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RESEARCH PAPER

Biplot Analysis of Genotype-Environment Interaction in Rapeseed (Brassica napus L.) in Two Normal and Stress Condition Using the AMMI Model

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Abstract

The standard yield stability used to measure changes is the potential yield and actual yield of a genotype in different environments. The aim of this research was to evaluate the genotype and environment interaction (GE) and detecting the sustainable genotypes in rapeseed. Also, this study aimed to determine genotypes with stable grain yield using parameters of equivalence (Wi), regression coefficient (bi), deviations mean square (S2di) and coefficient of variation (CV), (first model), and AMMI model analysis (second model). For this pupose, a field experiments was carried out with 14 winter rapeseed genotypes for two consecutive years in two different irrigation and rainfed. The expriment was performmed in a randomized complete block design with three replications per the environment. Combined analysis of variance showed that difference between the genotype-environment interaction was significant. positive correlation and significant parameters of Wi and S2di showed that both of these parameters can be used independently. According to the AMMI model, the genotypes Geronimo and ARC2 had the highest stability with a high average yield. These genotypes can be used in future breeding programs.

Keywords: Rapeseed, Stability, AMMI model, Biplot analysis

Introduction

Interpreting the results of the interaction between genotype and environment (GE) has been considered aa a challenge in trait studies. One of the problems in plant breeding is selecting genotypes in one environment and then using them in another environment (Happ et al., 2021). Breeders are trying to find genotypes with higher yield stability in different environments. These genotypes are used for breeding varieties for biotic and a biotic stress (Yohane et al., 2021). The interaction between genotype and environment leads to the differences between genotypes in other fields (Singh et al., 2020). In fact, this interaction delays the breeding programs and introducing the cultivar (Hajjarpoor et al., 2021). A multiplicative model is the principal component analysis that cannot describe the main effects of the addition effects. In general, their interaction with the leading results significantly reduces experiments power (Reckling et al., 2021).

The main effect of addition and multiplication is a multivariate statistical model (AMMI) used for experiments in several different environments (Islam et al., 2020). Several models have been

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introduced to determine other parameters and classification stability resulting from genotype and environment interaction. The most statistical model for measuring the strength of different products has been found to be Eberhart and Russell’s model (Reckling et al., 2021).

Stability measurements could be performed using the addition and multiplication principle effects model analysis (AMMI) or other methods (Balcha et al., 2020). One of the multivariate statistical methods evaluating the cumulative effects of environmental genotype and the multiplicative effects of genotype and environment is the method of principal additive effects and multiplicative interaction (Reckling et al., 2021). AMMI model analysis combines both ANOVA and PCA and makes a single analysis (Balcha et al., 2020). Plant breeders in breeding programs seek for genotypes that are compatible with a wide range of environments. Lin et al., 1986 identified four groups for sustainability statistics; Group A includes genotype variance in all environments: S^2x (lin et al., 1986) and coefficient of variation: CV (Francis and Kannenberg, 1978); Group B includes variance: $\delta^2 i$ (Shukla, 1972) and equivalence: Wi (Wricke, 1962); Group C have the regression coefficient: bi (Finlay and Wilkinson, 1963) and Group D comprises deviations mean square from the regression line: S^2di (Eberhart and Russell, 1966).

The current work aimed to use additive main effects and multiplicative interaction models to determine the best winter rape genotype in terms of grain yield stability.

Materials and Methods

Plant materials of this study consisted of 16 genotypes of winter oilseed rape. The experiments were carried out for two consecutive years in 2006/2007 and 2007/2008 in different irrigations (normal condition) and rainfeds (stress condition with one supplementary irrigation) in the research farm of the Campus of Agriculture and Natural Resources of the Razi University of Agriculture in Kermanshah, Iran, which offers a total of four environments. The experiment for each environment consisted of a randomized complete block design with three replications. Planting was done manually with four rows of 4-m long, the distance between the rows was 30 cm, and the distance between the pieces was 60 cm. The test site is located at 46℃ and 20΄ east longitude and 34℃ and 20΄ north longitude. The soil of the test site has a silty clay texture. Random factors (environments) and fixed factors (genotypes) were considered. Combined analysis of variance (by Bartlett's test) and comparison of mean (by Duncan's multiple range test) were performed using MSTAT-C and SPSS software.

Data for each plot and for each cultivar were collected separately. Stability assessment was performed using four parameters, namely Wricke's equivalence (wi), regression coefficient (bi), deviations mean square (s^2di), and CV. Interpretation of the results was performed using Haufe and Geidel (1978; according to Becker and Leon, 1988) models.

The correlation between the parameters was calculated. The AMMI model was employed to determine the effect of treatment, sites, and the interaction of treatment and sites. The sources of variability for genotype× environment effect were split through the analysis of the main components (interaction IPCA) (Gauch and Zobel, 1990). Analysis and interpretation of the results were based on the procedure of Zobel *et al*. (1988). The IRRISTAT program was used for analyzing the AMMI model.

Results and Discussion

Homogeneity of variance error was confirmed in four environments for grain yield and then combined analysis of variance was performed. The results of the combined analysis of variance (Table 1) showed a significant difference between genotypes (fix factor) and environment (random factor) in terms of grain yield. This results indicated the diversity in genotypes and diversity in different places. The interaction of genotype and environment (GEI) can be expressed through the difference between the phenotypic values and the amount of genotype and environment expected (Chavarría-Perez et al., 2020).

Table 1. Combined analysis of variance of grain yield in irrigated and rainfed conditions

Source of variation	Degree of freedom	Mean square
Treatments	13	0.810235**
Locations	3	0.629949**
Treatments × sites	39	0.358360**
Source of variation	Degree of freedom	Mean square
Trt × site reg	13	0.723544**
Deviation from regression	26	0.175769**
Total	55	

**: significant at the 1% level of probability; ns: non-significant

Grain yield expression, as a quantitatively important trait, is determined by the effect of genotype, environment, and genotype interaction (Eltaher et al., 2021). As a result, researchers have always tried to study genotypes' stability in a wide range of different environments. The data obtained from this research were critical and helpful for plant breeders. Determining the linear and nonlinear effects of the interaction between genotype and environment (GE), a significant difference was observed between environments, indicating the environment's genotypic response (Falcon et al., 2020). The regression coefficient results (Table 2) showed that the regression coefficient for genotypes 5, 9, 10, and 12 was more than one and the regression coefficient for genotypes 7, 8, and 14 was equal to one. The regression coefficient for genotypes 1, 2, 3, 4, 6, and 11 was less than one, indicating general adaptation to irrigated and rainfed conditions and specific adaptation to rainfed conditions (Amiri et al., 2020).

Table 2. Regression analysis in irrigated and rainfed conditions

Source of variance	Degree of freedom	Mean square
Year	1	1267905.990 **
Location	1	43315338.004**
YL	1	2017560.931**
R(LY)	8	389681.037**
Factor A	13	1322300.280**
YA	13	1114558.705**
LA	13	141888.479^{ns}
YLA	13	267021.417**
Error	104	80809.055
Total	167	

**: significant at the 1% level of probability

According to Eberhart and Russell (1966), a genotype with a single slope, low deviation from regression (S^2d), and high potential yield in different environments is called stable. Regression coefficients in this study ranged from 0.68 to 1.29. Genotypes Dante and SLM046, with low deviation from regression (S^2di) and regression coefficient (bi>1), had a desirable grain yield. Genotypes Sunday with low deviation from regression (S^2di) and regression coefficient (bi>1) had poor average yield. Genotypes Geronimo and ARC2, with low deviation from regression (S^2di), regression coefficient (bi~ 1), and average yield, were stable with relatively poor general adaptability for irrigated and rainfed conditions (Amiri et al., 2020), (Table 3).

Table 3. Stability of rapeseed seed yield

Genotype	Yield (kg/ha)	Wi	bi	CVi	S^2di
Geronimo	3474	23047.83	0.914	17.69	314113.7
Celecious	3609	410049.3	0.86	21.01	402656.3
Milena	2235	468545.9	0.685	21.69	293047.9
Sahra	2649	812831.2	0.928	25.94	58724.5
Sunday	3161	49340.51	1.14	26.16	489984.2
Zarfam	4276	659151.3	0.876	21.03	498050.2
Dante	4042	140375.6	1.03	19.23	435820.3
SLM-046	3665	23914.94	1.05	18.57	412044.5
Talaye	3213	425999.5	1.29	29.06	729927.8
Talent	2357	730609.8	1.28	34.84	817281.1
ARC2	3695	490724.8	0.819	21.23	399322.9
Opera	2794	672134.6	1.28	33.40	800025.2
ARC5	2264	480877.2	0.849	26.24	418539.9
Licord	4179	12140.95	1.01	29.02	780374.2

Stability assessment was performed using the four previously mentioned parameters (Wricke's equivalence (wi), regression coefficient (bi), deviations mean square (s2di), and CV). Based on these indicators, genotype ARC2 was selected.

The results of AMMI analysis of variance (Table 4) implied that the mean of squares due to treatments, locations, and treatments × sites interactions (GEI) was significant, suggesting a high diversity between genotypes (Popović et al., 2020).

Table 4. AMMI analysis in *Brassica napus*

Source of variation	Degree of freedom	Mean square
Treatments	13	0.810235^{**}
locations	3	0.629949^{**}
Treatments × sites	39	0.358360^{**}
Source of variation	Degree of freedom	Mean square
AMMI COMPONENT 1	15	0.679471^{**}
AMMI COMPONENT 2	13	0.255363^{**}
AMMI COMPONENT 3	11	6.48342^{ns}
Total	55	

**: significant at the 1% level of probability

The AMMI2 biplot explained 96% of the GE interaction (Figure 1); it is a practical and accurate interaction test. The results revealed that most genotypes and environments were scattered around with biplot. Environments A, B, and C were further away from the center of the biplot. The D environment was closer to center of the biplot. Genotype 8 for environment A, genotype 10 for environment B, genotype 11 for environment C, and genotype 5 for environment D with closer to center of the biplot; thus, they had specific adaptability in these environments. Genotype 8 had the most negative genotype × environment interaction with environment D. Genotype 9 had a negative interaction with environment A and specific adaptability to environment D was on the side opposite environment B.

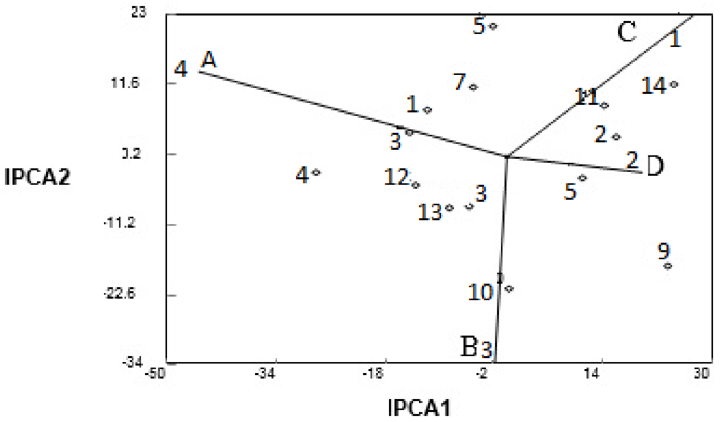

Figure 1. Biplot analysis for the AMMI2 model in *Brassica napus*

A strong and highly significant positive correlation was estimated between **the** regression coefficient with S^2di (0.785**) and Cvi (0.681**). The complete, positive, highly significant correlation between equivalence (Wi) and deviations mean square (S^2di) (0.644**) indicated that either of these two parameters could be used independently without affecting the accuracy of estimation (Table 5).

Table 5. Correlation coefficient of stability parameters in rapeseed

Stability parameters	bi	S^2di	Cvi	Wi
bi	1			
S^2di	0.785**	1		
Cvi	0.681**	0.891**	1	
Wi	0.032	0.644**	0.596*	1

** F test significant at level P<0.01; * F test significant at level P<0.05

Discussion

Due to the difference between the phenotype value and the expected genotype and environment quantity, the interaction between genotype and environment could be expressed (Mengistu et al., 2020). The amount of genetic diversity observed in the interaction of genotype and environment (GEI) varies from one environment to another; accordingly, in stronger and superior environments, this amount of diversity is more than that in weaker environments (Przystalski et al., 2008). Environmental factors play an important role in the expression of genes that control quantitative traits (Wang et al., 2020). This is why there are different phenotypic expressions in different places. The interaction between genotype and environment makes it difficult for breeders to select suitable genotypes since a suitable genotype for one location may not similarly function in different locations (Ahakpaz et al., 2020). By determining the linear and nonlinear effects of the interaction between genotype and environment (GE), a significant difference between environments indicates the environment's genotypic response (Falcon et al., 2020). According to Eberhart and Russell (1966), a genotype with a single slope, low deviation from regression (S^2d), and high potential yield in different environments is called stable.

Conclusion

Genotypes Dante and SLM046, with low deviation from regression (S^2di) and regression coefficient (bi>1), had a desirable grain yield. Genotypes Sunday, with low deviation from regression (S^2di) and regression coefficient (bi>1), had poor average yield. Genotypes Geronimo and ARC2, with low deviation from regression (S^2di), regression coefficient (bi~ 1), and average yield, were a stable genotype. The AMMI2 biplot explained 96% of the GE interaction, which is a practical and accurate interaction test. The results implied that most genotypes and environments were scattered around with biplot. Sites Environments A, B, and C were further away from the center of the biplot. Site D was closet to the center of the biplot. Genotype 8 for site A, genotype 10 for site B, genotype 11 for site C, and genotype 5 for site D with closer to the center of the biplot; thus, they have specific adaptability in these sites. Due to the positive and significant correlation between equivalent (Wi) and mean square deviation (S2di) (0.644**) parameters, these two could be used independently of each other without affecting the accuracy of evaluation and estimation.The treatment and sites main effects and treatment by sites interaction effect were significant for yieldseed rape cultivars studied in this study. Genotype Dante is recommended for further inclusion in the breeding program due to its desirable grain yield.

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Reference

Becker HC, Leon J. 1988. Stability analysis in plant breeding. Plant breeding, 101(1);1-23.

Crossa J, Gauch JR, Zobel HG. 1990. Additive main effects and multiplicative interaction analysis of two international maize cultivar trials. Crop science, 30(3);493-500.

Eberhart ST, Russell WA. 1966. Stability parameters for comparing varieties 1. Crop science, 6(1);36-40.

Finlay KW, Wilkinson GN. 1963. The analysis of adaptation in a plant-breeding programme. Australian journal of agricultural research, 14(6);742-754.

Francis TR, Kannenberg LW. 1978. Yield stability studies in short-season maize. I. A descriptive method for grouping genotypes. Canadian Journal of Plant Science, 58(4);1029-1034.

Lin CS, Binns MR, Lefkovitch LP. 1986. Stability analysis: where do we stand? 1. Crop science, 26(5);894-900.

Shukla GK. 1972. Some statistical aspects of partitioning genotype environmental components of variability. Heredity, 29(2);237-245.

Tuck G, Glendining MJ, Smith P, House JI, Wattenbach M. 2006. The potential distribution of bioenergy crops in Europe under present and future climate. Biomass and Bioenergy, 30(3);183-197.

Haufe W, Geidel H. 1978. To assess the yield security of varieties and breeding lines. i. definitions, stability parameters and their interpretation possibilities. Z plant breeding .

Ahakpaz F, Abdi H, Neyestani E, Hesami A, Mohammadi B, Mahmoudi KN, Abedi-Asl G, Noshabadi MRJ, Ahakpaz F, Alipour H. 2021. Genotype-by-environment interaction analysis for grain yield of barley genotypes under dryland conditions and the role of monthly rainfall. Agricultural Water Management, 245;106665.

Amiri SR, Deihimfard R, Eyni-Nargeseh H. 2020. Toward dormant seeding of rainfed chickpea as an adaptation strategy to sustain productivity in response to changing climate. Field Crops Research, 247;107674.

Balcha A. 2020. Additive main effects and multiplicative interaction and other stability analyses of Tef [Eragrostis tef (Zucc.) Trotter] grain yield. American Journal of Plant Sciences, 11(06);793.

Chavarría-Perez LM, Giordani W, Dias KOG, Costa ZP, Ribeiro CAM, Benedetti AR, Cauz-Santos LA, Pereira GS, Rosa JRBF, Garcia AAF, Vieira MLC. 2020. Improving yield and fruit quality traits in sweet passion fruit: Evidence for genotype by environment interaction and selection of promising genotypes. PloS one, 15(5);0232818.

Eltaher S, Baenziger PS, Belamkar V, Emara HA, Nower AA, Salem KF, Alqudah AM, Sallam A. 2021. GWAS revealed effect of genotype× environment interactions for grain yield of Nebraska winter wheat. BMC genomics, 22(1);1-14.

Falcon CM, Kaeppler SM, Spalding EP, Miller ND, Haase N, AlKhalifah N, Bohn M, Buckler ES, Campbell DA, Ciampitti I, Coffey L. 2020. Relative utility of agronomic, phenological, and morphological traits for assessing genotype-by-environment interaction in maize inbreds. Crop Science, 60(1);62-81.

Hajjarpoor A, Kholová J, Pasupuleti J, Soltani A, Burridge J, Degala SB, Gattu S, Murali TV, Garin V, Radhakrishnan T, Vadez V. 2021. Environmental characterization and yield gap analysis to tackle genotype-by-environment-by-management interactions and map region-specific agronomic and breeding targets in groundnut. Field Crops Research, 267;108160.

Happ MM, Graef GL, Wang H, Howard R, Posadas L, Hyten DL. 2021. Comparing a Mixed Model Approach to Traditional Stability Estimators for Mapping Genotype by Environment Interactions and Yield Stability in Soybean [Glycine max (L.) Merr.]. Frontiers in plant science, 12;542.

Islam SS, Anothai J, Nualsri C, Soonsuwon W. 2020. Analysis of genotype-environment interaction and yield stability of Thai upland rice (*'Oryza sativa'L.*) genotypes using AMMI model. Australian Journal of Crop Science, 14(2);362-370.

Mengistu SB, Mulder HA, Benzie JA, Khaw HL, Megens HJ, Trinh TQ, Komen H. 2020. Genotype by environment interaction between aerated and non-aerated ponds and the impact of aeration on genetic parameters in Nile tilapia (Oreochromis niloticus). Aquaculture, 529;735704.

Popović V, Ljubičić N, Kostić M, Radulović M, Blagojević D, Ugrenović V, Popović D, Ivošević B. 2020. Genotype× Environment Interaction for Wheat Yield Traits Suitable for Selection in Different Seed Priming Conditions. Plants, 9(12);1804.

Reckling M, Ahrends H, Chen TW, Eugster W, Hadasch S, Knapp S, Laidig F, Linstädter A, Macholdt J, Piepho HP, Schiffers K. 2021. Methods of yield stability analysis in long-term field experiments. A review. Agronomy for Sustainable Development, 41(2);1-28.

Singh B, Das A, Parihar AK, Bhagawati B, Singh D, Pathak KN, Dwivedi K, Das N, Keshari N, Midha RL, Kumar R. 2020. Delineation of Genotype-by-Environment interactions for identification and validation of resistant genotypes in mungbean to root-knot nematode (Meloidogyne incognita) using GGE biplot. Scientific reports, 10(1);1-14.

Wang Y, Bo K, Gu X, Pan J, Li Y, Chen J, Wen , Ren Z, Ren H, Chen X, Grumet R. 2020. Molecularly tagged genes and quantitative trait loci in cucumber with recommendations for QTL nomenclature. Horticulture research, 7(1);1-20.

Yohane EN, Shimelis H, Laing M, Mathew I, Shayanowako A. 2021. Genotype-by-environment interaction and stability analyses of grain yield in pigeonpea [Cajanus cajan (L.) Millspaugh]. Acta Agriculturae Scandinavica, Section B-Soil & Plant Science, pp.1-11.