Research Article

AMMI Biplot Analysis for Genotype X Environment Interaction on Yield Trait of High Fe content Lentil Genotypes in Terai and Mid-Hill Environment of Nepal

Darai R1*, Sarker A2, Sah RP3, Pokhrel K4 and Chaudhary R5

1Senior Scientist, Senior Technical officer and Technical Assistance, Nepal Agricultural Research Council, GLRP, Khajura, Nepal
2Principal Food Legumes Breeder and Coordinator, ICARDA South Asia and China Regional Program, NASC Complex, Pusa Campus, India
3Technical Officer, Nepal Agricultural Research Council, Surkhet, Nepal
4Corresponding author: Darai R, Senior Scientist, Senior Technical Officer and Technical Assistance, Nepal Agricultural Research Council, Khajura, India

Received: March 01, 2017; Accepted: April 26, 2017; Published: May 03, 2017

Abstract

Adolescence covers 10-19 years of human age and is the transition period of life. The prevalence of iron (Fe) deficiency in Nepal is around 23% population. High Fe content biofortified lines had developed to overwhelm the problem. This study aimed to explore the effect of Genotype (G) and Genotype x Environment Interaction (GxE) on yield of 16 high Fe content lentil genotypes under four different environments (Nepalgunj, Banke, Dashrathpur, Surkhet, Parwanipur, Bara and Itahari, Sunsari). The research was conducted at the winter season cropping period of the year 2014 and 2015 following randomized complete block design with three replications in each location. Combined analysis of variance showed that there were highly significant differences in genotype and location but not genotype x environment interaction at 5% probability level, where G and GxE captured totally 87.4% of total variability. These four environments had good discriminative and representativeness for yield trait of high Fe content lines. Mean yield performances indicated that biofortified lentil genotypes HUL-57, PL-4, RL-11 and LG-12 were the best performers across the environments over the years and stability of genotypes indicated that they were satisfactorily stable with high yield.

Keywords: AMMI Biplot and triplot analysis; GxE; Stability; Lentil

Introduction

Lentil (Lens culinaris Medikus subsp. culinaris) is a self-pollinating, diploid (2n = 2x = 14) pulse crop with a relatively large genome of 4,063 Mpb [1]. Generally, lentil varieties are distinguished by seed size and color. Lentil seed sizes are grouped into two types: macrosperma and microsperma. In Nepal, it is the main pulse crop accounting for 62.64% in area and 64.35% in production of the total legume area and production [2]. Lentil statistics showed that area, production and productivity had increased by 100.1%, 270.80% and 85.32% in between 1984/85 and 2012/13 respectively. This crop is also recognized as one of the major agricultural product with high export potential by Nepal Trade Integration Strategy. Obviously Nepalese lentils are rich in micronutrients like iron and zinc and have a great role in nutritional security of low-income people. Nepal has retained its position as the world’s sixth largest producer of lentil in 2012 after it logged 0.64 percent rise in production according to the FAO of the United Nations [3]. In fact, it is the largest exported agricultural item with a share of about 2.3% of total national export from Nepal and about 3.2% of the total world export (ITC, 2010). Nepal ranks fifth (3.2%) in lentil export after Canada (69.5%), USA (10.3%), Turkey (7.3%) and Australia (3.8%). The interplay in the effect of genetic and non-genetic on development is termed as Gx E interaction. G x E interactions are of major consequences to the breeder in the process of evolution of improved varieties. So, phenotypes are the mixture of Genotype (G), Environment (E) components and interactions (GxE) between them. It was reported that the prevalence of Fe deficiency anemia was estimated to be 55.1% in children under five, 31% in school age children, 63.5% in pregnant women, and 35% in manual laborer (Directorate of Public Nutrition, 1993). The problem for women and children is more severe because of their physiological need. The prevalence of Fe deficiency in Nepal is around 23% population. Breeding lentil with high micronutrient content dubbed as ‘biofortification’ provides a cost effective and sustainable solution to combat malnutrition. Yield is a quantitative trait that is strongly affected by environment. GxE study on yield trait of the high Fe and Zn rice lines would give information about the yield and stability, so that it could be selected the best genotypes with high yield and stable across environment. Advanced micronutrient rich breeding materials must be evaluated in multi-location and more than one year. Selection based on the yield performances are the two major phases of varietal development and the later one is highly influenced by the locations and years of testing. The main Environmental effects (E) and Genotype by Environment Interaction (GxE) have been reported as the most important sources of variation for the measured yield of crops [4]. For this reason, multi-location trials are conducted throughout the country for major crops every year. Although the measured yield is a combined result of the effects of the genotype (G), E and GE interaction, only G and GxE are relevant to cultivar evaluation and mega environment identification. Typically, E explains mostly (80% or higher) of the total yield variation, while G and GE are usually small [5]. However, effective interpretation and utilization of MET data in making selection decisions remain a major challenge to researchers. Some important concepts such as mega environment, specific adaptation, and stability all originate from the GE interaction. A significant GE interaction...
Table 1: Combine variance analysis of yield trait of high Fe content lentil in 4 sites

| Source of variation | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|---------------------|----|--------|---------|---------|--------|
| ENV                 | 3  | 17440986 | 5813662 | 56.4975 | 9.972e-06 |
| REP(ENV)            | 8  | 823210  | 102901  | 1.8164  | 0.07713 |
| GEN                 | 15 | 2849535 | 189969  | 3.3532  | 6.042e-05 |
| ENV:GEN             | 45 | 2570246 | 57117   | 1.0082  | 0.46809 |
| Error               | 168| 9517633 | 56653   |         |         |
| CV%                 | 24.58 |

Table 2: Analysis of variance of principle components of biplot genotype and location of the trial of high Fe lentil lines in four sites, 2014 and 2015.

| Principle component | percent | acum | Df | Sum.Sq | Mean.Sq | F.value | Pr.F |
|---------------------|---------|------|----|--------|---------|---------|------|
| PC1                  | 62.3    | 62.3 | 17 | 1292529.7 | 763031.16 | 1.34    | 0.1736 |
| PC2                  | 25.1    | 87.4 | 15 | 521788.9 | 34785.93  | 0.61    | 0.8641 |
| PC3                  | 12.6    | 100.0| 13 | 260968.4 | 20074.49  | 0.35    | 0.9824 |

Materials and Methods

The present experiment material comprised a total of 16 Fe rich genotypes of lentil were selected on the basis of lab analysis report, for grain yield can reduce the usefulness of subsequent analysis and limit the feasibility of selecting superior cultivars. Development of widely adapted and or location specific adapted genotypes is the goal of all breeding programs. For this purpose, the genotypes are grown in different environments and their yield stability is estimated before giving any recommendations for variety release. A genotype may be considered to be stable if its environment variance is small. Various methods have been introduced to assume cultivar reaction in different situations. Additive Main Effects and Multiplicative Interaction (AMMI) analysis is one of the popular parametric of multivariate methods to predict adaptation and stability of cultivars. The usefulness of the method to be applied to some different crops has been noted by many researchers [6-8]. Zobel et al, proposed the name AMMI first time. The AMMI model is a hybrid model involving both additive and multiplicative components of two way data structure which enabled a breeder to get precise prediction on genotypic potentiality and environmental influences on it. AMMI uses ordinary ANOVA to analyze the main effects (additive part) and Principal Component Analysis (PCA) to analyze the non-additive residual left over by the ANOVA [9]. Purchase et al., 2000 [10], developed a quantitative stability value to rank genotypes through the AMMI model, named the AMMI Stability Value (ASV). During the analysis of cultivars stability they found a significant correlation between the stability measures ASV with Shukla and Wricke (Wi), and Eberhart and Russel (S2d), while Finlay and Wilkinson (b), and Linn and Binns (Pi) showed limited correspondence with any of the other methods [11,12]. The developed ASV was considered to be the most appropriate single method of describing the stability of genotypes. The breeders want to develop and select high yield and high stability lines which is highly desirable but some time, high yield but low stability lines which is desirable for specific selection, low yield and low stability (desirable for special breeding purposes, e.g. drought resistance selection) while low yield but high stability is undesirable and no one wants to select such types.

Table 3: AMMI analysis of variance for yield and yield attributing traits of lentil genotypes across 4 environments.

| SN | Name of entries | DF | DM | Plht | P/P | Grain Yield (kg/ha) | HSWT |
|----|-----------------|----|----|------|-----|---------------------|------|
| 1  | ILL-8006        | 83 | 134| 29   | 77  | 963                 | 2    |
| 2  | RL-6            | 81 | 131| 30   | 66  | 1042                | 1    |
| 3  | RL-12           | 84 | 133| 30   | 77  | 1070                |      |
| 4  | ILL-7715        | 85 | 133| 31   | 76  | 1039                | 1    |
| 5  | ILL-7164        | 85 | 133| 31   | 76  | 1029                | 2    |
| 6  | ILL-3490        | 84 | 134| 30   | 78  | 884                 | 1    |
| 7  | Khajura-2       | 84 | 132| 30   | 85  | 984                 | 2    |
| 8  | Simal           | 86 | 133| 29   | 67  | 851                 | 1    |
| 9  | Shital          | 81 | 130| 30   | 75  | 996                 | 1    |
| 10 | Sagun           | 86 | 131| 29   | 68  | 1013                | 2    |
| 11 | HUL-57          | 85 | 133| 31   | 76  | 1179                | 1    |
| 12 | LG-12           | 84 | 131| 30   | 77  | 1061                | 1    |
| 13 | PL-4            | 82 | 133| 30   | 70  | 1119                | 2    |
| 14 | RL-11           | 84 | 134| 31   | 74  | 1077                | 2    |
| 15 | RL-4            | 85 | 133| 29   | 69  | 912                 | 2    |
| 16 | ILL-4605        | 88 | 126| 25   | 55  | 610                 | 3    |
| Mean|                | 83 | 132| 30   | 73  | 989                 | 2    |

F-pr

Genotype <.001 <.001 <.001 <.001 <.001 <.001 <.001
Environment <.001 <.001 <.001 <.001 <.001 <.001 <.001
GxE <.001 <.001 0.008 0.707 0.075 175.1 <.001
CV% 4.9 2.4 13.7 31.2 27.7 16.4 0.1915
LSD 2.957 2.29 2.919 16.57 175.1 0.1915
to silty loam, poor in organic carbon and available N, but medium in available P₂O₅ and K₂O, pH varies from 7.2-7.5. The trials were conducted in a Randomized Complete Block Design (RCBD) with three replications. The plot size was of 4 meter length of four rows (1m wide) of 25cm spacing between rows and continues between plants. Important quantitative traits i.e. Days to 50% Flowering (DF), Days to 90% Maturity (DM), Plant Height (PH) in cm, number of Pods per Plant (PP), number of Seeds per Pod (SP), 100 Seed Weight (SW) in gram, and grain yield metric ton/ha (GY kg ha⁻¹) were recorded. Five plants randomly selected from each plot to take the data of yield attributing traits. Grain yields were recorded on the plot basis and their ranks are presented in Table 4. The highest mean grain yield of genotypes averaged over environments was produced by HUL-57 (1179 kgha⁻¹) followed by PL-4 (1119 kg ha⁻¹) and ILL4605 (1042 kg ha⁻¹) while lowest by ILL7164 (1029 kg ha⁻¹). The pooled mean yields and yield attributing traits of all the genotypes averaged over environments were produced by HUL-57 (1119 kg ha⁻¹) followed by PL-4 (1119 kg ha⁻¹) and RL-12 (1077 mt ha⁻¹) while lowest by ILL4605 (610 kg ha⁻¹). Different genotypes showed in consistent performance across all environments. The highest environments mean grain yield of genotypes averaged over environments was produced by HUL-57 (1179 kg ha⁻¹) followed by PL-4 (1119 kg ha⁻¹) and RL-11 (1077 mt ha⁻¹) while lowest by ILL4605 (610 kg ha⁻¹). Different genotypes showed in consistent performance across all environments. The highest environments mean grain yield of genotypes averaged over environments was produced by HUL-57 (1179 kg ha⁻¹) followed by PL-4 (1119 kg ha⁻¹) and RL-11 (1077 mt ha⁻¹) while lowest by ILL4605 (610 kg ha⁻¹). Different genotypes showed in consistent performance across all environments.

Results and Discussions

AMMI analysis of variance

Variance analysis showed that the genotype and environment was found highly significant differences for the yield and yield attributing traits except plant height and pod per plant but non-significant differences in genotype x environment interaction indicating distinct features of genotype and environments but not distinct the genotype x environment interactions [14] on phenotypic expression. High estimate of Sum of Square (SS) for all the traits are expressed by environment (Table 1). Yield variation was observed due to the environment effect indicated that the environments were diverse and a major part of variation in grain yield can be resulted from environmental changes. These data had compiled the requirements for biplot analysis. Biplot analysis was conducted and visualized to determine the differences among the environments, to evaluate stable and wide adaptable line, and to evaluate the environments if a certain graph representing the appropriate environment to select genotypes based on yield. The presence of Genotype Environment Interaction (GEI) was clearly demonstrated by the AMMI model, when the interaction was partitioned among the first three Interaction Principal Component Axis (IPCA). All PCA 1, PCA 2 and PCA 3 were non-significant. PC1 contribute 62.3 % variation to the total. PC2 contribute 25.1 % to the total variation and IPC3 contribute 12.6 % variation of the total with Pr. F value more than 0.005. It means that by using PC1 and PC2, the analysis could explain 87.4 % variation (Table 2).

Mean yield and yield attributing traits comparison

The pooled mean yields and yield attributing traits of all the environments are presented in Table 3. AMMI analysis variance for yield and yield attributing traits indicated that significant differences were observed in genotype, environment and Genotype environment interaction in the days to flowering, days to maturity, hundred seed weight and plant height while significant differences was genotype and environment but in Genotype x Environment interaction in the yield trait. Only nine genotypes have produced grain yield above the grand mean yield, while all the checks produced below the grand mean. The highest mean grain yield of genotypes averaged over environments was produced by HUL-57 (1179 kg ha⁻¹) followed by PL-4 (1119 kg ha⁻¹) and RL-11 (1077 mt ha⁻¹) while lowest by ILL4605 (610 kg ha⁻¹). Different genotypes showed in consistent performance across all environments. The highest environments mean grain yield of genotypes averaged over environments was produced by HUL-57 (1179 kg ha⁻¹) followed by PL-4 (1119 kg ha⁻¹) and RL-11 (1077 mt ha⁻¹) while lowest by ILL4605 (610 kg ha⁻¹). Different genotypes showed in consistent performance across all environments. The highest environments mean grain yield of genotypes averaged over environments was produced by HUL-57 (1179 kg ha⁻¹) followed by PL-4 (1119 kg ha⁻¹) and RL-11 (1077 mt ha⁻¹) while lowest by ILL4605 (610 kg ha⁻¹). Different genotypes showed in consistent performance across all environments. The highest environments mean grain yield of genotypes averaged over environments was produced by HUL-57 (1179 kg ha⁻¹) followed by PL-4 (1119 kg ha⁻¹) and RL-11 (1077 mt ha⁻¹) while lowest by ILL4605 (610 kg ha⁻¹). Different genotypes showed in consistent performance across all environments. The highest environments mean grain yield of genotypes averaged over environments was produced by HUL-57 (1179 kg ha⁻¹) followed by PL-4 (1119 kg ha⁻¹) and RL-11 (1077 mt ha⁻¹) while lowest by ILL4605 (610 kg ha⁻¹). Different genotypes showed in consistent performance across all environments.

The AMMI Stability Value (ASV) and AMMI stable index are calculated as suggested by Zobel et al, 1998 and Purchase et al. [10] and their ranks are presented in Table 4. The highest mean grain yield of genotypes averaged over environments were produced by HUL-57 (1179 kg ha⁻¹) followed by PL-4 (1119Kg ha⁻¹) and RL-11 (1077 mt ha⁻¹) while lowest by ILL4605 (610 kg ha⁻¹). The genotypes which has low stability value (ASV) is said to be stable and the breeder chose the stable genotypes, having grain yield above the mean grand yield. In this experiment genotype HUL-57 ranked 1st instability followed by RL-12, RL-11 and LG-12 and suitable for all environment but out of test genotypes; genotypes HUL-57, RL-12, RL-11, LG-12, Sagun, PL-...
the origins are sensitive and have large interaction. In the present study genotype PL-4, simal (Nepalgunj), ILL3490 (Itahari), Sagun (Surkhet) and, RL-4 and Khajura-2 (Parwanipur) are more responsive to the environment given in parenthesis and are specific adopted. The genotypes ILL-8006, RL-11, and RL-12 are less affected by the G x E interaction and thus would perform well across a wide range of environments.

Conclusion

Yield is a quantitative trait that is strongly affected by environment. AMMI statistical model might be a great tool to select the most suitable and stable high yielding genotypes for specific as well as for diverse environments. In the present study, AMMI model has shown that the largest proportion of the total variation in grain yield was attributed to environments. The genotype HUL-57, PL-4, RL-11 and LG-12 showed higher grain yield than all other genotypes across all the environments and performed well at all the environment. The genotypes ILL-8006, RL-11, and RL-12 are less affected by the G x E interaction and thus would perform well across a wide range of environments.

Acknowledgment

The research was supported collaboratively by ICARDA through Harvest plus Biofortification Project on Development of Lentil Cultivars with High Concentration of Iron and Zinc for Nutritional Security. We are highly acknowledged to Dr. A. Sarker, Regional Coordinator, ICARDA and China Regional program for bringing such a wonderful project. We would like to give special thanks to NARC ED Dr. YR Pandey, CHD Dr. YP Giri and Planning Director Dr. AK Gautam for his continuing support to the program. Most importantly we would like to thanks all the staffs that directly and indirectly help to conduct the experiments.

References
1. Arumuganathan K, Earle ED. Nuclear DNA content of some important plant species. Plant Mol Biol. 1991; 9: 208-218.
2. Statistical Information on Nepalese Agriculture 2013/14. Ministry of Agriculture and Development business promotion and agriculture statistics division. Nepal. MOAD. 2014.
3. FAOSTAT. Statistical Database. FAO. 2010.
4. Dehghani H, Ebadi A, Yousefi A. Biplot analysis of genotype by environment interaction for barley yield in Iran. Agron J. 2006; 98: 388-393.
5. Yan W, Kang MS. GGE-biplot analysis: Agraphical tool for breeders, geneticists, and agronomists. CRC Press, USA. 2003.
6. Abay F, Bjornstad A. Specific adaptation of Barley varieties in different locations in Ethiopia. Euphytica. 2009; 167: 181-195.
7. Alwala S, Kwolek T, McPherson M, Pellow J, Meyer D. A comprehensive comparison between Eberhart and Russell joint regression and GGE biplot analyses to identify stable and high yielding maize hybrids. Field Crops Res. 2010; 119: 225-230.
8. Annicchiarico P, Haricz N, Camoni AM. Adaptation, diversity, and exploitation of global white lupin (Lupinus albus L.) landrace genetic resources. Field Crops Res. 2010; 119: 114-124.
9. Gauch HG. AMMI and related analysis for two way data matrices. Microcomputer power, Ithaca, New York. USA J. 1993; 80: 388-339.
10. Purchase JL, Hatting H and Van Deventer CS. Genotype x environment interaction of winter wheat (T. aestivum) in South Africa: Stability analysis of yield performance. S Afr J Plant Soil. 2000; 17: 101-107.
11. Eberhart SA, Russell WA. Stability parameters for comparing varieties. Crop Sci. 1966; 6: 36-40.

12. Finlay KW, Wilkinson GN. The analysis of adaptation in a plant breeding programme. Aust J Agric Res. 1963; 14: 742-754.

13. Yadav NK, Ghimire SK, Sah BP, Sarker A, Shrestha SM, Sah SK. Genotype x environment interaction and stability analysis in lentil (Lens culinaris Medik.). Paper published in the International Journal of Environment, Agriculture and Biotechnology (IJEAB). 2016; 1: 2456-1878.

14. Freeman GH. Statistical methods for the analysis of Genotype X Environment Interactions. Heredity. 1973; 31: 339-354.

15. Kempton RA. The use of biplots in interpreting variety by environment interactions. Journal of Agricultural Science. 1984; 103: 123-135.

16. Ebdon J, Gauch H. Additive main effect and multiplicative interaction analysis of national turfgrass performance trials: I. Interpretation of genotype X Environment Interaction. Crop Sci. 2002; 42: 489-496.

17. Gauch HG, Zobel RW, Kang MS & Gauch HG. AMMI analysis of yield trials. Genotype by-environment interaction, pp: 85-122. Gujrat Agric Uni Res J. 1996; 22: 101-102.