

Evaluation of genotype \times environment interaction for grain yield of promising genotypes of rice (*Oryza sativa* L.) derived from mutation induction using the GGE-biplot method

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Abstract

The existence of genotype \times environment interaction complicates the evaluation of cultivar performance and reduces gain to selection. One of the multivariate methods for interpreting genotype by environment interaction is GGE-Biplot, in which the main effect of genotype and genotype by environment interaction are investigated simultaneously. In this study, 13 mutant genotypes of rice along with three check cultivars Tarrom-Mahalli, Tarrom-Jelodar and Neda were evaluated for grain yield stability in the two locations of Sari and Tonekabon during the years 2016 and 2017 using randomized complete block design with three replications within each environment. The results of GGE-biplot analysis showed that the two first components explained 92.52% of the total yield variation. According to the polygon view, all four environments of the experiment were located in the place that the Neda cultivar was at the top. Genotypes 33, 30, 26, 31 were highly stable genotypes and genotypes 18, 16 and 25 were highly unstable. In this study, we found only one mega-environment. Also following Neda and Jelodar cultivars, genotype 31 was closest to the ideal genotype. Ton 95 was the most desirable environment.

Keywords: Genotype by environment interaction; GGE-biplot; Mutant rice; Stability

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Introduction

The genotype by environment interaction (GE) refers to the relative yield of cultivars in different environments, indicating differences in the ranking of genotypes or other words, differences in the expression levels of the genetic structure under varying environmental conditions (Li *et al.* 2017). Due to the presence of genotype \times environment interaction, no crop cultivar performs the best in all years and locations (Yan 2019), so they should be evaluated in multi-

environment yield trials to investigate the genotype \times environment interaction and grain yield stability. GGE-biplot simultaneously uses the main effect of the genotype and the genotype by environment interaction, unlike the more conventional multivariate method of stability analysis (Yan *et al.* 2000). This method helps breeders by the graphical demonstration of $G \times E$ interaction to evaluate the stability of different genotypes together with their performance in different environments. Also, it provides the

possible relationship between environments and identifies target environments in breeding programs (Yan *et al.* 2001). The GGE-biplot method has been used in rice for the simultaneous selection of yield and stability (Raza Khan *et al.* 2019; Jadhav *et al.* 2019; Bana *et al.* 2020; Bii *et al.* 2020; Chandrashekhar *et al.* 2020).

The main objectives of this study were to: (1) evaluate the stability of promising rice genotypes under four different environmental conditions (2) rank the genotypes in the environments and determine the appropriate genotype(s) for each environment and (3) examine the relationship between the tested locations.

Materials and Methods

In this study, 13 mutant rice genotypes (from the eighth generation, derived from the Tarrum Mahalli rice cultivar using ethyl methane sulfonate with the concentration of 150 mM) along with three check cultivars, Tarrum-mahalli, Tarrum-Jelodar and Neda were evaluated for grain yield stability in two locations of Sari and Tonekabon during the two cropping years of 2016 and 2017. The experimental design was randomized complete block design with three replications within each environment. The GGE-biplot method based on the two-dimensional data, which is an effective tool for visualization and graphical analysis, was used for the analysis by the following equation (Yan *et al.* 2000):

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{1j} + \lambda_2 \xi_{i2} \eta_{2j} + \varepsilon_{ij}$$

Y_{ij} = Yield of the i th genotype in the j th environment.

μ = Grand mean.

β_j = Main effect of the j th environment.

λ_1, λ_2 = Singular values of the first and second principal components.

ξ_1, ξ_2 = The eigenvectors for the j th genotype for the first and second principal components, respectively.

η_{1j}, η_{2j} = The eigenvectors for the j th environment for the first and second principal components, respectively.

ε_{ij} = The residual values of the i th genotype in the j th environment.

In the GGE-biplot analysis, Sari 95, Tonekabon 95, Sari 96 and Tonekabon 96 were considered as the first to fourth environments, respectively.

For performing the combined analysis of variance, SAS 9.1.3 software and for GGE-biplot analysis, R 3.3.2 software (R Development Core Team 2016) including the GGE-Biplot GUI package were used.

Results and Discussion

Combined analysis of variance showed that the effects of environment, genotype (G) and genotype \times environment interaction were significant for grain yield (Table 1). Therefore, it was indicated that GGE biplot could be used to evaluate G and GE interaction effects. The results of GGE-biplot analysis showed that the two first components explained 92.52% of the total yield variation which was higher than the results reported by Oladosu *et al.* (2017) in mutant rice genotypes. In their research, the first two principal components justified about 71% of the total variation.

The relationship among environments was demonstrated in Figure 1. Lines connecting the

Table 1. Combined analysis of variance of grain yield of rice genotypes studied in four environments.

Source of variation	df	SS	MS	% of SS from the total SS for E, G and G × E interaction
Environment	3	26.68	8.89**	17.01
Error 1	8	4.43	0.55	
Genotype	15	87.49	5.83**	55.79
Genotype G × E interactions	45	42.64	0.94**	27.19
Error 2	120	36.95	0.30	
Total	191	198.20		

^{ns}, * and **not significant and significant at the 5 and 1% probability levels, respectively.

biplot origin to the environment markers are environment vectors. The cosine of the angle between two environment vectors determines their correlation coefficient approximately (Kroonenberg 1995). Acute, obtuse and right angles imply positive, negative and lack of correlation between vectors (Yan and Tinker 2006). There were positive correlations between Sari 95 and Sari 96 (acute angle). Negative correlations were observed between Sari 95 and Ton 96 (obtuse angle). On the other hand, Sari 96 and Ton 96 were not associated (right angle).

Grain yield performance and stability of rice mutant genotypes were graphically shown in Figure 2 based on the average environment coordinate (AEC) method (Yan 2002). The arrowed line passing through the origin of the biplot is the AEC abscissa, it points to higher mean yield across environments (Yan and Tinker 2006). Thus, the Neda cultivar was the high-yielding genotype, followed by Tarrow-Jelodar, 31, 26 and 33, showing the yield above the grand mean. The perpendicular line that passes through the biplot origin, is the AEC ordinate. It shows greater variability in both directions (Yan and

Tinker 2006). Genotypes 33, 30, 26, 31 were highly stable genotypes and genotypes 18, 16 and 25 were highly unstable.

The polygon view of the GGE biplot was represented in Figure 3. Polygon view not only is an effective tool to identify the best genotype(s) for each environment but also determines the mega-environment(s) by dividing the test environments into groups (Yan and Kang 2003). The polygon view was constructed joining the furthest genotypes from the biplot origin, and then all other genotypes were located inside the polygon. These vertex genotypes have either the best or poorest yield at some or all of the environments. Also, some perpendicular lines were drawn from the biplot origin to each side of the polygon, such that some sectors were made on the graph (Yan and Rajcan 2002). The length of the genotype vector from the biplot origin is a measure of responsiveness to environments (Yan and Kang 2003) Accordingly, the Neda cultivar was the best genotype and the most responsive cultivar in all four environments and the other genotypes in Neda's sector such as 33, 26, 31 and Tarrow-Jelodar were less responsive in these

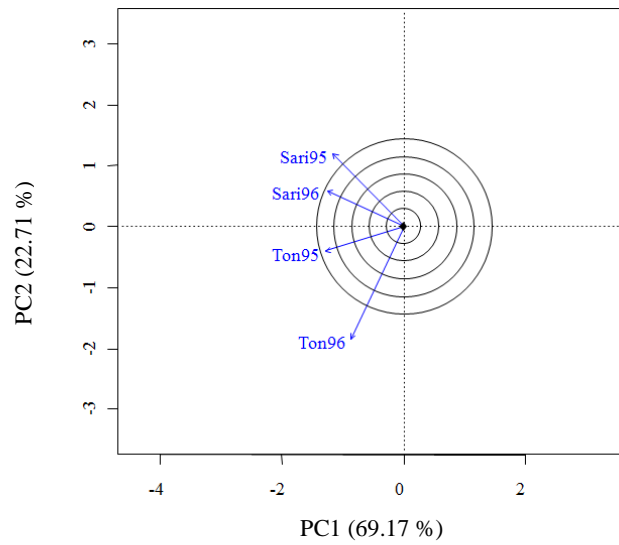


Figure 1. The vector view of the GGE biplot to show the relationship among the environments.

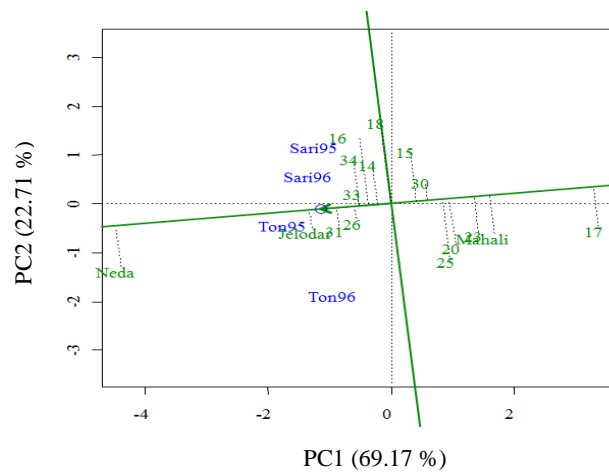


Figure 2. Average-environment coordinate (AEC) view of the GGE biplot for ranking of 14 rice genotypes based on mean and stability in four environments.

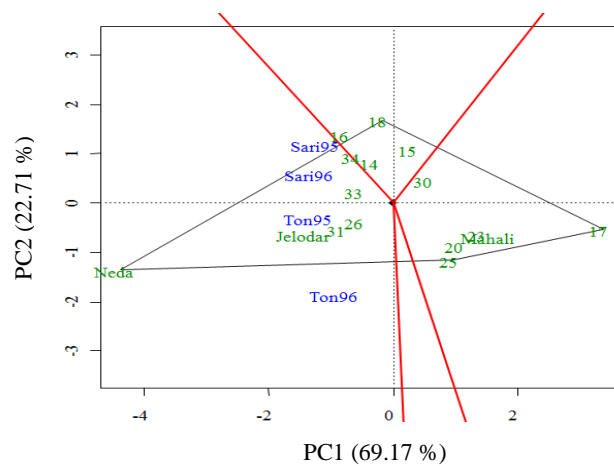


Figure 3. Polygon view of the GGE biplot shows the "which-won-where pattern".

environments. Also, only one mega-environment was found because all environments fell into one sector and the Neda cultivar was the best genotype in this mega-environment. A mega-environment consists of a group of environments that share the same best genotype (Yan and Rajcan 2002). The vertex genotypes 17, 18 and 25 had the poorest yield in any environment because no environment fell into their sectors.

A comparison of the test environments with the ideal environment was represented in Figure 4. The small circle on the AEC abscissa, with an arrow pointing to it, represents the ideal environment. It is the most discriminating and representative of all test environments. The ideal environment is situated in the center of concentric circles (Yan and Kang 2003). Thus, according to

Figure 4, Ton 95 was the closest to the ideal environment, so it was the most desirable environment.

An ideal genotype has the highest yield and is the most stable (Yan and Kang 2003). A comparison of the test genotypes with the ideal genotype was graphically shown in Figure 5. Similar to the ideal environment, the ideal genotype was also located in the center of concentric circles on the AEC view (Yan and Kang 2003). Thus, the Neda cultivar followed by the Jelodar cultivar and genotype 31, were close to the ideal genotype. Ahmadi *et al.* (2012) in barley and Karimizadeh *et al.* (2013) in lentils have also used the GGE-biplot method to identify ideal genotypes.

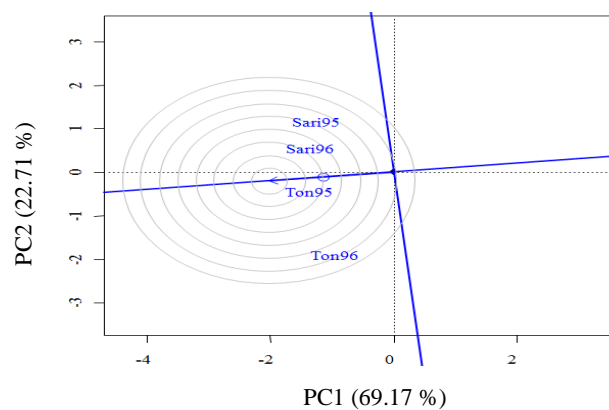


Figure 4. Ranking the environments based on the ideal environment.

Conclusion

In this study, GGE-biplot was utilized to assess yield stability and test environments for mutant rice genotypes. The relationship between Sari 95 and Sari 96 had positive correlations. Neda cultivar was the high-yielding genotypes, followed by Tarrom-Jelodar, 31, 26 and 33, as well as genotypes 33, 30, 26, 31 were highly

stable genotypes. Ton 95 was the most desirable environment for selecting mutant rice genotypes.

Conflict of Interest

The authors declare that they have no conflict of interest with any organization concerning the subject of the manuscript.

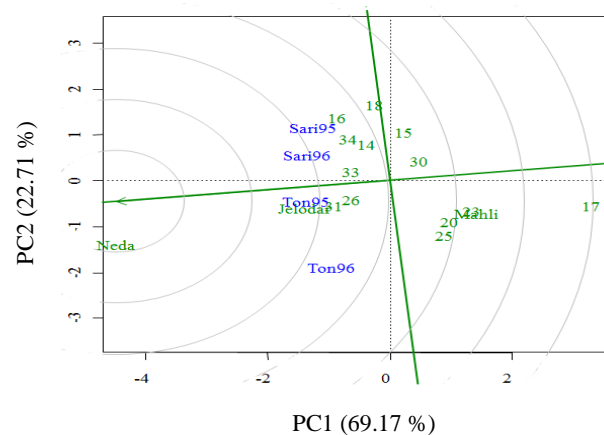


Figure 5. Ranking the rice genotypes based on the ideal genotype.

References

- Ahmadi J, Vaezi B and Fotokian MH, 2012. Graphical analysis of multi-environment trials for barley yield using AMMI and GGE-Biplot under rain-fed conditions. *Journal of Plant Physiology and Breeding* 2(1): 43-54.
- Bana RS, Singh D, Nain MS, Kumar H, Kumar V and Sepat S, 2020. Weed control and rice yield stability studies across diverse tillage and crop establishment systems under on-farm environments. *Soil & Tillage Research* 204: 104729.
- Bii CL, Ngug K, Kimani JM, George N and Chemining W, 2020. Genotype by environment analysis of rice (*Oryza sativa* L.) populations under drought stressed and well-watered environments. *Australian Journal of Crop Science* 14: 259-262.
- Chandrashekhar S, Babu R, Jeyaprakash RU, Bhuvaneshwari K and Manonmani S, 2020. Yield stability analysis in multi-environment trials of hybrid rice (*Oryza sativa* L.) in northern India using GGE Biplot analysis. *Electronic Journal of Plant Breeding* 2: 665-673.
- Jadhav S, Balakrishnan D, Shankar G, Beerelli K, Chandu G and Neelamraju S, 2019. Genotype by environment (G×E) interaction study on yield traits in different maturity groups of rice 22: 425-449.
- Karimizadeh R, Mohammadi M and Sabaghnia N, 2013. Site regression biplot analysis for matching new improved lentil genotypes into target environments. *Journal of Plant Physiology and Breeding* 3(2): 51-65.
- Kroonenberg PM, 1995. Introduction to biplots for $G \times E$ Tables. Department of Mathematics, Res. Rep. 51. University of Queensland, Australia.
- Li Y, Suontama M, Burdon RD and Dungey HS, 2017. Genotype by environment interactions in forest tree breeding: review of methodology and perspectives on research and application. *Tree Genetics & Genomes* 13: 1-18.
- Oladosu Y, Rafli MY, Abdullah N, Magaji U, Miah G, Hussin G and Ramli A, 2017. Genotype × environment interaction and stability analyses of yield and yield components of established and mutant rice genotypes tested in multiple locations in Malaysia. *Acta Agriculturae Scandinavica, Section B- Soil & Plant Science* 7: 590-606.
- R Development Core Team, 2016. R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria. URL <http://www.R-project.org/>.

- Raza Khan RA, Ramzan M, Haider Z, Akter M, Riaz M, Ali SS, Awan TH and Mahmood A, 2019. Stability and adaptability analysis in advance fine grain rice (*Oryza sativa* L.) genotypes for yield. *Journal of Agriculture and Aquaculture* 2: 1-9.
- Yan W, 2002. Singular-value partitioning in biplot analysis of multi-environment trial data. *Agronomy Journal* 94: 990-996.
- Yan W, 2019. LG biplot: a graphical method for mega-environment investigation using existing crop variety trial data. *Scientific Reporters* 9: 7130. doi.org/10.1038/s41598-019-43683-9.
- Yan W, Cornelius PL, Crossa J and Hunt LA, 2001. Two types of GGE biplots for analyzing multi-environment trial data. *Crop Science* 41: 656-663.
- Yan W, Hunt LA, Sheng Q and Szlavnic Z, 2000. Cultivar evaluation and mega environment investigations based on the GGE biplot. *Crop Science* 40: 597-605.
- Yan W and Kang MS, 2003. *GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists*. CRC Press, Boca Raton, FL, USA, 271p.
- Yan W and Rajcan, 2002. Biplot analysis of test sites and trait relations of soybean in onatario. *Crop Science* 42: 11-20.
- Yan W and Tinker NA, 2006. Biplot analysis of multi-environment trial data: principles and applications. *Canadian Journal of Plant Science* 86: 623-645.

ارزیابی اثرات متقابل ژنوتیپ و محیط برای عملکرد دانه تعدادی از ژنوتیپ‌های امیدبخش برنج (*Oryza sativa* L.) حاصل از القای جهش با استفاده از روش GGE-biplot

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چکیده

وجود اثرات متقابل ژنوتیپ و محیط باعث پیچیده کردن ارزیابی عملکرد ارقام و کاهش سودمندی انتخاب می شود. یکی از روش‌های چند متغیره برای تفسیر اثرات متقابل ژنوتیپ و محیط GGE-biplot نام دارد که اثرات اصلی ژنوتیپ‌ها و اثرات متقابل ژنوتیپ و محیط را به طور هم‌زمان مورد بررسی قرار می‌دهد. در مطالعه حاضر ۱۳ ژنوتیپ حاصل از القای جهش در برنج به همراه سه رقم شاهد طارم-محلی، طارم-جلودار و ندا در قالب طرح بلوک‌های کامل تصادفی با سه تکرار در دو منطقه ساری و تنکابن طی دو سال زراعی ۱۳۹۵ و ۱۳۹۶ از نظر پایداری عملکرد دانه مورد ارزیابی قرار گرفتند. نتایج حاصل از تجزیه GGE-biplot نشان داد که دو جزء اول در مجموع توانستند ۹۲/۵۲ درصد از تغییرات عملکرد دانه را توجیه نمایند. مطابق با نمودار چندوجهی حاصل از این روش هر چهار محیط به کار رفته در این آزمایش هم مکان با رقم پرمحصول ندا (شاهد) در قسمت بالا قرار گرفتند. ژنوتیپ‌های ۳۳، ۳۰، ۲۶ و ۳۱ پایداری بالایی داشتند و ژنوتیپ‌های ۱۸، ۱۶ و ۲۵ ناپایدار بودند. در این مطالعه تنها یک محیط بزرگ شناسایی شد. همچنین به دنبال ارقام ندا و جلودار، ژنوتیپ ۳۱ به ژنوتیپ ایده‌آل نزدیک‌تر از بقیه بود. محیط تنکابن ۹۶ به عنوان مطلوبترین محیط شناخته شد.

واژه‌های کلیدی: اثر متقابل ژنوتیپ محیط؛ برنج موتانت؛ پایداری؛ GGE-biplot

