finger millet genotypes for Ear Length, Fingers per Ear and Productive Tillers per Plant for Season 2

Genotype No.	Ear Length		Fingers per Ear		Productive tillers per plant	
	Season 1	**Season 2**	**Season 1**	**Season 2**	**Season 1**	**Season 2**
G1	8.53	6.96	6.70	7.04	1.67	1.86
G2	9.13	10.56	5.36	5.11	1.85	1.65
G4	9.23	7.96	7.36	6.26	1.75	1.80
G5	8.43	6.56	7.55	5.25	1.68	2.24
G6	8.63	8.96	5.51	5.85	1.68	1.68
G7	8.73	6.56	6.37	6.96	1.74	1.40
G8	10.13	9.96	6.65	7.15	2.60	1.60
G9	11.23	10.46	5.91	7.17	1.77	1.96
G10	9.23	7.66	8.78	5.46	1.74	1.38
G11	8.83	7.06	7.42	5.62	1.59	1.45
G13	9.23	8.96	4.67	5.04	1.57	1.66
G14	10.13	9.96	8.75	8.79	1.69	1.75
G15	10.03	9.66	7.48	5.55	1.65	1.14
G16	8.33	9.76	5.69	5.29	1.53	1.67
G17	10.53	11.46	7.27	6.31	1.18	1.97
G18	7.13	8.56	5.95	6.95	2.49	2.30
G19	7.00	6.62	5.47	7.45	2.73	2.35
G20	7.70	7.32	8.27	6.59	1.17	2.16
G21	6.70	7.92	8.54	7.40	1.94	2.03
G22	7.40	7.92	5.70	6.03	1.57	1.84
G23	8.00	7.62	7.57	7.29	1.75	1.66
G24	8.60	9.73	8.48	7.82	1.79	2.15
G25	8.70	7.83	5.53	7.00	2.57	2.27
G26	9.40	9.03	7.46	7.81	1.85	1.43
G27	8.10	8.43	6.75	7.46	1.73	1.27
G28	8.00	8.13	7.49	7.73	1.21	1.46
G29	8.40	9.02	5.34	6.41	1.69	1.68
G30	9.50	10.23	7.75	7.69	1.33	1.79

G31	10.00	10.63	7.95	7.79	2.44	2.14
G33	10.50	9.63	8.35	7.85	1.51	1.73
G34	8.60	9.32	7.70	8.40	1.60	1.81
G35	7.80	6.62	7.37	6.01	2.01	1.99
G36	7.00	7.42	5.89	5.63	2.11	2.15
G37	10.03	9.09	7.26	7.97	2.06	2.09
G38	8.23	8.69	6.62	6.19	2.03	2.10
G39	10.13	9.69	5.48	6.02	2.49	2.21
G42	11.23	9.59	6.14	5.58	2.33	1.96
G43	8.73	11.29	7.42	7.37	2.03	2.45
G46	11.53	7.54	7.08	6.61	2.15	2.12
G47	10.13	10.59	6.55	6.69	2.29	1.96
G48	9.43	9.69	8.04	7.19	2.06	2.12
G49	8.33	11.29	5.95	8.38	2.39	1.85
G51	10.33	8.09	5.03	7.21	1.85	2.14
G52	9.83	9.69	8.06	5.32	1.99	1.66
G54	10.33	8.79	7.15	8.22	2.48	2.10
G55	9.20	7.59	7.64	7.70	2.26	2.03
G56	8.40	8.49	6.70	7.63	1.22	2.18
G57	9.20	8.39	6.24	6.67	2.18	1.69
G58	11.50	8.49	7.93	6.52	0.97	1.95
G59	10.90	10.09	7.19	7.13	1.42	1.10
G60	9.10	10.39	5.75	6.03	2.14	1.59
G61	11.20	9.89	8.62	5.87	2.17	1.94
G62	10.40	10.69	5.81	8.08	1.79	2.10
G63	9.30	9.19	4.66	6.39	2.10	1.95
G65	8.90	9.89	6.70	5.38	2.29	2.14
G66	7.90	9.99	5.55	5.71	1.88	2.13
G67	9.60	8.09	5.63	6.48	2.48	2.21
G68	9.60	9.79	6.70	5.03	2.28	2.69
G69	8.30	9.09	7.72	6.03	2.20	1.94
G70	11.30	8.89	7.74	7.17	2.47	2.13
G72	11.50	10.49	6.79	8.51	2.21	2.45
G73	7.47	8.09	6.48	8.22	1.99	2.23
G74	11.17	6.79	7.30	6.37	2.20	2.31

G75	9.57	10.69	6.54	7.69	2.35	2.02
G76	11.17	9.49	5.58	6.42	2.51	2.63
G77	9.17	11.69	8.11	6.16	2.42	2.64
G78	8.27	8.79	7.44	8.71	2.42	2.26
G82	7.47	9.09	5.32	8.60	2.65	2.02
G83	10.07	8.19	6.08	7.27	1.74	2.24
G84	10.87	10.29	6.31	7.12	1.53	1.93
G85	9.57	11.09	8.38	7.26	2.35	1.72
G86	8.27	9.49	7.49	8.95	1.77	2.06
G87	7.37	9.09	6.44	6.98	2.58	1.68
G88	7.27	7.99	5.38	7.52	1.88	2.05
G89	9.87	8.09	7.64	6.86	1.60	2.08
G90	11.07	9.69	6.44	7.63	2.13	1.66
G91	8.83	8.99	7.51	7.75	1.91	1.99
G92	10.33	10.69	7.65	7.03	1.91	1.73
G93	11.43	9.79	5.71	7.19	2.71	1.60
G94	11.63	10.89	5.67	7.20	1.86	2.62
G95	9.73	9.79	6.56	6.81	1.61	1.80
G96	6.93	8.79	8.33	8.29	1.74	1.92
G97	9.43	7.99	6.54	7.50	1.86	1.60
G98	8.63	8.19	8.45	8.60	2.57	1.95
G99	9.63	10.19	7.71	7.48	1.72	1.88
G100	11.33	10.89	7.35	7.90	1.86	1.51
G101	10.43	11.59	7.77	7.73	1.64	1.54
G102	11.33	11.19	7.45	8.01	1.77	1.88
G103	9.53	9.29	4.97	6.29	1.71	1.89
G104	10.73	9.19	5.82	6.82	1.47	2.07
G106	8.73	9.69	5.85	6.70	1.66	2.51
G107	9.83	10.49	8.01	8.71	1.82	1.74
G108	9.93	10.09	8.43	8.82	2.69	1.79
G109	9.40	10.39	5.39	5.89	1.47	2.39
G111	10.90	10.89	6.48	6.56	1.94	1.94
G112	11.60	10.59	7.16	6.47	1.91	1.72
G113	10.30	9.89	5.55	4.32	2.09	1.52
G114	7.40	8.69	8.38	6.86	2.74	2.59

G115	6.70	7.29	7.47	6.38	1.51	1.74
G116	6.20	5.89	5.41	5.10	1.81	1.60
G117	7.10	6.89	5.28	4.97	1.87	2.03
G118	9.40	11.39	7.54	6.77	1.61	1.70
G121	10.20	9.59	6.35	5.36	1.41	1.63
G122	9.30	8.99	5.56	5.43	2.54	2.38
G123	10.50	10.49	6.09	5.01	1.67	1.78
G125	11.20	10.89	7.35	6.77	2.27	2.22
G126	10.60	11.29	5.26	5.81	1.81	2.74
G127	8.43	9.06	5.68	5.08	1.73	2.03
G128	10.43	10.16	6.97	6.07	2.47	1.97
G129	9.63	9.36	6.35	6.37	1.87	1.68
G130	10.13	9.66	5.75	5.14	2.40	2.36
G132	11.23	11.46	7.04	6.49	2.60	2.21
G133	10.23	10.36	4.86	4.81	1.87	1.68
G135	9.73	8.56	7.04	6.10	2.47	1.86
G136	10.13	9.66	6.19	5.07	2.47	1.78
G137	9.23	8.96	4.99	4.92	1.73	1.86
G138	9.93	10.26	6.37	5.49	1.93	1.78
G139	11.23	11.46	7.75	7.17	2.47	2.32
G141	9.33	10.36	4.86	5.09	1.13	1.32
G142	10.93	11.16	4.80	5.68	1.40	1.62
RAU-8 (check-1)	9.42	9.59	8.20	7.66	2.09	2.12
GPU-67 (Check-2)	7.62	8.57	7.05	7.50	2.76	2.35
VL-376 (Check-3)	8.15	7.91	7.93	7.49	1.88	2.10

APPENDIX-III

DATA FOR QUALITATIVE MORPHOLOGICAL TRAITS

Genotype No.	Plant growth habit	Ear shape	Finger multiple whorl	Finger branching	Position of finger branching	Seed colour	Seed shape	Glume colour	Stem culm branching	Seed shattering	Pericarp persistence after threshing
G1	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G2	ERECT	COMPACT	PRESENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G4	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	PRESENT
G5	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	PRESENT
G6	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	PRESENT
G7	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G8	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G9	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	LIGHT PURPLE	ABSENT	ABSENT	PRESENT
G10	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT

G11	ERECT	FIST-TYPE	ABSENT	PRESENT	IN THUMB FINGER	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G13	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G14	DECUMBENT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G15	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	LIGHT BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	ABSENT
G16	ERECT	FIST-TYPE	ABSENT	ABSENT	ABSENT	LIGHT BROWN	ROUND	LIGHT GREEN	PRESENT	ABSENT	ABSENT
G17	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	LIGHT BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G18	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	PRESENT
Check 1 (RAU 8)	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
Check 2 (GPU 67)	DECUMBENT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	PRESENT	PRESENT
Check 3 (VL 376)	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	ABSENT
G19	ERECT	FIST-TYPE	ABSENT	PRESENT	IN THUMB FINGER	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G20	ERECT	SEMI-COMPACT	PRESENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G21	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	LIGHT PURPLE	ABSENT	ABSENT	PRESENT
G22	ERECT	OPEN	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT

G23	DECUMBENT	SEMI-COMPACT	PRESENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	PRESENT
G24	ERECT	OPEN	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	PRESENT
G25	ERECT	FIST-TYPE	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	PRESENT
G26	ERECT	OPEN	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	PRESENT	PRESENT
G27	ERECT	FIST-TYPE	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	PRESENT
G28	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	LIGHT GREEN	PRESENT	ABSENT	PRESENT
G29	ERECT	COMPACT	PRESENT	PRESENT	IN THUMB FINGER	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G30	ERECT	OPEN	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G31	ERECT	OPEN	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G33	ERECT	OPEN	PRESENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G34	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G35	ERECT	FIST-TYPE	ABSENT	ABSENT	ABSENT	LIGHT BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G36	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	LIGHT BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
Check 1	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT

Check 2	DECUMBENT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	PRESENT	PRESENT
Check 3	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	ABSENT
G37	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	LIGHT PURPLE	ABSENT	ABSENT	ABSENT
G38	ERECT	OPEN	PRESENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G39	ERECT	OPEN	PRESENT	ABSENT	ABSENT	WHITE	ROUND	WHITE	PRESENT	ABSENT	ABSENT
G42	DECUMBENT	OPEN	PRESENT	ABSENT	ABSENT	LIGHT BROWN	ROUND	LIGHT GREEN	PRESENT	ABSENT	PRESENT
G43	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	LIGHT BROWN	ROUND	LIGHT GREEN	PRESENT	ABSENT	PRESENT
G46	ERECT	OPEN	PRESENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G47	ERECT	FIST-TYPE	ABSENT	PRESENT	IN THUMB FINGER	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G48	ERECT	FIST-TYPE	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G49	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G51	DECUMBENT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	LIGHT PURPLE	PRESENT	ABSENT	PRESENT
G52	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	LIGHT GREEN	PRESENT	ABSENT	PRESENT
G54	PROSTRATE	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT

Check 1	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
Check 2	DECUMBENT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	PRESENT	PRESENT
Check 3	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	ABSENT
G55	ERECT	OPEN	PRESENT	ABSENT	ABSENT	LIGHT BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G56	ERECT	COMPACT	ABSENT	PRESENT	IN THUMB FINGER	LIGHT BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G57	ERECT	FIST-TYPE	ABSENT	ABSENT	ABSENT	WHITE	ROUND	LIGHT GREEN	PRESENT	ABSENT	PRESENT
G58	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	WHITE	ROUND	WHITE	PRESENT	PRESENT	PRESENT
G59	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	PRESENT
G60	ERECT	OPEN	PRESENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G61	ERECT	OPEN	PRESENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G62	ERECT	OPEN	PRESENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G63	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G65	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	LIGHT BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G66	ERECT	COMPACT	ABSENT	PRESENT	IN THUMB FINGER	COPPER BROWN	ROUND	LIGHT GREEN	PRESENT	ABSENT	PRESENT

G67	ERECT	OPEN	PRESENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	PRESENT
G68	DECUMBENT	OPEN	PRESENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G69	DECUMBENT	OPEN	PRESENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	ABSENT
G70	ERECT	OPEN	PRESENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	ABSENT
G72	ERECT	SEMI-COMPACT	PRESENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
Check 1	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
Check 2	DECUMBENT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	PRESENT	PRESENT
Check 3	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	ABSENT
G73	ERECT	OPEN	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G74	ERECT	OPEN	PRESENT	ABSENT	ABSENT	COPPER BROWN	ROUND	LIGHT PURPLE	ABSENT	PRESENT	PRESENT
G75	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	LIGHT PURPLE	ABSENT	ABSENT	PRESENT
G76	ERECT	OPEN	PRESENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	PRESENT
G77	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	PRESENT
G78	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	PRESENT	PRESENT

G82	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	PRESENT	PRESENT
G83	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G84	ERECT	OPEN	PRESENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	ABSENT
G85	ERECT	COMPACT	ABSENT	PRESENT	IN THUMB FINGER	COPPER BROWN	ROUND	DARK GREEN	PRESENT	PRESENT	ABSENT
G86	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G87	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G88	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	LIGHT GREEN	ABSENT	ABSENT	ABSENT
G89	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	LIGHT BROWN	ROUND	DARK GREEN	ABSENT	PRESENT	ABSENT
G90	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	WHITE	ROUND	LIGHT GREEN	ABSENT	ABSENT	ABSENT
Check 1	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
Check 2	DECUMBENT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	PRESENT	PRESENT
Check 3	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	ABSENT
G91	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	WHITE	ROUND	LIGHT GREEN	ABSENT	ABSENT	PRESENT
G92	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	LIGHT BROWN	ROUND	LIGHT PURPLE	ABSENT	ABSENT	PRESENT

G93	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G94	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	LIGHT GREEN	ABSENT	ABSENT	PRESENT
G95	DECUMBENT	OPEN	PRESENT	ABSENT	ABSENT	DARK BROWN	ROUND	LIGHT GREEN	ABSENT	ABSENT	ABSENT
G96	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	PRESENT	ABSENT
G97	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	ABSENT
G98	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	PRESENT
G99	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G100	ERECT	OPEN	PRESENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G101	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G102	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G103	ERECT	FIST-TYPE	ABSENT	PRESENT	IN THUMB FINGER	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G104	ERECT	OPEN	PRESENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G106	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	PRESENT	PRESENT
G107	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	LIGHT BROWN	ROUND	DARK GREEN	ABSENT	PRESENT	PRESENT

G108	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
Check 1	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
Check 2	DECUMBENT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	PRESENT	PRESENT
Check 3	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	ABSENT
G109	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G111	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G112	ERECT	FIST-TYPE	ABSENT	PRESENT	IN THUMB FINGER	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G113	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G114	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	ABSENT
G115	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G116	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	LIGHT GREEN	ABSENT	ABSENT	PRESENT
G117	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G118	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	PRESENT	PRESENT
G121	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	LIGHT GREEN	ABSENT	ABSENT	PRESENT

G122	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	LIGHT GREEN	ABSENT	ABSENT	PRESENT
G123	DECUMBENT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G125	ERECT	COMPACT	ABSENT	PRESENT	IN THUMB FINGER	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G126	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
Check 1	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
Check 2	DECUMBENT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	PRESENT	PRESENT
Check 3	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	ABSENT
G127	ERECT	OPEN	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G128	ERECT	OPEN	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G129	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G130	ERECT	FIST-TYPE	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	LIGHT PURPLE	ABSENT	ABSENT	ABSENT
G132	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
G133	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G135	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	PRESENT

G136	ERECT	COMPACT	ABSENT	PRESENT	IN THUMB FINGER	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	ABSENT
G137	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	ABSENT
G138	ERECT	FIST-TYPE	ABSENT	ABSENT	ABSENT	WHITE	ROUND	WHITE	PRESENT	ABSENT	ABSENT
G139	ERECT	OPEN	PRESENT	ABSENT	ABSENT	LIGHT BROWN	ROUND	LIGHT GREEN	ABSENT	ABSENT	ABSENT
G141	DECUMBENT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G142	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	ABSENT
Check 1	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
Check 2	DECUMBENT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	PRESENT	PRESENT
Check 3	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	ABSENT
G139	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
G142	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	DARK GREEN	PRESENT	ABSENT	PRESENT
Check 1	ERECT	COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
Check 2	DECUMBENT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	COPPER BROWN	ROUND	DARK GREEN	ABSENT	ABSENT	PRESENT
Check 3	ERECT	SEMI-COMPACT	ABSENT	ABSENT	ABSENT	DARK BROWN	ROUND	LIGHT PURPLE	ABSENT	ABSENT	PRESENT

APPENDIX-IV

MONTHLY WEATHER DATA-2022

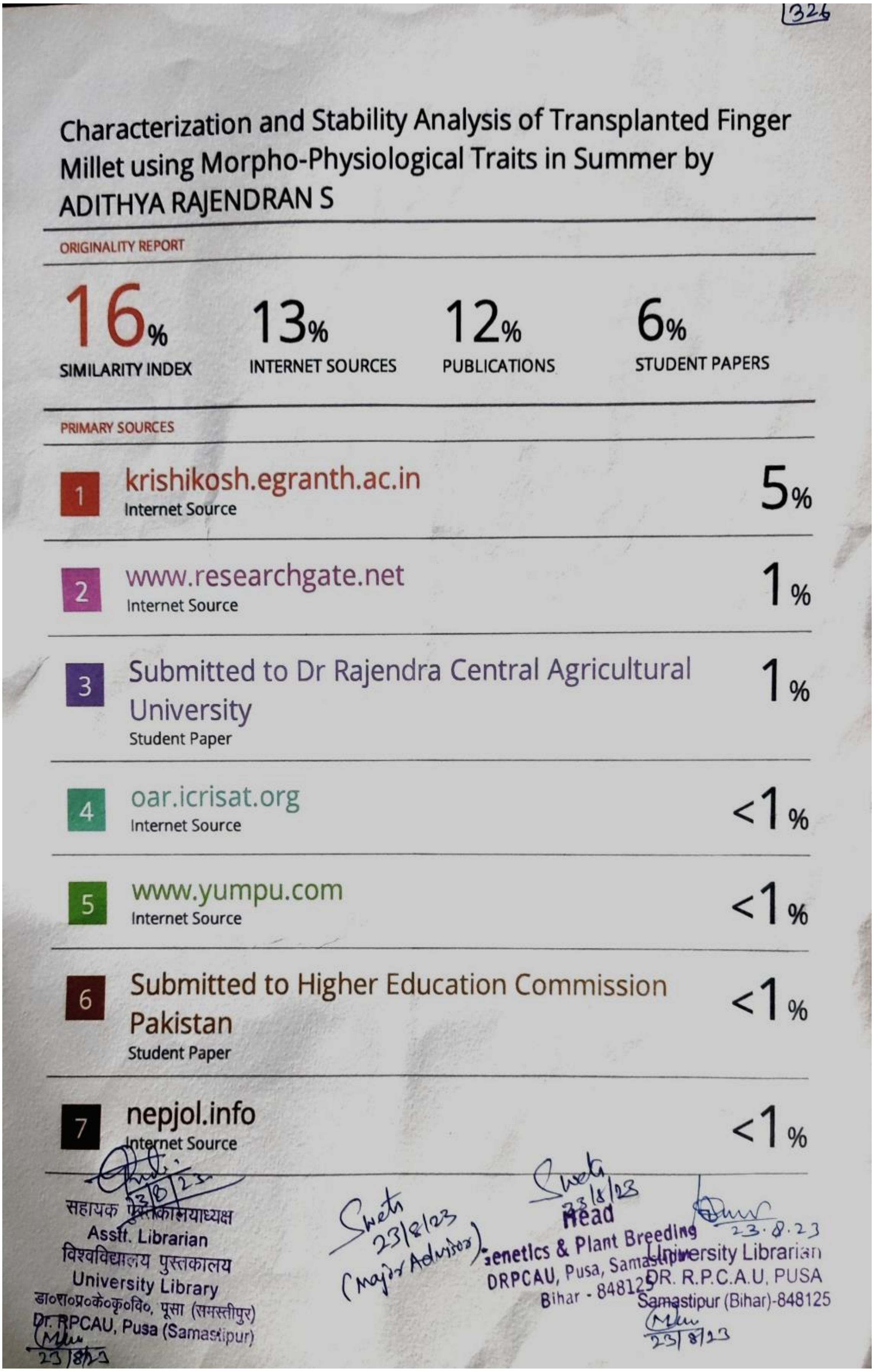
MONTH	TEMPERATURE(℃)		RELATIVE HUMIDITY (%)		RAINFALL(mm)
	MIN.	MAX.	MORNING	EVENING	
February	11.3	24.4	94.5	57.8	0.0
March	18.9	33.1	90.8	53.0	0.0
April	21.7	35.1	85.0	52.5	9.4
May	24.1	35.2	86.4	62.0	17.7
June	25.3	35.7	88.3	67.3	20.1

APPENDIX-V

MONTHLY WEATHER DATA – 2023

MONTH	TEMPERATURE (℃)		RELATIVE HUMIDITY (%)		RAINFALL (mm)
	MIN.	MAX.	MORNING	EVENING	
February	11.1	26.8	97	51	0.0
March	15.7	30.6	91	50	19.8
April	18.1	35.7	74	31	1.4
May	21.3	35.5	79	45	37.4
June	24.6	38.3	79	46	92.6

✠✠✠



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