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Identification of stable lentil (*Lens culinaris* Medik) genotypes through GGE biplotand AMMI analysis for North Hill Zone of India

Muniyandi Samuel Jeberson[1]*, Kadanamari Sankarappa Shashidhar[2], Shabir Hussain Wani[3], Amit Kumar Singh[4] and Sher Ahmad Dar[5]

Plant Breeding, AICRP on MULLaRP, DoR,
Central Agricultural University, Imphal 795 004 Manipur, India.
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ABSTRACT

In the present investigation with 24 lentil genotypes, first two Principal components revealed more than 90 per cent of the variability for the yield which indicates that G and GE together accounted for more than 10 per cent of total variability. Based on the present analysis of using GGE biplot models, considering simultaneous mean yield and stability, the genotypes G4, G12, G6, G13 and G2 were relatively stable in all the environments. The environment E1(Berthin) was discriminative (informative). This environment contributed most to the variability in grain yield. Hence, GGE biplot method is suitable to discriminate the genotypes based on their stable and instability nature across the environments. The AMMI analysis revealed that G13, G14, G12, G2, G23, G16 and G9 had wide adaptation and not be affected by the Genotype x environment interaction (GxE); hence mayyieldedgood across the environments. E2 and E3 could be considered as good selection sites for identifying broad based and most adaptable lentil genotypes. This study has clearly and by far aided in identification of stable and superior genotypes in graphical representation.

Key words: AMMI, GGE, Lentil, Stability, Yield.

INTRODUCTION

Lentil (*Lens culinaris* Medik.) is the fourth most important legume crop in the world. Its grain is rich in protein for human consumption and the straw is a valued animal feed. In most lentil producing areas yield seems to be not more than one-half of potential yields while improved genotypes contribute to increase lentil production(Erskine, 2009). Selecting genotypes for high mean yield and yield stability has been a challenge for lentil breeders. The requirement for stable genotypes that perform well over a wide range of environments becomes increasingly important as farmers need reliable production quantity (Gauch *et al*., 2008). Therefore, identifying most stable genotypes is an important objective in many plant breeding programs for all crops, including lentil. The performance of a genotype is determined by three factors: genotypic main effect (G), environmental main effect (E) and their interaction (Yan *et al.,* 2007). Understanding genotype by environment (GE) interactions is necessary to accurately determine stability in lentil genotypes and help breeding programs by increasing efficiency of selection (Sabaghnia *et al*., 2008). The complexities of genotype × environment interaction (GEI) make selection difficult to identify the best performing and most stable genotypes (Yau, 1995). Thus, first we need to identify the stable genotypes for their yield and yield component traits. Stability of genotypes over wide range of environments is desirable and depends upon GEI (Ali and Sawar, 2008). AMMI analysis has been shown to improve both the postdictive and predictive success of yield trials by altering the noise (random variation) from the data pattern, thereby improving predictive accuracy (Gauch and Zobel, 1988).Understanding the structure and nature of GEI is of utmost significance in crop improvement programmes because the significant GEI can seriously impair efforts in selecting the superior genotypes (Danyali*et al*., 2012).The objectives of this investigation were: (1) to apply a GGE biplotand AMMI model to evaluate the magnitude of the effect of GE interaction on grain yield of 24 lentil genotypes tested across three locations, and (2) to evaluate relationships between test environments for identification of favourable genotypes for lentil production areas in NHZ conditions.

MATERIALS AND METHODS

Twenty-four improved lentil genotypes were used as experimental materials (Table 1). These genotypes were evaluated at three locations Berthin, Srinagar and Imphal; during *rabi*, 2013-14. The test locations were selected as

*Corresponding author's e-mail: samuel8142@gmail.com, shabirhwani@skuastkashmir.ac.in
[1]Plant Breeding, AICRP on MULLaRP, DoR, Central Agricultural University, Imphal 795 004 Manipur, India.
[2]Agronomy, AICRP on MULLaRP, DoR, Central Agricultural University, Imphal 795 004 Manipur, India.
[3]Plant Breeding, Mountain Research Centre For Field Crops, Khudwani Anantnag-192 101, Sher-e-Kashmir, University of Agricultural Sciences and Technology of Kashmir, J&K, India, [4]Agronomy, AICRP on RM, Central Agricultural University, Imphal-795 004, Manipur, India.
[5]Plant Breeding, DARS, Budgam, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, J&K, India.

samples of lentil growing areas of North Hill Zone having variation in latitude, rainfall, soil type, temperature and other agro-climatic factors (Table 2). At each location, the genotypes were evaluated in a completely randomized block design with three replications.Each plot was 5.4 m^2 (1.35 × 4 m plots consisting of 6 rows) in size. Sowing was done manually in rows 22.5 cm apart. Plot means were used for further analysis. The data were subjected to analysis of variance. AMMI model was used to study GE interaction (Zobel *et al*.,1988). The basic model of the analysis is given below-

$$Y_{ij} = \mu + \beta_j + \sum_{n=1}^{k} \lambda_{in}\xi_{in}\eta_{in} + \varepsilon_{ij}$$

where Y_{ij} is the mean of genotype i in environment j; μ is the grand mean; β_j is the environment j main effect; n is the singular value; λ in and ζ in are, the singular vectors for genotype and environment for n = 1, 2, ..., respectively and åij is the residual effect. GGE biplots were generated using the first two symmetrically scaled principal components (PC) for an average tester coordinate and polygon view biplots. To visualize correlations between locations, a vector view biplot was made. These graphic analyses were done using the PBTools, version 1.4. which was used in yield stability in rice(STAR, 2014).

RESULTS AND DISCUSSION

The average yield (Table 1) of all genotypes over all the locations was 1215.86 kg/ha among the locations, the average yield of genotypes was highest in Imphal (1462.70 kg/ha), which was closely followed by Berthin (1427.45 kg/ha), the average at Srinagar was the least (757.41 kg/ha). Among the genotypes, G3 was the highest yielder followed by G8 and G11 in that order. G5 was the lowest yielder followed by G22, G21 and G20 in that order. Variations among the yields of the genotypes across the locations were found indicating the presence of g x e interaction. For example, the top average yielding genotypes G3 and G17 were found to be among the top yielders in two out of three locations, although in Berthin they were the lowest yielders.

Which-won-where: The polygon formed by connecting the markers of genotypes that are farthest away from the biplot origin,such that all other genotypes are contained in the polygon. Fig 1 (left) also contain a set of lines perpendicular its side of the polygon.The winning genotype of its sector is the one located at the respective vertex. Genotype located at the vertices of the polygon reveals the best or the poorest in one or other environment;Yan and Tinker (2006). There are six sectors with genotypes G20, G9, G5, G13 and G19 as the corner or vertex genotypes. EnvironmentE1 (Berthin) fell in the sector in which G9 and G5 were the vertex cultivars. This means G9 and G5 was best genotypes for E1 (Berthin). The environments E2 (Srinagar) and E3 (Imphal) fell in the genotype G17 andG20 were the vertex cultivars. So, these two genotypes G17 and G20were best cultivar for these two environments.Advantage of graphical presentation of GEI is that genotypes closest to ideal genotype can be identified conveniently (Rakshit *et al*., 2012). Genotypes present closer to the 'ideal genotype' are more desirable than others. The genotypes, G5, G23 and G12 were nearer to the ideal genotype followed by G20.

Mean performance and stability of the genotypes: Fig 1(right) depicts the average-environment coordination (AEC) view of the GGE biplot, which has the following

Table 1: Mean yield (Kg /Ha) of lentil genotypes for Three locations.

Genotypes	Name	Berthin (E1)	Srinagar (E2)	Imphal (E3)
G1	PL 4	764	644	1710
G2	VL 126	1042	792	1494
G3	L 4147	2384	741	1722
G4	VL 4	1412	787	1673
G5	RL 7-2	301	750	1247
G6	L 4712	1019	810	1537
G7	DL 13-5	1204	514	1451
G8	IPL 225	2477	806	1370
G9	DKL 55	1551	597	1469
G10	PL 153	1944	778	1475
G11	VL 147	2222	769	1593
G12	KLS 13-5	1157	769	1451
G13	KLS 13-1	1412	824	1463
G14	VL 146	1319	819	1438
G15	IPL226	741	796	1512
G16	PL 166	1620	764	1537
G17	LL 1209	2083	792	1586
G18	RLG 161	1620	833	1877
G19	PL 165	1991	838	1679
G20	DL 13-1	949	801	1278
G21	DKL 50	1204	810	732
G22	RL 6-4	440	773	1377
G23	L 4713	1806	778	1494
G24	LL1277	1597	593	940

Table 2: Analysis of variance.

Source	DF	SS	MSS	Explained (%)
Environment	2	22.7432	11.3716	44.87
Genotypes	23	11.3419	0.4931	22.37
Environment X Genotype	46	16.5983	0.3608	32.74
AMMI1	24	14.5605	3.83921	87.72
AMMI2	22	2.0378	0.58616	12.27
Total	71	50.6834		

interpretation (Yan and Tinker, 2006). The single arrowed line is the AEC abscissa (AEA) and points to higher mean yield across environments. Thus,G9 had the highest mean yield,followed by G23 andG5 etc., where G19 had the lowest mean yield.G5 was highly unstable, whereas G22 was highly stable. On the contrary, G4, G12, G6, G13 and G2 were relatively stable even though they are not higher grain yielders. Lentil is grown in a wide range of environmental conditions in India from temperate to tropical, so the yield of several genotypes tested across environments differed due to high GE interactions (Sabaghnia *et al*.,2008). Keeping in view yield and stability, G12, G6, G13 and G2 showed the best performance, suggesting their adaptation to a wide range of environments. This result is corroborated with the studies by Hassan *et al*. (2013) in wheat.

In GGE biplot analysis, the complex nature of GEI were simplified in various PC (Yan and Tinker, 2006). If the first two PC explain more than 60% of the (G+GL) variability in the data, and the combined (G+GL) effect account for more than 10% of the total variability, then the biplot adequately approximates the variability in GxE data (Yang, 2007). In the present study, first two PC revealed more than 90% of the variability for the yield. From the Table 2, it indicates that G and GE together accounted for more than 10% of total variability. Thus, the GGE biplots may safely be interpreted as effective graphical representation of the variability in the multi-location trial data. The graphical representation of PCI and PC2 (Fig 1) has rightly brought out the complexity in the data set.

From the mean yield table, the genotypes nearer to the ideal genotypes were comparatively high yielding. However, these genotypes are lesser yielders in one or other locations. Similar kinds of observations were reported by different authors in different food crops (Sabaghnia *et al.* 2008 and Dehghani *et al*. 2008). Using biplot, relationship significant effect of cropping season rainfall and temperature on grain yield, contributing to the GEI was reported by Saed and Francis (1984), between the testing locations can be understood easily considering their angle between their vectors (Rakshit *et al.* 2012). The present study indicates that, except E1 (Berthin) all other locations were related. Projections of the locations with respect to the concentric circles were indicative of their discriminating ability (Yan, 2001). Thus E1 (Berthin) with higher vector length were more discriminating than E2 (Srinagar) and E3 (Imphal). Presence of wide obtuse angles between environment vectors (Fig 4) which shows strong negative correlation among the testing locations suggests existence of strong crossover GE across some environment for grain yield. This reveals the genotypes yielding better in one location might be performing poor in other locations. Comprising of crossover and non-crossover GEI in multilocation data is of very common occurrence (Kamut *et al.* 2013). Which-won-where is the most important feature of GGE biplot, which graphically addresses crossover GE, mega environment differentiation and specific adaptation etc. (Hoyos-Villegas *et al.* 2016; Bhartiya *et al*. 2017 and Negash *et al*. 2017). Based on this GGE biplot analysis, the testing environments were portioned in to three mega environments. ME1 represents E1 (Berthin) with G5 and G9 as the winning genotypes. ME2 comprises of E2(Srinagar) and E3 (Imphal) with G20 is the winning genotype. Thus, the cost of testing may be reducing significantly as given by Rakshit *et al.* (2012). The lentil genotypes which were used in the present investigation separated in to stable and unstable to different environments.

AMMI analysis: The AMMI analysis of variance showed that all the components were highly significant (Table 2). The environment had the greatest influence and showed for 45.22% of the total sum of squares; genotype shared for 20.43% of the total sum of squares and GEI had shared for 34.35% which is the next highest contribution after environment. The environment has the large sum squares

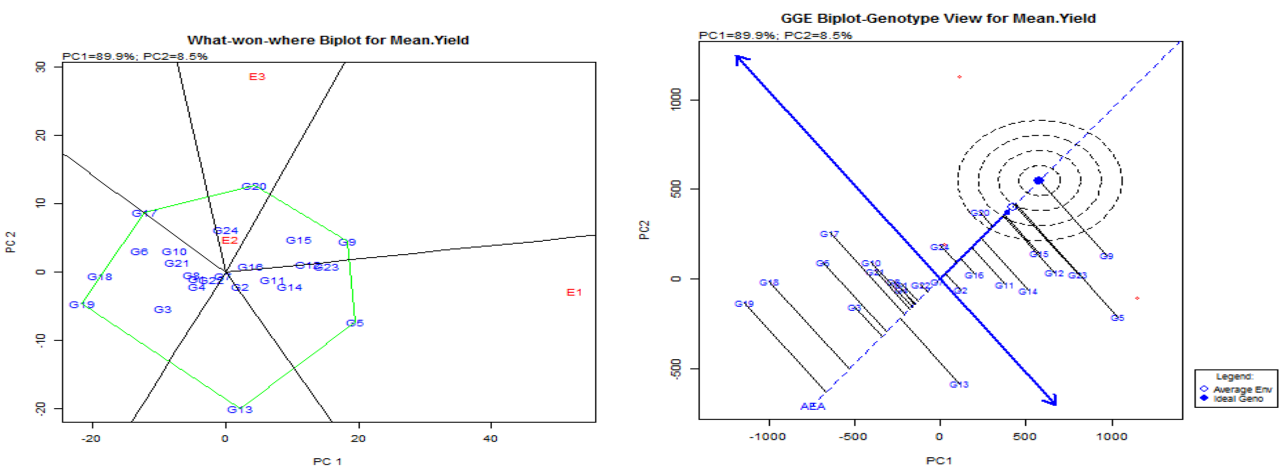

Fig 1: The which-won-where view of the GGE biplot for NHZ data (left) and AEC view for NHZ data (right).

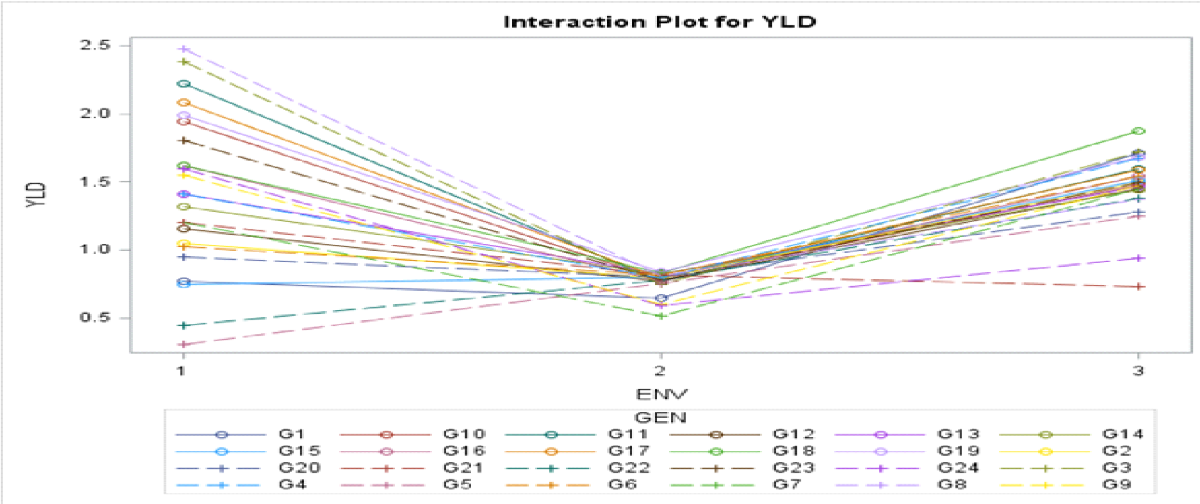

Fig 2: Interaction plot for yield in lentil.

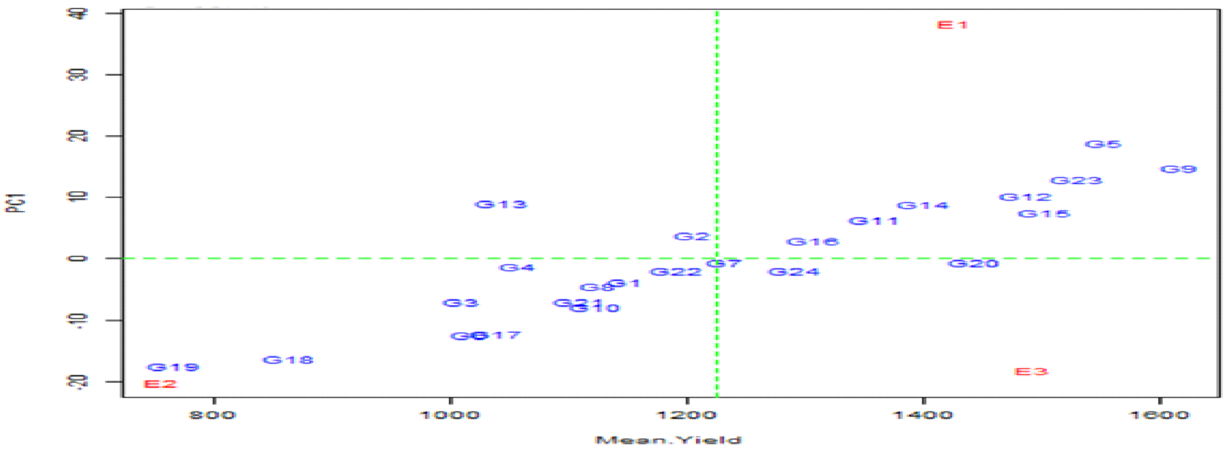

Fig 3: AMMI Biplot 1 for grain mean yield in lentil.

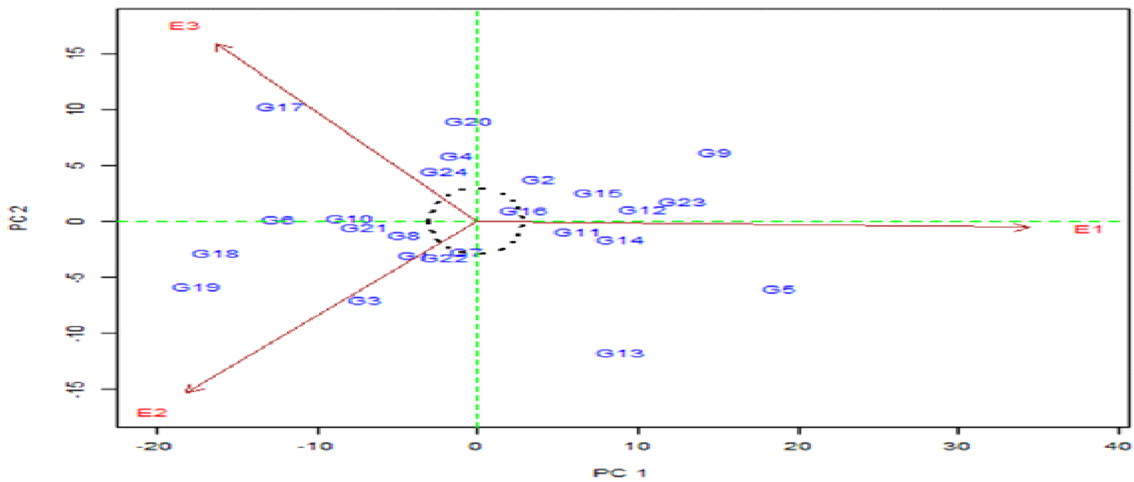

Fig 4: AMMI biplot 2 for grain mean yield in lentil.

which indicates that the environments were dissimilar, with large difference among environmental means causing larger variation in seed yield in lentil. The magnitude of GEI sum of squares was 1.5 times more than the genotypes, revealing that the differential expression of the genotypes across the environments. Genotypes with IPCA1 scores near to zero had little interaction across environments, while genotypes with very high IPCA1 values had considerable interaction with environments. Similar findings were reported by Zali *et al*. (2012) in chickpea and Rezene *et al*. (2014) in fieldpea.The GEI was portioned into two interaction PC on analysis axis (IPCA). This shows that the interaction of the lentil genotypes with three locations were predicted by the first two components of genotypes and environments. The findings further show that the first two interaction PC (IPCA1 and IPCA2) were very much important in explaining the interactions while the other IPCA's were not significant and thus constituted a residual noise component. IPCA 1 explained 87.72% of the variability relating to GEI and 24% of the interaction degrees of freedom. Likewise, the second PC axis (IPCA2) amount for 12.27% of the variability of the GEI sum of squares as shown in Table 2. The first two IPCA axis jointly accounted for almost 100% of the GE interaction sum of squares. According to Crossa *et al*. (1991) and Zobel *et al*. (1988) in the AMMI, the first two interaction PCA are best predictive model to explain the interaction sum of squares. The average grain yield distribution in the examined environments was as follows: E1>E3>E2 (Fig 2). In AMMI (Fig 3) biplot (Fig 4) the locations scores are joined to the origin by side lines. Locations with short vector might not influence strong interactive forces. Those with long vector exert strong interaction. The locations E1, E2 and E3 had long vectors, they exert strong interactive forces. In the present investigation, the genotypes, G1, G5, G22, G21, G24, G8 and G13 had large interaction since they were away from the origin whereas the genotypes G13, G14, G12, G2, G23, G16 and G9 were close the origin and hence they were not influenced by location's effect. Similarly, the locations close together exert same pattern of interaction. But in the present investigation, all the locations were falling on plot and they found to have different interaction pattern on genotypes.

CONCLUSION

Based on the present analysis of using GGE biplot models, considering simultaneous mean yield and stability, G4, G12, G6, G13 and G2 were relatively stable in all the environments. The environment E1(Berthin) was more discriminative (informative). The environment contributed most to the variability in grain yield. In conclusion, the GGE biplot methods is a suitable on to discriminate the genotypes based on their stable and instability nature across nature across the environments. The AMMI analysis revealed that G13, G14, G12, G2, G23, G16 and G9 had wide adaptation. The present study revealed that the location specific breeding effort should be strengthen rather than wider adaptability. Lentil breeders across India need to ponder on this fact while, developing genotypes for varied geographical and agro-climatic region.

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