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Title of thesis	:	"Stability analysis in promising bio-fortified red kernel genotype of rice (*Oryza sativa* L.) by using AMMI model"
Name of the student	:	Mr. Chavan Mahadeo Rajaram
Regd. No.	:	2419
Degree	:	M. Sc. (Ag.)
Discipline	:	Genetics and Plant Breeding
Name of the Research Guide	:	Dr. B. D. Waghmode Officer Incharge, Agricultural Research Station, Shirgaon, Dist. Ratnagiri
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ABSTRACT

The present investigation entitled **"Stability analysis in promising bio-fortified red kernel genotype of rice (*Oryza sativa* L.) by using AMMI model"** was conducted at the experimental farm of Agricultural Research Station, Shirgaon,Agricultural Research Station,Phondaghat and College of Agriculture, Dapoli (M.S.) during *Kharif* 2016. Stability analysis of twenty genotypes of bio-fortified red kernel rice at three environments and at three locations.The results indicated that, Genotypes, RTN-1201-51-2-1-5-48,RTN-1211-5-1-3-5 and RTN-1201-5-1-3-14 are high yielding and stable at Dapoli and Shirgaon location. Genotypes, RTN-1201-13-2-2-1-32, RTN-1201-51-2-1-5-48 andRTN-1211-6-1-3-1-8 are Favourable for characters *viz.,* Spikelet fertility, test weight, plant height, panicle length and micronutrients and stable at Shirgaon location

In interaction principle axis of AMMI biplot, first interaction principle axis (IPCA I) are favourable for all characters but second

interaction principle axis (IPCA II) are favourable for characters such as spikelets fertility, grain yield plot-1 (kg), number of panicles square meter-1, protein and amylose content (%), iron content (ppm), grain yield plant^{-1} (g) and total number of spikelets panicle^{-1}. In AMMI 1 biplot, Dapoli location favourable for characters *viz.,* day to 50 per cent flowering, number of panicles square meter^{-1}, grain yield plant^{-1}, total number of spikelets panicle^{-1}, and number of filled spikelets panicle^{-1}. Phondaghat location favourable for characters *viz.,*spikelets fertility, amylose content, protein content and Shirgaon location favourable for number of tillers plant^{-1}, panicle length, test weight, grain yield plot-1, straw yield plot-1 and plant^{-1}, plant height, iron and zinc content.

Genotype, RTN-1211-4-2-1-1 is stable for grain yield plot-1, grain yield plant^{-1} and protein content. Genotype, RTN-1201-13-2-2-1-32 is most favourable for all the characters in the entire three environments, they give high yield. More plant height, more content of micronutrients.

CHAPTER I

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important staple food crops for more than two-thirds of the world population and it has become a synonym of food itself. India (27.70 %) is second of the world's largest producers of white rice, accounting for about 21.49 per cent of all world rice production after China. The India's rice production reached to a record high of 159.20 million tonnes from an area of 43.94 million hectares in 2015-16 crop years (Anonymous, 2016).

In Maharashtra state, rice is cultivated on 1.55 million hectares area in almost all four regions *viz.* Vidharbha (8.24 lakh ha), Konkan (3.69 lakh ha), Western Maharashtra (3.55 lakh ha) and Marathwada (0.08 lakh ha) with annual production of 2.93 million tonnes of rice, accounting for about 2.79 per cent of all India rice production.

Highest productivity was observed in Konkan region i.e. 2.93 tonnes per hectares milled rice and 4.25 tonnes per hectares rough rice by production of 15.69 lakh tonnes rough rice (10.82 lakh tonnes milled rice) from 3.69 lakh hectares area (Anonymous, 2016).

Rice is a monocotyledonous angiosperm. It is princess among the cereals have 24 recognized species belonging to genus *Oryza* and tribe *Oryzeae* in the family Poaceae (Gramineae). *Oryza sativa* L. and *Oryza glaberrima* L. are the only two cultivated species. *Oryza sativa* L. is believed to have originated in Asia in the region encompassing North-Eastern India, Northern Bangladesh, and the triangle adjoining Burma, Thiland, Laos, Vietnam and Southern

China. *Oryza glaberrima,* Steud is believed to have originated on the swampy upper Niger River basin in Africa. Both the cultivated species of rice are diploid with 2n=24 chromosomes.

The earliest record of colored rice is found in the Taittiriya Samhita of the Yajurveda [1200 BC(c. 7000 BC – editors)]. During this period, rice formed an important part of the ritual offering to God. Different types of rice's were offered to different and specific divinities. In India, red rice's have occupied a special position since time immemorial. In their respective treatises, the founding fathers of ancient Ayurveda – Susruta (c. 400 BC), Charaka (c. 700 BC), and Vagbhata (c. 700 AD) refer to the medicinal value of *shali*, *vrihi*, and *shastika* rice's, and list the rice's according to their relative medicinal value, with the most useful type at the top of the list. Charaka, the author of Charaka Samhita, and other, later authorities classify the *rakta shali* or *lohit shali* rice (with red husk and grain) as the best; this variety is considered the most efficacious and subdues the three deranged *doshas* (Kumar, 1988 and Krishnamurthy, 1991).

The origin of colored rice is as old as rice itself. Rice with a red bran layer is called red rice. Though the color is confined to the bran layer, a red tinge remains even after a high degree of milling. The color of the bran ranges from light to dark red. The bran layer contains polyphenols and anthocyanin, and possesses antioxidant properties. The zinc and iron content of red rice is 2–3 times higher than that of white rice (Ramaiah and Rao, 1953).

Before the advent of high yielding varieties, which are mostly white, red rice's formed an important group in almost all the rice growing Asian countries such as Sri Lanka, Philippines, Korea, China, Japan, and India. In India, red rice was prevalent in the South, East, and the hilly tracts of the Northeast and West. Red rice cultivars showed high tolerance to such unfavorable environments as infertile soils, deep water, and mountain lands. Few red varieties were reported from the plains of Haryana, Punjab, Rajasthan, western Uttar Pradesh, and Gujarat. A number of red-grained varieties were cultivated in Kerala, Tamil Nadu, Karnataka, Bihar, Orissa, Bengal, Madhya Pradesh, and the northeastern states with areas having unfavorable conditions such as deep water, drought, sandy soils, salinity, and cold conditions. Some of the famous red varieties include Matta of Kerala, Patni of Maharashtra, and Jatu and Matali of the Kulu valley in Himachal Pradesh.

In some areas of India, red rice are considered highly nutritive and medicinal. The rice is eaten as whole grain; Red gunja is preferred for making bread and *chapati* (Rani and Krishnaiah, 2001). Glutinous rice is used in making *puttu* in South India. In Himachal Pradesh, Jatu red rice is prized for its aroma and taste. Matali and Lal dhan of Himachal Pradesh are used for curing blood pressure and fever. Kafalya, from the hills of Himachal Pradesh and Uttar Pradesh, is used for treating leucorrhea and abortion complications. Kari kagga and Atikaya of Karnataka are used for coolness and as tonic, while Neelam samba is used for lactating mothers in Tamil Nadu (Arumugasamy *et al.*, 2001). In addition of being nutritive and having medicinal value, red rice possesses many other special features. It is common experience that red and black husked rice is comparatively more resistant to storage insect pests than brown husked rice. The Patni rice of Maharashtra and the Jatu of Himachal Pradesh are well known for such hardiness and resistance. In Maharashtra, particularly in Sindhudurg, Ratnagiri, Raigad and Thane districts, local red kernel types are grown since ancient years. These varieties are Patni, Munga, Bela, Valai, Halga Red, Kala Rata, Bura Rata, Jaddu, Varangal etc. These local red rice's are mainly having bold grain type, tall and grassy stature, seed dormancy, sparse plant type, lodging and low yields. However, these varieties are having low amylose, high zinc, iron, and riboflavin and antioxidant properties. Their nutritional and physico-chemical properties are used for making soup; locally known as *Pej* and served to children, women and patients for their daily breakfast.

The introduction of high-yielding varieties in the 1970s and the market demand of white rice have resulted in a drastic reduction of the area under red rice in India. However, scientists in the states of Kerala and Tamil Nadu tried to improve the yield of red rice, and a number of red rice varieties have been developed and released. In white rice varietal improvement programs, red rice varieties have proved to be useful donors for sources of resistance or tolerance to many stress environments and for imparting resistance to important pests and diseases.

With the sharp increase in lifestyle related health issues and diseases such as diabetes, cancer, and heart problems scientists are looking at quality traits other than carbohydrates, protein, and fat in foodstuffs. Evaluation of foodstuffs now places greater focus on their antioxidant properties, glycemic index, and mineral content. Scientists are looking at rice as more than just starchy food, and are analyzing the antioxidant properties of colored rice. Also, the mineral content of rice varieties is gaining importance. Red rice has been found to have greater antioxidant property than black and white rice. With this rediscovery of their nutritive and medicinal value, red rice has begun to regain their old position and prestige.

It is now known that flavonoid and anthocyanin compounds are closely related to the anti-oxidation properties of black rice (Zhang *et al.*, 2005). Oki *et al.* (2005) found that the DPPH (1-1-

diphenyl-2-picrylhydrazyl) radical scavenging activity is higher in red rice than in black and white rice, and that this activity is correlated with polyphenols and proanthocyanidin content.

By keeping these facts in view, the present research programme entitled **“Stability analysis in promising bio-fortified red kernel genotype of rice (*Oryza sativa* L.) by using AMMI model**" with the following objectives:

1. To study the G X E interaction for grain yield and quality attributes in promising bio-fortified lines of rice.
2. To study the specificity in adaptability of rice genotypes to specific environment.
3. To identify stable bio-fortified rice genotypes for yield and quality traits.

CHAPTER II

REVIEW OF LITERATURE

The present investigation was undertaken to study the **Stability analysis in promising bio-fortified red kernel genotypes of rice (*Oryza sativa* L.) by using AMMI model**. In this chapter, efforts have been made to review the work done in India and abroad on rice in relation to study the G X E interaction for grain yield and quality attributesand adaptability of rice genotypes to specific environment, and identifying the stable bio-fortified rice genotypes for yield and quality traits. The relevant literature is presented under the following suitable headings.

2.1 G X E interaction for grain yield and quality attributes

Shrestha *et al.* (2007) studied yield stability and genotype X environment interactions of upland rice in altitudinal gradient in madagascar. According to climate change prediction, it is easy to expect positive effects on upland rice production systems in high altitude. The rise in temperature will increase productivity mainly via reduced spikelet sterility, considering that other climatic parameters such as rainfall patterns will not have adverse effects. Climate change will increase the number of genotypes which can be cultivated in upland areas; however genotypes still will be sensitive to weather experienced during sensitive physiological and phenological periods. This study was to compare contrasting genotypes which cover a broad range of phenological and physiological traits across a temperature gradient in Madagascar in order to quantify the extent of genotype by environment interaction and to characterize yield stability and adaptability across different environments.

Weikai *et al.* (2007) compared GGE biplot vs. AMMI analysis of genotype-by-environment data. This study gave four main conclusions: (i) Both GGE biplot analysis and AMMI analysis combine rather than separate G and GE in mega-environment analysis and genotype evaluation, (ii) The GGE biplot is superior to the AMMI graph in mega-environment analysis and genotype evaluation because it explains more G+GE and has the inner-product property of the biplot, (iii) The discriminating power vs. representativeness view of the GGE biplot is effective in evaluating test environments, which is not possible in AMMI analysis, and (iv) Model diagnosis for each dataset is useful, but accuracy gain from model diagnosis should not be overstated.

Adugna *et al.* (2011) studied genotype-by-environment interaction and yield stability analysis in finger millet (*Elucine coracana* L. gaertn) in Ethiopia. A total of 44 indigenous accessions selected in previous evaluations and two check varieties were tested in two sets (mixed and colored) each containing 22 entries in a total of 11 environments.The result showed that 2.5 percent, 79.1 percent and 18 .3 percent of the total sum of squares in the mixed set and 2.1 percent, 86.9 percent and 11.0 percent in the colored set was attributed to genotype, environment, and genotype × environment interaction (GEI) effects, respectively. A white seed accession from the mixed set and three other accessions from the colored set were most stable and also had above average mean grain yield across environment and thus are recommended for release as cultivars to improve finger millet production in these environments.

Hasan *et al.* (2011) investigated phenotypic stability of 12 rice genotypes for plant height, days to maturity and yield were assessed at five different locations through regression and deviation from regression using Additive Main Effect and Multiplicative Interaction

(AMMI) model. The result showed highly significant genotypic and G x E interaction. The G x E interaction influenced the relative ranking of the genotypes tested, BR1A/BR827R, Teea, BRRI dhan 33 and Mayna showed low interaction effect with score nearest to zero with above average yield. While two genotypes BRRI hybrid dhan4 and Heera995 exhibited high positive interaction effect, gave mean grain yield around 5 tonne per ha and was better suited to favorable environments. Similarly AMMI characterized the environments and identified Satkhira as a favorable environment for the better expression of the trait studied

Dewi *et al.* (2013) studied genotype × environment interaction, and stability analysis in ten lowland rice promising genotypes and two Indonesian rice varieties were grown in six environments during 2011 cropping season to determine the grain yield stability and adaptability. The study severed that, among rice promising genotypes that identified for superior performance genotypes i.e. IPB 107-F-5-1-1, IPB 115-F-3-2-1, and IPB 149-F-8-1-1 were stable for two or more stability parameters and combination with high yield potential based on AMMI biplot analysis, genotypes IPB 116-F-3-1-1, IPB 116-F-46-1-1, IPB 116-F-44-1-1 and IPB 149-F-8-1-1 were found to be more stable and have minimal interaction with environment. Whereas, genotypes IPB 117-F-4-1-1 and IPB 107-F-5-1-1 gave indication to adapt at specific environmental condition.

Emmanuel *et al.* (2013) studied genotype x environment interaction (GEI) and stability analysis of backcross inbred lnes (BILs) derived from Swarna x WAB 450 inter cross under rainfed ecosystem in North Karnataka state of India. Multi-location yield trials of nineteen superior BILs and three checks selected for earliness, productivity, reaction to blast diseases and grain size were conducted at three locations in six environments. Result of AMMI analysis showed that genotypes, environments and GEI components were significant. Out of twenty two genotypes evaluated for GEI effect in this study, six genotypes were found suitable for all environments; six genotypes for favorable environments while ten genotypes were identified as suitable for unfavorable environments.

Kulsum *et al.* (2013) investigated genotype-environment interaction and stability performance on amylose, protein and grain yield with 13 hybrid rice promising combinations in five environments. The Additive Main Effects and Multiplicative Interaction (AMMI) biplot for yield clearly indicated that the hybrids BR10A/BR12R, II32A/BR15R, II32A/BR16R, II32A/BR10R, BR9A/BR15R, BRRI hybrid dhan-2 and BRRI hybrid dhan-3 were high yielding, stable and had general adaptability at all locations. The AMMI estimation had a profound effect in producing sharp and stratified ranking patterns and on this basis BRRI hybrid dhan-2 found more adapted to a wide range of environments than the rest of the genotypes. The biplot technique was used to identify appropriate genotype to special locations. The hybrid combination II32A/BR12R was found more suitable for Gazipur location and the hybrid combination BR10A/BR13R was found suitable for Comilla region.

Tariku *et al.* (2013) reported in their genotype by environment interaction and grain yield stability analysis of rice (*Oryza sativa* L.). They studied sixteen rainfed lowland rice genotypes which were evaluated at three locations of eight environments in north western Ethiopia. The AMMI analysis of variance indicated that the genotype-by-environment interaction sum of squares was about 3.5 times larger than that for genotypes, which determined substantial differences in genotypic response across environments. On the basis of AMMI model, when the interaction was partitioned among the first four interaction principal component axis (IPCA) which cumulatively captured 91.13 percent of the total GEI. The stability study indicated that among the tested genotypes, no variety was found to be stable; however, genotypes such as GEN13, GEN12, GEN10 and GEN9 showed high yield potential in favorable environments. In this study, environments (testing locations) fell into three sections, where most of the tested genotypes showed specificity.

Akter *et al.* (2014) studied genotype x environment interaction and stability performance on grain yield with 12 rice genotypes in five environments. The ANOVA for grain yield revealed highly significant ($P < 0.01$) for genotypes, environments and their interactions. The significant interaction indicated that the genotypes respond differently across the different environments. In AMMI analysis, AMMI 1 biplot showed the hybrids G1, G2, G3 and (G4) have higher average mean yields with high main (additive) effects with positive IPCA1 score, but the hybrid (G3) being the overall best. Hence, the genotype G3 considered more adapted to a wide range of environments than the rest of genotypes. Environments, Gazipur and Jessore identified as regarded as a more stable site for high yielding hybrid rice improvement than other location for grain yield due to IPCA score near zero which had no interaction effect. In AMMI 2 biplot, Comilla and Rangpur showed the most discriminating environments, while BRRI 1A/ BRRI 827R (G1) and Heera 99-5 were found most responsive genotypes.

Islam *et al.* (2014) investigated on genotype-environment interaction and stability performance on grain yield with five rice genotypes at five locations. The ANOVA for grain yield revealed highly significant ($P<0.01$) variation among genotypes, environments and their interactions. In AMMI analysis, AMMI biplot showed that

Biswanath and Baniachang were favorable environments; Sunamganj and Sylhet Sadar were unfavorable environments. Among genotypes, BR7840-54-3-1 and BRRI dhan55 produced higher average mean yields. In AMMI-2 biplot, Habiganj Sadar and Sylhet Sadar were the most discriminating environments. The most suitable genotypes BR7840-54-3-1; BRRI dhan28 for Sylhet Sadar; BR7840-54-2-5-1 for Baniachang while genotypes BR7840-54-1-2-5 was suitable for Habiganj Sadar. Among the tested genotypes, BR7840-54-2-5-1had higher mean grain yield values coupled with small IPCA 1 scores and hence it is recommended for all environments.

Kumar *et al.* (2014) in their genotype (g) × environment (e) interaction of nine rice genotypes possessing cold tolerance at seedling stage tested over four environments was analyzed to identify stable high yielding genotypes suitable for boro environments. The results of AMMI (additive main effect and multiplicative interaction) analysis indicated that the first two principal components (PC1 and PC2) were highly significant ($P<0.05$). The partitioning of TSS (total sum of squares) exhibited that the genotype effect was a predominant source of variation followed by G×E interaction and environment. The genotype effect was nine times higher than that of the G×E interaction, suggesting the possible existence of different environment groups. The study revealed that, genotypes GEN6 and GEN4 were found to be stable based on all stability statistics. Grain yield (GY) is positively and significantly correlated with rank-sum (RS) and yield stability index (YSI).

Bose *et al.* (2015) evaluated genotype by environment interactions for grain yield in 18 rainfed upland breeding lines of rice under direct seeded conditions across four environments. The

AMMI model was applied, with additive effects for the 18 breeding lines of rice genotypes (G) and four seasons of testing (Environments = E), and multiplicative term for genotype × environment interaction. The AMMI statistical model has shown that more than 50% proportion of the total variation in grain yield was attributed due to genotype × environment interaction. Most of the breeding lines showed environment specificity. CR2897-11-1 and CR28818-1 were found to be favorable during 2011 (En. 4) and CR2908-12-5-1 and CR2899-7-1 were found to be favorable in the year 2010 (En. 3) with grain yield more than 3 t ha^{-1}.

Verma *et al.* (2016) analyzedthe highly significant effects of different environments, genotypes and interactions were observed for forage and grain yield of barley by AMMI model. The result indicated that the environments were diverse and a major part of variation in yield resulted from environmental changes. The highly significant interaction effects partitioned into IPCA1, IPCA2 and IPCA3, IPCA4; which explained 30.4, 19.4, 14.8 & 13.2 percent for forage and 37.0, 17.2, 16.1 and 12.5 percent for harvested grain yield. AMMI stability value (ASV) identified promising genotypes BH 971 and RD 2857, BH 971and NDB 1570 for forage and grain yield respectively. AMMI distance (D) marked RD 2035, BH 970 and RD 2857 for former while genotypes RD 2856, NDB 1570, BH 971for grain yield. GSI score advocated NDB 1570, RD 2035, RD2715 and BH 971, desirable genotypes for selection with forage and grain yield. Genotypes with IPCA-1 scores close to zero identified UPB 1036, BH 971, NDB 1566 and NDB 1570for forage and grain yield respectively would have wider adaptation to the tested environments as per AMMI graphical plots.

2.2 Adaptability of rice genotypes to specific environment

Mark Cooper (1999) studied and nominated Putative adaptive traits. However, there is little consensus on the definition of appropriate trait-based selection criteria to complement direct selection for yield. The complexity of the target population of environments, and the incidence of large genotype-by-environment (G × E) interactions, has stimulated interest in analysis and interpretation of yield variation in multi-environment trials as part of the process of examining the adaptation of rainfed lowland rice.

Samonte *et al.* (2004) identified the highest yielding cultivar for a specific environment on the basis of both genotype (G) and genotype × environment they demonstrated the stability and adaptability of specific cultivars were assessed by plotting their nominal grain yields at specific environments in an AMMI biplot, which aided in the identification of mega environments (environments with the same highest yielding cultivar). Appropriate check cultivars for all locations or for specific locations were identified. Through GGE biplots of SREG model analysis results, the relative yield performance of cultivars at a specific environment were illustrated, the performance of a cultivar at different environments were compared, the highest yielding cultivars at the different mega environments were identified, and ideal cultivars and test locations were identified.

Anandan *et al.* (2009) studied AMMI Analysis of yield performances in rice genotypes under coastal saline environments. They evaluated germplasm in multi-environment to access the performance and adaptation for specific or general environment. The objective of the present investigation was to analyse the pattern of Genotype x Environment (G x E) interaction for grain yield of 46 genotypes by Additive Main effects and Multiplicative Interaction

(AMMI) model using the data generated from three saline stress environments of east coastal region of Tamil Nadu, India. The results showed highly significant genotypic and G x E interaction. The G x E interaction influenced the relative ranking of the genotypes across saline stress environment condition. Among the genotypes tested, G45, G26, G27, G35 and G34 showed low interaction effect, with score nearest to zero with above average yield. While two genotypes, G36 and G19 exhibited high positive interaction effect, gave the highest mean grain yield and are better suited to favorable environment. Similarly, AMMI characterized the environments and identified E2 as a favorable environment for the better expression of the trait studied.

Michiel *et al.* (2011) studied adaptability of irrigated rice to temperature change in sahelian environments. They conducted experiment at two locations, Ndiaye and Fanaye, along the Senegal River, rice was sown on 15 consecutive dates at one month intervals starting in February 2006. Rice yield was very sensitive to sowing date and the associated temperature regimes. Spikelet sterility due to cold stress ($T < 20\ ^{0}C$) was observed when the crops were sown in August (Ndiaye), September (Ndiaye and Fanaye) and October (Ndiaye and Fanaye), and heat stress ($T > 35\ ^{0}C$) resulted in spikelet sterility when sowing took place in month of April (Ndiaye and Fanaye) and May (Fanaye). For all experiments the source and sink balance was quantified and showed that yield was most limited by sink size when sowing between July and October.

Anputhas *et al.* (2012) studied stability and adaptability analysis of rice cultivars using environment centered yield in two ways ANOVA model. In this study they used variance component analysis (VCA) technique to make the varietal recommendation for wider adaptability for many varying environments and the location specific recommendations. In this method variety × environment interaction is portioned into components for individual varieties using yield deviation approach. The average effect of variety (environment centered yield deviation - Dk) and the stability measure of each variety (variety interaction variance) are used to make the recommendations. Based on the experimental results the variety At581 gave the highest Dk value with wide adaptability selected for general recommendation. Varieties Bg305 and At303 also had relatively higher Dk and thus these two can also be selected for general cultivation purpose.

Castillo *et al.* (2013) analyzed the adaptability, stability, and genotype × environment (G×E) interaction effect, grain yield, sedimentation and wet gluten content of 13 spring wheat cultivars sown in six environments in the central-south and southern zones of Chile during two seasons. The data were analyzed by regression analysis, additive main effects and multiplicative interaction (AMMI), and the sites regression (SREG) model. By this was thus established that SREG analysis is the most efficient for this type of study since, in addition to analyzing stability, adaptability, and effect (G×E), it allows identifying the best cultivar. In this case, 'Pandora-INIA' stands out by exhibiting the best yield (7.38 tha-1), high sedimentation (36.95 cm3), and wet gluten (41.54%) indices in all the environments, and this positions it as a variety having both high yield and quality.

Hasan *et al.* (2014) identified the stable and adaptable hybrid rice genotypes and developed varieties of hybrid rice with high yield potential coupled with wide adaptability. This development by studying was under taken to assess yield performance, stability and adaptability of seventeen hybrid rice genotypes evaluated over 12 environments. The analysis of variance for growth duration and grain yield (t ha^{-1}) for genotype, environment year, environment × genotype, year × environment, year × genotype and year × environment × genotype were highly significant ($p<0.01$) showing the variable response of the genotype across environments and years. GE interaction patterns revealed by AMMI biplot analysis indicated that the hybrid rice genotypes are broadly adapted. Genotypes BRRI53A/BRRI26R, Jin23A/507R, Jin23A/BR7881-25-2-3-12 and IR79156A/F2277R were best for the environment: Gazipur and Rangpur at second and third year. Genotypes Jin23A/PR344R, BRRI11A/AGR and IR79156A/BRRI20R showing high yield performance and widely adapted to all environments.

Rumanti *et al.* (2016) studied the adaptation of hybrid rice varieties mostly are in three specific locations and two seasons. Data across location and season were analyzed by using AMMI and Eberhart Russel methods. The AMMI analysis showed that the IR79156A/PK88 was adaptable to favorable environments but unstable. This hybrid is always performing well and produces the higher yield as compared to check variety. Some of other hybrids were good only in specific location, i.e. IR62829A/BP2280-1E-12-22 and IR58029A/ BP2280-1E-12-22. Those hybrids produced higher yield in Salatiga and Malang, respectively seem to AMMI analysis, the result of Eberhart and Russell method also showed that IR79156A/PK81 was the best hybrid with regression slope (b) around 1 with the yield average higher than average of all hybrids. It indicated that this hybrid has a wide adaptation and probably can be cultivated in the wider ecosystem.

2.3Stable bio-fortified rice genotypes for yield and quality traits

Ogunbayo *et al.* (2011) investigated the comparative performance of grain yield and stability among forty-eight lowlandrice genotypes in diverse environments using the AMMI and

GGE biplot analysis. The analysis of variance revealed significant (p = 0.05) GEI effect. They tested mean grain yield of the different rice genotypes from these NERICA-L33, NERICA-L42 and NERICA-L56 were established as the most promising and stable genotypes across the test environments. FKR 19, NERICA-L49 and NERICA-L48 performed best for the grain thickness and test weight mega traits while FARO 51 performed best for grain width mega-trait. The best genotype for the grain length was NERICA-L55. Stability model of AMMI biplot was observed to be more effective and informative in mega-environment analysis compared to GGE analysis.

Padmavathi *et al.* (2012) studied on fourcms lines which were crossed with 13 restorers in a line x tester fashion for studying stability analysis of rice (*Oryza sativa* L.) hybrids, utilizing regression and AMMI models during kharif, 2010. Whereas in AMMI analysis the hybrids *viz.*, apms 10a x mtu 1071, apms 10a x mtu ii -187-6-1-1, apms 9a x mtu ii -187-6-1-1, apms 10a x mtu ii-190-1-1-1-1-1 and ir 58025a x mtu ii-110-9-1-1-1-1 were more stable as they recorded IPCA score near zero and less interaction with environments. AMMI model ANOVA brings out Gx E interaction through IPCAwhich gets combined with error in the other ANOVA and points out the utility of AMMI models in studying the G X E interaction and identifying stable genotypes for characters which so undetected in the earlier analysis.

Bose *et al.* (2014) studied additive main effects and multiplicative interaction (AMMI) analysis and genotype × environment interaction of 17 early duration rice genotypes tested over four seasons was analyzed to identify stable high yielding genotypes. AMMI analysis of variance showed highly significant genotype and environment mean squares. The biplot generated using genotypes and environmental scores for first two IPCAs revealed positioning of the four genotype groups (GG) into three sectors of the biplot.

Jambhulkar *et al.* (2014) identified the stable genotypes of rice across the different environments. The Field experiments were conducted with nine rice genotypes for four consecutive years. AMMI model was used which showed that 95 percent of the variance was explained by the first two interaction principal component analysis axis. Another new approach called AMMI Stability Index (ASI) was proposed which provides quantitative value for stability analysis which helps in the interpretation of the results. Based on ASI genotype GEN6 was found to be most stable followed by GEN4; whereas GEN3, GEN7 and GEN9 were highly unstable. Based on the ASI score and grain yield, the nine genotypes were classified into three clusters. Due to low ASI score and good average grain yield over tested environments GEN6 can be considered as a universal variety with good and stable performance over the years.

Lakew *et al.* (2014) conducted field experiment at Woreta, Metema and Pawe of North West Ethiopia during the 2008 - 09 and 2009-10 cropping seasons by using, sixteen upland rice genotypes and two standard checks were evaluated for selecting stable and high-yielding, disease-resistant and early maturing varieties. Data is analyzed with AMMI model exhibited, variations due to environments accounted for 52.48 percent of the treatment sum of square (SS) while genotypes and genotype × environment interaction explained 12.06 percent and 35.45 percent of SS, respectively. In GGE biplot, G15 and G7 respectively were the best genotypes in E1, E2, and E6. The Genotype G15 was relatively stable in grain yield across environments and it also showed relatively better resistance to major rice diseases.

Ramanjaneyulu *et al.* (2014) studied ten popular low land rice genotypes in 2007, 2008 and 2009 and were evaluated for variability, genetic divergence, stability and suitability under aerobic conditions on Alfisols. Results showed that low variability in some of the growth and yield attributes like plant height, tillers plant^{-1}, spikelet length and harvest index, whereas high heritability (broad sense) estimates were observed for quantitative characters such as test weight and grain yield. There was a significant and positive correlation of grain yield with number of tillers plant^{-1} (1.11), number of productive tillers plant^{-1} (0.99), number of grains spikelet^{-1} (0.84) and spikelet length (0.59 cm), indicating that grain yield and these traits have the same physiological basis for expression.

Temesgen *et al.* (2015) evaluated twenty bread wheat genotypes and two checks were evaluated at six test locations of Central and South Eastern Ethiopia during main growing season.The study was to quantify the magnitude of genotype by environment interaction and yield stability of bread wheat genotypes. The AMMI analysis revealed significant difference at (P=0.01) for genotype, location and genotype by location interaction for the response variable grain yield. The AMMI model clearly indicated the genotype by environment interaction by partitioning into three significant component taking 89.70 percent of genotype by environment variation 20.68 percent of the variation in the genotype by environment interaction. In general, the results of the analysis showed that bread wheat is highly sensitive to environmental changes and this necessitates screening of cultivars for wide and specific adaptation.

CHAPTER III

MATERIAL AND METHODS

The information pertaining to the experimental details and analytical methodology followed during the present investigation entitled **"Stability analysis in promising bio-fortified red kernel genotypes of rice (*Oryza sativa*L.) by using AMMI model.**"has been presented below.

3.1 Experimental site, Climate and Weather conditions:

The present investigation was carried out at three locations *viz.,* Educational and Research Farm, Department of Agricultural Botany, College of Agriculture, Dapoli,Agricultural Research Station, Shirgoan Dist. Ratnagiri, Agricultural Research Station, Phondaghat Dist. Sindhudurg during *Kharif*2016.The detail information of experimental site is given below:

3.1.1 Educational and Research Farm, Department of Agricultural Botany, College of Agriculture, Dapoli, Dist. Ratnagiri

Geographically Dapoli is situated in the tropical region on the $17^{0}45'$ North latitude and 73^{0} 12' East longitude having elevation of 250 meter above the mean sea level with warm and humid condition throughout the year.The mean annual precipitation is 4000mm which was received during the month from June to October at the location. The soil of the experimental site was lateritic. The meteorological data during the period of experimentation i.e., from June to October, 2016 was recorded at the meteorological observatory of the, College of Agriculture, Dapoli. The detail of the meteorological data is presented in Appendix I.

3.1.2 Agricultural Research Station, Shirgoan, Dist. Ratnagiri.

Geographically, Shirgaon is situated in the tropical region on the 17^0 50' North latitude and 73^0 00' East longitude having elevation of 10 meters above the mean sea level with warm and humid conditions throughout the year. The mean annual precipitation was 3000 mm which was received during the month from June to October at the location. The soil of the experimental site was lateritic. The meteorological data during the period of experimentation i.e., from June to November, 2016 was recorded at the meteorological observatory of the, Agricultural Research Station, Shirgoan. The detail of the meteorologicaldata is presented in Appendix II.

3.1.3Agricultural Research Station, Phondaghat, Tal. Kankavli, Dist. Sindhudurg.

Geographically, Phondaghat is situated in the tropical region on the $16^0$35’ North latitude and 73^0 18' East longitude having elevation of 145.11 meters above the mean sea level with warm and humid conditions throughout the year. The mean annual precipitation was3500mmwhich was received during the month from June to October at the location. The soil of the experimental site was lateritic. The meteorological data during the period of experimentation i.e., from June to November, 2016 was recorded at the meteorological observatory of the, Agricultural Research Station, Phondaghat The details of the meteorological data is presented in AppendixIII.

Biochemical analysis was done at Regional Agricultural Research Station, Karjat and Indian Institute of Rice Research

(IIRR), Hyderabad. Statistical analysis was done at Department of Agricultural Economics, College of Agriculture, Dapoli

3.2 Experiment material:

Experimental material was obtained from ARS, Shirgaon. Developed and maintained at ARS, Shirgaon (Ratnagiri).

Table1: The list of promising bio-fortified red kernel lines are given below

Sr. No.	Designation of cultures	Cross combination	Source
1	RTN-1201-13-2-2-1-32	KJT-4/Patani-6	ARS, Shirgaon
2	RTN-1201-23-2-2-1-43	KJT-4/Patani-6	ARS, Shirgaon
3	RTN-1201-51-2-1-5-48	KJT-4/Patani-6	ARS, Shirgaon
4	RTN-1209-10-1-2-1-9	RTN-13A/ MO-17	ARS, Shirgaon
5	RTN-1211-6-1-3-1-8	RTN-1A/ MO-9	ARS, Shirgaon
6	RTN-1211-6-1-4-1-11	RTN-1A/ MO-9	ARS, Shirgaon
7	RTN-1211-6-1-4-3-13	RTN-1A/ MO-9	ARS, Shirgaon
8	RTN-1211-6-1-5-1-14	RTN-1A/ MO-9	ARS, Shirgaon
9	RTN-1211-15-1-4-2-23	RTN-1A/ MO-9	ARS, Shirgaon
10	RTN-1212-4-1-2-4	RTN-13A/ MO-17	ARS, Shirgaon
11	RTN-1211-4-2-2-2	RTN-1A/ MO-9	ARS, Shirgaon
12	RTN-1210-3-1-4-5	RTN-1A/ MO-13	ARS, Shirgaon
13	RTN-1211-5-1-3-5	RTN-1A/ MO-9	ARS, Shirgaon

14	RTN-1211-6-1-2-7	RTN-1A/ MO-9	ARS, Shirgaon
15	RTN-1212-4-3-5-5	RTN-13A/ MO-17	ARS, Shirgaon
16	RTN-1201-5-1-3-14	KJT-4/Patani-6	ARS, Shirgaon
17	RTN-1211-4-2-1-1	RTN-1A/ MO-9	ARS, Shirgaon
18	RTN-1211-9-1-2-12	RTN-1A/ MO-9	ARS, Shirgaon
19	Red kernel check -1	Bela	ARS, Shirgaon
20	Red kernel check -2	Patni-6	ARS, Shirgaon

3.3 Methodology:

The experiment was conducted in the Randomized Block Design (RBD) with three replications at three locations *viz.,* Educational and Research farm Department of Agricultural Botany, College of Agriculture, Dapoli, Agricultural Research Station, Shirgoan Dist. Ratnagiri, Agricultural Research Station, Phondaghat during *Kharif* 2016. The plot size was3m x 2m along with 20 cm x 15 cm spacing and two seedlings hill^{-1}. Line to line distance was 20 cm and plant to plant was 15 cm.There were 10 lines per plot and 20 hills per line with 200 hills in each plot were transplanted.

3.4 Observations recorded on different characters:

The data of different characters was recorded on five plants mean and plot basis as follows.

3.4.1Days to 50 percent flowering:

Days to 50 percent flowering were recorded on commencement of flowering in fifty per cent on plants in the plots from the date of sowing of the plot.

3.4.2Plant height (cm):

Plant height was measured in centimeter (cm) from base of the plant (at ground level) to the tip of the main panicle at maturity stage and calculated the average for randomly selected five plants.

3.4.3Number of tillers plant^{-1}:

At the time of maturity, number of tillers was counted from randomly selected five plants and calculated the average for those randomly selected five plants.

3.4.4Number of panicles square meter^{-1}:

At the time of maturity, panicles were counted from randomly selected twenty plants and calculated the average for those randomly selected twenty plants.

3.4.5 Panicle length (cm):

The length of panicle was measured from base to the tip of panicle in centimeters at the time of maturity and calculated the average for randomly selected five panicles from five observation plant.

3.4.6 Total Number of spikeletspanicle^{-1}:

Total number of spikeletspanicle^{-1} which were matured and fully developed were counted after harvesting of five plants and calculated the average for those randomly selected five panicles from five observation plant.

3.4.7 Number of filled spikeletspanicle^{-1}:

Number of matured and developed filled spikeletspanicle^{-1}wascounted after harvesting of each of the five plants under observation and mean was calculated.

3.4.8 Spikelet fertility (%):

Spikelet fertility was obtained by using following formula.

$$\text{Spikelet fertility}(\%) = \frac{\text{Number of filled spikelets panicle}^{-1}}{\text{Total number of spikeletspanicle}^{-1}} \times 100$$

3.4.9 Test weight (g):

The harvested fully filled,matured and clean dry 1000 seed of each genotypewere collected. These were weighted and recorded in grams.

3.4.10 Grain yieldplant^{-1}(g) andplot^{-1}(kg):

The harvested fully filled, matured and clean dry panicles of the randomly selected five plants were threshed and cleaned. Then grains were weighted and recorded in grams and mean was calculated.The net plot grain yield was recorded by removing the two border lines and 20 hills each from both sides.

3.4.11 Straw yieldplant^{-1} (g) andplot^{-1}(kg):

After removing the panicles the dry matter (straw) obtained from five plants were dried in sunlight, weighted and recorded in grams and mean was calculated. The net plot straw yield was recorded by removing the two borderlines and 20 hills each from both sides.

3.4.12 Iron content (ppm):

Iron contents in the samples were estimated by using the X-ray Fluorescence Spectrophotometer (XRF) Anuradha(2012).

3.4.13 Zinc content (ppm):

Zinc contents in the samples wereestimated by using the X-ray Fluorescence Spectrophotometer (XRF) Anuradha(2012).

3.4.14Protein content (%):

The grain samples were subjected to nitrogen content analysis by modified Micro-Kjeldahl's method (Tandon, 1993). Then the protein content was calculated by multiplying the nitrogen content (%) in grains by 6.25 (AOAC, 1975).

The per cent protein was calculated by theformula:

Protein (%) = Nitrogen (%) × 6.25

3.4.15Amylose content (%):

Amylose contents of the milled rice samples were estimated by following the method suggested by Juliano (1971) involving the spectrophotometer.

Amylose content was assigned as per its contents as given below:

Property	Amylose content (%)
Waxy	1-2
Very Low	2-9
Low	9-20
Intermediate	20-25

High	25-33

3.4.16 Statisticalanalysis:

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

3.4.16.1 Stability analysis

The combined analysis of variance was proceeded to look at G × E and stability of the genotypes across all environment. The AMMI model, which combines standard analysis of variance with IPC analysis (Zobel*et al.,* 1988), was used to investigate G × E interaction. In AMMI model the contribution of each genotype and each environment to the GEI is assessed by use of the biplot graph display in which yield means are plotted against the scores of the IPCA1 (Zobel *et al.,*1988*)*.

The AMMI model is:

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

Where,

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

μ is the general mean

G_i and E_j represent the effects of the genotype and environment

λ_k is the singular value of the kth axis in the PCA

α_{ik} is the eigenvector of the ith genotype for the kth axis

γ_{jk} is the eigenvector of the jth environment for the kth axis

n is the number of principal components in the model

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

The member of the AMMI family with IPCA I axis denoted AMMI 1; whileAMMI 2 retainsIPCA II axes and so on. In general, AMMINdenotes the AMMI model with PCA axes 1 to N. AMMI 0 has no IPCA axes and is identically ANOVA**.**

3.4.16.2Steps in Computation

Environment wise analysis and pooled analysis of variance were conducted as per normal procedure. Ifgenotype, Environment and GXE interactionweresignificant; the analysis may proceed further for AMMI analysis.

Table2:Analysis of variance (ANOVA) of AMMI model for stability analysis.

Source	**DF**	**MSS**	**F**
Total	(ger-1)		
Treatment	(ge-1)		
Genotype	(g-1)	MS1	MS1/Mse3
Environment	(e-1)	MS2	MS2/Mse3
Genotype x Environment	(g-1)(e-1)	MS3	MS3/Mse3
IPCA 1	(G+E-1-2n)	MS 4	MS4/Mse3
IPCA 2	(G+E-1-2n)		

Residual			
Blocks	(r-1)		
Error	(r-1)(ge-1)	MSe	

Where,

g = Genotype,

e = Environment,

r = Replication,

MS =Mean sum of square,

MS =Mean sum of square for error

If IPCA mean sum of square are significant and residual mean square is non-significant, the step may be conducted for development of biplot. TheAMMI biplot developed by placing both genotype and environment mean value on X-axis and the respective IPCA axis eigenvector on the Y-axis.

3.4.17.3Interpretation of Biplot

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

In AMMI 2 interaction biplot between IPCA I and IPCAII, the environmentscore are joined to the origin by side lines. Site with short spokes do not exert strong interactiveforces. Those with long spokes exert strong interaction. The genotype occurring close together on the origin of centre on bipolt will tend to have similar yield in all environments while genotype far apart from origin of centre on bipolt may either differ in mean yield or show different pattern of response over the environments.

3.4.17.4Soil analysis

Available nitrogen

Available nitrogen was determined by alkaline permanganate (0.32% KMn04) method (Bubbiah and Asija, 1956),

Available phosphorus

Available phosphorus was determined by extracting the soil P with 0.5M $NaHCO_3$at pH 8.5. The soil: extractant ratio was 1:20 and shaking time was 30 minutes.

Phosphorus in the extract was determined colorimetrically by using Spectrophotometer at 660 nm wavelength as outlined by Olsen ***et al*** (1954).

Available potassium

It ***was*** estimated on Systronics Flame Photometer-128 using neutral-normal-ammonium acetate (pH 7.0) as per procedure given by Jackson (1973).

CHAPTER IV

EXPERIMENTAL RESULTS

The results obtained from the present investigation was undertaken to study the stability analysis in promising bio-fortified red kernel genotypes of rice (*Oryza sativa* L.) by using AMMI model have been presented under the following heads:

4.1 Stability analysis

Results obtained from the experiment conducted for stability analysis of twenty genotypes of rice during *Kharif* 2016, are interpreted on the basis of statistical analysis and documented graphically wherever, necessary. The results are subsequently discussed in light of the available pertinent literature for stability analysis. The experimental results on stability analysis are presented under the following sub-heads.

4.1.1 Mean performance and environmental indices of deferent characters are:

4.1.1.1 Days to 50 per cent flowering

The days to 50 per cent flowering ranged from 87.33 to 118.67 days at Dapoli (E1), 88 to 120.67 days at Phondaghat (E2) and 87 to 119.67 days at Shirgaon (E3) location (table 3). While overall mean of three environments it ranged between 87.44 to 119.67 days. Genotype, RTN-1212-4-3-5-5(120.67 days) recorded highest days to 50 per cent flowering at Phondaghat (E2) followed at Shirgaon (E3)(119.67 days) and at Dapoli (E1)(118.67 days) location. Genotype, RTN-1211-4-2-1-1(87 days) recorded lowest days to 50 per cent flowering on the basis of over all the three environments. On the basis of mean maximum days to 50 per cent flowering was recorded at Phondaghat (E2) (101.60 days) followed by Shirgaon (E3) (100.38 days) and Dapoli (E1) (100.02 days) location.

Table 3. Mean performance of genotypes over three environments for days to 50 per cent flowering and plant height (cm)

GENOTYPES	Days to 50 per cent flowering				Plant height (cm)			
	E 1	**E2**	**E 3**	**Mean**	**E 1**	**E2**	**E 3**	**Mean**
RTN-1201-13-2-2-1-32	111.00	112.33	112.67	112.00	113.97	113.63	113.60	113.73
RTN-1201-23-2-2-1-43	98.00	102.00	97.67	99.22	106.18	106.40	106.41	106.33
RTN-1201-51-2-1-5-48	88.67	89.00	88.00	88.56	109.82	110.15	110.18	110.05
RTN-1209-10-1-2-1-9	94.00	95.33	94.33	94.56	95.60	95.99	95.18	95.59
RTN-1211-6-1-3-1-8	103.33	102.00	101.00	102.11	101.47	101.50	101.50	101.49
RTN-1211-6-1-4-1-11	91.67	91.67	90.67	91.33	101.60	101.97	102.24	101.94
RTN-1211-6-1-4-3-13	95.33	96.67	95.67	95.89	106.27	106.60	106.47	106.44
RTN-1211-6-1-5-1-14	112.33	113.67	112.67	112.89	100.19	100.57	100.12	100.29
RTN-1211-15-1-4-2-23	102.00	103.33	102.33	102.56	88.53	88.87	88.01	88.47
RTN-1212-4-1-2-4	106.33	107.33	106.33	106.67	99.50	100.20	98.97	99.56
RTN-1211-4-2-2-2	94.67	95.67	94.67	95.00	96.96	97.29	95.83	96.70
RTN-1210-3-1-4-5	95.33	98.67	97.67	97.22	96.49	96.89	96.04	96.48
RTN-1211-5-1-3-5	97.33	99.00	98.00	98.11	97.18	96.85	97.57	97.20
RTN-1211-6-1-2-7	112.00	112.00	111.67	111.89	93.20	92.53	92.77	92.83
RTN-1212-4-3-5-5	118.67	120.67	119.67	119.67	98.66	98.53	99.69	98.96
RTN-1201-5-1-3-14	97.33	99.00	98.00	98.11	99.27	98.60	100.03	99.30
RTN-1211-4-2-1-1	87.33	88.00	87.00	87.44	97.57	96.53	98.66	97.59
RTN-1211-9-1-2-12	100.33	102.33	101.67	101.44	93.87	93.53	94.54	93.98
Ch-1 (Bela)	104.67	105.67	106.67	105.67	134.93	135.90	134.19	135.01
Ch-2 (Patni-6)	90.00	96.67	92.33	93.00	139.56	138.09	140.10	139.25
Mean	100.02	101.60	100.38	100.67	103.54	103.53	103.61	103.56
CD at 5 %	16.61	16.36	16.85		11.71	9.95	13.26	
CV at 5 %	10.05	9.74	10.16		6.84	5.81	7.74	

4.1.1.2 Plant height (cm)

The plant height ranged from 88.53 to 139.56 cm at Dapoli (E1), 88.87 to 138.09 cm at Phondaghat (E2), 88.01 to 140.10 cm at Shirgaon (E3) location. While overall mean over three environments it ranged between 88.47 to 139.25 cm. Genotype, Patni-6 recorded highest plant height in all three environments 140.10, 139.56 and 138.09 cm at Shirgaon (E3), Dapoli (E1) and Phondaghat (E2) location respectively. Genotype, Patni-6 (140.10 cm) given highest plant height while as the genotype, RTN-1210-3-1-2-3 (88.01 cm) given shortest plant height over all basis of three environments.

4.1.1.3 Number of tillers plant^{-1}

The total number of tillers plant^{-1} of red rice ranged from 4.40 to 8.07 at Dapoli (E1), 4.60 to 8.00 at Phondaghat (E2), 5.97 to 7.67 at Shirgaon (E3) location. While overall mean over three locations it ranged between 5.31 to 7.62. Genotype, RTN-1201-23-2-2-30 recorded highest number of tillers plant^{-1} (8.07) at Dapoli (E1) location followed by RTN-1211-4-2-1-1 at Phondaghat (E2) and RTN-1201-14-1-1-26 (7.67) at Shirgaon (E3) location. On the basis of pooled mean, genotype, RTN-1201-23-2-2-30 (8.07) given maximum number of tillers plant^{-1}While the RTN-1209-15-2-1-15 (4.40) given minimum number of tillers plant^{-1} over all the three environments.

Table 4.Mean performance of genotypes over three environments for number of tillers plant^{-1} and number of panicles square meter^{-1}

GENOTYPES	Number of tillers plant^{-1}				Number of panicles square meter^{-1}			
	E 1	**E 2**	**E 3**	**Mean**	**E 1**	**E 2**	**E 3**	**Mean**
RTN-1201-13-2-2-1-32	8.07	8.00	6.80	7.62	124.33	122.33	119.33	122.00
RTN-1201-23-2-2-1-43	4.80	6.40	6.20	5.80	107.00	106.00	106.67	106.56
RTN-1201-51-2-1-5-48	6.47	6.93	6.07	6.49	101.33	112.33	98.00	103.89
RTN-1209-10-1-2-1-9	7.33	6.27	6.93	6.84	128.67	119.00	114.67	120.78
RTN-1211-6-1-3-1-8	5.53	5.20	5.97	5.57	115.67	109.00	109.67	111.44
RTN-1211-6-1-4-1-11	6.13	4.60	5.97	5.57	104.67	102.00	101.33	102.67
RTN-1211-6-1-4-3-13	7.00	5.33	6.47	6.27	110.67	111.00	108.67	110.11
RTN-1211-6-1-5-1-14	6.87	4.73	6.62	6.07	111.67	113.00	111.67	112.11
RTN-1211-15-1-4-2-23	6.73	5.07	6.43	6.08	100.33	102.00	102.00	101.44
RTN-1212-4-1-2-4	7.53	5.07	6.10	6.23	127.33	122.33	131.33	127.00
RTN-1211-4-2-2-2	6.80	5.07	6.53	6.13	118.00	115.67	117.00	116.89
RTN-1210-3-1-4-5	7.40	6.07	7.67	7.04	120.00	114.67	119.33	118.00
RTN-1211-5-1-3-5	6.20	6.80	7.13	6.71	130.00	122.33	129.33	127.22
RTN-1211-6-1-2-7	6.73	6.00	6.53	6.42	121.00	124.33	124.67	123.33
RTN-1212-4-3-5-5	5.60	6.13	5.97	5.90	127.00	127.00	120.67	124.89
RTN-1201-5-1-3-14	6.13	5.40	7.20	6.24	122.00	121.67	127.67	123.78
RTN-1211-4-2-1-1	6.47	5.20	6.60	6.09	116.67	117.00	120.00	117.89
RTN-1211-9-1-2-12	7.00	5.87	7.87	6.91	133.33	132.67	134.33	133.44
Ch-1 (Bela)	4.57	3.97	7.40	5.31	131.00	128.67	129.33	129.67
Ch-2 (Patni-6)	4.40	4.73	7.67	5.60	105.00	106.00	101.67	104.22
Mean	6.39	5.64	6.71	6.25	117.78	116.45	116.37	116.87
CD at 5 %	1.72	1.64	1.11		9.74	11.10	10.70	
CV at 5 %	16.33	17.64	10.03		5.01	5.77	5.56	

4.1.1.4 Number of panicles square meter^{-1}

The number of panicles square meter^{-1} of red rice ranged from 100.33 to 133.33 at Dapoli(E1), 102 to 128.67 at Phondaghat(E2), 98 to 134.33 at Shirgaon(E3) location. While overall mean over three environments it ranged between 101.44 to 133.44. Genotype, RTN-1211-9-1-2-12 recorded higher number of panicles square meter^{-1} (134.33) at Shirgaon(E3) location followed by RTN-1211-9-1-2-12 (133.33) at Dapoli(E1) and Bela (128.67) at Phondaghat(E2) location. On the basis of pooled mean, genotype, RTN-1211-9-1-2-12 (134.33) given higher number of panicles square meter^{-1}WhileRTN-1201-44-1-1-31 (98) given lower number of panicles square meter^{-1} over all the three environments.

4.1.1.5 Panicle length (cm)

The panicle length ranged from 19.63 to 28.43 cm at Dapoli(E1), 21.13 to 28.50 cm at Phondaghat(E2) and 21.73 to 28.33 cm at Shirgaon(E3) location (table 5). While overall mean over three environments it ranged between 19.33 to 27.08 cm. Genotype, Bela recorded longest panicle length (28.50 cm) at Phondaghat(E2) location followed by RTN-1211-6-1-2-7 (28.43 cm) at Dapoli(E1) and Patni-6 (20)-6 (28.33 cm) at Shirgaon(E3) location. Genotype, RTN-1211-6-1-2-7 (28.50 cm) given longest panicle length mean While the genotype, RTN-1210-3-1-2-3 (19.63 cm) given shortest panicle length mean over all the three environments. On the basis of pooled mean, Genotype, Bela (28.50 cm) showed longest panicle length mean across all the three enivironments.

Table 5.Mean performance of genotypes over three environments for panicle length (cm) and total number of spikelets panicle^{-1}

GENOTYPES	Panicle Length (cm)				Total number of spikeletspanicle^{-1}			
	E 1	E2	E 3	Mean	E 1	E 2	E 3	Mean
RTN-1201-13-2-2-1-32	23.90	23.77	25.33	24.33	169.00	180.00	193.67	180.89
RTN-1201-23-2-2-1-43	24.53	22.67	25.57	24.26	236.00	181.67	163.00	193.56
RTN-1201-51-2-1-5-48	24.10	27.50	26.30	25.97	175.67	140.00	171.33	162.33
RTN-1209-10-1-2-1-9	24.80	25.27	26.00	25.36	173.33	212.33	210.67	198.78
RTN-1211-6-1-3-1-8	25.20	24.30	26.87	25.46	204.33	164.33	201.33	190.00
RTN-1211-6-1-4-1-11	22.20	24.07	21.73	22.67	161.33	186.00	172.00	173.11
RTN-1211-6-1-4-3-13	22.07	27.53	27.27	25.62	187.33	197.67	101.67	162.22
RTN-1211-6-1-5-1-14	20.80	25.80	23.00	23.20	226.00	136.67	160.00	174.22
RTN-1211-15-1-4-2-23	19.63	23.90	22.93	22.16	163.00	170.67	171.00	168.22
RTN-1212-4-1-2-4	26.60	24.87	24.53	25.33	227.33	177.67	168.00	191.00
RTN-1211-4-2-2-2	24.73	23.67	22.67	23.69	218.33	155.00	138.33	170.56
RTN-1210-3-1-4-5	28.43	24.97	22.53	25.31	216.00	133.67	162.00	170.56
RTN-1211-5-1-3-5	23.07	21.13	22.07	22.09	200.00	131.33	184.67	172.00
RTN-1211-6-1-2-7	22.73	22.37	24.13	23.08	177.00	111.00	162.33	150.11
RTN-1212-4-3-5-5	24.10	25.03	24.07	24.40	166.00	131.67	165.33	154.33
RTN-1201-5-1-3-14	28.17	22.50	26.53	25.73	186.33	139.00	135.33	153.56
RTN-1211-4-2-1-1	25.20	22.70	24.20	24.03	251.33	221.00	197.33	223.22
RTN-1211-9-1-2-12	23.53	22.03	24.67	23.41	192.00	109.67	149.00	150.22
Ch-1 (Bela)	24.47	28.50	28.27	27.08	180.33	151.33	149.33	160.33
Ch-2 (Patni-6)	26.60	4.73	28.33	19.89	184.67	133.33	110.67	142.89
Mean	24.24	23.37	24.85	24.15	194.77	158.20	163.35	172.11
CD at 5 %	4.06	4.08	3.70		48.44	29.23	47.66	
CV at 5 %	10.12	10.03	9.01		15.05	11.18	17.65	

4.1.1.6 Total number of spiklets panicle^{-1}

The total number of spiklets panicle^{-1} of red rice ranged from 161.33 to 236 at Dapoli(E1), 109.67 to 221 at Phondaghat(E2), 101.67 to 210.67 at Shirgaon(E3) location. While overall mean over three environments it ranged between 162.33 to 223.22. Genotype, RTN-1201-23-2-2-30 recorded highest total number of spiklets panicle^{-1} (236) at Dapoli(E1) location followed by RTN-1211-4-2-1-1 (221) at Phondaghat(E2)and RTN-1201-14-1-1-26 (210.67) at Shirgaon(E3) location. On the basis of pooled mean, genotype, RTN-1201-23-2-2-30(236) given highest total number of spiklets panicle^{-1}While the genotype, RTN-1209-15-2-1-15 (101.67) given lower total number of spiklets panicle^{-1} over all the three environments.

4.1.1.7 Number of filled spiklets panicle^{-1}

The number of filled spiklets panicle^{-1}ranged from 111.67 to 199.67 at Dapoli(E1), 87.33 to 187 at Phondaghat(E2), 82.33 to 175.33 at Shirgaon(E1) location (table 6)While overall mean over three environments it ranged between 117.33 to 167.11. Genotype, RTN-1211-6-1-2-7 recorded maximum number of filled spiklets panicle^{-1}(199.67) at Dapoli location followed by RTN-1201-14-1-1-26 (187) at Phondaghat and RTN-1201-5-1-3-14 (175.33) at Shirgaon location. Genotype, RTN-1211-4-2-2-2 (199.67) given maximum number of filled spiklets per panicle mean,WhileRTN-1209-15-2-1-15 (82.33) given minimum number of filled spiklets panicle^{-1} over all basis mean of three environments.

Table 6. Mean performance of genotypes over three environments for number of filled spikletes panicle^{-1} and spikelet fertility (%)

GENOTYPES	Number of filled spikletes panicle^{-1}				Spikelet fertility (%)			
	E 1	E2	E 3	Mean	E 1	E 2	E 3	Mean
RTN-1201-13-2-2-1-32	151.33	159.00	169.67	160.00	87.68	87.84	85.08	86.87
RTN-1201-23-2-2-1-43	196.67	159.00	145.67	167.11	93.97	85.18	81.99	87.05
RTN-1201-51-2-1-5-48	158.00	117.67	148.00	141.22	90.36	87.08	87.90	88.45
RTN-1209-10-1-2-1-9	147.00	187.00	166.00	166.67	81.49	91.98	84.60	86.02
RTN-1211-6-1-3-1-8	168.00	147.67	175.33	163.67	88.26	89.93	87.37	88.52
RTN-1211-6-1-4-1-11	111.67	162.67	150.00	141.44	79.16	88.54	77.38	81.70
RTN-1211-6-1-4-3-13	156.00	183.33	82.33	140.56	86.33	92.09	80.58	86.33
RTN-1211-6-1-5-1-14	197.00	119.67	108.33	141.67	87.05	89.92	75.86	84.28
RTN-1211-15-1-4-2-23	130.33	150.33	95.33	125.33	83.54	87.12	75.66	82.11
RTN-1212-4-1-2-4	157.00	158.00	152.33	155.78	69.39	87.67	88.42	81.83
RTN-1211-4-2-2-2	179.00	130.00	99.33	136.11	79.09	81.47	73.55	78.04
RTN-1210-3-1-4-5	169.33	113.67	134.33	139.11	77.89	82.36	75.18	78.48
RTN-1211-5-1-3-5	171.33	105.00	153.00	143.11	85.75	79.63	85.06	83.48
RTN-1211-6-1-2-7	155.67	87.33	109.00	117.33	87.84	77.70	68.65	78.06
RTN-1212-4-3-5-5	144.33	114.00	115.33	124.56	87.19	88.40	81.37	85.65
RTN-1201-5-1-3-14	152.67	103.33	101.33	119.11	79.04	86.17	81.42	82.21
RTN-1211-4-2-1-1	199.67	183.33	129.67	170.89	79.79	81.99	70.92	77.57
RTN-1211-9-1-2-12	163.67	99.00	131.67	131.44	85.36	87.30	84.03	85.57
Ch-1 (Bela)	155.67	134.00	119.33	136.33	85.51	89.50	86.17	87.06
Ch-2 (Patni-6)	153.67	122.00	102.33	126.00	82.83	91.87	88.73	87.81
Mean	160.90	136.80	129.42	142.37	83.88	86.69	81.00	83.85
CD at 5 %	36.98	29.52	30.01		9.93	7.58	11.15	
CV at 5 %	13.90	13.05	14.03		7.16	5.29	8.33	

4.1.1.8 Spiklet fertility (%)

The spiklet fertility of rice ranged from 77.89 to 93.97 per cent at Dapoli(E1), 77.70 to 92.09 per cent at Phondaghat(E1), 68.65 to 88.73 per cent at Shirgaon(E1) location. While overall mean over three environments it ranged between 78.04 to 88.52 per cent. Genotype, RTN-1210-3-1-2-3 recorded maximum spiklet fertility (93.97 %) at Dapoli followed by RTN-1209-15-2-1-15 (92.09 %) at Phondaghat and Patni-6 (88.73 %) at Shirgaon location. On the basis of pooled mean, RTN-1210-3-1-2-3 (93.97 %) given maximum spiklet fertility, WhileRTN-1211-9-1-3-13 (68.65 %) given minimum spiklet fertility over all the three environments.

4.1.1.9 Test weight (g)

The test weight ranged from 17.74 to 29.70 g at Dapoli(E1), 18.74 to 32.91 g at Phondaghat(E1)and 19.71 to 33.34 g at Shirgaon(E1) location. While overall mean over three environments it ranged between 18.84 to 31.04 g. Genotype, Patni-6 recorded highest test weight (33.34 g) at Shirgaon location followed by Patni-6 (32.91 g) at Phondaghat and Bela(29.70 g) at Dapoli location. Genotype, Patni-6 (33.34 g) given highest test weight mean While the RTN-1201-12-1-2-21 (17.74 g) given lowest test weight mean over all the three environments.

4.1.1.10 Grain yield plant^{-1} (g)

The grain yield plant^{-1} of rice ranged from 8.17 to 10.73 g at Dapoli(E1), 5.60 to 10.50 g at Phondaghat(E), 6.97 to 12.37 g atShirgaon(E1) location (table 7).While overall mean over three environments it

Table 7. Mean performance of genotypes over three environments for test weight (g) and grain yield plant-1

GENOTYPES	Test weight (g)				Grain yield plant^{-1}			
	E 1	**E2**	**E 3**	**Mean**	**E 1**	**E 2**	**E 3**	**Mean**
RTN-1201-13-2-2-1-32	17.74	20.36	22.13	20.08	10.00	10.50	8.53	9.68
RTN-1201-23-2-2-1-43	18.08	19.90	19.93	19.30	9.47	8.87	6.97	8.43
RTN-1201-51-2-1-5-48	23.88	25.89	24.67	24.81	10.73	7.87	10.73	9.78
RTN-1209-10-1-2-1-9	22.08	24.05	26.31	24.15	10.17	8.33	9.00	9.20
RTN-1211-6-1-3-1-8	20.94	21.95	23.58	22.16	9.40	7.43	11.20	9.34
RTN-1211-6-1-4-1-11	21.10	22.55	22.91	22.19	8.20	6.93	9.63	8.26
RTN-1211-6-1-4-3-13	21.29	22.32	22.57	22.06	8.17	6.93	8.63	7.91
RTN-1211-6-1-5-1-14	21.88	22.74	22.20	22.27	10.20	7.50	9.80	9.17
RTN-1211-15-1-4-2-23	20.90	24.55	24.56	23.34	9.17	7.77	12.37	9.77
RTN-1212-4-1-2-4	19.18	22.96	23.14	21.76	9.00	6.73	11.30	9.01
RTN-1211-4-2-2-2	17.99	20.42	19.89	19.43	8.63	7.80	7.80	8.08
RTN-1210-3-1-4-5	20.44	21.07	23.80	21.77	9.87	8.43	8.07	8.79
RTN-1211-5-1-3-5	18.50	20.22	25.33	21.35	9.47	8.93	10.97	9.79
RTN-1211-6-1-2-7	20.92	19.98	22.08	20.99	10.17	9.40	7.87	9.14
RTN-1212-4-3-5-5	22.10	21.87	20.47	21.48	9.37	8.40	7.80	8.52
RTN-1201-5-1-3-14	21.51	23.12	21.60	22.08	10.23	9.40	10.10	9.91
RTN-1211-4-2-1-1	18.07	18.74	19.71	18.84	10.37	7.53	8.00	8.63
RTN-1211-9-1-2-12	20.55	19.93	18.76	19.74	8.73	5.60	8.13	7.49
Ch-1 (Bela)	29.70	31.43	31.98	31.04	8.67	6.67	10.20	8.51
Ch-2 (Patni-6)	26.61	32.91	33.34	30.95	6.77	6.50	8.67	7.31
Mean	21.17	22.85	23.45	22.49	9.34	7.88	9.29	8.84
CD at 5 %	3.51	3.87	4.59		1.33	1.85	1.71	
CV at 5 %	10.02	10.24	11.85		8.60	14.22	11.11	

ranged between 7.31 to 9.91 g. RTN-1210-3-1-2-3 (12.37 g) recorded highest grain yield plant^{-1} at Shirgaon location followed by RTN-1201-44-1-1-31 (10.73 g) at Dapoli and RTN-1201-12-1-2-21(10.50 g) at Phondaghat location. On the basis of pooled mean, genotype, RTN-1210-3-1-2-3 (12.37 g) given highest grain yield plant^{-1}While RTN-1211-9-1-2-12 (5.60 g) given lowest grain yield plant^{-1} over all the three environments.

4.1.1.11 Straw yield plant^{-1} (g)

The straw yield plant^{-1} of red rice ranged from 15.07 to 22.07 g in Dapoli(E1), 19.46 to 23.50 g in Phondaghat(E2), 15.60 to 24.53 g in Shirgaon(E1)location. While overall mean over three environments it ranged between 18.17 to 21.25 g. Genotype, Bela recorded highest straw yield plant^{-1} (24.53 g) at Shirgaon location followed by RTN-1211-6-1-2-7 (23.50 g) at Phondaghat and RTN-1211-6-1-2-7 (22.07 g) at Dapoli location. Genotype, Bela (24.53 g) give highest straw yield plant^{-1} while as the RTN-1209-15-2-1-15 (15.07 g) giveminimum straw yield plant^{-1} over all the three environments. On the basis of pooled, Bela (24.53 g) showed highest straw yield plant^{-1} across all the three enivironments.

4.1.1.12 Grain yield plot^{-1} (kg)

The grain yield plot^{-1} of red rice ranged from 1.67 to 2.77 kg at Dapoli(E1), 1.82 to 2.44 kg at Phondaghat(E2), 1.68 to 2.72 kg at Shirgaon(E3)location (table 8).While overall mean over three environments it ranged between 1.92 to 2.34 kg. Genotype, RTN-1211-6-1-2-7 recorded highest grain yield plot^{-1} (2.77 kg) at Dapoli followed by

Table 8. Mean performance of genotypes over three environments for straw yield plant^{-1} and grain yield plot^{-1}

	Straw yield plant^{-1}				Grain yield plot^{-1}			
GENOTYPE	**E 1**	**E2**	**E 3**	**Mean**	**E 1**	**E 2**	**E 3**	**Mean**
RTN-1201-13-2-2-1-32	17.93	20.37	21.07	19.79	2.10	1.82	2.17	2.03
RTN-1201-23-2-2-1-43	20.80	21.80	19.13	20.58	2.03	2.08	2.22	2.11
RTN-1201-51-2-1-5-48	17.47	23.20	18.83	19.83	2.43	2.15	1.68	2.09
RTN-1209-10-1-2-1-9	15.07	19.46	19.97	18.17	1.67	2.33	1.95	1.98
RTN-1211-6-1-3-1-8	17.67	22.35	20.80	20.27	2.04	1.88	2.67	2.20
RTN-1211-6-1-4-1-11	16.77	22.97	17.80	19.18	2.10	2.32	1.82	2.08
RTN-1211-6-1-4-3-13	15.97	23.37	15.60	18.31	1.73	2.35	2.08	2.06
RTN-1211-6-1-5-1-14	17.20	20.00	18.60	18.60	2.13	2.03	2.08	2.08
RTN-1211-15-1-4-2-23	15.20	21.00	18.43	18.21	1.93	2.19	2.13	2.08
RTN-1212-4-1-2-4	17.73	21.60	16.35	18.56	2.03	1.85	2.72	2.20
RTN-1211-4-2-2-2	18.20	22.93	17.70	19.61	2.10	1.99	2.05	2.05
RTN-1210-3-1-4-5	22.07	23.50	18.18	21.25	2.77	2.44	1.71	2.30
RTN-1211-5-1-3-5	20.43	20.97	15.99	19.13	2.60	1.90	1.99	2.16
RTN-1211-6-1-2-7	20.30	21.03	16.27	19.20	2.63	2.11	2.29	2.34
RTN-1212-4-3-5-5	17.90	22.30	16.37	18.86	2.37	2.02	2.57	2.32
RTN-1201-5-1-3-14	20.30	22.77	15.60	19.56	2.17	1.92	2.28	2.12
RTN-1211-4-2-1-1	20.03	19.97	18.01	19.34	2.08	1.91	2.43	2.14
RTN-1211-9-1-2-12	21.20	20.23	18.00	19.81	1.70	1.98	2.08	1.92
Ch-1 (Bela)	20.60	18.90	20.07	19.86	2.27	1.85	2.57	2.23
Ch-2 (Patni-6)	17.40	21.30	24.53	21.08	1.70	1.85	3.10	2.22
Mean	18.51	21.50	18.37	19.46	2.13	2.05	2.23	2.14
CD at 5 %	3.37	2.74	3.39		0.43	0.34	0.66	
CV at 5 %	11	7.71	11.18		12.17	10.05	17.97	

RTN-1211-4-2-2-2 (2.72 kg) at Shirgaon and RTN-1211-6-1-2-7 (2.44 kg) at Phondaghat location. On the basis of pooled mean, RTN-1211-6-1-2-7 (2.77 kg) given highest grain yield plot^{-1}WhileRTN-1201-14-1-1-26 (1.67 kg) given lowest grain yield plot^{-1} over all the three environments.

4.1.1.13 Straw yield plot^{-1} (kg)

The straw yield plot^{-1} of red rice ranged from 2.83 to 5.37 kg in Dapoli(E1), 3.30 to 5.43 kg in Phondaghat(E2), 2.48 to 4.00 kg in Shirgaon(E3) location. While overall mean over three environments it ranged between 3.56 to 4.43 kg. Genotype, RTN-1209-15-2-1-15 recorded highest straw yield plot^{-1} (5.43 kg) at Phondaghat location followed by RTN-1209-15-2-1-15 (5.37 kg) at Dapoli and RTN-1201-12-1-2-21 (4.00 kg) at Shirgaon location. Genotype, RTN-1209-15-2-1-15 (5.43 kg) given highest mean straw yield plot^{-1}WhileRTN-1211-9-1-3-13 (2.48 kg) given lower straw yield plot^{-1} mean over all the three environments.

4.1.1.14 Iron content (ppm)

The total iron content in rice ranged from 4.60 to 10.47 ppm at Dapoli(E1), 5.83 to 11.27 ppm at Phondaghat(E2), 5.77 to 11.10 ppm at Shirgaon(E3)location (table 9).While overall mean over three environments it ranged between 5.40 to 10.52 ppm. Genotype, Bela (11.27 ppm) recorded highest total iron content at Phondaghat followed by RTN-1210-3-1-4-5 (11.10 ppm) at Shirgaon and Bela (10.47 ppm) at Dapoli location. On the basis of pooled mean, , Bela (11.27 ppm) given highest total iron content, While

Table 9. Mean performance of genotypes over three environments for straw yield plot^{-1} and iron content (ppm)

GENOTYPES	Straw yield plot^{-1}				Iron content (ppm)			
	E 1	E2	E 3	Mean	E 1	E2	E 3	Mean
RTN-1201-13-2-2-1-32	4.03	4.00	4.00	4.01	5.97	6.60	7.07	6.54
RTN-1201-23-2-2-1-43	4.07	4.33	3.41	3.93	5.33	6.37	6.57	6.09
RTN-1201-51-2-1-5-48	3.57	4.92	3.53	4.00	8.97	9.23	9.10	9.10
RTN-1209-10-1-2-1-9	2.83	3.88	3.70	3.47	6.37	6.87	6.90	6.71
RTN-1211-6-1-3-1-8	3.30	3.84	3.85	3.66	7.77	8.63	8.23	8.21
RTN-1211-6-1-4-1-11	3.20	4.72	3.05	3.66	7.97	8.97	9.00	8.64
RTN-1211-6-1-4-3-13	5.37	5.43	2.50	4.43	7.50	8.70	9.30	8.50
RTN-1211-6-1-5-1-14	3.13	4.01	3.53	3.56	6.47	7.73	7.27	7.16
RTN-1211-15-1-4-2-23	3.30	3.89	3.24	3.48	6.00	7.60	7.07	6.89
RTN-1212-4-1-2-4	3.63	4.76	2.80	3.73	4.60	5.83	5.77	5.40
RTN-1211-4-2-2-2	3.90	4.53	3.21	3.88	9.67	10.80	11.10	10.52
RTN-1210-3-1-4-5	4.50	4.37	3.00	3.96	9.53	10.57	10.60	10.23
RTN-1211-5-1-3-5	3.93	3.95	2.80	3.56	6.63	8.63	9.77	8.34
RTN-1211-6-1-2-7	3.93	3.79	2.48	3.40	9.00	9.93	10.57	9.83
RTN-1212-4-3-5-5	3.67	4.17	3.64	3.82	8.57	9.70	10.13	9.47
RTN-1201-5-1-3-14	4.33	4.90	2.99	4.08	9.57	10.13	10.03	9.91
RTN-1211-4-2-1-1	4.03	4.00	3.44	3.82	8.57	9.53	10.13	9.41
RTN-1211-9-1-2-12	4.20	3.55	2.94	3.56	9.23	9.90	10.90	10.01
Ch-1 (Bela)	4.30	3.30	3.33	3.64	10.47	11.27	10.70	10.81
Ch-2 (Patni-6)	3.30	3.85	3.90	3.68	9.23	10.00	10.53	9.92
Mean	3.83	4.21	3.27	3.77	7.87	8.85	9.04	8.59
CD at 5 %	1.03	0.75	0.81		1.32	1.91	1.68	
CV at 5 %	16.35	10.82	15.09		10.17	13.07	11.27	

the genotype, RTN-1211-4-2-2-2 (4.60 ppm) given lowest total iron content over all the three environments.

4.1.1.15 Zinc content (ppm)

The total zinc content in red rice ranged from 11.57 to 28.27 ppm in Dapoli(E1), 14.10 to 27.57 ppm in Phondaghat(E2), 13.12 to 28.67 ppm in Shirgaon(E3)location. While overall mean over three environments it ranged between 13.12 to 28.16 ppm. Genotype, RTN-1211-9-1-2-12 (28.67 ppm) recorded highest total zinc content at Phondaghat followed by RTN-1211-9-1-2-12 (28.27 ppm) at Shirgaon and RTN-1211-9-1-2-12 (27.57 ppm) at Dapoli location. WhileRTN-1201-12-1-2-21 (11.57 ppm) given lowest total zinc content over all the three environments.

4.1.1.16 Protien content (%)

The total protien content in red rice genotype ranged from 6.133 to 8.80 per cent at Dapoli(E1), 5.80 to 8.23 per cent at Phondaghat(E2), 5.86 to 8.56 per cent at Shirgaon(E3) location (table 10).While overall mean over three environments it ranged between 5.96 to 8.53 per cent. Genotype, Patni-6 (8.80 %) recorded highest total protien content at Dapoli followed by Bela (8.56 %) at Shirgaon and Phondaghat (8.23 %) location. On the basis of pooled mean, genotype, RTN-1211-9-1-3-13 (8.80 %) given highest total protien content, while as the, RTN-1210-3-1-2-3 (5.80 %) given lowest total protien content over all the three environments. The highest total protien content mean was

Table 10. Mean performance of genotypes over three environments for total zinc content (ppm) and protein content

GENOTYPES	**Zinc content (ppm)**				**Protein content (%)**			
	E 1	**E 2**	**E 3**	**Mean**	**E 1**	**E2**	**E 3**	**Mean**
RTN-1201-13-2-2-1-32	11.567	13.700	14.100	13.122	7.950	8.067	8.133	8.050
RTN-1201-23-2-2-1-43	15.467	16.033	17.467	16.322	7.700	7.467	8.167	7.778
RTN-1201-51-2-1-5-48	13.667	14.100	15.400	14.389	7.200	7.667	6.967	7.278
RTN-1209-10-1-2-1-9	14.067	15.000	15.700	14.922	6.133	5.900	5.867	5.967
RTN-1211-6-1-3-1-8	16.333	15.800	16.500	16.211	7.667	8.000	7.667	7.778
RTN-1211-6-1-4-1-11	11.867	15.800	18.333	15.333	6.400	6.000	6.100	6.167
RTN-1211-6-1-4-3-13	18.533	19.067	19.267	18.956	7.200	7.067	7.233	7.167
RTN-1211-6-1-5-1-14	16.333	17.067	17.233	16.878	7.600	7.433	7.800	7.611
RTN-1211-15-1-4-2-23	19.933	19.633	19.633	19.733	6.133	5.800	6.367	6.100
RTN-1212-4-1-2-4	16.467	17.467	17.900	17.278	7.367	7.167	7.367	7.300
RTN-1211-4-2-2-2	20.533	20.733	20.167	20.478	6.800	7.300	7.833	7.311
RTN-1210-3-1-4-5	18.833	19.300	18.900	19.011	7.333	7.367	7.633	7.444
RTN-1211-5-1-3-5	15.133	16.167	15.467	15.589	8.533	7.900	7.933	8.122
RTN-1211-6-1-2-7	15.400	14.500	15.667	15.189	6.500	6.400	6.933	6.611
RTN-1212-4-3-5-5	17.467	18.833	19.267	18.522	7.367	7.367	7.100	7.278
RTN-1201-5-1-3-14	17.867	17.733	17.667	17.756	7.367	8.000	7.000	7.456
RTN-1211-4-2-1-1	17.667	18.600	18.967	18.411	7.233	7.800	7.100	7.378
RTN-1211-9-1-2-12	28.267	27.567	28.667	28.167	7.200	7.067	6.767	7.011
Ch-1 (Bela)	15.300	15.200	15.567	15.356	8.467	8.233	8.567	8.422
Ch-2 (Patni-6)	15.967	14.967	20.567	17.167	8.800	8.300	8.500	8.533
Mean	16.833	17.363	18.122	17.439	7.348	7.315	7.352	7.338
CD at 5 %	3.090	2.910	4.210		1.180	0.620	0.610	
CV at 5 %	11.090	10.130	14.060		9.730	5.120	5.030	

Table 11. Mean performance of genotypes over three environments for amylose content (%)

GENOTYPES	**Amylose content (%)**			
	E 1	**E 2**	**E 3**	**Mean**
RTN-1201-13-2-2-1-32	18.92	18.99	20.02	19.31
RTN-1201-23-2-2-1-43	20.66	20.77	22.25	21.23
RTN-1201-51-2-1-5-48	19.84	19.47	20.96	20.09
RTN-1209-10-1-2-1-9	19.63	18.99	16.71	18.44
RTN-1211-6-1-3-1-8	20.55	21.72	21.15	21.14
RTN-1211-6-1-4-1-11	20.14	21.39	20.82	20.78
RTN-1211-6-1-4-3-13	20.44	22.28	21.36	21.36
RTN-1211-6-1-5-1-14	23.68	24.56	24.31	24.18
RTN-1211-15-1-4-2-23	19.41	20.60	20.56	20.19
RTN-1212-4-1-2-4	18.74	19.92	19.51	19.39
RTN-1211-4-2-2-2	19.21	20.48	20.36	20.01
RTN-1210-3-1-4-5	22.26	23.49	23.26	23.00
RTN-1211-5-1-3-5	20.85	22.12	21.46	21.48
RTN-1211-6-1-2-7	15.32	16.26	15.85	15.81
RTN-1212-4-3-5-5	19.97	20.58	21.03	20.53
RTN-1201-5-1-3-14	21.69	22.49	22.52	22.23
RTN-1211-4-2-1-1	19.79	21.31	20.86	20.66
RTN-1211-9-1-2-12	18.03	18.63	18.97	18.54
Ch-1 (Bela)	18.50	18.47	18.81	18.59
Ch-2 (Patni-6)	16.93	17.00	17.01	16.98
Mean	19.73	20.48	20.39	20.20
CD at 5 %	3.29	3.81	3.92	
CV at 5 %	10.08	11.27	11.62	

recorded at Shirgaon (7.35 %) followed by Dapoli (7.34 %) and then at Phondaghat (7.31 %) location.

4.1.1.17 Amylose content (%)

The total amylose content in red rice ranged from 15.32 to 23.68 per cent in Dapoli(E1), 16.26 to 24.56 per cent in Phondaghat(E1), 15.85 to 24.31 per cent in Shirgaon(E1) location. While overall mean over three environments it ranged between 15.81 to 24.18 per cent. Genotype, RTN-1210-3-1-4-5 (24.56 %) recorded highest total amylose content at Phondaghat followed by RTN-1210-3-1-4-5 (24.31 %) at Shirgaon and RTN-1210-3-1-4-5 (23.68 %) at Dapoli location. On the basis of pooled mean, genotype, RTN-1210-3-1-4-5 (24 %) given highest total amylose content, WhileRTN-1211-9-1-3-13 (15.32 %) lowest total amylose content over all the three environments. The highest total amylose content mean was recorded at Phondaghat (20.48 %) followed by Shirgaon (20.39 %) and Dapoli (19.73 %) location (table 11).

4.1.2 Phenotypic stability analysis based on AMMI biplot

To investigate the main effects and interactions across different environments, AMMI 1 and AMMI 2 biplots were constructed for yield and yield component traits. AMMI 1 biplot of main effects (Genotype and environments) are shown along the abscissa and the ordinate represents the first IPCA. The interpretation of a biplot assay is that if main effects have IPCA score close to zero, it indicates negligible interaction effects and when a genotype and an environment have the same sign on the IPCA axis, their interaction is positive; if different, their interaction is negative. The IPCA 1 versus IPCA 2 biplot (*i.e.*, AMMI II biplot), explain the magnitude of interaction of each Genotype, and environment. The Genotypes and environments that are farthest

Table 12. AMMI ANOVA of twenty genotypes of bio-fortified red kernel rice for eight different characters pooled over three environments

Sources	DF	MSS							
		Days to 50 per cent flowering	Plant height (cm)	Number of tillers plant^{-1}	Number of panicles seq.meter^{-1}	Panicle length	Total number of spikelets panicle^{-1}	Number of filled spiklets panicle^{-1}	Spikletfartility (%)
Trial	59	80.2825	161.3355	0.9316	99.9669	4.5440	1068.2733	865.4731	32.4021
Genotypes	19	246.8928*	500.3409*	0.9894*	287.0940*	7.5536*	1164.0221*	823.4865*	40.3687*
Environments	2	13.7388	0.0320	5.9769	12.6396	1.8547	7835.5103	5421.7485	161.8888
GxE Interaction	38	0.4796	0.3225	0.6372	10.9995	3.1807	664.2286	646.6625	21.6037
PCA I	20	0.7976	0.5605	0.6808	12.5624	4.5338	693.3206	677.0439	30.3390
IPCA II	18	0.1264	0.0581	0.5887	9.2629	1.6773	631.9041	612.9053	11.8977
Error	120	35.1944	16.6527	0.2860	13.2352	1.9059	217.5963	126.0370	11.3811
Total	179	50.0559	64.3415	0.4988	41.8227	2.7754	497.9870	369.7618	18.3098

Source	DF	MSS								
		Test weight (g)	Grain yield plant^{-1} (g)	Straw yield plant^{-1} (g)	Grain yield plot $^{-1}$ (kg)	Straw Yield plot^{-1}	Iron content (ppm)	Zinc content (ppm)	Protein content (%)	Amylose content (%)
Trial	59	12.5594	1.9203	5.6701	0.4148	0.0907	2.8721	10.6581	0.5452	4.0399
Genotypes	19	32.5145*	1.8107*	2.3732*	0.1930*	0.0375*	7.8107*	30.2011*	1.528*	11.530*
Environments	2	27.8066	13.8245	62.6267	4.4888	0.1647	7.8545	8.3859	0.0082	3.3320
GxE Interaction	38	1.7793	1.3485	4.3208	0.3113	0.1134	0.1406	1.0062	0.0817	0.3320
PCA I	20	2.5208	2.1734	5.3027	0.4069	0.1564	0.2182	1.4023	0.1015	0.4204
PCA II	18	0.9554	0.4320	3.2298	0.2050	0.0656	0.0545	0.5661	0.0596	0.2339
Error	120	2.0103	0.3536	1.2168	0.0983	0.0302	0.3446	1.4909	0.0852	1.7039
Total	179	5.4873	0.8700	2.6847	0.2026	0.0502	1.1777	4.5125	0.2368	2.4738

*significant for 5%

from the origin being more responsive fit the worst. Genotypes and environments that fall into the same sector interact positively; negatively if they fall into opposite sectors (Anandan*et al.*, 2009).

4.1.2.1 Days to 50 per cent flowering

The AMMI analysis of variance for Days to 50 per cent flowering of the twenty genotypes tested in three environments showed that 13.7388 of the total sum of square was attributable to environmental effects, 246.8928 to genotypic effects, and 0.4796 to GEI effects (Table 12). IPCA I captured 0.7976 sum of square and the IPCA II explained a further 0.1264 of the GEI sum of square and cumulatively contributed to 0.9240 of the total GEI. The mean square for the IPCA I was significant at P = 0.01 but IPCA II was non-significant. Therefore, only AMMI 1 biplot analysis between main effects and first IPCA was performed.

AMMI 1 biplot analysis for Days to 50 per cent flowering showed that the relative variability due to genotypes was less than the variability due to most of the environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 1). Genotypes or environments on left hand side of the vertical line showed early flowering than those on the right hand side. Thus, eight out of twenty Genotypes namely, RTN-1201-51-2-1-5-48 (3), RTN-1209-10-1-2-1-9 (4), RTN-1211-6-1-4-1-11 (6), RTN-1211-6-1-4-3-13 (7), RTN-1211-4-2-2-2 (11), RTN-1210-3-1-4-5 (12), RTN-1211-4-2-1-1 (17) and RTN-1211-9-1-2-12 (18) were found to show early flowering with RTN-

1201-51-2-1-5-48 (3) being the overall best with general mean of 88.56. In contrast, remaining of the genotypes was observed to show late flowering as they occupied the place right hand side of the main effect mid line on the biplot. Among the test environments, Dapoli environment occupied position on the left hand side of the midpoint of the main effect axis and seems to be most favourable environment.

Genotypes or environments with larger negative or positive IPCA I scores have high interactions, while those with IPCA I scores near zero (close to horizontal line) have little interaction across environments. Only genotypes, RTN-1201-5-1-3-14 (16) fell almost on the horizontal line indicating their uniform performance across the environments. However, it is to mention that eight genotype namely, RTN-1209-10-1-2-1-9 (4), RTN-1211-6-1-4-3-13 (7),1, RTN-1211-6-1-5-1-14 (8), RTN-1211-15-1-4-2-23 (9), RTN-1211-9-1-2-12 (18) and RTN-1212-4-3-5-5 (15) were quite close to IPCA I axis therefore considered to be stable against the environmental changes. The genotype, RTN-1211-4-2-1-1 (17) had flowering on left half of the main effect axis but with large negative score on IPCA II and therefore, expected to perform better under Dapoli environment but variable performance across the different environments. Similarly, RTN-1201-23-2-2-1-43 (2) also had early flowering but positive score on IPCA I and therefore, expected to perform better under Phondaghat environment since it had positive interaction with these environment.

4.1.2.2 Plant height (cm)

The AMMI analysis of variance for plant height illustrated that 0.0320 of the total sum of square was attributable to environmental effects, only 0.0320 to genotypic effects, and 0.3225 to GEI effects (Table 12). The IPCA I captured 0.5605 of the interaction sum of square. Similarly, IPCA II explained a further 0.0581 of the GEI sum of square and together with IPCA I and IPCA II contributed 0.6186 of the total GEI. The mean square for the IPCA I was significant at P = 0.01 but IPCA II was non-significant. Therefore, only AMMI 1 biplot analysis between main effects and first IPCA was performed.

AMMI 1 biplot analysis for plant height depicted that the relative variability due to genotypes was greater than the variability due to environments as indicated by the distribution as well as position occupied by the twenty Genotypes and three environments on biplot display (Fig. 2). Genotypes or environments on right hand side of the vertical line showed higher plant height than those on the left hand side. Thus, three out of twenty genotypes namely, RTN-1201-13-2-2-1-32 (1), Bela (19) and Patni-6 (20)-6 (20)were identified to have higher plant height with Patni-6 (20)-6 (20) being the overall best with general mean of 139.25. In contrast, the remaining of the genotypes were observed to show shorter plant height as they occupied the place farther from the left hand side of the main effect mid line on the biplot. Among the test environments, all three environments such as Dapoli, Shirgaon and Phondaghat they not show significant or non significant plant height. These three environments were identified to be average environments.

Perusal of Fig. 2 revealed that, genotypes namely, RTN-1201-23-2-2-1-43 (2),RTN-1211-6-1-3-1-8 (5)and RTN-1201-51-2-1-5-48 (3) fell almost on the horizontal line indicating uniform plant height across the three environments. However, it is to mention that four genotypes namely, RTN-1211-6-1-2-7 (14), RTN-1211-6-1-4-1-11 (6), RTN-1211-6-1-4-3-13 (7) and RTN-1201-13-2-2-1-32 (1) was quite close to IPCA I axis therefore considered to be stable against the environmental changes. The Genotype, RTN-1201-13-2-2-1-32 (1) and Bela (19) fell on right hand side of the main effect axis but with large negative score on IPCA I and therefore, expected to perform better under Dapoli and Phondaghat environments. Similarly, Patni-6 (20)-6 (20) had higher plant height but positive score on IPCA I and therefore, expected to perform better on under Shirgaon environment showing positive interaction with these environment.

4.1.2.3 Number of tillers plant^{-1}

The AMMI analysis of variance for number of tillers plant^{-1}of the twenty genotypes tested in three environments showed that 5.9769 of the total sum of square was attributable to environmental effects, 0.9894 to genotypic effects, and 0.6372 to GEI effects (Table 12). IPCA I captured 0.6808 of the interaction sum of square. Similarly, the IPCA II explained a further 0.5887 of the GEI sum of square and cumulatively contributed to 1.2695 of the total GEI. The mean square for the IPCA I was significant at $P = 0.01$ but IPCA II was non-significant. Therefore, only AMMI 1 biplot analysis between main effects and IPCA I was performed.

AMMI 1 biplot analysis for number of tillersplant^{-1}showed that the relative variability due to genotype was less than the variability due to most of the environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 3). Genotypes or environments on right hand side of the vertical line showed higher number of tillers than those on the left hand side. Thus, five out of twenty genotype namely, RTN-1210-3-1-4-5 (12), RTN-1211-9-1-2-12 (18), RTN-1209-10-1-2-1-9 (4),RTN-1201-13-2-2-1-32 (1), and RTN-1211-5-1-3-5 (13) were found to show higher number of tillers plant^{-1}with RTN-1201-13-2-2-1-32 (1) being the overall best with general mean of 7.62 cm. In contrast, remaining of the genotypes except RTN-1201-51-2-1-5-48 (3) located quite close to vertical line, were observed to show less number of tillers plant^{-1}as they occupied the place left hand side of the main effect mid line on the biplot. Among the test environments, Shirgaon occupied position on the right hand side of the midpoint of the main effect axis and seems to be most favourable. The environments Dapoli and Phondaghat were identified to have relatively unfavourable environments as they occupied position farther from the left half of the midpoint axis.

Genotypes or environments with larger negative or positive IPCA I scores have high interactions, while those with IPCA I scores near zero (close to horizontal line) have little interaction across environments. Only three genotypes, RTN-1211-4-2-1-1 (17), RTN-1211-6-1-5-1-14 (8) and RTN-1211-6-1-3-1-8 (5) fell almost on the horizontal line indicating their uniform performance across the environments. However, it is to mention that two genotypes namely, RTN-1210-3-1-4-5 (12) and RTN-1211-5-1-3-5 (13) were quite close to IPCA I axis and also placed on right hand side of the midpoint axis of main effect and therefore considered to be stable against the environmental changes with minor positive and negative interactions. The genotype, RTN-1201-13-2-2-1-32 (1) had flowering on right half of the main effect axis but with large negative score on IPCA I and therefore, expected to perform better under Dapoli environment but variable performance across the different environments. Similarly, RTN-1211-9-1-2-12 (18) and RTN-1210-3-1-4-5 (12) also had more number of tillers plant^{-1}but positive score on IPCA I and therefore, expected to perform better under Shirgaon environments since it had positive interaction with these environments.

4.1.2.4 Number of panicles square meter^{-1}

The AMMI analysis of variance for number of panicles square meter^{-1} of the twenty genotypes tested in three environments showed that 12.6396 of the total sum of square was attributable to environmental effects, 287.0940 to genotypic effects, and 10.9995 to GEI effects (Table 12). The IPCA I captured 12.5624 of the interaction sum of square. Similarly, the IPCA II explained a further 9.2629 of the GEI sum of square and cumulatively contributed to 21.8253 of the total GEI. The mean square for the IPCA I was significant at P = 0.01 but IPCA II was non-significant. Therefore, only AMMI1 biplot analysis between main effects and first IPCA was performed.

AMMI 1 biplot analysis for number of panicles square meter^{-1} showed that the relative variability due to genotypes was less than the variability due to most of the environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 4). Genotypes or environments on right hand side of the vertical line showed higher number of panicles square meter^{-1} than those on the left hand side. Thus, nine out of twenty genotypes namely, RTN-1212-4-1-2-4 (10), RTN-1211-5-1-3-5 (13), RTN-1201-5-1-3-14 (16), RTN-1211-6-1-2-7 (14), RTN-1211-9-1-2-12 (18), Bela (19), RTN-1201-13-2-2-1-32 (1), RTN-1209-10-1-2-1-9 (4) and RTN-1212-4-3-5-5 (15) were found to show higher number of panicles square meter^{-1} with RTN-1211-9-1-2-12 (18) being the overall best with general mean of 133.44. In contrast, remaining of the genotype were observed to show less number of panicles square meter^{-1} as they occupied the place left hand side of the main effect mid line on the biplot. Among the test environments, all three environment show close to vertical line therefore they show average performance.

Genotypes or environments with larger negative or positive IPCA I scores have high interactions, while those with IPCA I scores near zero (close to horizontal line) have little interaction across environments. Genotype, RTN-1211-15-1-4-2-23 (9) fell almost on the horizontal line indicating their uniform performance across the environments. However, it is to mention that three genotypes namely, RTN-1211-6-1-2-7 (14), RTN-1211-9-1-2-12 (18) and Bela (19) were quite close to IPCA I axis therefore considered to be stable against the environmental changes with minor positive and negative interactions. The genotypes, RTN-1212-4-1-2-4 (10), RTN-1211-5-1-3-5 (13), RTN-1201-5-1-3-14 (16), and RTN-1211-9-1-2-12 (18) had on right half of the main effect axis but with large negative score on IPCA I and therefore, expected to perform better under Dapoli and

Shirgaon environment but variable performance across the different environment. Similarly, RTN-1212-4-3-5-5 (15), RTN-1209-10-1-2-1-RTN-1211-15-1-4-2-23 (9) and RTN-1201-13-2-2-1-32 (1) also had more number of panicles square meter^{-1} but positive score on IPCA I and therefore, expected to perform better under Dapoli environments since it had positive interaction with these environments.

4.1.2.5 Length of panicle (cm)

The AMMI analysis of variance for panicle length illustrated that 1.8547 of the total sum of square was attributable to environmental effects, only 7.5536 to genotypic effects, and 3.1807 to GEI effects (Table 12). The IPCA I captured 4.5338 of the interaction sum of square. Similarly, the IPCA II explained a further 1.6773 of the GEI sum of square and together with IPCA I and IPCA II contributed 6.2111 of the total GEI. The mean square for the IPCA I was significant at P = 0.01 but IPCA II was non-significant. Therefore, only AMMI 1 biplot analysis between main effects and first IPCA was performed.

AMMI 1 biplot analysis for panicle length depicted that the relative variability due to genotypes was greater than the variability due environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 5). Genotypes or environments on right hand side of the vertical line showed higher panicle length than those on the left hand side. Thus, seven out of twenty genotypes namely, RTN-1211-6-1-4-3-13 (7), RTN-1201-51-2-1-5-48 (3), RTN-1209-10-1-2-1-9 (4), RTN-1211-6-1-3-1-8 (5), RTN-1212-4-1-2-4 (10), RTN-1210-3-1-4-5 (12) and RTN-1201-5-1-3-14

(16) were identified to have higher panicle length with RTN-1211-6-1-4-3-13 (7) being the overall best with general mean of 25.62 cm. In contrast, the remaining of the genotypes were observed to show shorter panicle length as they occupied the place farther from the left hand side of the main effect mid line on the biplot. Among the test environments, Shirgaon they not show significant panicle length.

Perusal of Fig. 5 revealed that, genotypes RTN-1209-10-1-2-1-9 (4), RTN-1201-13-2-2-1-32 (1) and RTN-1212-4-3-5-5 (15) fell almost on the horizontal line indicating uniform panicle length across the environments. However, it is to mention that three genotypes namely, RTN-1211-6-1-3-1-8 (5), RTN-1211-6-1-2-7 (14) and RTN-1211-6-1-4-1-11 (6) were quite close to IPCA I axis therefore considered to be stable against the environmental changes. The genotypes, RTN-1201-51-2-1-5-48 (3), and RTN-1211-6-1-4-3-13 (7) fell on right hand side of the main effect axis but with large negative score on IPCA I and therefore, expected to perform better under Phondaghat and Shirgaon environments. Similarly, RTN-1201-5-1-3-14 (16), RTN-1210-3-1-4-5 (12) and RTN-1212-4-1-2-4 (10) had higher panicle length but positive score on IPCA I and therefore, expected to perform better on under Dapoli environments showing positive interaction with these environments.

4.1.2.6 Total number of spikelets panicle^{-1}

The AMMI analysis of variance for total number of spikelets panicle^{-1}illustrated that 7835.5103 of the total sum of square was attributable to environmental effects, only 1164.0221 to genotypic effects, and 664.2286 to GEI effects

(Table 12). The IPCA I captured 693.3206 of the interaction sum of square. Similarly, the IPCA II explained a further 631.9041 of the GEI sum of square and together with IPCA I and IPCA II contributed 1325.2247 of the total GEI. Both AMMI 1 and AMMI 2 biplot analysis was performed for total number of spikelets panicle^{-1} since mean square for the IPCA I and IPCA II were found to be significant.

AMMI 1 biplot analysis for total number of spikelets panicle^{-1} depicted that the relative variability due to genotypes was less than the variability due environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 6). Genotypes or environments on right hand side of the vertical line showed higher total number of spikelets panicle^{-1} than those on the left hand side. Thus, six out of twenty genotypes namely, RTN-1201-13-2-2-1-32 (1), RTN-1209-10-1-2-1-9 (4), RTN-1211-6-1-3-1-8 (5), RTN-1212-4-1-2-4 (10), RTN-1201-23-2-2-1-43 (2) and RTN-1211-4-2-1-1 (17) were identified to have higher total number of spikelets panicle^{-1} with RTN-1209-10-1-2-1-9 (4)being the overall best with general mean of 198.78. In contrast, the remaining of the genotypes were observed to show slightly low total number of spikelets panicle^{-1} as they occupied the place farther from the left hand side of the main effect mid line on the biplot. Among the test environments, one out of three environments namely, Dapoli seems to be most favourable environment as these occupied position on the right hand side of the midpoint of the main effect axis. The Shirgaon and Phondaghat environments were identified to be relatively slightly unfavourable environments as they occupied position farther from the left hand side of the midpoint axis.

Perusal of Fig. 6 revealed that, genotype Bela (19) fell almost on the horizontal line indicating uniform total number of spikelets panicle^{-1} across the environments. However, it is to mention that two genotypes, RTN-1211-4-2-1-1 (17) and RTN-1211-6-1-3-1-8 (5)were quite close to IPCA I axis and also plotted right hand side of the midpoint axis of main effect and therefore considered to be stable against the environmental changes with minor positive and negative interactions. The RTN-1212-4-1-2-4 (10), RTN-1201-23-2-2-1-43 (2) and RTN-1211-4-2-1-1 (17) fell on right hand side of the main effect axis but with large negative score on IPCA II and therefore, expected to perform better under Shirgaon environment. Similarly, RTN-1211-6-1-3-1-8 (5), RTN-1201-13-2-2-1-32 (1) and RTN-1209-10-1-2-1-9 (4)had higher total number of spikelets panicle^{-1} but positive score on IPCA I and therefore, expected to perform better on under Dapoli environment showing positive interaction with these environment.

The AMMI 2 biplot was generated using genotypes and environments scores of the first two IPCA and presented as Fig. 7 the genotypes and environments that are farthest from the origin being more responsive fit the worst. The closer genotypes are more stable than the score of the genotypes away from the centre. The angles between the genotype and environment vectors determine the nature of the interaction as it is positive for acute angles, negligible for right angles, and negative for obtuse angles. Perusal of the Fig. 7 indicated that the Shirgaon environment had large interaction as indicated by large scores on both IPCA I and IPCA II whereas Dapoli were quite close to IPCA II but large score on IPCA I. The environment Phondaghat was quite close to IPCA I but has large score on IPCA II.

Orthogonal projection of genotypes on the environmental vector showed that the best genotypes with respect to Dapoli location were RTN-1211-6-1-4-1-11 (6), RTN-1209-10-1-2-1-9 (4), RTN-1211-15-1-4-2-23 (9) and RTN-1201-13-2-2-1-32 (1) as indicated by close acute angles with this environment. The genotypes, RTN-1211-5-1-3-5 (13), RTN-1210-3-1-4-5 (12), RTN-1211-6-1-2-7 (14), RTN-1211-9-1-2-12 (18) and RTN-1211-6-1-5-1-14 (8) were best adapted to Shirgaon environments showing quite close acute angles with this environment. The genotypes, RTN-1211-6-1-4-3-13 (7), RTN-1211-4-2-1-1 (17), RTN-1211-4-2-2-2 (11) and RTN-1201-23-2-2-1-43 (2) were best adapted to Phondaghat environment showing quite close acute angles with this environment. The genotypes RTN-1212-4-1-2-4 (10), RTN-1201-5-1-3-14 (16), RTN-1201-51-2-1-5-48 (3), RTN-1212-4-3-5-5 (15) and RTN-1211-6-1-3-1-8 (5) were found to scattered relatively close to the origin point in the AMMI 2 biplot indicating minimal interactions of these genotypes with the environments. The total number of spikelets panicle^{-1} of genotype RTN-1201-5-1-3-14 (16) was lower than the overall mean and therefore did not qualify for stable genotypes. The other three genotypes namely, RTN-1212-4-1-2-4 (10), RTN-1201-51-2-1-5-48 (3) and RTN-1212-4-3-5-5 (15) had higher total number of spikelets panicle^{-1} as well as low IPCA I and IPCA II scores and therefore assumed to be stable across three different environments.

4.1.2.7 Number of filled spikelets panicle^{-1}

The AMMI analysis of variance for number of filled spikelets panicle^{-1} of the twenty genotypes tested in three environments showed that 5421.7485 of the total sum of square was attributable to environmental effects, 823.4865 to genotypic effects, and 646.6625 to GEI effects (Table 12). The IPCA I captured 677.0441 of the interaction sum of square. Similarly, the IPCA II explained a further 612.9053 of the GEI sum of square and cumulatively contributed to 1289.9494 of the total GEI. The mean square for the IPCA I was significant at $P = 0.01$ but IPCA II was non-significant. Therefore, only AMMI 1 biplot analysis between main effects and first IPCA was performed.

AMMI 1 biplot analysis for number of filled spikelets panicle^{-1} showed that the relative variability due to genotypes was less than the variability due to most of the environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 8). Genotypes or environments on right hand side of the vertical line showed higher number of filled spikelets panicle^{-1} than those on the left hand side. Thus, nine out of twenty genotypes namely, RTN-1211-6-1-5-1-14 (8), RTN-1211-5-1-3-5 (13), RTN-1201-51-2-1-5-48 (3), RTN-1212-4-1-2-4 (10), RTN-1201-13-2-2-1-32 (1), RTN-1211-6-1-3-1-8 (5), RTN-1201-23-2-2-1-43 (2), RTN-1211-4-2-1-1 (17) and RTN-1209-10-1-2-1-9 (4) were found to show higher number of filled spikelets panicle^{-1} with RTN-1201-23-2-2-1-43 (2) being the overall best with general mean of 167.11. In contrast, remaining of the genotypes were observed to show less number of filled spikelets panicle^{-1} as they occupied the place left hand side of the main effect mid line on the biplot. Among the test environments, Dapoli environment occupied position on the right hand side of the midpoint of the main effect axis and seems to be most favourable environment. The Phondaghat and Shirgaon environments were identified to have relatively unfavourable environments as they occupied position farther from the left half of the midpoint axis.

Genotypes or environments with larger negative or positive IPCA I scores have high interactions, while those with IPCA I scores near zero (close to horizontal line) have little interaction across environments. Only two genotypes, Bela (19) and RTN-1211-6-1-3-1-8 (5) fell almost on the horizontal line indicating their uniform performance across the environments. However, genotypes, RTN-1201-23-2-2-1-43 (2) and RTN-1211-4-2-1-1 (17) were quite close to IPCA I axis therefore considered to be stable against the environmental changes with minor positive and negative interactions. The genotypes, RTN-1201-23-2-2-1-43 (2), RTN-1211-5-1-3-5 (13) and RTN-1211-9-1-2-12 (18) had on right half of the main effect axis but with large negative score on IPCA I and therefore, expected to perform better under Dapoli environment but variable performance across the different environments. Similarly, RTN-1211-6-1-4-1-11 (6), RTN-1211-6-1-4-3-13 (7), RTN-1212-4-1-2-4 (10), RTN-1211-6-1-2-7 (14), and RTN-1211-4-2-1-1 (17) also had more number of filled spikelets panicle^{-1} but positive score on IPCA I and therefore, expected to perform better under

Phondaghat environment since it had positive interaction with these environment.

4.1.2.8Spikelets fertility (%)

The AMMI analysis of variance for spikelets fertility illustrated that 161.8888 of the total sum of square was attributable to environmental effects, only 40.3687 to genotypic effects, and 21.6037 to GEI effects (Table 12). IPCA I captured 30.3390 of the interaction sum of square. Similarly, IPCA II explained a further 11.8987 of the GEI sum of square and together with IPCA I and IPCA II contributed 42.2377 of the total GEI. Both AMMI 1 and AMMI 2 biplot analysis was performed for spikelets fertility since mean square for the IPCA I and IPCA II were found to be significant.

AMMI 1 biplot analysis for spikelets fertility depicted that the relative variability due to genotypes was less than the variability due environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 9). Genotypes or environments on right hand side of the vertical line showed higher spikelet fertility than those on the left hand side. Thus, eleven out of twenty genotypes namely, RTN-1211-15-1-4-2-23 (9), RTN-1201-5-1-3-14 (16), RTN-1211-5-1-3-5 (13),RTN-1211-6-1-5-1-14 (8),10, RTN-1212-4-3-5-5 (15), RTN-1211-6-1-4-3-13 (7), RTN-1201-13-2-2-1-32 (1), RTN-1211-6-1-3-1-8 (5), RTN-1201-51-2-1-5-48 (3), RTN-1209-10-1-2-1-9 (4) andRTN-1211-9-1-2-12 (18) were identified to have higher spikelets fertility with RTN-1211-6-1-3-1-8 (5)being the overall best with general mean of 88.52 per cent. In contrast, the remaining of the genotypes were observed to show slightly low spikelets fertility as they occupied the place farther from the left hand side of the main effect mid line on the biplot. Among the test environments, two out of three environments namely, Dapoli and Phondaghat seems to be most favourable environments as these occupied position on the right hand side of the midpoint of the main effect axis.

Perusal of Fig. 9 revealed that, genotypes, RTN-1201-13-2-2-1-32 (1)and RTN-1210-3-1-4-5 (12)fell almost on the horizontal line indicating uniform spikelets fertility across the environments. However, it is to mention that three genotypes namely, RTN-1211-5-1-3-5 (13), RTN-1211-9-1-2-12 (18), and RTN-1211-6-1-3-1-8 (5)were quite close to IPCA I axis and also plotted right hand side of the midpoint axis of main effect and therefore considered to be stable against the environmental changes with minor positive and negative interactions. The RTN-1211-6-1-5-1-14 (8), RTN-1201-23-2-2-1-43 (2), RTN-1212-4-3-5-5 (15), RTN-1211-6-1-4-3-13 (7), RTN-1201-13-2-2-1-32 (1) andRTN-1201-51-2-1-5-48 (3)fell on right hand side of the main effect axis but with large negative score on IPCA I and therefore, expected to perform better under Phondaghat environment. Similarly, RTN-1209-10-1-2-1-9 (4), RTN-1211-6-1-3-1-8 (5), RTN-1211-9-1-2-12 (18)had higher Spikelets fertility but positive score on IPCA I and therefore, expected to perform better on under Dapoli environment showing positive interaction with these environment.

The AMMI 2 biplot was generated using genotypes and environments scores of the first two IPCA and presented as Fig.10. To demonstrate the relative magnitude of the G x E for specific genotypes and environments. The genotypes and environments that are farthest from the origin being more responsive fit the worst. The closer genotypes are more stable than the score of the genotypes away from the centre. The angles between the genotype and environment vectors determine the nature of the interaction as it is positive for acute angles, negligible for right angles, and negative for obtuse angles. Perusal of the Fig. 10 indicated that the Shirgaon environment had large interaction as indicated by large scores on both IPCA I and IPCA II whereas Dapoli were quite close to IPCA II but large score on IPCA I. The Phondaghat environment was quite close to IPCA I but has large score on IPCA II.

Orthogonal projection of genotypes on the environmental vector showed that the best genotypes with respect to Dapoli location were RTN-1201-5-1-3-14 (16), RTN-1212-4-1-2-4 (10), and RTN-1209-10-1-2-1-9 (4) as indicated by close acute angles this environment. The genotypes, RTN-1201-5-1-3-14 (16) and RTN-1211-6-1-4-3-13 (7) were best adapted to Shirgaon environment showing quite close acute angles with this environment. The genotypes, RTN-1211-5-1-3-5 (13), RTN-1201-23-2-2-1-43 (2), and RTN-1201-51-2-1-5-48 (3) were best adapted to Shirgaon environment showing quite close acute angles with this environment. The genotypes RTN-1212-4-3-5-5 (15), RTN-1211-4-2-2-2 (11), RTN-1211-9-1-2-12 (18), RTN-1201-5-1-3-14 (16), and RTN-1211-6-1-3-1-8 (5) were found to scattered relatively close to the origin point in the AMMI 2 biplot indicating minimal interactions of these genotypes with the environment. The spikelets fertility of genotype

RTN-1211-6-1-3-1-8 (5) was lower than the overall mean and therefore did not qualify for stable genotypes. The other five genotypes namely, RTN-1212-4-3-5-5 (15), RTN-1211-4-2-2-2 (11), RTN-1211-9-1-2-12 (18), RTN-1201-5-1-3-14 (16) and RTN-1201-13-2-2-1-32 (1) had higher spikelets fertility as well as low IPCA I and IPCA II scores and therefore assumed to be stable across three different environments.

4.1.2.9 Test weight (g)

The AMMI analysis of variance for test weight of the twenty genotypes tested in three environments showed that 27.8066 of the total sum of square was attributable to environmental effects, 32.5145 to genotypic effects, and 1.7793 to GEI effects (Table 12). The IPCA I captured 2.5208 of the interaction sum of square. Similarly, the IPCA II explained a further 0.9554 of the GEI sum of square and cumulatively contributed to 3.4762 of the total GEI. The mean square for the IPCA I was significant at P = 0.01 but IPCA II was non-significant. Therefore, only AMMI 1 biplot analysis between main effects and first IPCA was performed.

AMMI 1 biplot analysis for test weight showed that the relative variability due to genotypes was less than the variability due to most of the environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 11). Genotypes or environments on right hand side of the vertical line showed higher test weight than those on the left hand side. Thus, four out of twenty genotypes namely, RTN-1201-51-2-1-5-48 (3), RTN-1209-10-1-2-1-9 (4), RTN-1212-4-1-2-4 (10), and Patni-6 (20) were found to show higher test weight with Patni-6 (20) being the overall best with general mean of 87.81 g. In contrast, remaining of the genotypes were observed to show less test weight as they occupied the place left hand side of the main effect mid line on the biplot. Among the test environments, Shirgaon occupied position on the very close to vertical line therefore they close to favourable.

Genotypes or environments with larger negative or positive IPCA I scores have high interactions, while those with IPCA I scores near zero (close to horizontal line) have little interaction across environments. Only genotype, RTN-1212-4-1-2-4 (10) fell almost on the horizontal line indicating their uniform performance across the all environments. However, it is to mention that four genotype namely, RTN-1211-6-1-3-1-8 (5), RTN-1211-6-1-4-1-11 (6), RTN-1211-4-2-2-2 (11) and RTN-1201-23-2-2-1-43 (2) were quite close to IPCA I axis therefore considered to be stable against the environmental changes with minor positive and negative interactions. The genotype, RTN-1201-51-2-1-5-48 (3) had on right half of the main effect axis but with large negative scores on IPCA I and therefore, expected to perform better under Dapoli environment but variable performance across the different environments. Similarly, Patni-6 (20) and RTN-1209-10-1-2-1-9 (4) also had more test weight but positive score on IPCA I and therefore, expected to perform better under Shirgaon and Phondaghat environments since it had positive interaction with these environments.

4.1.2.10 Grain yield plant^{-1} (g)

The AMMI analysis of variance for grain yield plant^{-1}illustrated that 13.8245 of the total sum of square was attributable to environmental effects, only 1.8107 to genotypic effects, and to 0.0817 GEI effects (Table 12). The IPCA I captured 2.1734 of the interaction sum of square. Similarly, the IPCA II explained a further 0.4320 of the GEI sum of square and together with IPCA I and IPCA II contributed 2.6054 of the total GEI. Both AMMI 1 and AMMI 2 biplot analysis was performed for grain yield plant^{-1}since mean square for the IPCA I and IPCA II were found to be significant.

AMMI 1 biplot analysis for grain yield plant^{-1}depicted that the relative variability due to genotypes was less than the variability due environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 12). Genotypes or environments on right hand side of the vertical line showed higher grain yield plant^{-1}than those on the left hand side. Thus, RTN-1212-4-3-5-5 (15) out of twenty genotypes, except RTN-1211-4-2-2-2 (11), RTN-1211-9-1-2-12 (18), RTN-1211-6-1-4-3-13 (7) and RTN-1211-6-1-4-1-11 (6) were identified to have higher grain yield plant^{-1}with RTN-1201-5-1-3-14 (16)being the overall best with general mean of 9.91 g. In contrast, the genotypes, Patni-6 (20), RTN-1211-4-2-2-2 (11), RTN-1211-9-1-2-12 (18), RTN-1211-6-1-4-3-13 (7) and RTN-1211-6-1-4-1-11 (6) they present on line were observed to show slightly low grain yield plant^{-1}as they occupied the place farther from the left hand side of the main effect mid line on the biplot. Among the test environments, all the three environments *viz.,*Dapoli, Phondaghat and Shirgaon seems to be most favourable environments as this occupied position on the right hand side of the midpoint of the main effect axis.

Perusal of Fig. 12 revealed that, no anyone genotype, fell almost on the horizontal line indicating uniform grain yield plant^{-1}across the three environments. However, it is to mention that four Genotypes namely, RTN-1201-5-1-3-14 (16), RTN-1201-51-2-1-5-48 (3), RTN-1211-5-1-3-5 (13), RTN-1211-6-1-5-1-14 (8) and RTN-1209-10-1-2-1-9 (4)were quite close to IPCA I axis and also plotted right hand side of the midpoint axis of main effect and therefore considered to be stable against the environmental changes with minor positive and negative interactions. The RTN-1211-4-2-1-1 (17), RTN-1210-3-1-4-5 (12), RTN-1211-6-1-2-7 (14), RTN-1209-10-1-2-1-9 (4), and RTN-1201-13-2-2-1-32 (1) fell on right hand side of the main effect axis but with large negative score on IPCA I and therefore, expected to perform better under Dapoli environment. Similarly, RTN-1212-4-1-2-4 (10), RTN-1211-6-1-5-1-14 (8), RTN-1211-6-1-3-1-8 (5), RTN-1211-5-1-3-5 (13), RTN-1211-15-1-4-2-23 (9), and RTN-1201-51-2-1-5-48 (3)had higher grain yield plant^{-1}but positive score on IPCA I and therefore, expected to perform better on under Shirgaon environment showing positive interaction with these environment.

The AMMI 2 biplot was generated using genotypes and environments scores of the first two IPCA and presented as Fig. 13. To demonstrate the relative magnitude of the G x E for specific genotypes and environments. The genotypes and environments that are farthest from the origin being more responsive fit the worst. The closer genotypes are more stable than the score of the genotypes away from the centre. The angles between the genotypes and environments vectors determine the nature of the interaction as it is positive for acute angles, negligible for right angles, and negative for obtuse angles. Perusal of the Fig. 13 indicated that the Phondaghat environment had large interaction as indicated by large scores on both IPCA I and IPCA II. The Dapoli location was quite close to IPCA I but has large score on IPCA II. The Shirgaon location was quite close to IPCA II but has large score on IPCA I.

Orthogonal projection of genotypes on the environmental vector showed that the best genotypes with respect to Dapoli location were RTN-1211-4-2-1-1 (17), RTN-1211-9-1-2-12 (18), and RTN-1211-6-1-5-1-14 (8) as indicated by close acute angles with this environment. The genotypes, RTN-1211-15-1-4-2-23 (9) and RTN-1212-4-1-2-4 (10) were best adapted to Shirgaon environment showing quite close acute angles with this environment. The genotypes, RTN-1201-13-2-2-1-32 (1), RTN-1211-5-1-3-5 (13) and Patni-6 (20) were best adapted to Phondaghat environment showing quite close acute angles with this environment. The remaining all genotypes were found to scattered relatively close to the origin point in the AMMI 2 biplot indicating minimal interactions of these genotypes with the environments. The grain yield per plant of genotype, Patni-6 (20) was lower than the overall mean and therefore did not qualify for stable genotypes. The other ten genotypes had higher grain yield plant^{-1} as well as low IPCA I and IPCA II scores and therefore assumed to be stable across three different environments.

4.1.2.11 Straw yield plant^{-1} (g)

The AMMI analysis of variance for straw yield plant^{-1}of the twenty genotypes tested in three environments showed that 62.6267 of the total sum of square was attributable to environmental effects, 2.3732 to genotypic effects, and 4.3208 to GEI effects (Table 12). The IPCA I captured 5.3027 of the interaction sum of square. Similarly, the IPCA II explained a further 3.2298 of the GEI sum of square and cumulatively contributed to 8.5325 of the total GEI. The mean square for the IPCA I was significant at P = 0.01 but IPCA II was non-significant. Therefore, only AMMI 1 biplot analysis between main effects and first IPCA was performed.

AMMI 1 biplot analysis for straw yield plant^{-1}showed that the relative variability due to genotypes was less than the variability due to most of the environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 14). Genotype or environments on left hand side of the vertical line showed lower straw yield plant^{-1}than those on the right hand side. Thus, RTN-1201-5-1-3-14 (16) out of twenty genotypes except RTN-1210-3-1-4-5 (12), RTN-1211-6-1-3-1-8 (5) and RTN-1201-23-2-2-1-43 (2) were found to show lower straw yield plant^{-1} with RTN-1209-10-1-2-1-9 (4) being the overall best with general mean of 18.17 g. In contrast, remaining of the genotypes was observed to show higher straw yield plant^{-1}as they occupied the place right hand side of the main effect mid line on the biplot. Among the test environments, Dapoli and Shirgaon environment occupied position on the left hand side of the midpoint of the main effect axis and seems to be most favourable environments.

Genotypes or environments with larger negative or positive IPCA I scores have high interactions, while those with IPCA I scores near zero (close to horizontal line) have little interaction across environments. No anyone genotype fell almost on the horizontal line indicating their uniform performance across the environments. However, it is to mention that four genotypes namely, RTN-1211-4-2-2-2 (11), RTN-1211-6-1-4-1-11 (6), RTN-1201-51-2-1-5-48 (3) and RTN-1211-4-2-1-1 (17) were quite close to IPCA I axis and left side of vertical line therefore considered to be stable against the environmental changes with minor positive and negative interactions. The genotypes, RTN-1201-5-1-3-14 (16), RTN-1211-5-1-3-5 (13), RTN-1211-6-1-2-7 (14), RTN-1212-4-3-5-5 (15), RTN-1212-4-1-2-4 (10) and RTN-1211-6-1-4-3-13 (7) had on left half of the main effect axis but with large negative score on IPCA I and therefore, expected to perform better under Dapoli environment but variable performance across the different environment. Similarly, RTN-1209-10-1-2-1-9 (4), RTN-1211-6-1-4-1-11 (6), RTN-1211-6-1-5-1-14 (8) and RTN-1201-13-2-2-1-32 (1) also had low straw yield plant^{-1}but positive score on IPCA I and therefore, expected to perform better under Shirgaon environments since it had positive interaction with these environments.

4.1.2.12 Grain yield plot^{-1} (kg)

The AMMI analysis of variance for grain yield plot^{-1}illustrated that 4.4888 of the total sum of square was attributable to environmental effects, only 0.1930 to genotypic effect, and 0.3113 to GEI effects (Table 12). The IPCA I captured 0.4069 of the interaction sum of square. Similarly, the IPCA II explained a further 0.2050 of the GEI sum of square and together with IPCA I and IPCA II contributed 0.6119 of the total GEI. Both AMMI 1 and AMMI 2 biplot analysis was performed for grain yield plot^{-1} since mean square for the IPCA I and IPCA II were found to be significant.

AMMI 1 biplot analysis for grain yield plot^{-1}depicted that the relative variability due to genotypes was less than the variability due environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 15). Genotypes or environments on right hand side of the vertical line showed higher grain yield plot^{-1}than those on the left hand side. Thus, eight out of twenty genotypes namely, RTN-1201-13-2-2-1-32 (1), RTN-1201-23-2-2-1-43 (2), RTN-1201-51-2-1-5-48 (3), RTN-1211-6-1-4-3-13 (7), RTN-1211-4-2-2-2 (11), RTN-1210-3-1-4-5 (12), 15, RTN-1201-5-1-3-14 (16), and RTN-1211-4-2-1-1 (17) were identified to have higher grain yield plot^{-1}with RTN-1211-6-1-4-3-13 (7)being the overall best with general mean of 4.43 kg. In contrast, the remaining of the genotypes were observed to show slightly low grain yield plot^{-1} as they occupied the place farther from the left hand side of the main effect mid line on the biplot. Among the test environments, two out of three environments namely, Phondaghat and Shirgaon seems to be most favourable environments as these occupied position on the right hand side of the midpoint of the main effect axis. The Dapoli environment was identified to be relatively unfavourable environment as they occupied position farther from the left hand side of the midpoint axis.

Perusal of Fig. 15 revealed that, genotypes, Bela (19)and RTN-1211-6-1-4-1-11 (6)fell almost on the horizontal line indicating uniform grain yield plot^{-1}across the three environments. However, it is to mention that three genotypes namely, RTN-1201-23-2-2-1-43 (2), RTN-1211-4-2-1-1 (17) and RTN-1211-4-2-2-2 (11)were quite close to IPCA I axis and also plotted right hand side of the midpoint axis of main effect and therefore considered to be stable against the environmental changes with minor positive and negative interactions. The genotypes, RTN-1201-13-2-2-1-32 (1), RTN-1201-51-2-1-5-48 (3), RTN-1211-4-2-1-1 (17) and RTN-1212-4-3-5-5 (15) fell on right hand side of the main effect axis but with large negative score on IPCA I and therefore, expected to perform better under Dapoli and Shirgaon environments. Similarly, RTN-1201-23-2-2-1-43 (2), RTN-1211-6-1-4-3-13 (7), RTN-1211-4-2-2-2 (11), RTN-1210-3-1-4-5 (12) and RTN-1201-5-1-3-14 (16), had higher grain yield plot^{-1}but positive score on IPCA I and therefore, expected to perform better on under Phondaghat and Shirgaon environments showing positive interaction with these environments.

The AMMI 2 biplot was generated using genotypes and environments scores of the first two IPCA and presented as Fig. 16.To demonstrate the relative magnitude of the G x E for specific genotype and environment. The genotypes and environments that are farthest from the origin being more responsive fit the worst. The closer genotypes are more stable than the score of the genotypes away from the centre. The angles between the genotypes and environments vectors determine the nature of the interaction as it is positive for acute angles, negligible for right angles, and negative for obtuse angles. Perusal of the Fig. 16 indicated that the Dapoli environment had large interaction as indicated by large scores on both IPCA I and IPCA II whereas Shirgaon were quite close to IPCA II but large score on IPCA I. The environment Phondaghat was quite close to IPCA I but has large score on IPCA II. Thus, the distribution of environments on AMMI 2 biplot exhibited specificity of each environment and large effect on genotypic performance.

Orthogonal projection of genotypes on the environmental vector showed that the best genotypes with respect to Dapoli location were RTN-1211-6-1-4-1-11 (6), RTN-1212-4-1-2-4 (10), RTN-1201-51-2-1-5-48 (3), and RTN-1209-10-1-2-1-9 (4) as indicated by close acute angles with this environment. The genotypes, RTN-1201-5-1-3-14 (16), RTN-1211-6-1-4-3-13 (7) were best adapted to Phondaghat environment showing quite close acute angles with this environment. The genotypes, Bela (19), RTN-1211-9-1-2-12 (18), and RTN-1201-13-2-2-1-32 (1) were best adapted to Shirgaon environment showing quite close acute angles with this environment. The genotype RTN-1201-23-2-2-1-43 (2), RTN-1212-4-3-5-5 (15), RTN-1211-15-1-4-2-23 (9),RTN-1211-4-2-2-2 (11), RTN-1211-5-1-3-5 (13), RTN-1211-4-2-1-1 (17) and RTN-1211-6-1-5-1-14 (8) were found to scattered relatively close to the origin point in the AMMI 2 biplot indicating minimal interactions of these genotypes with the environments. The grain yield plot^{-1} of genotypes RTN-1211-15-1-4-2-23 (9) was lower than the overall mean and therefore did not qualify for stable genotypes. The genotypes, RTN-1201-23-2-2-1-43 (2), RTN-1211-4-2-2-2

(11), RTN-1211-4-2-1-1 (17) and RTN-1212-4-3-5-5 (15) had higher grain yield plot^{-1} as well as low IPCA I and IPCA II scores and therefore assumed to be stable across three different environments.

4.1.2.13 Straw yield plot^{-1} (kg)

The AMMI analysis of variance for straw yield plot^{-1}of the twenty genotypes tested in three environments showed that 0.1647 of the total sum of square was attributable to environmental effects, 0.0375 to genotypic effects, and 0.1134 to GEI effects (Table 12). The IPCA I captured 0.1564 of the interaction sum of square. Similarly, the IPCA II explained a further 0.0656 of the GEI sum of square and cumulatively contributed to 0.2220 of the total GEI. The mean square for the IPCA I was significant at P = 0.01 but IPCA II was non-significant. Therefore, only AMMI 1 biplot analysis between main effects and first IPCA was performed.

AMMI 1 biplot analysis for straw yield plot^{-1}showed that the relative variability due to genotypes was less than the variability due to most of the environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 17). Genotypes or environments on left hand side of the vertical line showed low straw yield plot^{-1}than those on the right hand side. Thus, genotypes namely, RTN-1201-51-2-1-5-48 (3), RTN-1211-6-1-4-1-11 (6), RTN-1211-6-1-5-1-14 (8), RTN-1211-15-1-4-2-23 (9), RTN-1211-4-2-2-2 (11), RTN-1211-6-1-4-3-13 (7), RTN-1209-10-1-2-1-9 (4), RTN-1201-13-2-2-1-32 (1) and RTN-1211-9-1-2-12 (18) were found to show low straw yield plot^{-1} with RTN-1211-9-1-2-12 (18) being the overall best with general mean of 1.92 kg. In contrast, remaining of the genotypes was observed to show high straw yield plot^{-1}as they occupied the place right hand side of the main effect mid line on the biplot. Among the test environments, Phondaghat environment occupied position on the left hand side of the midpoint of the main effect axis and seems to be most favourable environment. The Dapoli and Shirgaon environment were identified to have relatively unfavourable environments as they occupied position farther from the right half of the midpoint axis.

Genotypes or environments with larger negative or positive IPCA I scores have high interactions, while those with IPCA I scores near zero (close to horizontal line) have little interaction across environments. Only three genotypes, RTN-1201-23-2-2-1-43 (2), RTN-1211-6-1-4-3-13 (7) and RTN-1211-15-1-4-2-23 (9) fell almost on the horizontal line indicating their uniform performance across the all environments. However, it is to mention that eight genotype namely, RTN-1201-5-1-3-14 (16), RTN-1211-6-1-5-1-14 (8), RTN-1211-4-2-2-2 (11), RTN-1209-10-1-2-1-9 (4), RTN-1201-13-2-2-1-32 (1) and RTN-1211-9-1-2-12 (18) were quite close to IPCA I axis therefore considered to be stable against the environmental changes. The genotypes, RTN-1201-51-2-1-5-48 (3), RTN-1209-10-1-2-1-9 (4), and RTN-1211-6-1-4-1-11 (6) had on left half of the main effect axis but with large negative score on IPCA I and therefore, expected to perform better under Phondaghat environment but variable performance across the different environments. Similarly, RTN-1211-9-1-2-12 (18) and RTN-1201-13-2-2-1-32 (1) also had low straw yield plot^{-1}but positive score on IPCA I and therefore, expected to perform better under

Phondaghat environment since it had positive interaction with these environments.

4.1.2.14 Iron content (ppm)

The AMMI analysis of variance for iron content illustrated that 7.8545 of the total sum of square was attributable to environmental effects, only 4.1212 to genotypic effects, and to 0.3150 GEI effects (Table 12). The IPCA I captured 0.3542 of the interaction sum of square. Similarly, the IPCA II explained a further 0.2714 of the GEI sum of square and together with IPCA I and IPCA II contributed 0.6256 of the total GEI. Both AMMI 1 and AMMI 2 biplot analysis was performed for iron content since mean square for the IPCA I and IPCA II were found to be significant.

AMMI 1 biplot analysis for iron content depicted that the relative variability due to genotypes was less than the variability due environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 18). Genotypes or environments on right hand side of the vertical line showed higher iron content than those on the left hand side. Thus, twelve out of twenty genotypes except RTN-1201-5-1-3-14 (16), RTN-1209-10-1-2-1-9 (4), RTN-1211-15-1-4-2-23 (9), RTN-1211-6-1-3-1-8 (5), RTN-1211-9-1-2-12 (18), RTN-1211-5-1-3-5 (13), RTN-1211-4-2-2-2 (11), Patni-6 (20)-6 (20), RTN-1211-6-1-4-1-11 (6), RTN-1211-6-1-4-3-13 (7), RTN-1210-3-1-4-5 (12) and Bela (19) were identified to have higher iron content with RTN-1211-5-1-3-5 (13)being the overall best with general mean of 10.200 ppm. In contrast, the remaining genotype were observed to show slightly low iron content as they occupied the place farther from the left hand side of the main effect mid line on the biplot. Among the test environments, two out of three environments *viz.,*Phondaghat and Shirgaon seems to be most favourable environments as this occupied position on the right hand side of the midpoint of the main effect axis.

Perusal of Fig. 18 revealed that, only one genotype, RTN-1211-6-1-3-1-8 (5) fell almost on the horizontal line indicating uniform iron content across the all environments. However, it is to mention that five genotypes namely, RTN-1201-5-1-3-14 (16), RTN-1209-10-1-2-1-9 (4), RTN-1211-4-2-2-2 (11), RTN-1211-5-1-3-5 (13) and RTN-1211-6-1-4-1-11 (6)were quite close to IPCA I axis and also plotted right hand side of the midpoint axis of main effect and therefore considered to be stable against the environmental changes with minor positive and negative interactions. The RTN-1211-9-1-2-12 (18), RTN-1211-6-1-4-3-13 (7), RTN-1210-3-1-4-5 (12), RTN-1211-6-1-4-1-11 (6) and RTN-1209-10-1-2-1-9 (4) fell on right hand side of the main effect axis but with large negative score on IPCA I and therefore, expected to perform better under and Phondaghat environment. Similarly, RTN-1211-4-2-2-2 (11), RTN-1211-5-1-3-5 (13), Patni-6 (20), RTN-1211-15-1-4-2-23 (9) and RTN-1201-5-1-3-14 (16)had higher iron content but positive score on IPCA I and therefore, expected to perform better on under Shirgaon environment showing positive interaction with these environment.

The AMMI 2 biplot was generated using genotypes and environments scores of the first two IPCA and presented as Fig. 19. To demonstrate the relative magnitude of the G x E for specific genotypes and environments. The genotypes and environments that are farthest from the origin being more responsive fit the worst. The closer genotypes are more stable than the score of the genotypes away from the centre. The angles between the genotypes and environments vectors determine the nature of the interaction as it is positive for acute angles, negligible for right angles, and negative for obtuse angles. Perusal of the Fig. 19indicated that the Shirgaon and Phondaghat environments had large interaction as indicated by large scores on both IPCA I and IPCA II. The environment Dapoli was quite close to IPCA I but has large score on IPCA II.

Orthogonal projection of genotypes on the environmental vector showed that the best genotypes with respect to Dapoli location was RTN-1211-4-2-2-2 (11) and RTN-1211-9-1-2-12 (18) as indicated by close acute angles with this environment. The Genotypes, RTN-1211-6-1-4-1-11 (6) and RTN-1201-23-2-2-1-43 (2) were best adapted to Phondaghat environment showing quite close acute angles with this environment. The genotypes, RTN-1211-6-1-5-1-14 (8), RTN-1212-4-3-5-5 (15) and RTN-1212-4-1-2-4 (10) were best adapted to Shirgaon environment showing quite close acute angles with this environment. The remaining all genotypes were found to scattered relatively close to the origin point in the AMMI 2 biplot indicating minimal interactions of these genotypes with the environment. The iron content of genotype, RTN-1212-4-1-2-4 (10) was lower than the overall mean and therefore did not qualify for stable genotype. The other eleven genotypes had higher iron content as well as low IPCA I and IPCA II scores and therefore assumed to be stable across three different environments.

4.1.2.15 Zinc content (ppm)

The AMMI analysis of variance for zinc content illustrated that 8.3859 of the total sum of square was attributable to environmental effects, only 30.2011 to genotypic effects, and to 1.0062 GEI effects (Table 12). The IPCA I captured 1.4023 of the interaction sum of square. Similarly, IPCA II explained a further 0.5661 of the GEI sum of square and together with IPCA I and IPCA II contributed 1.9684 of the total GEI. Both AMMI 1 and AMMI 2 biplot analysis was performed for zinc content since mean square for the IPCA I and IPCA II were found to be significant.

AMMI 1 biplot analysis for zinc content depicted that the relative variability due to genotypes was less than the variability due environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 20). Genotypes or environments on right hand side of the vertical line showed higher zinc content than those on the left hand side. Thus, two out of twenty genotypes except RTN-1211-4-2-2-2 (11) and RTN-1211-9-1-2-12 (18) were identified to have higher zinc content with RTN-1211-4-2-1-1 (17)being the overall best with general mean of 28.167 ppm. In contrast, the remaining genotypes were observed to show slightly low zinc content as they occupied the place farther from the left hand side of the main effect mid line on the biplot. Among the test environments, Shirgaon seems to be most favourable environment as these occupied position on the close to vertical axis therefore they show average performance.

Perusal of Fig. 20 revealed that, only two genotypes, RTN-1212-4-1-2-4 (10) and RTN-1211-4-2-1-1 (17) fell almost on the horizontal line indicating uniform zinc content across the all environments. However, it is to mention that three Genotypes namely, RTN-1212-4-3-5-5 (15), RTN-1211-6-1-4-1-11 (6), and RTN-1209-10-1-2-1-9 (4)were quite close to IPCA I axis therefore considered to be stable against the environmental changes with minor positive and negative interactions. The RTN-1211-4-2-2-2 (11) and RTN-1211-9-1-2-12 (18) fell on right hand side of the main effect axis but with large negative score on IPCA I and therefore, expected to perform better under and Dapoli environment.

4.1.2.16 Protein content (%)

The AMMI analysis of variance for protein content illustrated that 0.0082 of the total sum of square was attributable to environmental effects; only 1.5287 to genotypic effects and to 0.0817 GEI effects (Table 12). The IPCA I captured 0.1015 of the interaction sum of square. Similarly, the IPCA II explained a further 0.0596 of the GEI sum of square and together with IPCA I and IPCA II contributed 0.1611 of the total GEI. Both AMMI 1 and AMMI 2 biplot analysis was performed for protein content since mean square for the IPCA I and IPCA II were found to be significant.

AMMI 1 biplot analysis for protein content depicted that the relative variability due to genotypes was less than the variability due environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 21). Genotypes or environments on right hand side of the vertical line showed higher protein content than those on the left hand side. Thus, out of twenty genotypes, except RTN-1211-6-1-4-1-11 (6), RTN-1209-10-1-2-1-9 (4), RTN-1211-6-1-2-7 (14) and RTN-1211-15-1-4-2-23 (9) were identified to have higher protein content with Patni-6 (20)being the overall best with general mean of 8.533 per cent. In contrast, the genotypes, RTN-1211-6-1-4-1-11 (6), RTN-1209-10-1-2-1-9 (4), RTN-1211-6-1-2-7 (14) and RTN-1211-15-1-4-2-23 (9) except RTN-1211-9-1-2-12 (18) they present on line were observed to show slightly low protein content as they occupied the place farther from the left hand side of the main effect mid line on the biplot. Among the test environments, all the three environments *viz.,* Dapoli, Phondaghat and Shirgaon seems to be most favourable environments as this occupied position on the right hand side of the midpoint of the main effect axis.

Perusal of Fig. 21 revealed that, only one genotype, RTN-1211-6-1-4-1-11 (6) fell almost on the horizontal line indicating uniform protein content across the all environments. However, it is to mention that four genotypes namely, RTN-1211-5-1-3-5 (13), RTN-1201-13-2-2-1-32 (1), Patni-6 (20) and RTN-1211-6-1-4-3-13 (7)were quite close to IPCA I axis and also plotted right hand side of the midpoint axis of main effect and therefore considered to be stable against the environmental changes with minor positive and negative interactions. The RTN-1201-13-2-2-1-

32 (1), RTN-1201-23-2-2-1-43 (2), RTN-1211-4-2-2-2 (11) and RTN-1211-6-1-5-1-14 (8) fell on right hand side of the main effect axis but with large negative score on IPCA I and therefore, expected to perform better under Dapoli and Phondaghat environments. Similarly, RTN-1201-5-1-3-14 (16), RTN-1211-4-2-1-1 (17), RTN-1201-51-2-1-5-48 (3), RTN-1211-6-1-3-1-8 (5) and RTN-1212-4-3-5-5 (15)had higher protein content but positive score on IPCA I and therefore, expected to perform better under Shirgaon environment showing positive interaction with these environment.

The AMMI 2 biplot was generated using genotypes and environments scores of the first two IPCA and presented as Fig. 22. To demonstrate the relative magnitude of the G x E for specific genotypes and environments. The genotypes and environments that are farthest from the origin being more responsive fit the worst. The closer genotypes are more stable than the score of the genotypes away from the centre. The angles between the genotype and environment vectors determine the nature of the interaction as it is positive for acute angles, negligible for right angles, and negative for obtuse angles. Perusal of the Fig. 22indicated that the Shirgaon and Phondaghat environments had large interaction as indicated by large scores on both IPCA I and IPCA II. The Dapoli environment was quite close to IPCA I but has large score on IPCA II.

Orthogonal projection of genotypes on the environmental vector showed that the best genotype with respect to Dapoli location was RTN-1211-4-2-2-2 (11) as indicated by close acute angles with this environment. The genotypes, RTN-1201-5-1-3-14 (16), RTN-1211-4-2-1-1 (17) and RTN-1201-51-2-1-5-48 (3) were best adapted to Shirgaon environment showing quite close acute angles with this environment. The genotypes, RTN-1211-5-1-3-5 (13), Patni-6 (20) and RTN-1211-6-1-4-1-11 (6) were best adapted to Phondaghat environment showing quite close acute angles with this environment. The remaining all genotypes were found to scattered relatively close to the origin point in the AMMI 2 biplot indicating minimal interactions of these genotypes with the environments. The protein content of genotype RTN-1209-10-1-2-1-9 (4) was lower than the overall mean and therefore did not qualify for stable genotypes. The other twelve genotypes had higher protein content as well as low IPCA I and IPCA II scores and therefore assumed to be stable across three different environments.

4.1.2.17 Amylosecontent (%)

The AMMI analysis of variance for amylose content illustrated that 3.3320 of the total sum of square was attributable to environmental effects, only 11.5301 to genotypic effects, and 0.3320 to GEI effects (Table 12). IPCA I captured 0.4204 of the interaction sum of square. Similarly, IPCA II explained a further 0.4339 of the GEI sum of square and together with IPCA I and IPCA II contributed 0.8543 of the total GEI. Both AMMI 1 and AMMI 2 biplot analysis was performed for amylose content since mean square for the IPCA I and IPCA II were found to be significant.

AMMI 1 biplot analysis for amylose content depicted that the relative variability due to genotypes was less than the variability due environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 23). Genotypes or environments on right hand side of the vertical line showed higher amylose content than those on the left hand side. Thus, ten out of twenty Genotypes namely, RTN-1211-6-1-5-1-14 (8), RTN-1210-3-1-4-5 (12), RTN-1201-5-1-3-14 (16), RTN-1211-5-1-3-5 (13), RTN-1211-6-1-4-3-13 (7), RTN-1211-6-1-3-1-8 (5), RTN-1211-6-1-4-1-11 (6), RTN-1212-4-3-5-5 (15), RTN-1211-15-1-4-2-23 (9) and RTN-1211-4-2-1-1 (17) were identified to have higher amylose per cent with RTN-1210-3-1-4-5 (12)being the overall best with general mean of 23.00 per cent. In contrast, the remaining of the genotypes except RTN-1211-4-2-2-2 (11) and RTN-1201-51-2-1-5-48 (3) they present on line, were observed to show slightly low amylose per cent as they occupied the place farther from the left hand side of the main effect mid line on the biplot. Among the test environments, two out of three environments namely, Phondaghat and Shirgaon seems to be most favourable environments as these occupied position on the right hand side of the midpoint of the main effect axis

Perusal of Fig. 23 revealed that, genotype, RTN-1212-4-1-2-4 (10) and fell almost on the horizontal line indicating uniform amylose content across the environments. However, it is to mention that five Genotypes, RTN-1211-6-1-5-1-14 (8), RTN-1210-3-1-4-5 (12), RTN-1201-5-1-3-14 (16), RTN-1211-4-2-1-1 (17) and RTN-1211-6-1-4-3-13 (7)were quite close to IPCA I axis and also plotted right hand side of the midpoint axis of main effect and therefore considered to be stable against the environmental changes with minor positive and negative interactions. The RTN-1201-23-2-2-1-43 (2), RTN-1212-4-3-5-5 (15), RTN-1201-5-1-3-14 (16) and RTN-1210-3-1-4-5 (12) fell on right hand side of the main effect axis but with large negative score on IPCA I and therefore, expected to perform better under Phondaghat environment. Similarly, RTN-1211-5-1-3-5 (13), RTN-1211-6-1-3-1-8 (5), RTN-1211-6-1-4-3-13 (7), RTN-1211-6-1-4-1-11 (6) and RTN-1211-6-1-5-1-14 (8)had higher amylose per cent but positive score on IPCA I and therefore, expected to perform better on under Shirgaon environments showing positive interaction with these environment.

The AMMI 2 biplot was generated using genotypes and environments scores of the first two IPCA and presented as Fig. 24. The genotypes and environments that are farthest from the origin being more responsive fit the worst. The closer genotypes are more stable than the score of the genotypes away from the centre. The angles between the genotype and environment vectors determine the nature of the interaction as it is positive for acute angles, negligible for right angles, and negative for obtuse angles. Perusal of the Fig. 24 indicated that the Dapoli environment had large interaction as indicated by large scores on both IPCA I and IPCA II whereas Shirgaon were quite close to IPCA II but large score on IPCA I. The environment Phondaghat was quite close to IPCA I but has large score on IPCA II.

Orthogonal projection of genotypes on the environmental vector showed that the best genotypes with respect to Dapoli location were RTN-1211-6-1-4-3-13 (7) and

RTN-1211-4-2-1-1 (17) as indicated by close acute angles with this environment. The genotypes, RTN-1209-10-1-2-1-9 (4) and Patni-6 (20) were best adapted to Shirgaon environment showing quite close acute angles with this environment. The Genotypes, RTN-1201-51-2-1-5-48 (3), RTN-1201-23-2-2-1-43 (2), RTN-1201-13-2-2-1-32 (1) was best adapted to Phondaghat environment showing quite close acute angles with these environment. The remaining all genotypes were found to scattered relatively close to the origin point in the AMMI 2 biplot indicating minimal interactions of these genotypes with the environments. The amylose content of genotype, RTN-1211-9-1-2-12 (18) was lower than the overall mean and therefore did not qualify for stable genotypes. The other twelve genotypes had higher amylose content as well as low IPCA I and IPCA II scores and therefore assumed to be stable across three different environments.

CHAPTER V

DISCUSSION

The success of crop improvement activity largely depends on the identification of superior and stable variety. A variety can be considered superior, if it has potential for high yield under favorable environment, and at the same time a great deal of phenotypic stability. Stability refers to non erratic performance with respect to agronomics trait and stable cultivar show minimal or low interaction. (Padmavati*et al.* 2012)

Numerous methods have been used for an understanding of the causes of G × E interaction. Among the multivariate approaches AMMI model is widely used (Gauch, 1988). The AMMI model describes the GE interaction in more than one dimension and it offers better opportunities for studying and interpreting GE interaction than analysis of variance (ANOVA) and regression of the mean (Zobel*et al.,* 1992). In AMMI, the additive, portion is separated from interaction by ANOVA. Then the Interaction Principle Components Analysis (IIPCA), which provides a multiplicative model, is applied to analyze the interaction effect from the additive ANOVA model. The biplot display of IIPCA scores plotted against each other provides visual inspection and interpretation of the GE interactions. Integrating biplot display and genotypic stability statistics enables genotypes to group based on similarity of performance across diverse environments. In this study the result of AMMI analysis indicated that the AMMI model fits the data well and justifies the use of AMMI 2. This made it possible to construct the biplot and calculate genotypes and environments effects (Adugna*et al.,* 2011). The Interaction Principle Component Axes (IIPCA) scores of genotypes in the AMMI analysis indicate the stability of genotypes across environments. The mean closer the IIPCA scores to zero, the more stable the genotypes are across their testing environments.

5.1 Days to 50 per cent flowering

The AMMI analysis of variance showed that G X E interaction sum of square was very less than that for genotypes, so major difference was due to genotypic effect. The variance of GEI was partitioned among the first two interaction principle component axis (IIPCA). Of which IIPCA I exhibited 0.7976 sum of square of the total GEI, IIPCA II was 0.1264 sum of square, these implied that the interaction of the Patni-6 genotype with three environments was predicted by the only first component of IPCA I. These finding were in conformity to those of Islam *et al.* (2014) and Gauch*et al.* (1996).

AMMI 1 biplot relieved that interaction of environments was high and varied. Phondaghat and Shirgaon had negative interaction while Dapoli had positive interaction. Dapoli environment being on the left hand side of the midpoint of the main effect axis seemed to be favorable environment for Days to 50 per cent flowering, while Phondaghat and Shirgaon away from midpoint was found less favorable environments. Genotypes, RTN-1211-4-2-1-1, RTN-1211-6-1-4-1-11, RTN-1211-6-1-4-3-13, RTN-1211-4-2-2-2, RTN-1210-3-1-4-5 and RTN-1211-5-1-3-5 had low mean and positive interaction were adapted to Dapoli environment. Conversely, the Genotypes, RTN-1201-13-2-2-1-32, RTN-1211-6-1-3-1-8, RTN-1211-6-1-5-1-14, RTN-1211-15-1-4-2-23, RTN-1212-4-1-2-4, RTN-1211-6-1-2-7 and RTN-1212-4-3-5-5 with high mean and negative interaction was adapted to Shirgaon environment. Genotype that grouped together that has similar adaptation while environment which grouped together influence the genotype in the same way Castillo *et al.* (2013), Gauch and Zobel (1996). Genotypes, RTN-1211-9-1-2-12, RTN-1211-15-1-4-2-23 and RTN-1201-5-1-3-14 score near zero have had small interaction effect indicating that these verities were less influenced by environments. Among them, Genotype, RTN-1211-9-1-2-12 had high mean hence, found stable and recommended for the entire environment. Similar finding were also reported by Kulsum*et al.* (2013)

In AMMI 2 biplotPhondaghat and Dapoli had short spoks and they did not exert strong interactive force while environment Shirgaon having long spoks exert strong interaction. Similar finding were also reported by Gunjan (2015). Genotypes, RTN-1211-6-1-3-1-8, RTN-1201-23-2-2-1-43, RTN-1201-13-2-2-1-32, RTN-1210-3-1-4-5, and RTN-1211-6-1-2-7 had high IPCA score and away from origin were most responsive. Genotype, RTN-1210-3-1-4-5 were adapted to Phondaghat, genotype, RTN-1201-13-2-2-1-32 to Dapoli and Genotypes, RTN-1211-6-1-3-1-8, RTN-1201-23-2-2-1-43 and RTN-1211-6-1-2-7 to were adapted to Shirgaon

5.2 Plant height (cm)

The variation of plant height in all three environment explained by AMMI analysis. They showed that the genotypic interaction was higher than that for environment, so major difference was due to genotypes effect. The variance of GEI was partitioned among the IPCA I, which exhibited 0.56 sum of square of the total GEI. These finding were in conformity to those of Verma*et al.* (2016).

In AMMI 1 biplot, genotype, RTN-1201-13-2-2-1-32 had high mean and positive interaction were adapted to Dapoli environment. Weikai *et al.* (2007) showed similar finding, genotypes, RTN-1201-51-2-1-5-48, RTN-1211-6-1-4-3-13 and RTN-1201-23-2-2-1-43 score near zero have small interaction effect indicating that these verities were less influenced by environments.

5.3 Numberof tillers plant^{-1}

The AMMI analysis of variance showed that G X E interaction sum of square was very less than that for environment, so major difference was due to environment effect. The variance of GEI was partitioned among the first two interaction principle component axis (IPCA) of which IIPCA I exhibited 0.6808 sum of square of the total GEI and IIPCA II was 0.5887 sum of square. These finding were in conformity to those of Akter*et al.* (2014).

AMMI 1 biplot relieved that interaction of environments was high and varied. Phondaghat and Dapoli had negative interaction while Shirgaon had positive interaction. Shirgaon environment being on the right hand side of the midpoint of the main effect axis seemed to be favorable environment for number of tillers plant^{-1}, while Phondaghat and Dapoli away from midpoint was found less favorable environments. Genotypes, RTN-1201-51-2-1-5-48, RTN-1211-5-1-3-5, RTN-1210-3-1-4-5, RTN-1211-9-1-2-12, and RTN-1201-13-2-2-1-32 had high mean and positive interaction were adapted to Dapoli environment. These finding were in conformity to those of Dewi*et al.* (2014) and Bose *et al.* (2015). Genotypes, RTN-1211-6-1-2-7, RTN-1211-5-1-3-5 and RTN-1211-6-1-4-3-13 score near zero have small interaction effect indicating that these verities were less influenced by environments. Among them Genotype, RTN-1211-5-1-3-5 followed by RTN-1211-6-1-2-7 had high mean hence, found stable and recommended for the entire environments. Similar finding were also reported by Rumanti*etal.* (2016)

5.4 Numberof panicle square meter^{-1}

The variation of number of Panicle square meter^{-1} in all three environment explained by AMMI analysis. They showed that the genotypic interaction was higher than that for environment, so major difference was due to genotypes effect. These finding were in conformity to those of Ogunbayo*et al.* (2011). The variance of GEI was partitioned among the IPCA I, which exhibited 12.56 sum of square of the total GEI.

In AMMI 1 biplot, the interaction of genotype was high and varied. Phondaghat and Shirgaon had negative interaction while Dapoli environment was near to line which shows average interaction and seemed to be favorable environment for straw yield plot^{-1}. Temesgen*et al.* (2015) and Ramanjaneyulu*et al.* (2014) showed similar finding. Genotypes, RTN-1212-4-3-5-5, RTN-1201-51-2-1-5-48, RTN-1201-13-2-2-1-32, RTN-1211-6-1-2-7, RTN-1201-5-1-3-14, RTN-1211-5-1-3-5 and RTN-1212-4-1-2-4 had high mean and positive interaction were adapted to Dapoli environment. Genotypes, RTN-1211-4-2-2-2 and RTN-1211-4-2-1-1 score near zero have had small interaction effect indicating that these verities were less influenced by environments.

5.5 Panicle length (cm)

Present investigation showed that very low variations in panicle length of rice in between three environments. The AMMI analysis of variance showed that G X E interaction sum of square was very less than that for genotypes, so major difference was due to genotypic effect. The mean squares for the IPCA I was significant at P = 0.01 but IPCA II was non-significant. Therefore, the variance of GEI was partitioned among the only one interaction principle component axis (IPCA) of which IPCA I exhibited 4.5338 sum of square of the total GEI. These finding were in conformity to those of Shresta*etal.* (2007) and Lakew*etal.* (2014).

AMMI1 biplot relieved that interaction of environment was high and varied. Phondaghat and Dapoli had negative interaction while Shirgaon had positive interaction. Shirgaon environment being on the right hand side of the midpoint of the main effect axis seemed to be favorable environment for panicle length, while Phondaghat and Dapoli away from midpoint was found less favorable environments. Genotypes, RTN-1201-51-2-1-5-48, RTN-1201-51-2-1-5-48, RTN-1212-4-1-2-4, RTN-1211-6-1-3-1-8, RTN-1210-3-1-4-5 and RTN-1201-5-1-3-14 had high mean and positive interaction were adapted to Dapoli environment. These finding were in conformity to those of Anputhas*etal.* (2014) and Bose *etal.* (2015). Genotypes, RTN-1212-4-3-5-5, RTN-1201-13-2-2-1-32 and RTN-1201-51-2-1-5-48 score near zero have small interaction effect indicating that these verities were less influenced by environment. Among them genotype, RTN-1201-51-2-1-5-48 followed by RTN-1212-4-3-5-5 had high mean hence found stable and recommended for the entire environments. Similar finding were also reported by Rumanti*etal.* (2016).

5.6 Total number of spikeletspanicle^{-1}

The total number of spikeletspanicle^{-1} had more variation in each environment. Total number of spikeletspanicle^{-1} of Dapoli environment is higher than Shirgaon and Phondaghat environment, and these variation explained by AMMI analysis. They showed that the environment interaction was higher than that for genotypic, so major difference was due to environment effect. These finding were in conformity to those of Shrestha*et al.* (2007) and Gauch*et al.* (1996). The variance of GEI was partitioned among the first two interaction principle component axis (IPCA). Of which IPCA I exhibited 693.32 sum of square of the total GEI; IPCA II was 631.90 sum of square.

AMMI 1 biplot relieved that interaction of environments was high and varied. Shirgaon and Phondaghat had negative interaction while Dapoli had positive interaction, because they present right hand side of the midpoint of the main effect axis seemed to be favorable environment for total number of spikeletspanicle^{-1} Bose *et al.* (2015) and Tariku *et al.* (2013). Genotypes, RTN-1201-51-2-1-5-48, RTN-1211-4-2-1-1, RTN-1211-6-1-3-1-8, RTN-1212-4-1-2-4 and RTN-1201-23-2-2-1-43 had high mean and positive interaction were adapted to Dapoli environment. Genotype RTN-1211-5-1-3-5 score near zero have had small interaction effect indicating that these verities were less influenced by environments.

In AMMI 2 biplot, Shirgaon had short spoks and they did not exert strong interactive force while environments, Phondaghat and Dapoli having long spoks exert strong interaction. Genotypes, RTN-1211-6-1-4-3-13, RTN-1201-13-2-2-1-32, RTN-1211-6-1-4-3-13, RTN-1211-4-2-2-2, RTN-1211-6-1-5-1-14, RTN-1211-9-1-2-12, RTN-1211-5-1-3-5, and RTN-1211-6-1-2-7 had high IPCA score and away from origin were most responsive. Genotypes, RTN-1211-6-1-4-3-13 and RTN-1211-4-2-2-2 were adapted to Phondaghat, RTN-1201-13-2-2-1-32 and RTN-1201-51-2-1-5-48 to Dapoli and RTN-1211-6-1-2-7, RTN-1211-5-1-3-5, RTN-1211-9-1-2-12 and RTN-1211-6-1-5-1-14 to be adapted to Shirgaon.

5.7 Number of filled spikelets panicle^{-1}

The number of filled spikelets panicle^{-1} showed more difference in each environment, Dapoli environment showed more number of spikelets panicle^{-1} is higher than other two environments, and these variation explained by AMMI analysis. They showed that G X E interaction and genotypes sum of square was very less than that for environments, so major difference was due to environment effect. These finding were in conformity to those of Islam *et al.* (2014) and Gauch*et al.* (1996). The variance of GEI was partitioned among the IPCA I, which exhibited 677.04 sum of square.

In AMMI 1 biplot, the interaction of environment was high and varied. Shirgaon and Phondaghat had negative interaction while Dapoli environment was showed positive interaction and seemed to be favorable environment for number of filled spikelets panicle^{-1}Gauch and Zobel (1996). Genotypes, RTN-1212-4-1-2-4, RTN-1201-23-2-2-1-43, RTN-1211-4-2-1-1, RTN-1201-51-2-1-5-48, RTN-1211-6-1-3-1-8 and RTN-1201-13-2-2-1-32 had high mean and positive interaction were adapted to Dapoli environment. Genotype, RTN-1201-51-2-1-5-48 and Bela score near zero have had small interaction effect indicating that these verities were less influenced by environments. Similar finding were also reported by Kulsum*et al.* (2013).

5.8Spikelets fertility (%)

The fertility of spikelets slightly difference in each environment and these variation explained by AMMI analysis. They showed that G X E interaction and genotypes sum of square was very less than that for environments, so major difference was due to environmental effect. These finding were in conformity to those of Islam *etal.* (2014) and Gauche *etal.* (1996). The variance of GEI was partitioned among the first two interaction principle component axis (IIPCA) of which IIPCA I exhibited 30.3390 sum of square of the total GEI, IIPCA II was 11.8977 sum of square these implied that the interaction of the Patni-6 rice genotype with three environments was predicted by the both the IPCA I and IPCA II .

AMMI 1 biplot relieved that interaction of environments was high and varied. Only Shirgaon had negative interaction while Dapoli and Phondaghat had positive interaction. Dapoli and Phondaghat environments being on the right hand side of the midpoint of the main effect axis seemed to be favorable environment for spikelets fertility, while Shirgaon away from midpoint was found less favorable environment, Padmavati*et al.* (2013), Gauch and Zobel (1996). Genotypes, RTN-1201-13-2-2-1-32, RTN-1201-

23-2-2-1-43, RTN-1201-51-2-1-5-48, RTN-1201-51-2-1-5-48, RTN-1211-9-1-2-12 and RTN-1212-4-3-5-5 had high mean and positive interaction were adapted to Phondaghat environment. Genotypes, RTN-1211-5-1-3-5, RTN-1211-15-1-4-2-23 and RTN-1211-6-1-5-1-14 score near zero have small interaction effect indicating that these verities were less influenced by environment. Among them genotype, RTN-1211-6-1-5-1-14 followed by genotype, RTN-1211-5-1-3-5 had high mean hence, found stable and recommended for the entire environments. Similar finding were also reported by Kulsum*et al.* (2013).

In AMMI 2 biplotShirgaon had short spoks and they did not exert strong interactive force while environments Phondaghat and Dapoli having long spoks exert strong interaction. Genotypes, RTN-1212-4-1-2-4, RTN-1211-5-1-3-5, RTN-1201-23-2-2-1-43, RTN-1211-6-1-4-1-11, RTN-1211-6-1-5-1-14, RTN-1201-51-2-1-5-48 and RTN-1211-6-1-2-7 had high IPCA score and away from origin were most responsive. Genotypes, RTN-1211-5-1-3-5 and RTN-1201-23-2-2-1-43 were adapted to Phondaghat, genotype RTN-1212-4-1-2-4 to Dapoli and genotypes, RTN-1211-6-1-4-1-11, RTN-1211-6-1-5-1-14 and RTN-1211-6-1-2-7 to be adapted to Shirgaon.

5.9 Test weight (g)

The test weight of grain slightly difference in each environment, test weight of Shirgaon environment is higher than Dapoli and Phondaghat environment and these variation explained by AMMI analysis. They showed that G X E interaction and environments sum of square was very less than that for genotypes, so major difference was due to genotypic effect. These finding were in conformity to those of Hasan*et al.* (2014). The variance of GEI was partitioned among the IPCA I, which exhibited 2.5208 sum of square of the total GEI.

In AMMI1 biplot, the interaction of genotypes was high and varied. Dapoli and Phondaghat had negative interaction while Shirgaon environment was near to line which shows positive interaction and seemed to be favorable environment for test weight of grain Anandan*et al.* (2009). Genotypes, RTN-1201-51-2-1-5-48 and RTN-1201-51-2-1-5-48 had high mean and positive interaction were adapted to Phondaghat environment. Genotypes, RTN-1211-6-1-3-1-8 and RTN-1211-6-1-4-1-11 score near zero have small interaction effect indicating that these verities were less influenced by environments. Similar finding were also reported by Michiel*et al.* (2011)

5.10 Grain yield plant^{-1} (g)

The variation of grain yield plant^{-1} in all the three environments explained by AMMI analysis. They showed that the environment interaction was higher than that for genotypic, so major difference was due to environments effect. These finding were in conformity to those of Islam *et al.* (2014) and Gauch*et al.* (1996). The variance of GEI was partitioned among the first two interaction principle component axis of which IPCA I exhibited 2.1734 sum of square of the total GEI, IPCA II was 0.4320 sum of square these implied that the interaction of the 20 rice genotype with three environments was predicted by the both the IPCA I and IPCA II .

AMMI 1 biplot relieved that interaction of environments was high and varied. Phondaghat had negative interaction while Shirgaon and Dapoli had positive interaction, because they present right hand side of the midpoint of the main effect axis seemed to be favorable environments for grain yield plant^{-1}Padmavati*et al.* (2013), Gauch and Zobel (1996). Genotypes, RTN-1212-4-1-2-4, RTN-1211-6-1-3-1-8, RTN-1211-6-1-5-1-14, RTN-1201-51-2-1-5-48, RTN-1211-6-1-2-7, RTN-1201-13-2-2-1-32, RTN-1201-5-1-3-14, RTN-1201-51-2-1-5-48, RTN-1211-5-1-3-5 and RTN-1211-15-1-4-2-23 had high mean and positive interaction were adapted to Dapoli and Shirgaon environments. Genotype, Bela and RTN-1211-6-1-4-1-11 score near zero have had small interaction effect indicating that these verities were less influenced by environments.

In AMMI 2 biplot, Shirgaon had short spoks and they did not exert strong interactive force while environment Phondaghat and Dapoli having long spoks exert strong interaction. Genotypes, RTN-1211-15-1-4-2-23, RTN-1212-4-1-2-4, RTN-1211-9-1-2-12, RTN-1211-4-2-1-1, RTN-1201-23-2-2-1-43 and RTN-1201-13-2-2-1-32 had high IPCA score and away from origin were most responsive. Genotypes, RTN-1201-13-2-2-1-32 and RTN-1201-23-2-2-1-43 were adapted to Phondaghat, genotypes, RTN-1211-9-1-2-12 and RTN-1211-4-2-1-1 to Dapoli and RTN-1211-15-1-4-2-23 and RTN-1212-4-1-2-4 to be adapted to Shirgaon.

5.11 Straw yield plant^{-1} (g)

The variation of straw yield plant^{-1} in all the three environments explained by AMMI analysis. They showed that the environments interaction was higher than that for genotypes, so major difference was due to environmental effect. These finding were in conformity to those of Akter*et al.* (2014). The variance of GEI was partitioned among the IPCA I, which exhibited 5.30 sum of square of the total GEI.

In AMMI 1 biplot, all genotypes, except RTN-1211-6-1-3-1-8, RTN-1201-23-2-2-1-43 and RTN-1210-3-1-4-5 had high mean and positive interaction were adapted to Phondaghat environment. Anandan*et al.*(2009) and Gauch and Zobel (1996) showed similar finding genotype, RTN-1201-51-2-1-5-48 score near to zero have had small interaction effect indicating that these verities were less influenced by environments.

5.12 Grain yield plot $^{-1}$ (kg)

The yield of grain plot^{-1} showed slightly difference in each environment and these variation explained by AMMI analysis. They showed that the sum of square of environments is higher than the G X E interaction and genotypes, so major difference was due to environmental effect. These finding were in conformity to those of Temesgen*et al.* (2015). The variance of GEI was partitioned among the first two interaction principle component axis (IPCA). Of which IPCA I exhibited 0.4069 sum of square of the total GEI, IPCA II was 0.2050 sum of square.

AMMI 1 biplot relieved that interaction of environments was high and varied. Only Shirgaon had negative interaction while Dapoli and Phondaghat had positive interaction, because they present right hand side of the midpoint of the main effect axis seemed to be favorable environment for spikelets fertility Bose *et al.* (2014) Gauch and Zobel (1996). Genotypes, RTN-1201-13-2-2-1-32, RTN-1201-23-2-2-1-43, RTN-1201-51-2-1-5-48, RTN-1211-4-2-2-2, RTN-1210-3-1-4-5, RTN-1201-5-1-3-14, RTN-1211-4-2-1-1 and RTN-1212-4-3-5-5 had high mean and positive interaction were adapted to Phondaghat environment. Genotypes, RTN-1211-4-2-1-1, RTN-1211-4-2-2-2, RTN-1212-4-1-2-4 and RTN-1212-4-3-5-5 score near zero has small interaction effect indicating that these verities were less influenced by environment. Similar finding were also reported by Samonte*et al.* (2004)

In AMMI 2 biplotDapoli had short spoks and they did not exert strong interactive force while environment Phondaghat and Shirgaon having long spoks exert strong interaction. Genotypes, RTN-1211-6-1-4-3-13, RTN-1211-9-1-2-12, RTN-1201-13-2-2-1-32, RTN-1201-51-2-1-5-48, RTN-1211-6-1-4-1-11, RTN-1212-4-1-2-4 and RTN-1201-51-2-1-5-48 had high IPCA score and away from origin were most responsive. Genotypes, RTN-1211-6-1-3-1-8 and RTN-1201-13-2-2-1-32 were adapted to Phondaghat, genotypes, RTN-1212-4-1-2-4, RTN-1211-6-1-4-1-11 and RTN-1201-51-2-1-5-48 to Dapoli and RTN-1211-6-1-4-3-13 to be adapted to Shirgaon.

5.13 Straw yield plot^{-1} (kg)

There is very low difference in straw yield plot^{-1} in all three environment, and these variation explained by AMMI analysis. They showed that G X E interaction and genotypes sum of square was very less than that for environments, so major difference was due to environmental effect. These finding were in conformity to those of Jambhulkar *et al.* (2014) and Gauch*et al.* (1996). The variance of GEI was partitioned among the IPCA I, which exhibited 2.17 sum of square of the total GEI.

In AMMI 1 biplot, the interaction of genotypes was high and varied. Phondaghat had negative interaction while Dapoli and Shirgaon environment was near to line which shows positive interaction and seemed to be favorable environment for straw yield plot^{-1}. Lakew*et al.* (2014) showed similar finding. Genotypes, RTN-1210-3-1-4-5, RTN-1211-5-1-3-5, RTN-1211-6-1-2-7, RTN-1212-4-3-5-5, RTN-1211-6-1-3-1-8 and RTN-1212-4-1-2-4, had high mean and positive interaction were adapted to Phondaghat environment. Genotypes, RTN-1211-6-1-5-1-14, RTN-1211-15-1-4-2-23, RTN-1201-23-2-2-1-43 and RTN-1201-5-1-3-14 score near zero have small interaction effect indicating that these verities were less influenced by environments. Similar finding were also reported by Kurniawan*et al.* (2016).

5.14 Micronutrients content

The micronutrients viz. zinc, iron, protein and amylose content in red rice showed very low variation of mean at all three environments. The AMMI analysis of variance showed that G X E interaction environments sum of square was very less than that for genotypes, so major difference was due to genotypic effect on these four micronutrients. The variance of GEI was partitioned among the first two interaction principle component axis (IPCA) of which IPCA I exhibited viz. zinc, iron, protein and amylose respectively 1.4023, 0.2182, 0.1015 and 0.4204 sum of square of the total GEI, IPCA II was viz. zinc, iron, protein and amylose respectively, 0.5661, 0.0545, 0.0596 and 0.2339 sum of square these implied that the interaction of the 20 rice genotypes with three environments. These finding were in conformity to those of Kurniawan*et al.* (2016) and Kulsum*et al.* (2013).

AMMI 1 biplot relieved that interaction of environments was high and varied. Phondaghat and Shirgaon had positive interaction for iron, amylose and protein while for zinc showed negative interaction. Dapoli had negative interaction for all micronutrients. The environment being on the right hand side of the midpoint of the main effect axis seemed to be favorable environment for micronutrients viz. zinc, iron, protein and amylose. Genotypes, RTN-1211-9-1-2-12, RTN-1201-5-1-3-14, RTN-1211-4-2-2-2,12, RTN-1201-5-1-3-14, RTN-1211-6-1-5-1-14, RTN-1211-5-1-3-5, RTN-1211-6-1-4-3-13 and RTN-1201-23-2-2-1-43 had high mean and positive interaction were adapted to favorable environments. Genotype that grouped together that had similar adaptation while environments which grouped together influence the genotype in the same way Gauch and Zobel (1996). Genotypes, RTN-1211-6-1-4-1-11 for iron, RTN-1211-4-2-2-2 and RTN-1212-4-1-2-4 for amylose, RTN-1211-6-1-4-3-13 for zinc, and RTN-1211-6-1-4-3-13 for protein showed score near to zero have had small interaction effect indicating that these verities were less influenced by environments. All they found stable and recommended for all the three environments.

In AMMI2 biplot, for amylose, zinc and iron Dapoli environment and for protein, Phondaghat environment had short spoks and they did not exert strong interactive force while remaining all environments having long spoks exert strong interaction.

CHAPTER VI

SUMMARY AND CONCLUSION

The experimental trial entitled “Stability analysis in promising bio-fortified red kernel genotypes of rice (*Oryza* *sativa* L.) by using AMMI model” was conducted at three locations*viz.,* Agricultural Research Station, Phondaghat, Department of Agril. Botany, College of Agriculture, Dapoli and Agricultural Research Station, Shirgaon, during*Kharif* 2016. In respect of the fulfillment of following objectives:

1. To study the G X E interaction for grain yield and quality attributes in promising bio-fortified lines of rice.
2. To study the specificity in adaptability of rice genotypes to specific environment.
3. To identify stable bio-fortified rice genotypes for yield and quality traits.

The materials for the present study of twenty genotypes of promising bio-fortified red kernel rice were grown in randomized block design with three replications and three locations*viz.,* Dapoli, Shirgaon, Phondaghat, during *Kharif,* 2016. Observations were recorded on seventeen characters *viz.,* days to 50 per cent flowering, plant height (cm), number of tillers plant^{-1}, number of panicles square meter^{-1}, panicle length (cm), 1000 grain weight (g), number of spikelets panicle^{-1}, number of filled spikelets panicle^{-1}, spikelets fertility, straw yield plant^{-1} (g) and plot^{-1} (kg), and grain yield plant^{-1}(g) and plot^{-1}(kg), micronutrients*viz.,*zinc (ppm), iron (ppm), amylase (%), and protein content(%).

The GXE interaction was analyzed by AMMI model (Gauch 1988). The genotypes showed more interaction in characters*viz.,* Days to 50 per cent flowering, panicle length plant^{-1}, test weight (g), number of panicle square meter^{-1}, plant height (cm), amylose content (%), zinc content (ppm), and protein content (%). Environments showed more interaction in characters*viz.,* number of tillers plant^{-1}, spikelet fertility (%), grain yield plot-1 (kg), total number of spikelets panicle^{-1}, number of filled spikelets panicle^{-1}, grain yield plant^{-1} (g), straw yield plant^{-1} (g), and iron content (ppm).

Stability analysis (AMMI model, Gauch 1988) identified the following genotypes as stable: RTN-1201-5-1-3-14 for day to 50 per cent flowering, RTN-1201-51-2-1-5-48 for plant height, RTN-1209-10-1-2-1-9 for panicle length, RTN-1211-4-2-1-1 for grain yields plot-1 and grain yield plant^{-1}, RTN-1201-23-2-2-1-43 for straw yield plot-1, Bela for straw yield plant^{-1}, RTN-1211-6-1-4-3-13 for zinc content, RTN-1211-4-2-1-1 for protein content, RTN-1211-6-1-3-1-8 for iron content, RTN-1212-4-1-2-4 for amylose content and RTN-1211-6-1-4-1-11 for spikelets fertility, RTN-1211-5-1-3-5 for number of tillers plant^{-1}, RTN-1212-4-1-2-4 for test weight, RTN-1210-3-1-4-5 for number of panicles square meter^{-1}and RTN-1211-5-1-3-5 for total number of spikelets panicle^{-1}.

In AMMI 1 biplot, Dapoli location favorable for characters*viz.,* day to 50 per cent flowering, number of panicles square meter^{-1}, grain yield plant^{-1}, total number of spikelets panicle^{-1}, and number of filled spikelets panicle^{-1}. Phondaghat location favorable for characters*viz.,* spikelets fertility, amylose content, protein content and Shirgaon location favorable for number of tillers plant^{-1}, panicle length, test weight, grain yield plot-1, straw yield plot-1 and plant^{-1}, plant height, iron and zinc content.

In AMMI 2 biplot, genotypes, RTN-1211-6-1-3-1-8, RTN-1201-23-2-2-1-43, RTN-1201-13-2-2-1-32 and RTN-1211-6-1-2-7 for day to 50 per cent flowering, genotypes, RTN-1212-4-1-2-4, RTN-1211-5-1-3-5, RTN-1201-23-2-2-1-43 and RTN-1211-6-1-2-7 for spikelets fertility, genotypes, RTN-1211-6-1-4-3-13, RTN-1211-9-1-2-12, Bela and RTN-1201-51-2-1-5-48 for grain yield plot-1, genotypes, RTN-1211-6-1-4-3-13,1,RTN-1211-6-1-4-3-13 and RTN-1211-6-1-2-7 for number of panicles square meter^{-1} and RTN-1211-15-1-4-2-23, RTN-1212-4-1-2-4, RTN-1211-9-1-2-12 and Patni-6 for grain yield plant^{-1} had high PCA score and away from origin were most responsive.

CONCLUSION:

In interaction principle axis of AMMI biplot, first interaction principle axis (IPCA I) are favorable for all characters but second interaction principle axis(IPCA II) are favorable for characters such as spikelets fertility, grain yield plot-1 (kg), number of panicles square meter-1, protein content (%), iron content (ppm), amylose content (%), grain yield plant^{-1}(g) and total number of spikelets panicle^{-1}.

Table 13. Genotypes are high yielding stable performance for three environments

Sr. No.	Genotypes	Favourable for character	Stable environment
1	RTN-1201-51-2-1-5-48, RTN-1211-5-1-3-5 and RTN-1201-5-1-3-14	grain yield plant^{-1}, grain yield plot^{-1}and micronutrients	Dapoli and Shirgaon
2	RTN-1201-13-2-2-1-32	For all yield contributing character	Dapoli, Shirgaon and Phondaghat

3	RTN-1201-51-2-1-5-48 and RTN-1211-6-1-3-1-8	Spikelet fertility, test weight, plant height, panicle length and micronutrients	Shirgaon

Genotype,RTN-1201-13-2-2-1-32 is most favorable for all the characters in the entire three environments, with high yield,maximum plant height,and more content of micronutrients. Genotype,RTN-1211-4-2-1-1 is stable for grain yield plot-1, grain yieldplant^{-1}and protein content.

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Place : Dapoli

Date: / / 2014 *Mr. Mahadeo Rajaram Chavan*

APPENDIX-I

Meteorological observation during the period of experiment

Period	MW	T max	T min	RH I	RH II	Wind speed	Rain	RD	BSS
		(oC)	(oC)	(%)	(%)	(Km/ h)	(mm)	days	(hrs.)
28.05 - 03.06	22	34.7	25.6	83	59	7.1	5.1	1	9.2
04.06 - 10.06	23	34.0	24.8	91	70	6.0	40.0	2	3.2
11.06 - 17.06	24	31.4	24.9	91	76	6.9	93.5	5	4.7
18.06 - 24.06	25	29.6	23.1	98	93	4.9	298.7	7	1.4
25.06 - 01.07	26	27.2	22.6	98	97	6.2	792.5	7	0.0

02.07 - 08.07	27	28.5	23.6	94	92	8.5	462.6	7	0.2
09.07 - 15.07	28	28.4	23.3	95	89	10.3	256.8	7	1.4
16.07 - 22.07	29	27.3	22.4	99	95	4.5	403.0	7	0.6
23.07 - 29.07	30	28.8	22.4	98	85	3.3	268.0	6	0.7
30.07 - 05.08	31	27.6	22.7	97	94	11.8	481.5	7	0.6
06.08 - 12.08	32	27.7	23.6	94	92	10.5	182.7	7	0.4
13.08 - 19.08	33	29.3	24.3	91	84	8.5	39.0	4	1.8
20.08 - 26.08	34	28.9	23.4	95	87	5.9	73.6	6	2.0
27.08 - 02.09	35	28.4	22.6	95	88	3.5	138.4	7	1.1
03.09 - 09.09	36	29.4	21.6	94	72	3.7	36.9	3	5.3
10.09 - 16.09	37	29.9	22.2	93	82	2.9	55.8	2	3.3
17.09 - 23.09	38	27.0	22.5	98	94	7.7	582.4	7	1.0
24.09 - 30.09	39	29.1	22.6	96	82	5.1	88.1	2	3.5
01.10 - 07.10	40	27.7	21.4	97	83	3.6	189.1	6	2.4
08.10 - 14.10	41	30.4	22.3	94	83	3.6	10.2	1	5.8
15.10 - 21.10	42	33.7	21.4	93	81	2.1	0.0	0	6.7
22.10 – 28.10	43	32.6	18.8	96	72	2.0	0.0	0	8.2
29.10 – 04.11	44	34.5	15.7	92	69	1.5	0.0	0	8.8
05.11 – 11.11	45	33.0	13.5	95	63	0.7	0.0	0	8.3
12.11 – 18.11	46	33.2	16.5	92	63	1.6	0.0	0	6.9

Kharif-2016 at Dapoli location

Meteorological observation during the period of experiment *Kharif*-2016 at Shirgaon location

Period	MW	T max	T min	RH I	RH II	Wind speed	Rain	RD	BSS
		(°C)	(°C)	(%)	(%)	(Km/h)	(mm)	days	(Hrs)
28.05 - 03.06	22	34.7	28.5	79	73	2.1	38.8	2.0	0.3
04.06 - 10.06	23	32.5	34.8	87	82	2.0	62.4	4.0	0.4
11.06 - 17.06	24	30.3	26.1	89	83	1.9	231.4	5.0	0.3
18.06 - 24.06	25	38.2	23.9	97	88	2.4	277.9	6.0	0.1

25.06 - 01.07	26	29.5	23.3	95	97	2.2	650.7	7.0	0.2
02.07 - 08.07	27	30.2	25.2	92	91	3.7	280.0	7.0	0.5
09.07 - 15.07	28	30.0	25.2	90	88	6.2	173.4	6.0	0.6
16.07 - 22.07	29	29.3	24.6	96	90	2.6	431.5	6.0	2.0
23.07 - 29.07	30	29.0	23.9	97	87	1.5	198.6	4.0	1.0
30.07 - 05.08	31	29.1	24.3	96	89	5.2	471.2	7.0	0.5
06.08 - 12.08	32	30.4	25.8	89	86	7.5	74.9	5.0	1.6
13.08 - 19.08	33	30.5	25.7	87	81	4.6	51.8	2.0	3.5
20.08 - 26.08	34	31.0	24.7	97	81	2.2	46.4	6.0	3.8
27.08 - 02.09	35	31.3	24.3	93	93	0.8	140.9	6.0	1.9
03.09 - 09.09	36	31.2	23.2	96	80	1.4	43.7	4.0	5.9
10.09 - 16.09	37	31.1	23.9	97	79	1.0	46.5	3.0	7.0
17.09 - 23.09	38	29.0	23.8	97	89	1.5	262.6	7.0	1.6
24.09 - 30.09	39	30.1	24.1	99	84	1.1	246.8	3.0	2.9
01.10 - 07.10	40	29.7	23.1	95	86	0.7	25.4	3.0	4.1
08.10 - 14.10	41	30.3	24.2	94	86	1.7	82.1	1.0	6.3
15.10 - 21.10	42	32.9	22.3	95	75	0.6	0.0	0.0	8.2
22.10 –28.10	43	32.2	20.5	93	74	0.8	0.0	0.0	7.7
29.10 –04.11	44	35.1	18.5	95	80	0.7	0.0	0.0	9.0
05.11 –11.11	45	33.2	16.7	86	57	1.0	0.0	0.0	9.1
12.11 –18.11	46	35.2	19.9	85	58	0.6	0.0	0.0	8.2

Meteorological observation during the period of experiment
Kharif-2016 at Phondaghat location

Period	MW	T max	T min	RH I	RH II	Wind speed	Rain	RD	BSS
		(^{o}C)	(^{o}C)	(%)	(%)	(Km/h)	(mm)	days	(Hrs.)
28.05 - 03.06	22	34.0	23.4	81	78	2.0	31.0	1.0	0.4
04.06 - 10.06	23	31.5	33.7	89	80	2.0	176.0	4.0	0.3
11.06 - 17.06	24	29.9	26.8	90	81	1.7	112.8	6.0	0.4
18.06 - 24.06	25	38.7	23.0	98	87	2.1	470.0	7.0	0.2

25.06 - 01.07	26	28.3	22.5	97	98	1.9	155.2	5.0	0.1
02.07 - 08.07	27	30.9	22.8	90	95	3.1	25.4	4.0	0.4
09.07 - 15.07	28	31.1	23.2	92	90	4.9	98.4	7.0	0.4
16.07 - 22.07	29	29.8	23.7	98	93	2.0	140.8	7.0	2.3
23.07 - 29.07	30	25.3	21.5	94	90	1.1	204.0	7.0	0.9
30.07 - 05.08	31	27.8	22.4	90	81	3.2	147.5	7.0	0.8
06.08 - 12.08	32	32.9	22.1	95	89	4.5	153.4	7.0	1.1
13.08 - 19.08	33	30.1	25.0	84	79	3.5	72.6	5.0	3.0
20.08 - 26.08	34	31.8	24.1	92	87	1.8	107.8	6.0	3.0
27.08 - 02.09	35	33.3	22.1	91	98	0.7	123.6	6.0	1.1
03.09 - 09.09	36	28.7	23.1	92	83	0.8	31.2	2.0	5.1
10.09 - 16.09	37	30.0	20.0	98	81	0.8	169.8	7.0	4.8
17.09 - 23.09	38	27.8	22.7	94	87	1.4	109.2	4.0	1.0
24.09 - 30.09	39	30.2	22.6	97	87	1.3	250.3	3.0	2.1
01.10 - 07.10	40	29.7	23.5	97	85	0.5	95.6	5.0	3.9
08.10 - 14.10	41	30.0	22.2	92	84	1.4	24.0	2.0	4.9
15.10 - 21.10	42	32.1	22.9	99	85	0.9	7.8	1.0	6.2
22.10 –28.10	43	37.2	20.0	95	77	1.0	0.0	0.0	7.9
29.10 –04.11	44	33.9	17.3	98	90	0.9	0.0	0.0	8.1
05.11 –11.11	45	30.9	16.0	85	57	0.9	0.0	0.0	8.1
12.11 –18.11	46	31.1	19.0	89	67	0.9	0.0	0.0	7.8

APPENDIX II

ABREVIATIONS AND LOCAL TERMS USED

SYMBOLS **FULL FORM**

AMMI : Additive Main Effects and Multiplicative Interaction.

MSS : Mean Some of Square

RS : Rank-Sum

% : Per cent

$^{-1}$: Per
CMS : Cytoplasmic male sterile
°C : Degree Celsius
p.m. : Post meridian- After noon
viz., : Namely
et al., : And other
Mm : Mili meter
M meter
etc. : Et cetera
Cm : Centi meter
FAO : Food and Agricultural Organization
Kg : Kilo gram
i.e. : id est. (that is)
G : Gram
a.m. : Ante meridian- Before noon
B.C : Before Christian
Ppm : Part per million
A.C : AfterChristian
DPPH : 1-1-diphenyl-2-picrylhydrazyl
G X E : Genotype x Environment
IIRR : Indian Institute of Rice Research
ARS : Agriculture Research Station
RARS : Regional Agriculture Research Station
Ch : Chacke
DF : Degree of freedom

RBD	:	Randomized Block Design
XRF	:	X-ray Fluorescence Spectrophotometer
IPCA	:	Interaction principle component axis
GY	:	Grain yield
GEI	:	Genotype x Environment interaction
BILs	:	Backcross Inbred Lines
ASV	:	AMMI stability value
P	:	Probability
TSS	:	total sum of squares
YSI	:	Yield Stability Index
t ha–1	:	ton per hector
SRG	:	Sites Regression Model.
ANOVA	:	Analysis of Variance
Fe	:	Iron
Zn	:	Zinc
Dk	:	Environment centered yield deviation.
Di	:	Stability Index
ug	:	micro gram
mg	:	Mili gram
VCA	:	Variance Component Analysis

STABILITY ANALYSIS IN PROMISING BIO-FORTIFIED RED KERNEL GENOTYPES OF RICE (*Oryza sativa* L.) BY USING AMMI MODEL

By

Mr. Mahadeo Rajaram Chavan

B.Sc. (Ag.)

DEPARTMENT OF AGRICULTURAL BOTANY
FACULTY OF AGRICULTURE,
DR. BALASAHEB SAWANT KONKAN KRISHI
VIDYAPEETH, DAPOLI- 415 712,
DIST. RATNAGIRI (M.S.)

MAY, 2017

STABILITY ANALYSIS IN PROMISING BIO-FORTIFIED RED KERNEL GENOTYPES OF RICE (*Oryza sativa* L.) BY USING AMMI MODEL

A thesis submitted to the

DR. BALASAHEB SAWANT KONKAN KRISHI VIDYAPEETH, DAPOLI
(Agricultural University)
Dist. Ratnagiri (M.S.) India

In partial fulfilment of the requirements for the degree of

MASTER OF SCIENCE (AGRICULTURE)

In

Genetics and Plant Breeding

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Approved by the advisory committee

Chairman and Research Guide:

(B. D. Waghmode)
Officer incharge,
Agricultural Research Station,
Shirgaon, Dist. Ratnagiri.

Members:

(B. L. Thaware)
Professor,
Department of Agril. Botany,
College of Agriculture, Dapoli.

(T. J. Bedse)
Biochemist
Regional Agricultural
Research Station, Karjat

(J. S. Dhekale)
Associate professor,
Department of Agril. Economics,
College of Agriculture, Dapoli

MAY 2017

Dr. B. D. Waghmode
M.Sc. (Ag.) Ph.D. (Ag.),
Officer Incharge,
Agricultural Research Station,
Shirgaon, Dist. Ratnagiri- 415 629, (M.S.)

CERTIFICATE

This is to certify that the thesis entitled **“STABILITY ANALYSIS IN PROMISING BIO-FORTIFIED RED KERNEL GENOTYPES OF RICE (*Oryza sativa* L.) BY USING AMMI MODEL.”** submitted to the faculty of Agriculture, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, Dist. Ratnagiri, Maharashtra State in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING**, embodies the results of the piece of *bonafide* research carried out by **Mr. MAHADEO RAJARAM CHAVAN.** (Regd. No. 2419) under my guidance and supervision. No part of this thesis has been submitted for any other degree or diploma. All the assistance and help received during the course of investigation and the sources of literature have been duly acknowledged by him.

Place: Dapoli

Date: May, 2017

(B. D. Waghmode)
Chairman,
Advisory committee and
Research Guide

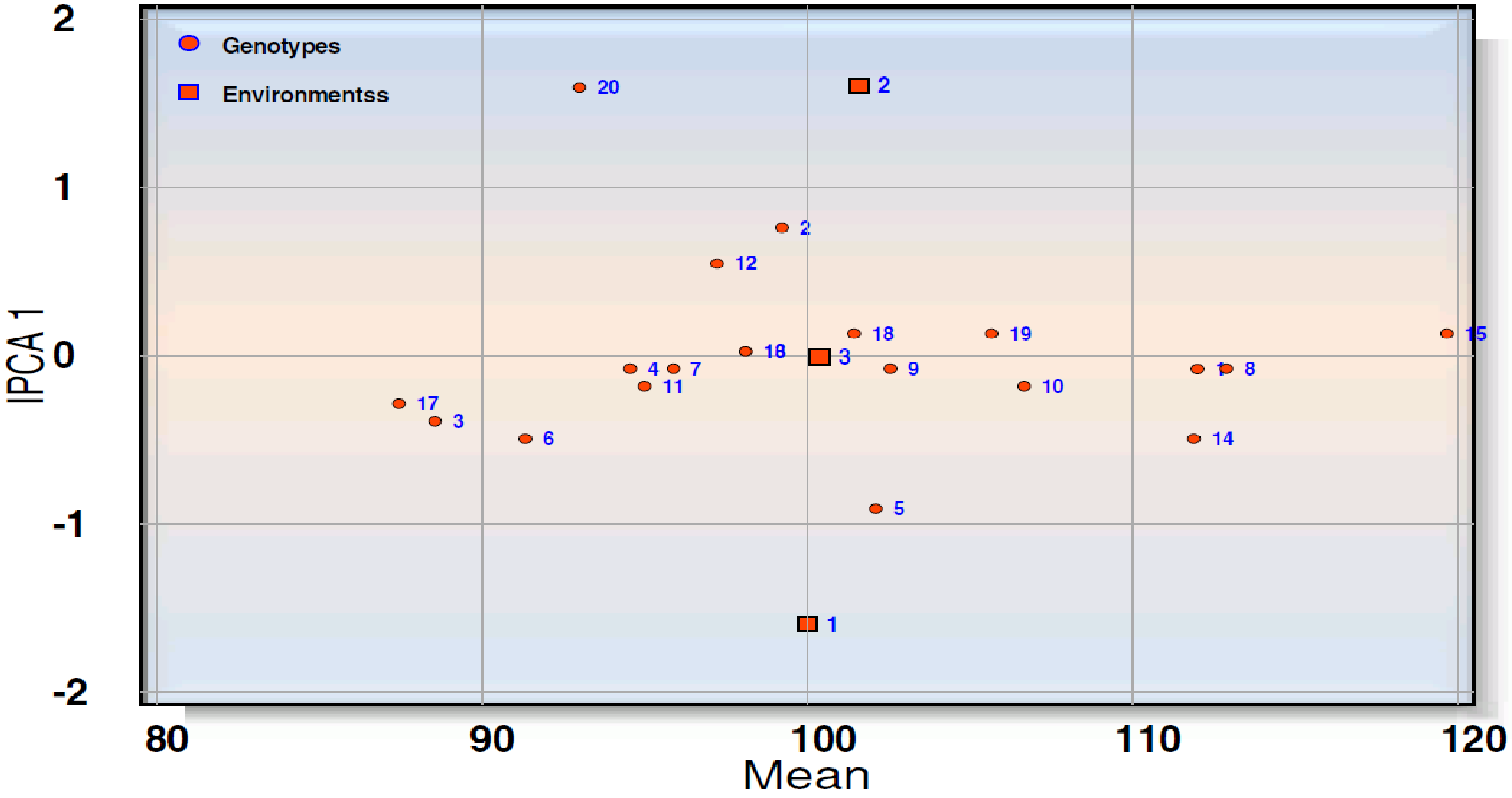


Fig 1. Biplot (AMMI 1) for days to 50 per cent flowering

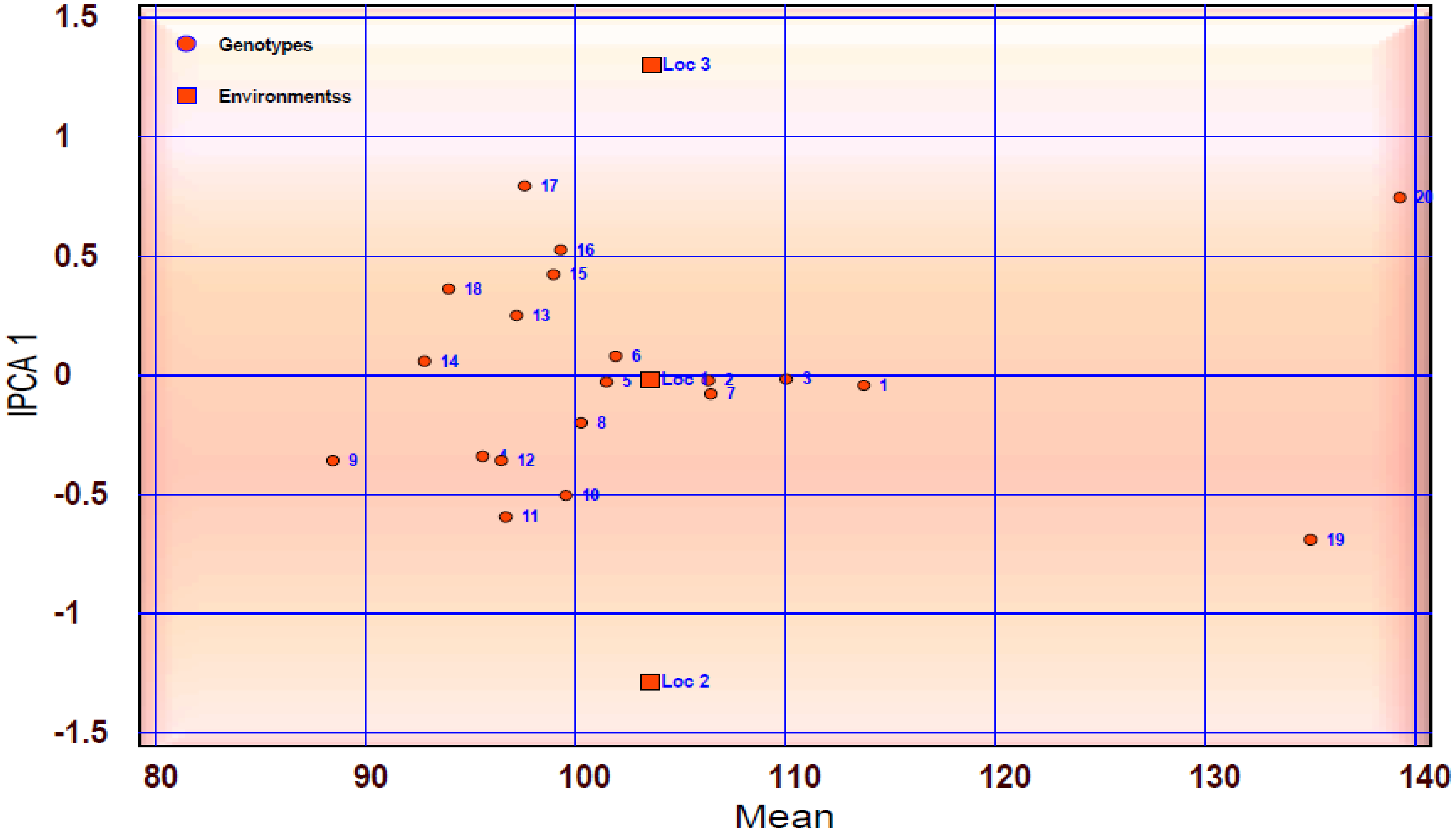


Fig 2. Biplot (AMMI 1) for plant height (cm)

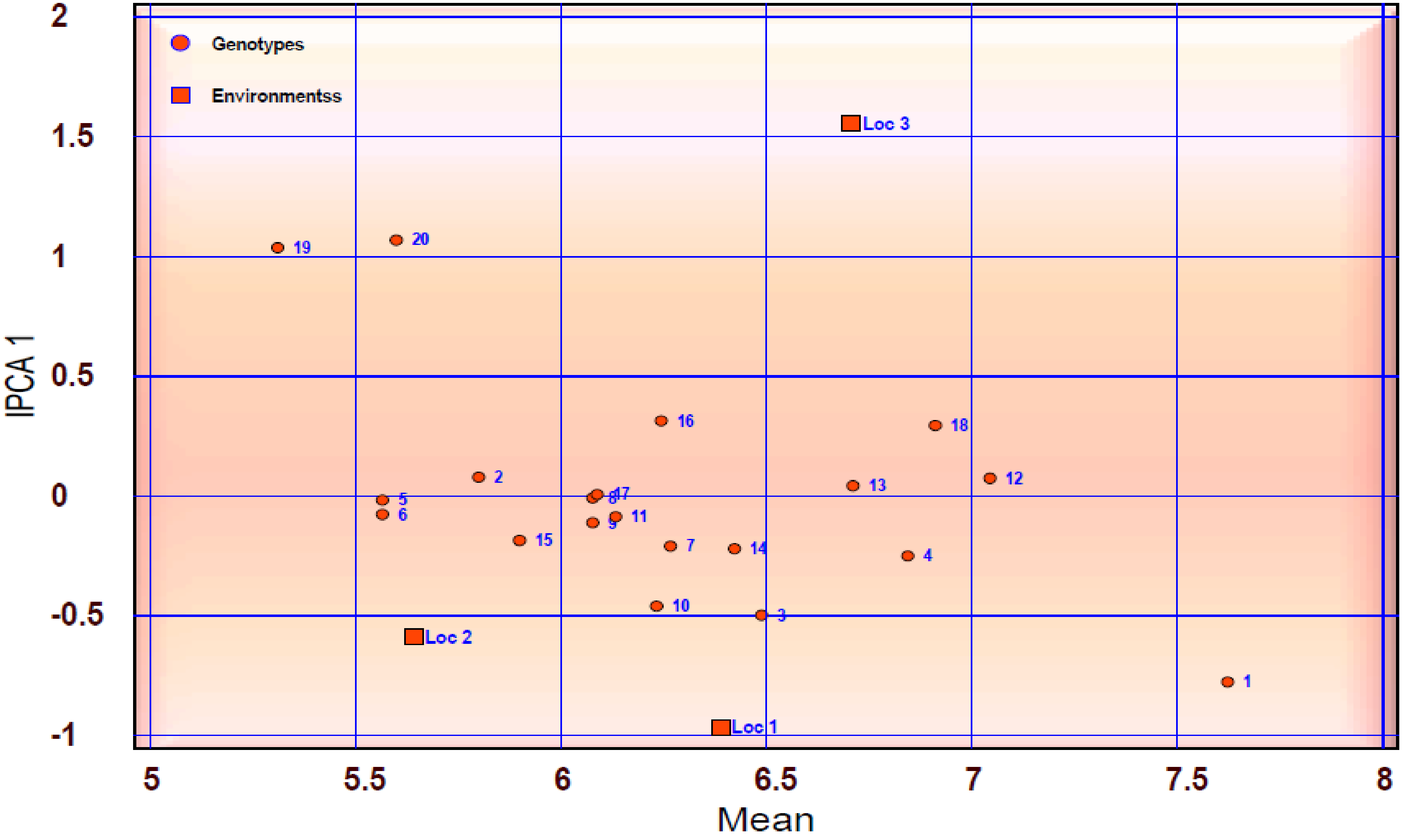


Fig 3. Biplot (AMMI 1) Number of tillers plant^{-1}

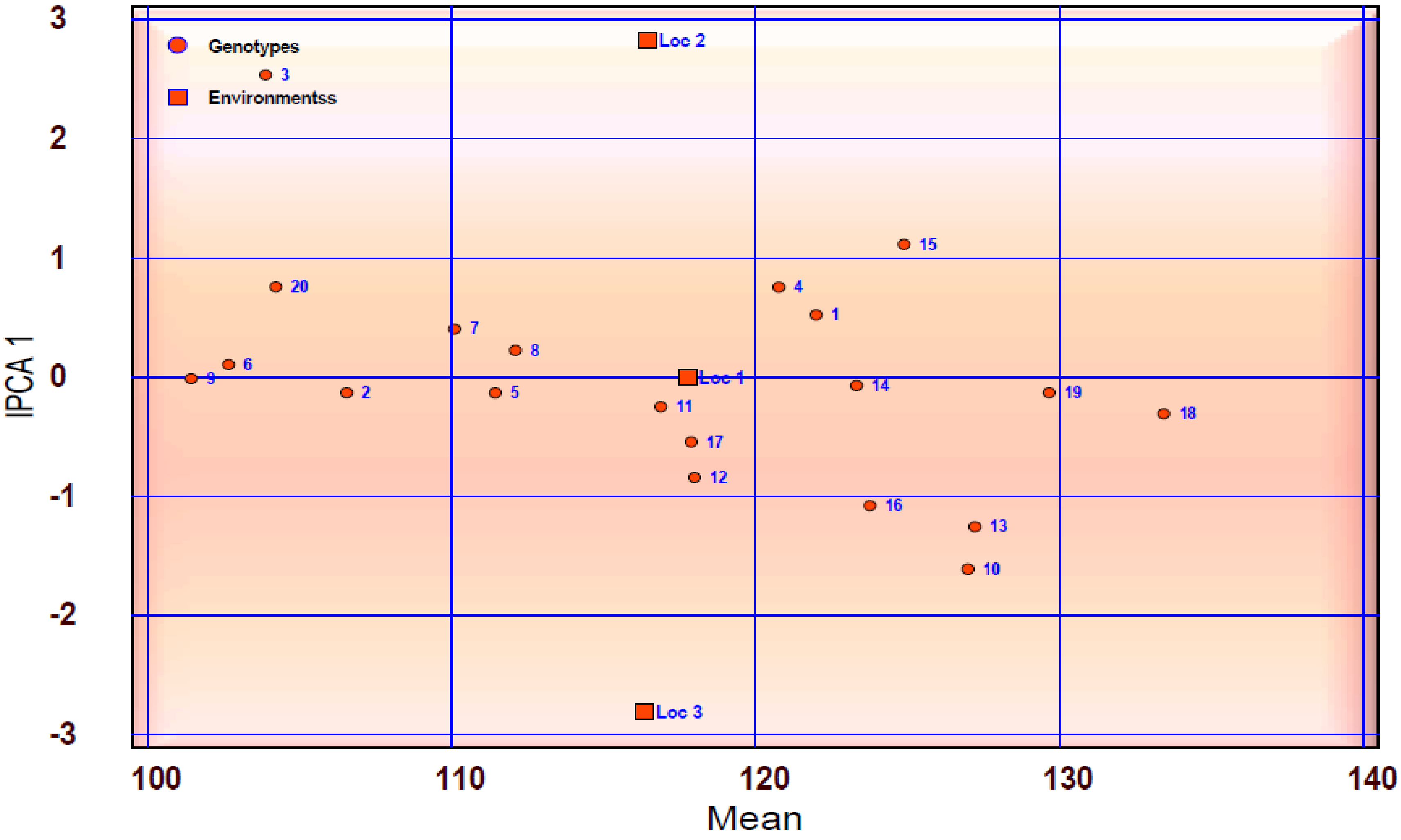

Genotypes
Environmentss
Loc 1
Loc 2
Loc 3
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
IPCA 1
3
2
1
0
-1
-2
-3
Mean
100
110
120
130
140

Fig 4. Biplot (AMMI 1) for panicle square meter^{-1}

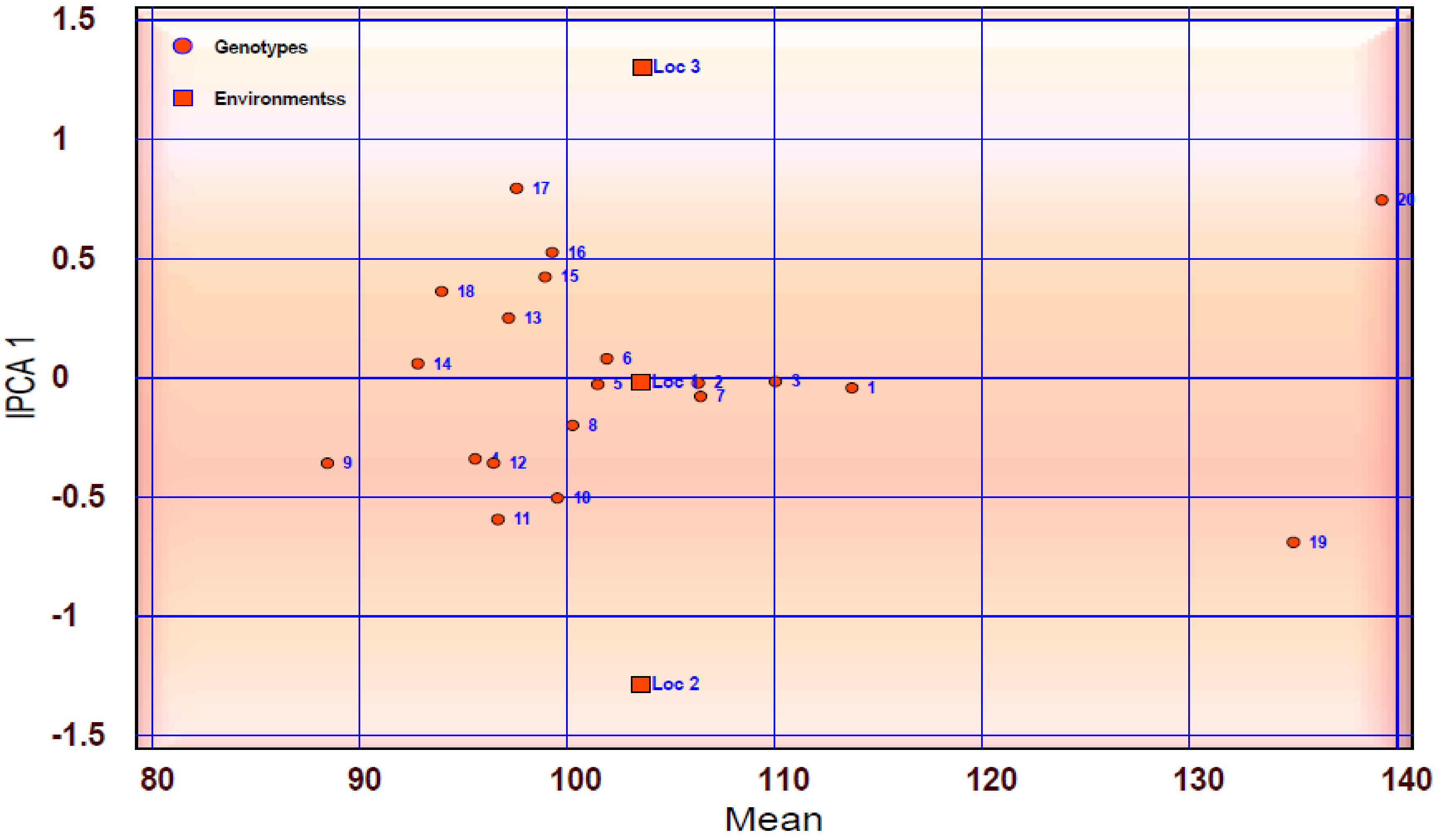
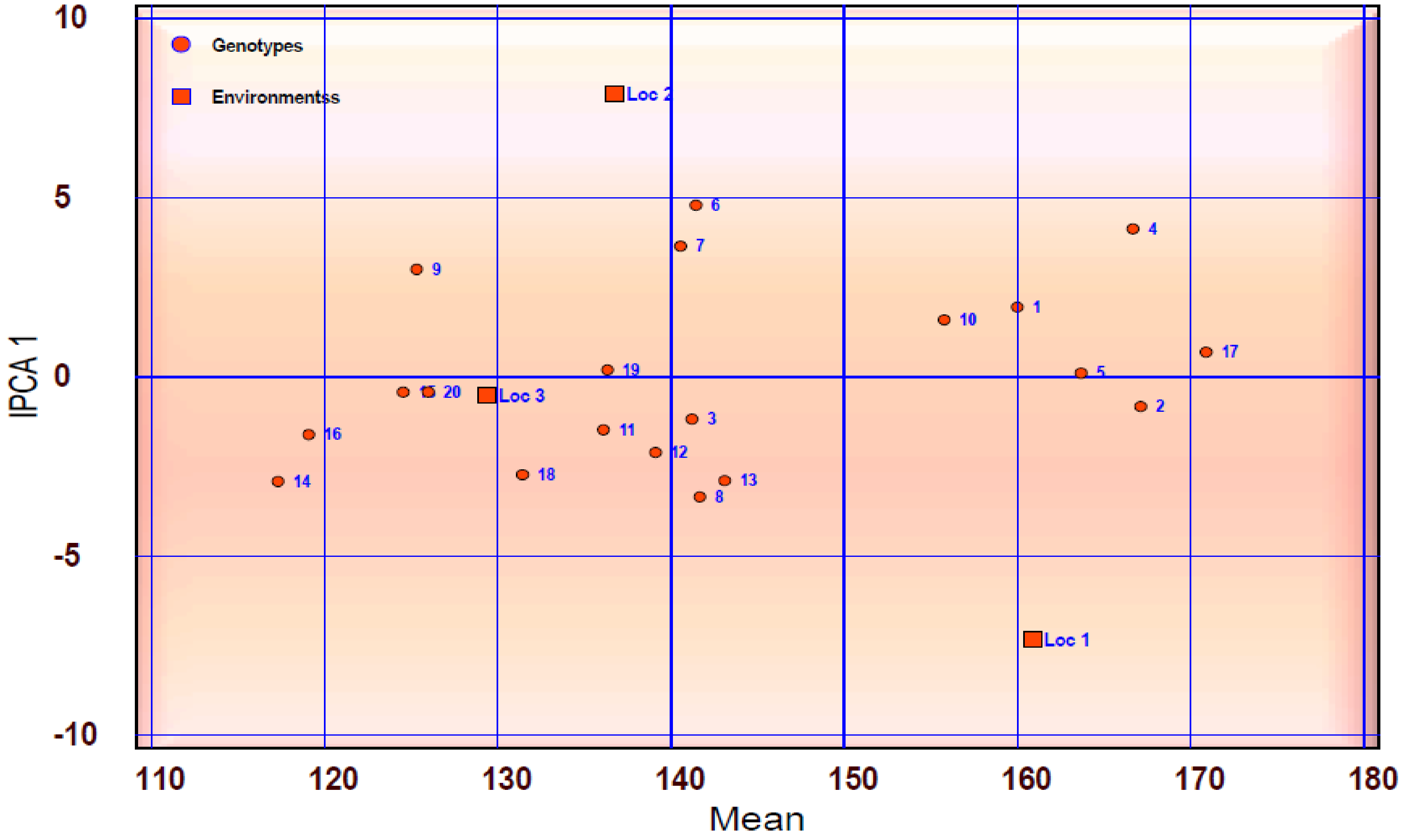


Fig 5. Biplot (AMMI 1) for panicle length (cm)



Fig

8. Biplot (AMMI 1) for number of filled spikelets panicle^{-1}

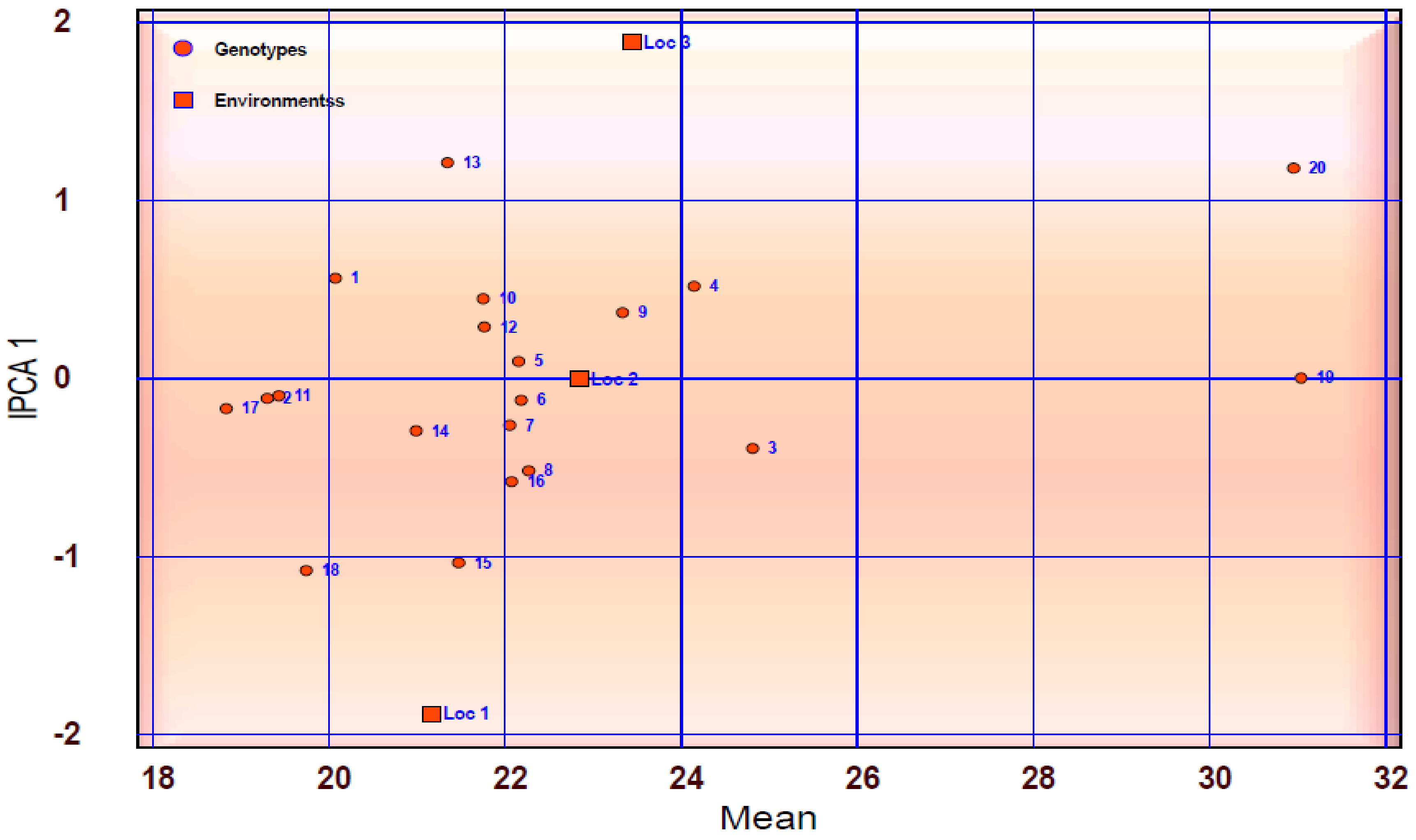


Fig 11. Biplot (AMMI 1) for test weight (g)

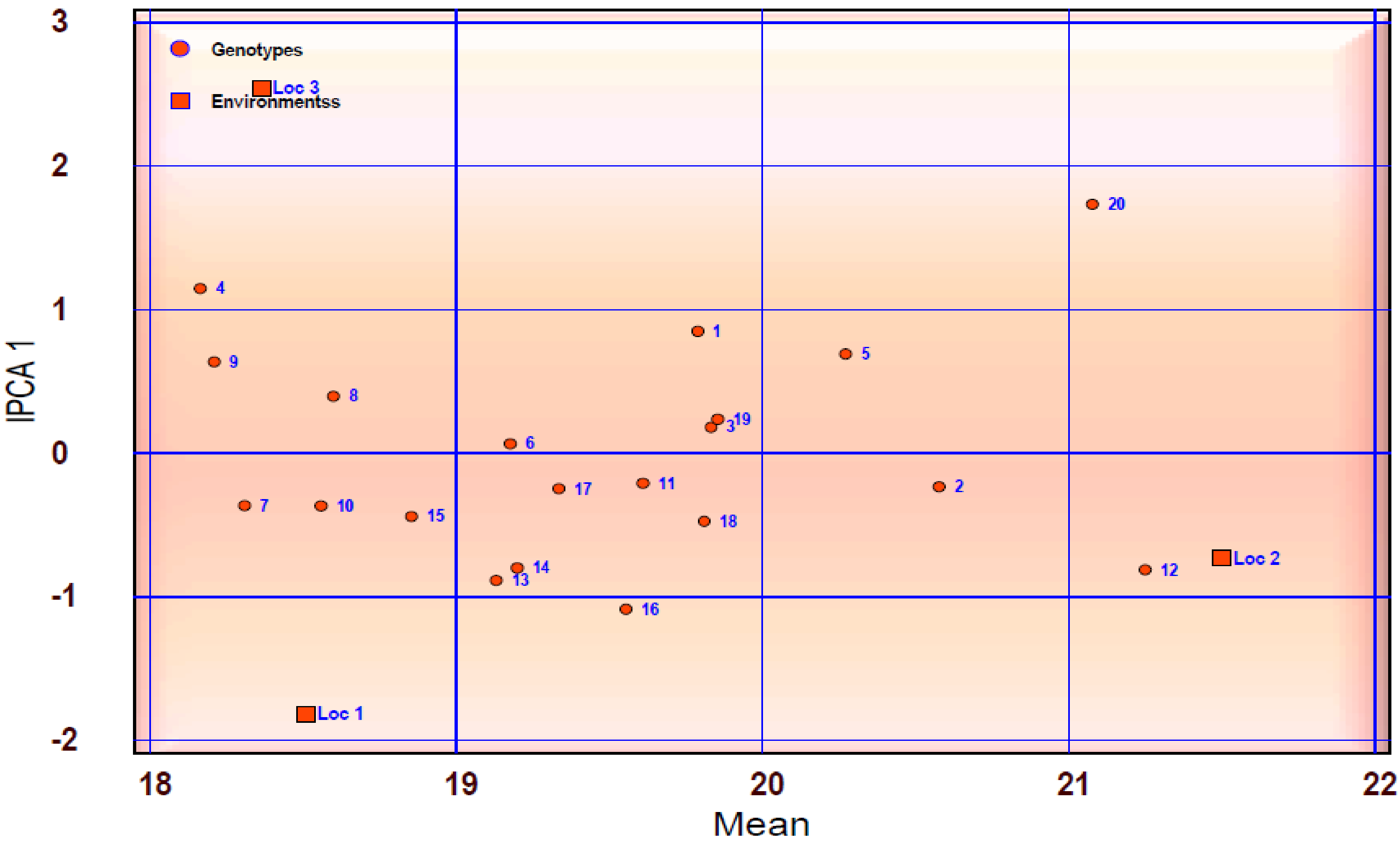


Fig 14. Biplot (AMMI 1) for straw yield plant^{-1}(g)

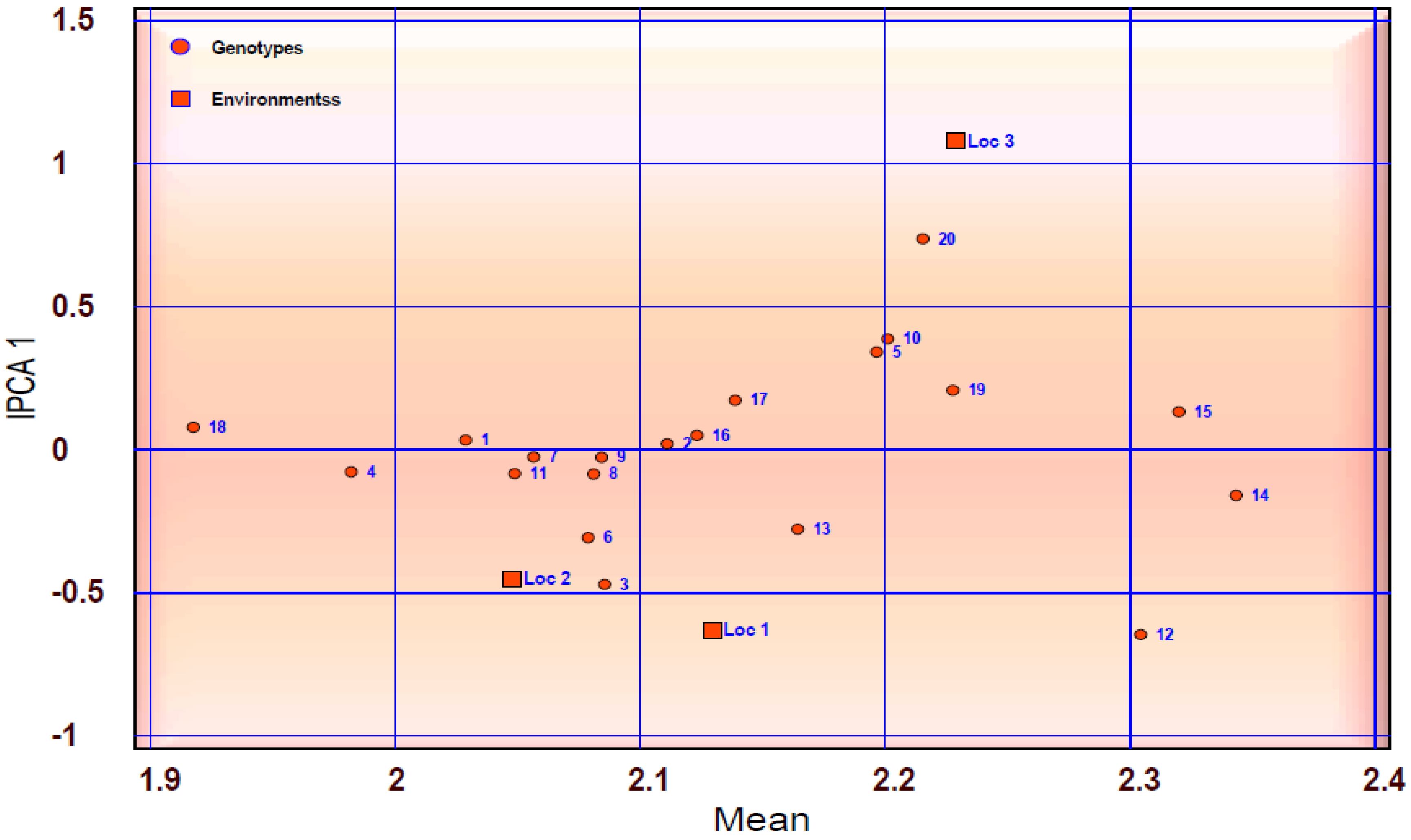


Fig 17. Biplot (AMMI 1) for straw yield plot^{-1}(g)

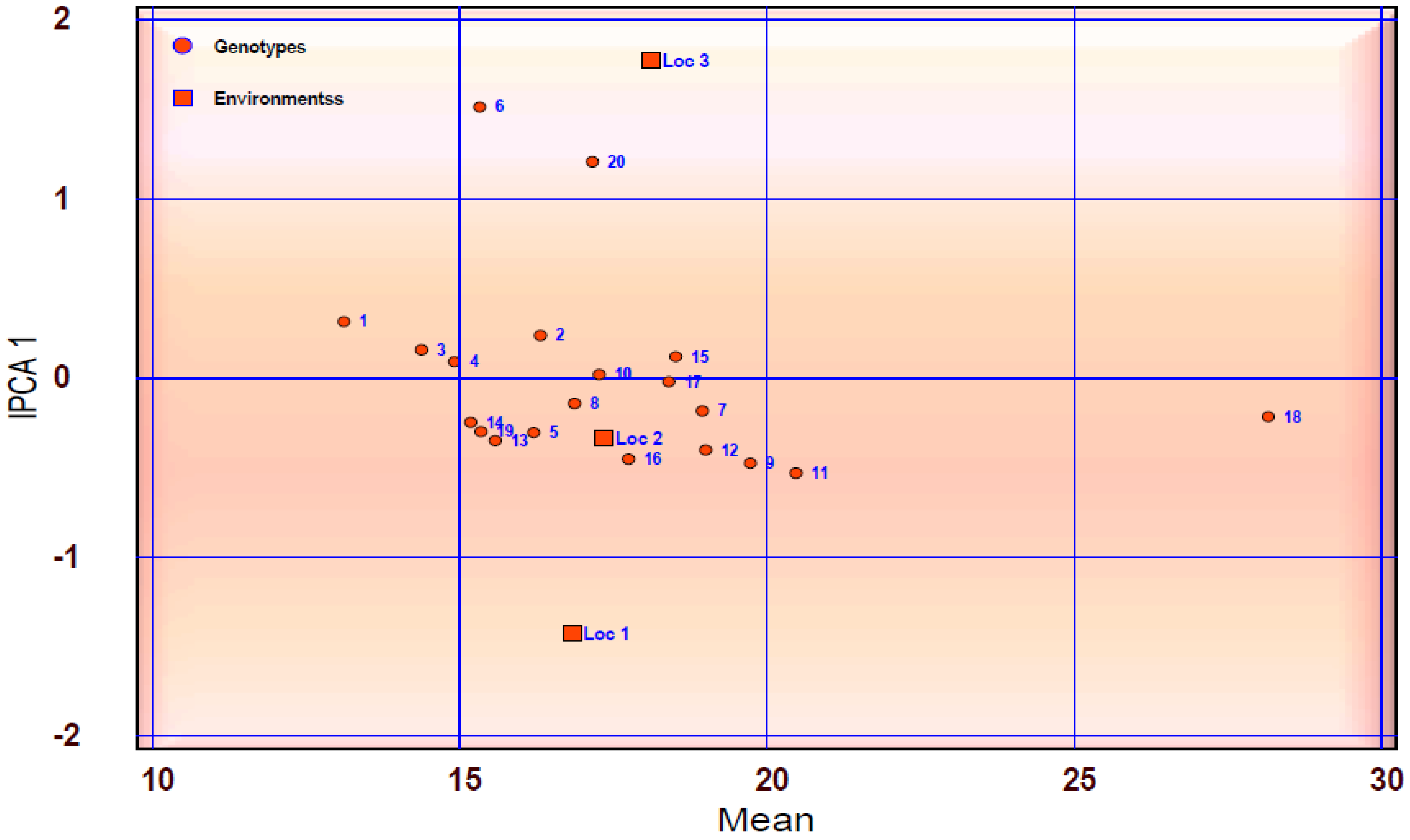


Fig 20. Biplot (AMMI 1) for zinc content (ppm)

Fig 6. Biplot (AMMI 1) for total number of spikelets panicle^{-1}

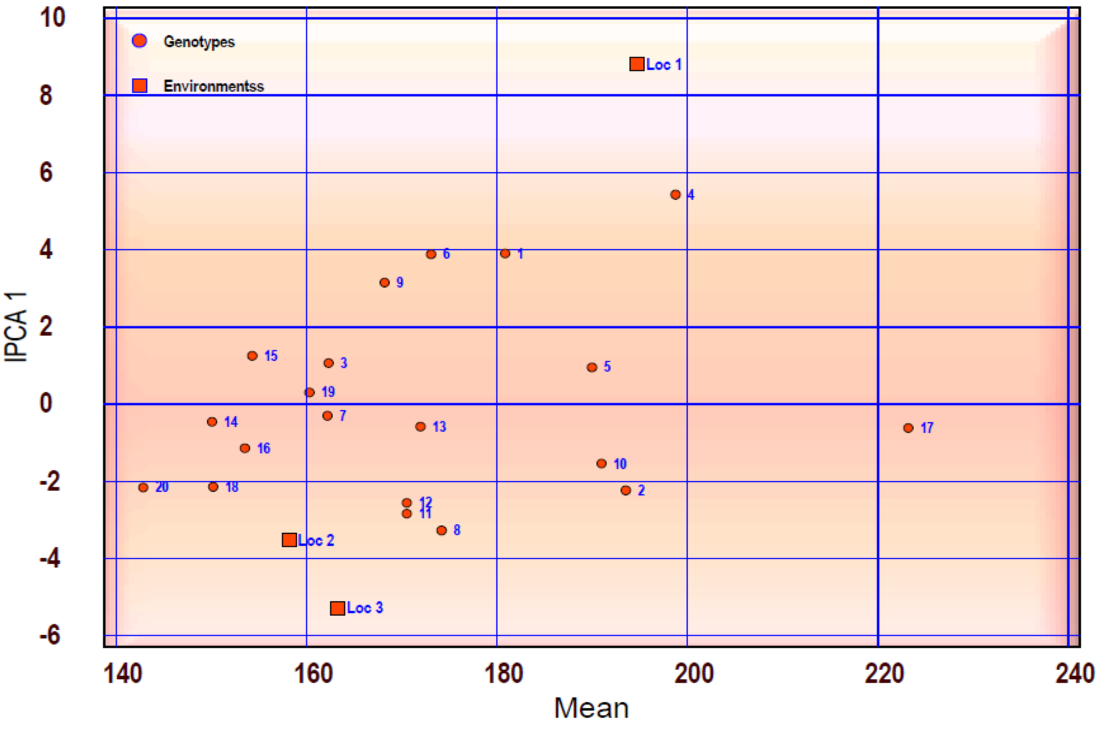
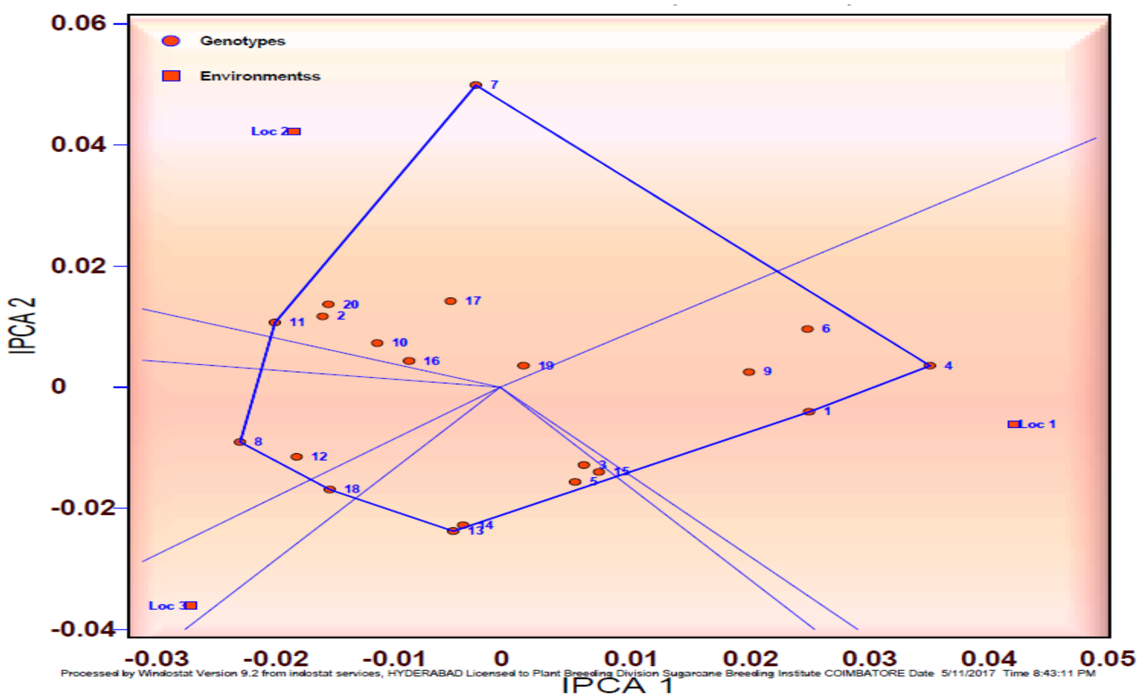


Fig 7. Intraction Biplot (AMMI 2) for total number of spikelets panicle^{-1}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0.04
0.02
0
-0.02
-0.04
IPCA 2
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7
20
2
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17
10
16
19
6
4
9
1
Loc 1
8
12
18
3
15
5
14
13
Loc 3
-0.03
-0.02
-0.01
0
0.01
0.02
0.03
0.04
0.05
Processed by Windostat Version 9.2 from indostat services, HYDERABAD Licensed to Plant Breeding Division Sugarcane Breeding Institute COIMBATORE Date 5/11/2017 Time 8:43:11 PM
IPCA 1

Fig 9. Biplot (AMMI 1) for spikelets fertility (%)

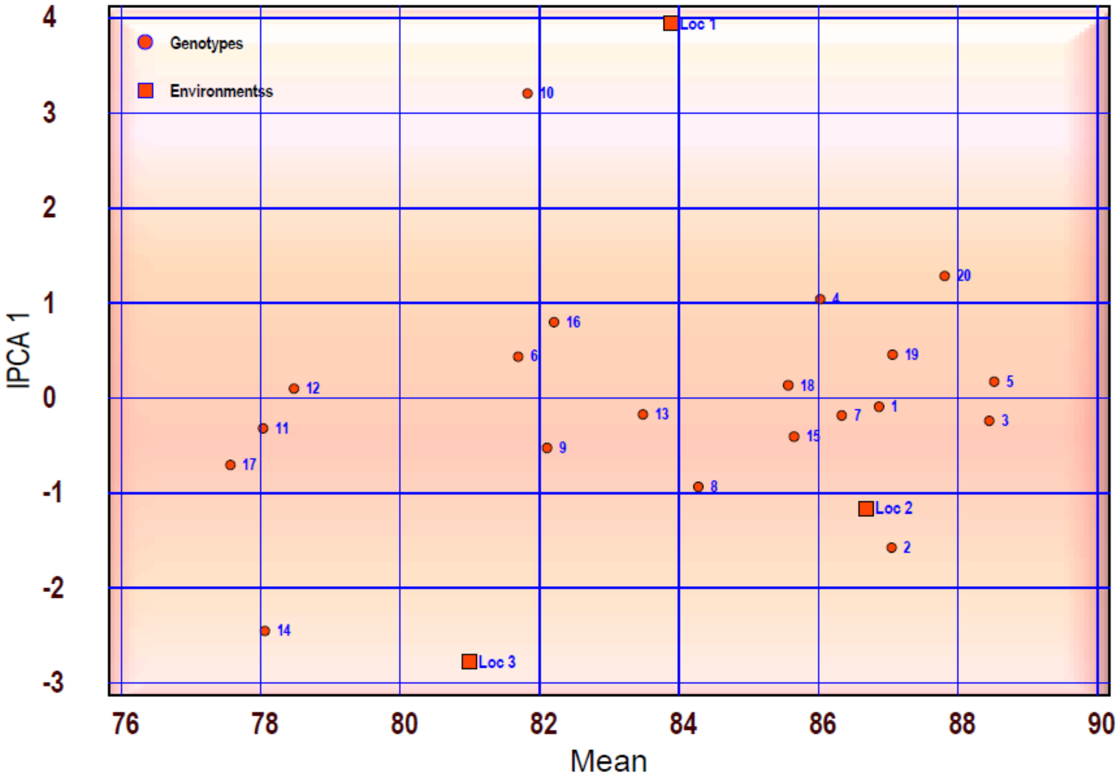
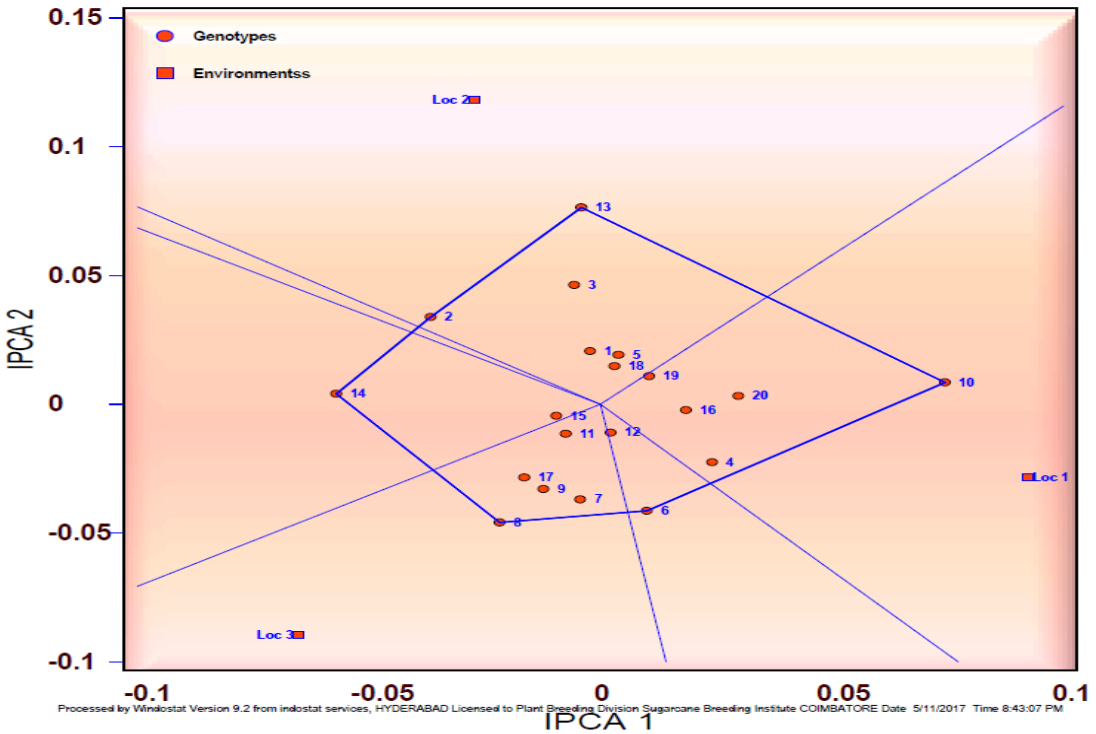


Fig 10. Intraction Biplot (AMMI 2) forspikelets fertility (%)


Genotypes
Environmentss
Loc 1
Loc 2
Loc 3
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4
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14
15
16
17
18
19
20
0.15
0.1
0.05
0
-0.05
-0.1
-0.1
-0.05
0
0.05
0.1
IPCA 2
IPCA 1
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Fig 12. Biplot (AMMI 1) for grain yield plant^{-1}(g)

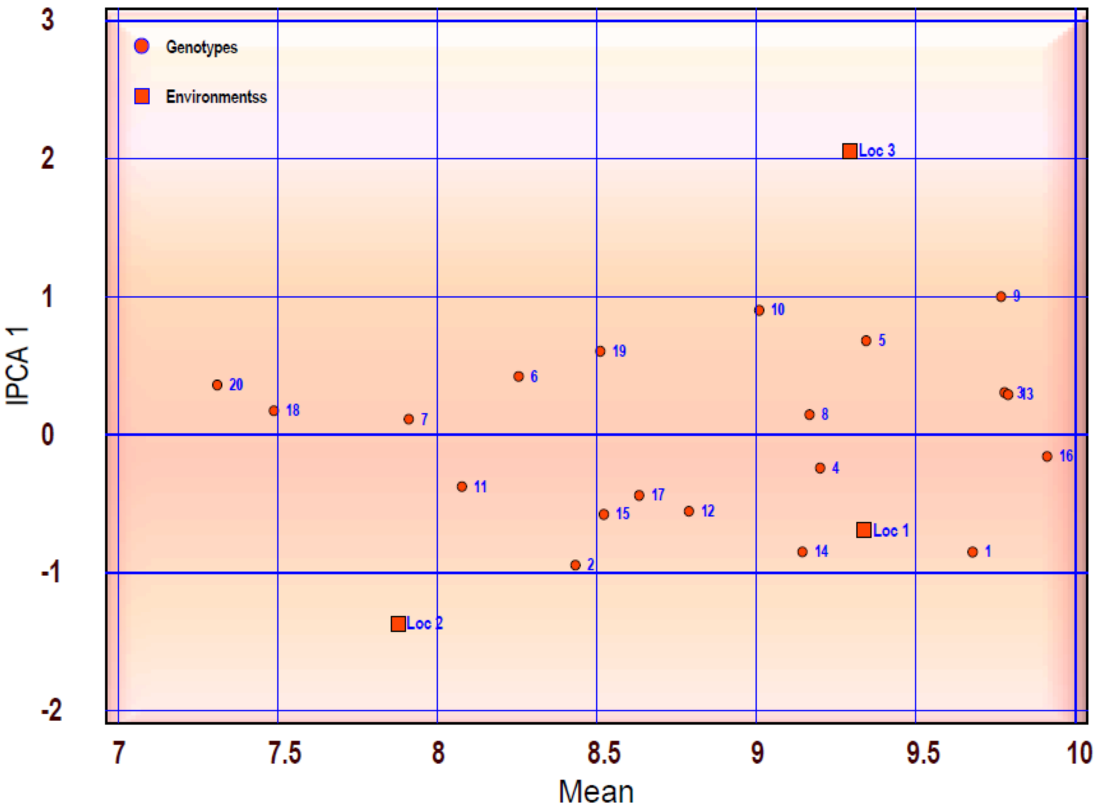

Fig 13. Intraction Biplot (AMMI 2) for grain yield plant^{-1}(g)

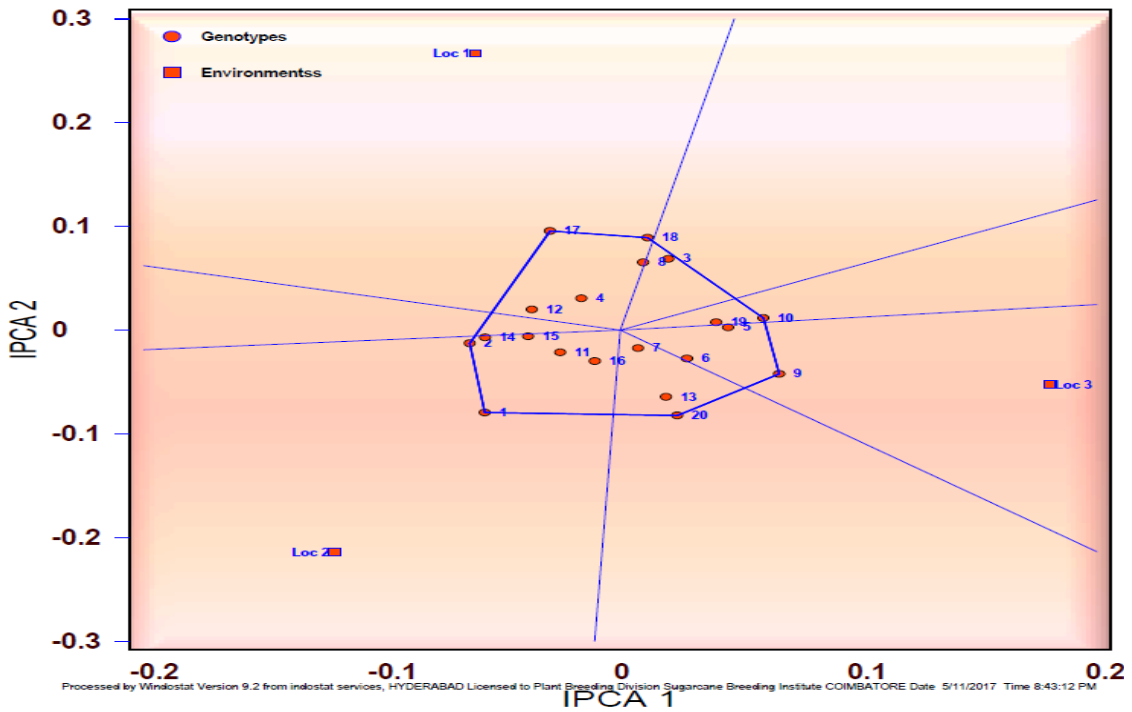
Genotypes
Environmentss
Loc 1
Loc 2
Loc 3
17
18
3
8
4
12
10
19
5
14
15
2
11
16
7
6
9
13
20
1
0.3
0.2
0.1
0
-0.1
-0.2
-0.3
IPCA 2
-0.2
-0.1
0
0.1
0.2
IPCA 1
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Fig 15. Biplot (AMMI 1) for grain yield plot^{-1}(g)

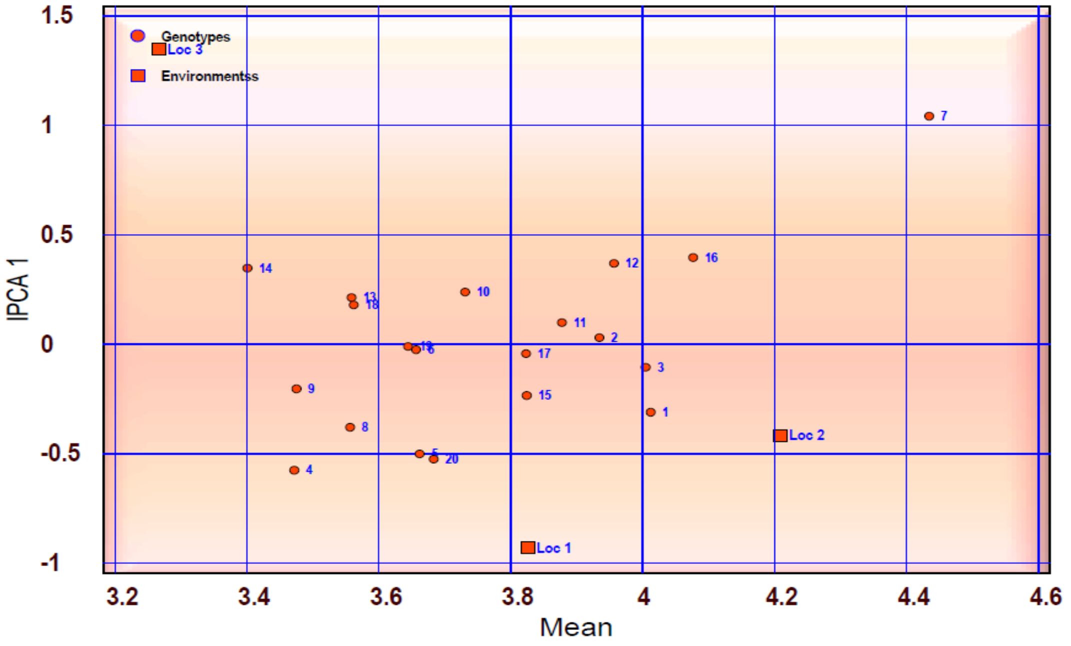


Fig 16. Intraction Biplot (AMMI 2) for grain yield plot^{-1}(g)

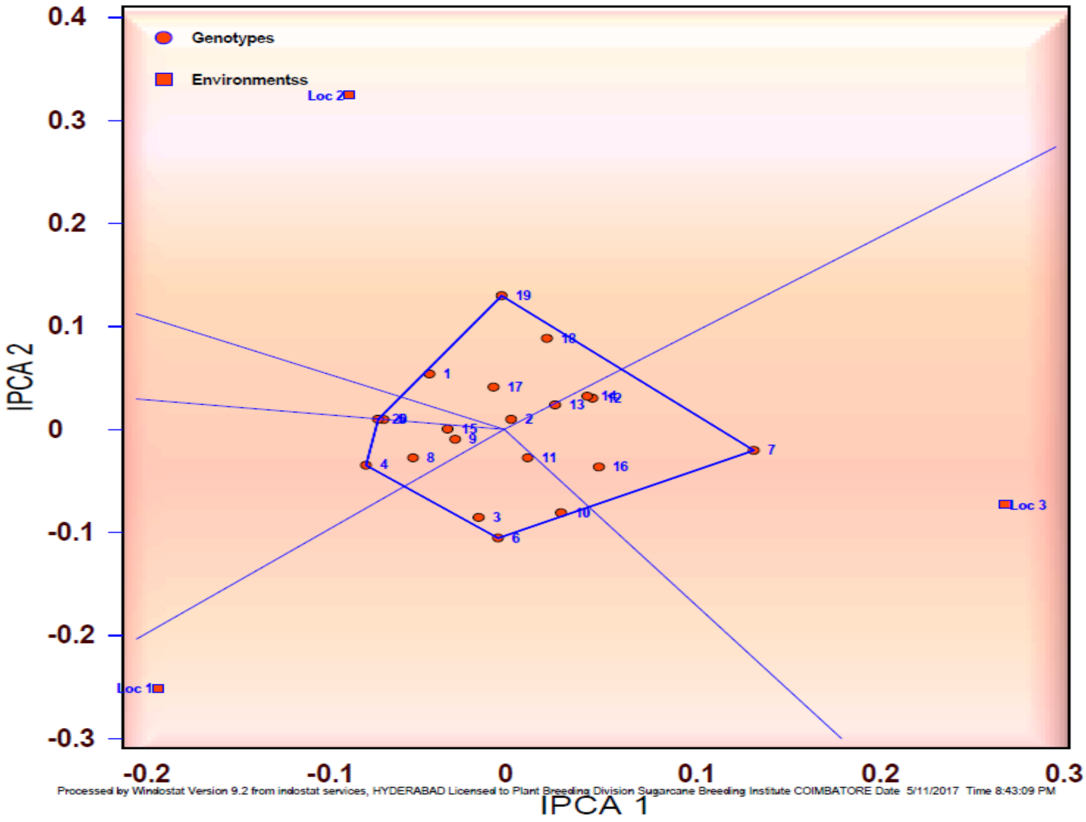

Genotypes
Environmentss
Loc 1
Loc 2
Loc 3
1
2
3
4
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
0.4
0.3
0.2
0.1
0
-0.1
-0.2
-0.3
IPCA 2
-0.2
-0.1
0
0.1
0.2
0.3
IPCA 1
Processed by Windostat Version 9.2 from indostat services, HYDERABAD Licensed to Plant Breeding Division Sugarcane Breeding Institute COIMBATORE Date 5/11/2017 Time 8:43:09 PM

Fig 18. Biplot (AMMI 1) for iron content (ppm)

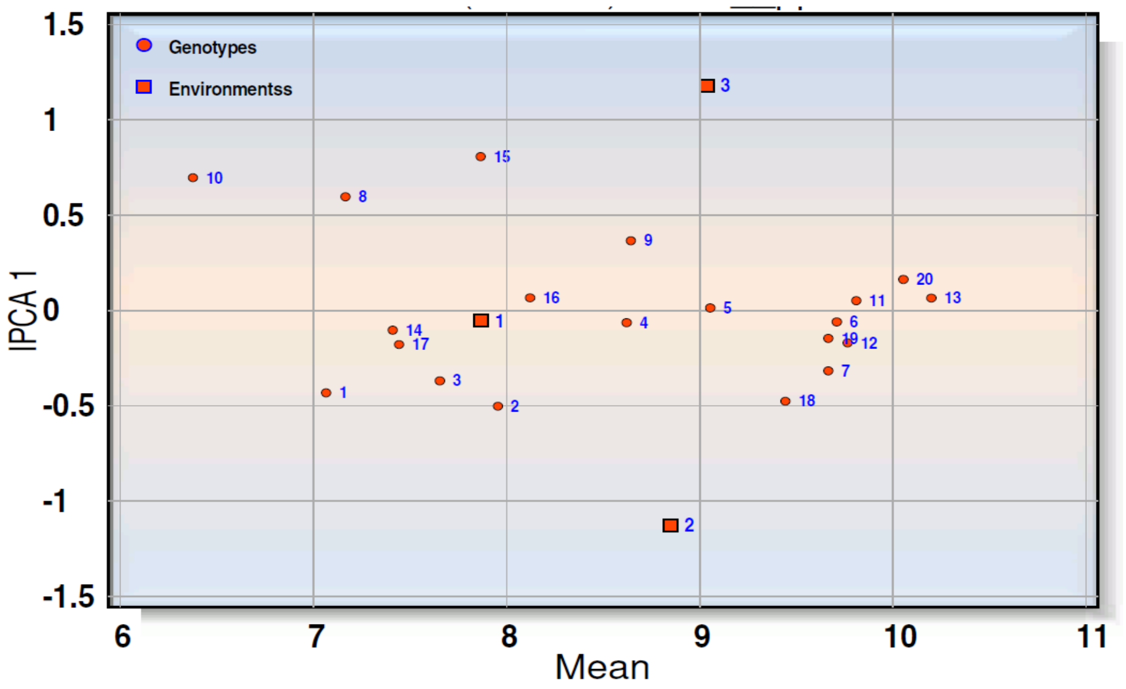


Fig 19. Intraction Biplot (AMMI 2)for iron content (ppm)

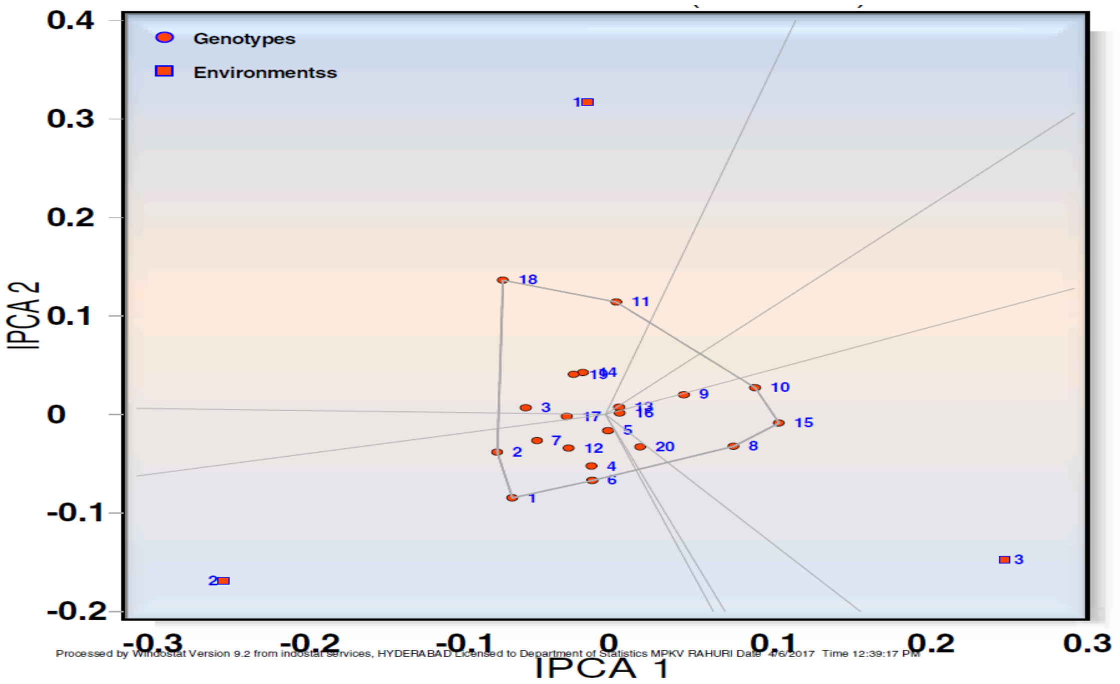


Fig 21. Biplot (AMMI 1) for protein content (%)

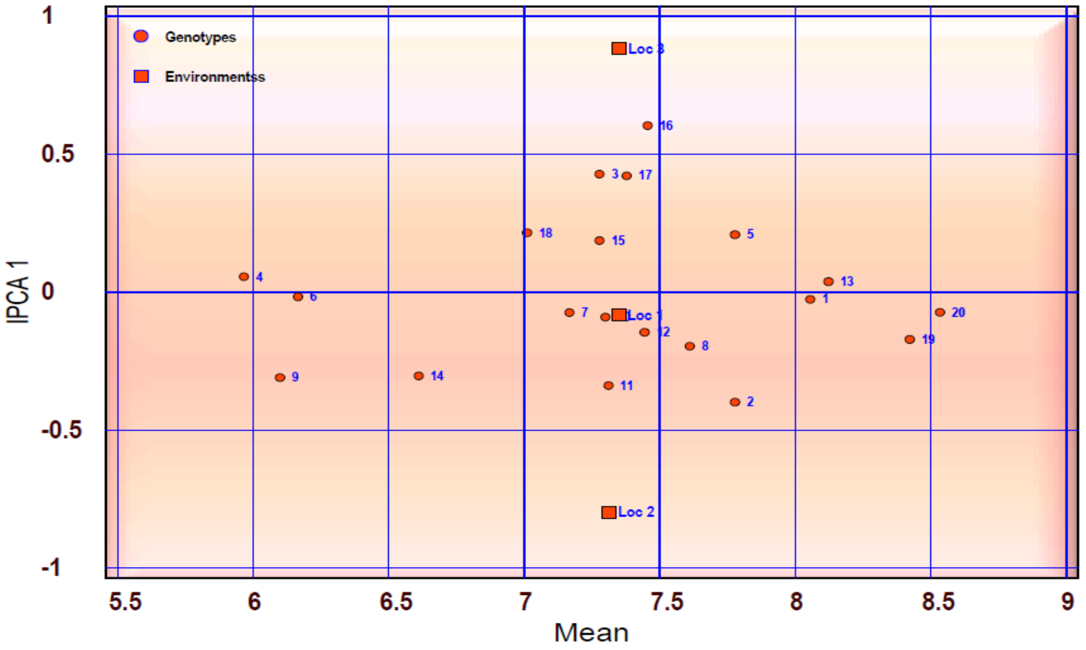
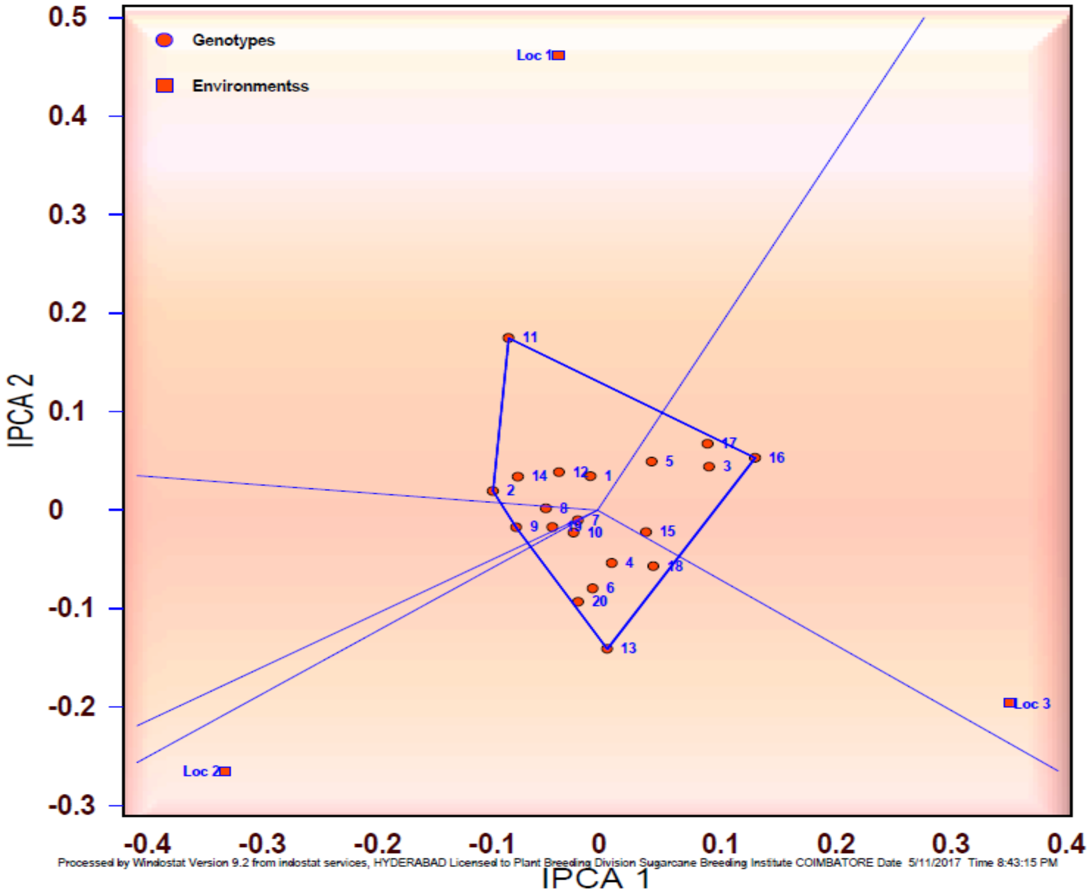


Fig 22. Intraction Biplot (AMMI 2)for protein content (%)


0.5
0.4
0.3
0.2
0.1
0
-0.1
-0.2
-0.3
IPCA 2
● Genotypes
■ Environmentss
Loc 1
Loc 2
Loc 3
11
17
16
5
3
14
12
1
2
8
7
9
19
10
15
4
18
6
20
13
-0.4
-0.3
-0.2
-0.1
0
0.1
0.2
0.3
0.4
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IPCA 1

Fig 23. Biplot (AMMI 1) for amylose content (%)

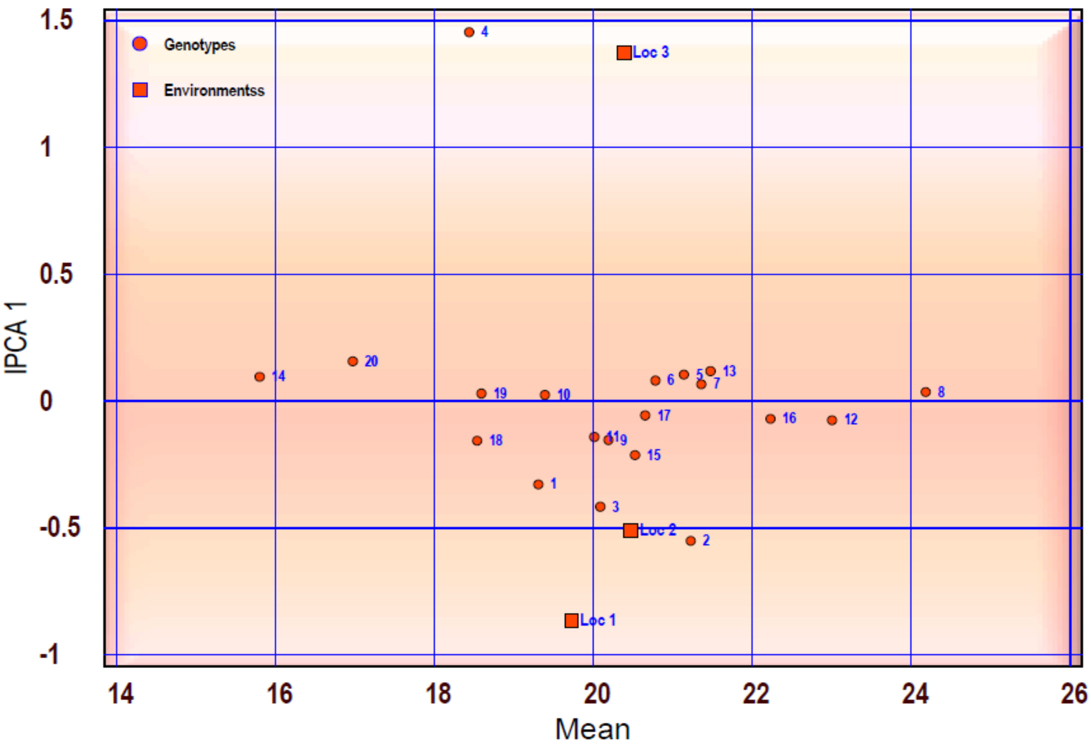
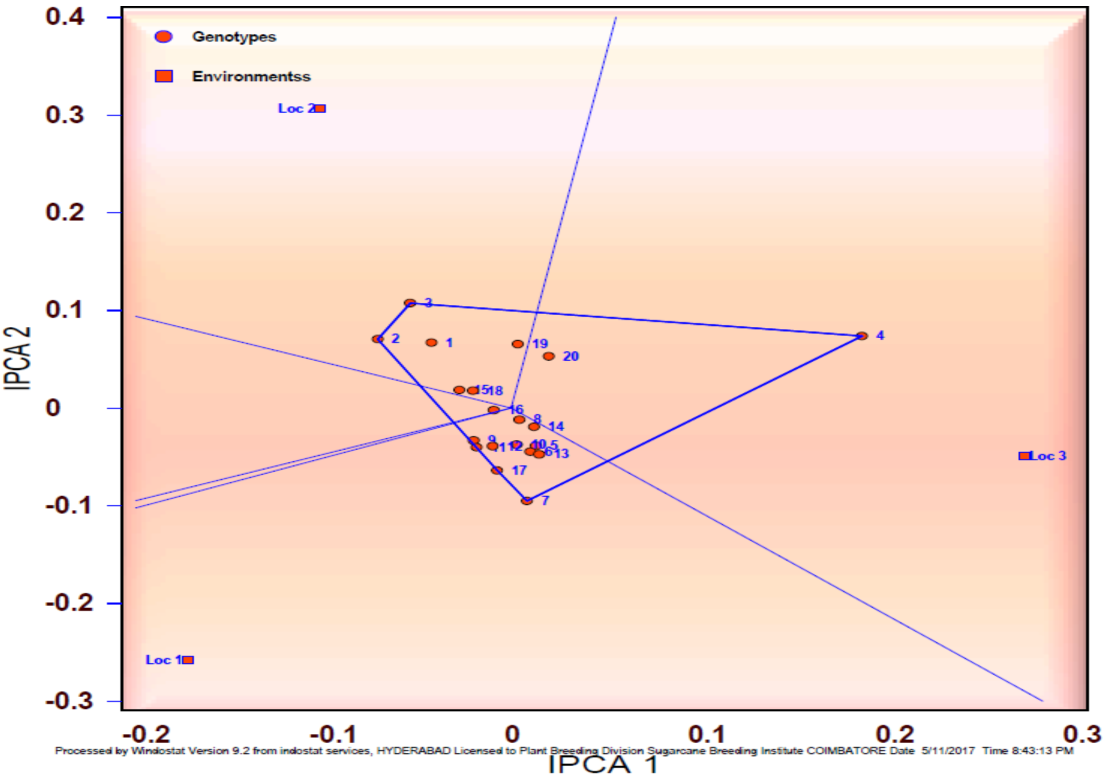


Fig 24. Intraction Biplot (AMMI 2)for amylose content (%)


0.4
0.3
0.2
0.1
0
-0.1
-0.2
-0.3
IPCA 2
Genotypes
Environmentss
Loc 2
Loc 1
Loc 3
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
-0.2
-0.1
0
0.1
0.2
0.3
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IPCA 1

CONTENTS

LIST OF FIGURES

LIST OF PLATES

LIST OF TABLES

Introduction

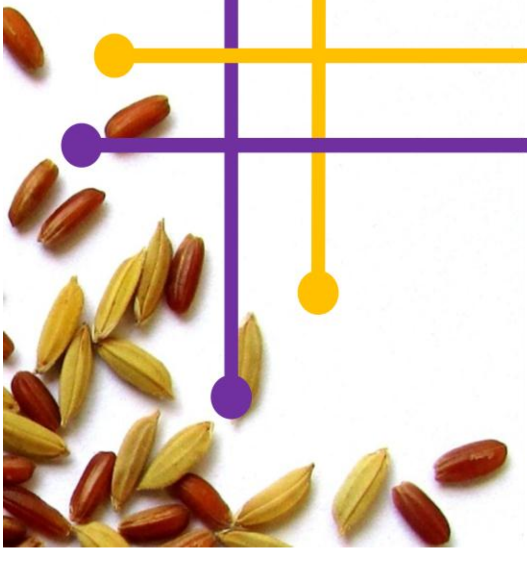
Review of Literature

Material & Methods

Experimental Results

Discussion

Summary & conclusion



Literature cited

Appendices

Abstract