

MULTIVARIATE ANALYSIS FOR ADAPTABILITY AND YIELD STABILITY OF RAPESEED (*Brassica napus* L.) STRAINS IN DIFFERENT AGRO-CLIMATIC ZONES

Tahira BIBI¹, Hafiz Saad Bin MUSTAFA^{1*}, Tariq MAHMOOD¹, Amir HAMEED²
and Qurban ALI^{3,4}

¹Directorate of Oilseeds, Ayub Agricultural Research Institute, Faisalabad, Pakistan

²Statistical Section, Ayub Agricultural Research Institute, Faisalabad, Pakistan

³Center of Excellence in Molecular Biology, University of the Punjab, Lahore, Pakistan

⁴Institute of Molecular Biology and Biotechnology, University of Lahore, Lahore, Pakistan

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Plant breeders always look for high yielding genotypes based on both genotype and $G \times E$ (interaction of genotype with environment) for stability and adaptability in diversified environmental conditions. This present study consists of eight *Brassica napus* L. strains using RCBD design with three replications and conducted at eight locations in Punjab province, Pakistan to determine general and specific adaptability in 2014-2015. Additive main effects and multiplicative interactions (AMMI) study showed that the environments (86.65%) have more influence to treatment sum of squares as compare to the interaction of genotype with environment (9.4%) and genotypes (2.65%) respectively, indicating the presence of adequate genetic variation for useful selection to identify stable genotypes. $G \times E$ interaction was further partitioned by principal component analysis (PCA). The first four multiplicative axis terms (IPCA1, IPCA2, IPCA3 and IPCA4) give detailed 54.0%, 28.0%, 9.9% and 5.6% of GEI sum of squares (SS), respectively. The AMMI method was used to recognize suitable genotype / genotypes to specific locations / environments. The results showed that genotypes RBN-08004, RBN-04021 and 11-CBN 006 were more stable with the lowest interaction and have general adaptability with yield near about their mean yield. Genotype RBN-08004 has more than average yield, IPCA value closer to zero (1.8), genotype selection index (GSI) is 4 and least AMMI stability value (ASV) of 3.6 therefore considered the most stable. According to AMMI analysis, KN-253, KN-256 and RBN-08004 (adaptive

Corresponding authors: Hafiz Saad Bin Mustafa, Directorate of Oilseeds, Ayub Agricultural Research Institute, Faisalabad, Pakistan, Email: saadpbg@gmail.com

group 1) exhibited specific adaptability for Bhakar and Khanpur with yield greater than mean and positive interaction. Genotype RBN-04047 (adaptive group 2) which has yield lesser than mean yield and positive interaction showed specific adaptability for Chakwal and Karore. It was observed that stability evaluation through AMMI analysis may be used for selection of genotypes from experiments performed under different environmental conditions.

Keywords: AMMI, brassica, GE interaction, stability analysis, seed yield

INTRODUCTION

The complex genotype \times environment interaction (GEI) influences the expression of yield traits. The main objective of the breeding programs is to find stable genotypes which have higher seed yield through their evaluation under different environmental conditions. The stability of genotypes can be estimated by using AMMI analysis (GAUCH and ZOBEL, 1996), or using other methods (AGUIRREZÁBAL *et al.*, 2002). ANOVA and PCA both can be combined in AMMI analysis (CROSSA, 1990). Stability of genotypes and their adaptability to environment can be assessed through biplot where the genotypes scattered according to their principal component values (DE VITA *et al.*, 2010). It is especially useful in making genotype recommendations (ZOBEL *et al.*, 1988), and it provides selection criteria for further genetic improvements in a specific area (SUDARIĆ *et al.*, 2003; MIJIĆ *et al.*, 2007; MARJANOVIĆ-JEROMELA *et al.*, 2011). However, high yield is habitually related with decline in yield stability (CALDERINI and SLAFER, 1999; PADI, 2004). Yield is a quantitative character (influence of many genes). Multi-locational yield trials are necessary to identify the most stable genotypes (AGUIRREZÁBAL *et al.*, 2002) because environment plays a significant role in the variation of their yield (KANG, 1993). These fluctuations are called as G \times E interaction (GEI). GEI influences the breeding progress because it explains stability of a genotype in different environments and the selection of superior genotypes through their interaction with environment (EBDON and GAUCH, 2002). Although, GEI reduces correlation between phenotypic and genotypic values which leads to preconception in the heritability estimation and forecast of genetic advance (COMSTOCK and MOLL, 1963; ALGHAMDI, 2004).

The aims of this research were;

- (i) Interpretation of genotype and environment interaction of 8 *Brassica napus* genotypes over eight locations.
- (ii) Observe fluctuations in yield performances across environments through biplot.

MATERIALS AND METHODS

In order to identify stable and high performance genotypes of *Brassica napus* (Table 1) Micro Yield Trial was carried out in randomized complete block design (RCBD) with three replications during growing season 2014-2015 at eight different agro-ecological environments (E1 to E8) in Punjab, Pakistan. Each plot consisted of four rows with 5 meter in length and 45 cm row to row distance was maintained. All recommended agronomical & cultural practices were done during whole growing period. Data for seed yield were recorded from each plot. At harvest seed yield was determined for each genotype at all locations.

*Biometrical genetic analysis**AMMI model*

GEI can be evaluated through the AMMI analysis. The AMMI equation is:

$$y_{ger} = \mu + \delta_g + \beta_e + \sum \lambda_n \gamma_{gn} \delta_{en} + P_{ge} + \varepsilon_{ger}$$

Where y_{ger} represents the seed yield of genotype (G) at each environment (E) for replicate (r), μ is the sum of mean yield, δ_g is the main effect of genotype or the genotype (G) mean deviation, β_e is the main effect of environment or the environment (E) mean deviation, $\sum \lambda_n \gamma_{gn} \delta_{en}$ is the singular value for IPCA axis N (N is the number of remain PCA axis in AMMI model: γ_{gn} and P_{ge} represents the genotype (G) and environment eigen vector value for IPCA axis N, respectively. ε_{ger} is the residual or noise and is the error (if the test has repetition)). It should be mentioned that eigen values are without unit. But the single value of eigen vector has a performance unit (GAUCH, 1992). Furthermore, AMMI stability value (ASV) was used to rank genotypes according to their stability as formula suggested by Purchase (PURCHASE, 1997). Based on the rank of mean yield of genotypes and rank of ASV a genotype selection index (GSI) was calculated for each genotype.

RESULTS AND DISCUSSION

The primary interaction principal component axis (IPCA 1) expressed maximum interaction (54%) of the total differences in the GEI SS and 13 of the interaction degrees of freedom (df). The second and third interaction principal component axis (IPCA 2 and IPCA 3) gave 28% and 9.9% of sum of squares (SS) of this GEI. The first four interaction principal component axes (IPCA 1-4) explained about 97.5% of total variation, leaving 2.5% of the variation in the GE interaction in the residual. Actually the residual accounts for only 0.057 % of total SS. AMMI analysis revealed that mean squares for the IPCA 1 and IPCA 2 were significant at 1% probability level and both contributed to 82% of the total GEI. It has also been reported that the first two principal component axes was the best predictive mode (ZOBEL *et al.*, 1988; YAN and RAJCAN, 2002; AFZAL *et al.*, 2016; AHMAD *et al.*, 2016) while another researcher has recommended the first four IPCAs to explain total variation (SIVAPALAN *et al.*, 2000). Variation in genotypes and range of environmental conditions will have an effect on the degree of complication (CROSSA, 1990; CROSSA *et al.*, 1990). Thus, results indicate that the AMMI analysis give sufficient details of the tested trial. So the interaction of the 8 brassica genotypes with eight environments was best predicted by the first two principal components (IPCA).

The IPCA scores (either positive or negative) of genotypes in the AMMI analysis indicate their stability or adaptability over environments (GAUCH and ZOBEL, 1996; PURCHASE, 1997; ALBERTS, 2004). The larger the IPCA scores indicate the specific adaptability of a genotype to certain environments. The genotypes having small IPCA scores (near to zero) showed the more stable or general adaptation of that genotype is all the environments. Distances from the origin (pivot) indicate the magnitude of interaction that displayed by either genotypes over environments or environments over genotypes (THANGAVEL *et al.*, 2011; MAHMOOD *et al.*, 2016). For example, the genotypes G1, G2, G5 and G7 and environments E2, E4, E6 and E8 expressed larger interaction, whereas the environments E1, E3, E5 and E7 showed low interaction.

Table 1. Seed Yield (kg/ha) of eight entries of *B. napus* in Micro Yield Trial conducted over 8 locations in Punjab, 2013-2014

Rank	Line/Variety	E 1 FSD	E 2 B/pur	E 3 BHAKAR	E 4 K/PUR	E 5 F/JG	E 6 CHKWAL	E 7 KARORE	E 8 PIPLAN	Mean
G1	KN-253	1531	3748	2019	2392	1061	2456	1586	2543	2167
G2	KN-256	2123	3459	2387	2292	357	1897	1665	2852	2129
G3	RBN-04047	1689	2985	2331	2160	773	1994	1452	2728	2014
G4	RBN-08004	1610	2848	1934	2045	834	2073	1622	2753	1965
G5	Faisal Canola	2040	2696	2108	2114	766	2139	1322	2284	1934
G6	11CBN006	1383	2319	1716	1944	1127	2383	1234	3062	1896
G7	RBN-08003	1501	2444	2411	1844	504	2211	1164	2840	1865
G8	RBN-04021	1817	2744	2181	2006	460	1953	1300	2259	1840
	LSD (5%)	86	162	146	177	182	165	35	78	71

Figure 1 interpreted that if genotypes have small IPCA score (close to zero), it indicates low interaction and stable. If genotype and environment have the same sign on the IPCA axis, it represents the positive interaction; if different, it indicated that their interaction is negative. Biplot of Figure 1 is divided into 4 sections. Upper and lower left (section 1 & 4) showed low yielding environments and upper and lower right (section 2 & 3) showed high yielding environments. Figure 1 put in the picture that the points for environment are more scattered than the point for genotypes showing that environments plays more role in inconsistency than that due to genotypes differences (Table 2). Genotypes which were at right hand side of grand mean value with IPCA scores close to zero showed high mean performance, low interaction, and general adaptation to all environments. However, the genotype with high average performance and larger IPCA score are considered as specific adaptability to the environments.

Figure 1 showed that G3 exhibited specific adaptability for E6 and E7 with seed yield less than mean and their interaction (G x E) is positive. Genotypes G1, G2, G4 exposed specific adaptation for E3, E4 with high seed yield more than mean yield and positive interaction (GEI). The genotype G6 and G8 with IPCA score close to zero showed stability and general adaptability with seed yield close to mean yield and low interaction. PURCHASE (1997) also reported that the genotypes close to pivot considered more stable. The genotypes G5, G7 were identified for specific adaptation for environment E1, E2 and E8 with positive interaction. AMMI model Analysis was also used in different crops for stability studies as in soybean (ZOBEL *et al.*, 1988), maize and wheat (CROSSA *et al.*, 1990), sorghum (ZAVALA-GARCIA *et al.*, 1992), barley (ROMAGOSA *et al.*, 2013) and chickpea (ZALI *et al.* 2011).

The environment E3 and E5 had same main effect but differed in interaction with genotypes. Therefore, variety recommendations in such environments would likely to be quite unpredictable. Further the environment E4 and E2 showed maximum deviation from the mean and larger interaction, hence most suitable only for those genotypes which were specifically adapted. Distance from the origin either for genotype or environment indicate interaction. When genotypes and environments be positioned into the same sector, indicating that they interact positively and vice versa (OSIRU *et al.*, 2009). A genotype which shows high positive association in an environment would be best representative of that specific environment. So AMMI analysis assists to find genotypes best suitable for specific environment.

The distribution of genotypes (G4 and G8) in the biplot revealed their minimum interaction with environments as they are close to the origin while other six genotypes spread away from the origin showing that these genotypes were more influenced by environment. The genotypes G5 and G8 had positive correlation with environments E5 and E8, exhibited specific adaptability in these environments. G6 exhibited positive association with environment E1 and E2. Genotypes G1 indicated more genotypic expression favored by environments E3, E4 and E7. G3 showed positive association with environments E6 and adapted specifically to it.

Table 2. Individual (separate) analysis of variance (RCB design) for a trial with 8 genotypes and three replications (by environment)

SOV	DF	Sum of Squares							
		E1	E2	E3	4	E5	E6	E7	E8
		FSD	B/pur	BHAKAR	K/PUR	F/JG	CHKWAL	KARORE	PIPLAN
Blocks	2	94540	20233	1406	22225	677	13408	813	132482
Genotypes	7	306373	1320798	801641	4017200	764349	661929	761460	561240
Error	14	124937	151219	142344	120575	28073	34058	5646	97044
Total	23	525850	1492250	945391	4160000	793099	709396	767919	790766
F ratio (Gen)		4.9	17.5	11.3	66.6	54.5	38.9	269.8	11.6
P-value (Gen)		0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CV (%)		7.4	15.7	4.4	3.6	2.5	4.3	1.4	5.8

Table 3. Combined analysis of variance (ANOVA) according to the AMMI model and Gollob's test of interaction PCs

Source	DF	SS	MS	P-value	G×E	explained (%)
Total	191	76299900	-			
Environment(E)	7	66115231	9445033.0	0.000		
Reps within E	16	285785	17861.6	0.001		
Genotype(G)	7	2023339	289048.4	0.078		
G×E	49	7171651	146360.2	0.000		
IPCA1	13	3874200	298015.4	0.003	54.0	
IPCA2	11	2008359	182578.1	0.004	28.0	
IPCA3	9	712743	79193.7	0.081	9.9	
IPCA4	7	401133	57304.7	0.067	5.6	
IPCA residual	9	175212.3	19468.0			
Residual	112	703895	6284.8			

IPCA=Interaction Principal Component Axis

The angle between the vectors of genotype and environment tells either the interaction is positive (for acute angles) or negative (for obtuse angle). Genotypes G8 and G5 showed acute (smaller) angle with E5, E6 and E8 vectors. Genotypes G7 showed acute angle with environments E1, E2 and E5 while obtuse angle (larger) with environments E4, E3, E7, E6 and E8. G1 revealed acute angle and positive correlation with E4, E3 and E7 vectors whereas obtuse angle and negative association with E1, E2, E5 and E8 vectors. The entries G2 and G3 displayed acute angle with the vectors of environments E6, E3, E4, E7 and E8 while showed negative interaction and obtuse angle with environments E5, E1 and E2. As the length of the vectors of

genotypes G4, G6, G3 and G8 is shorter than the other ones hence they are more adapted to their specified environments, while G1, G7, G5 and G2 with longer vectors indicated more deviation from their specified environments. Genotype or environment on the right side of the origin has higher yields than those on the left hand side. Regardless of IPCA 1 scores direction, environments on the right hand side of the midpoint of the main effect axis (E3, E4, E6 and E7) were seemed to be favorable environments for seed yield among the tested Brassica genotypes.

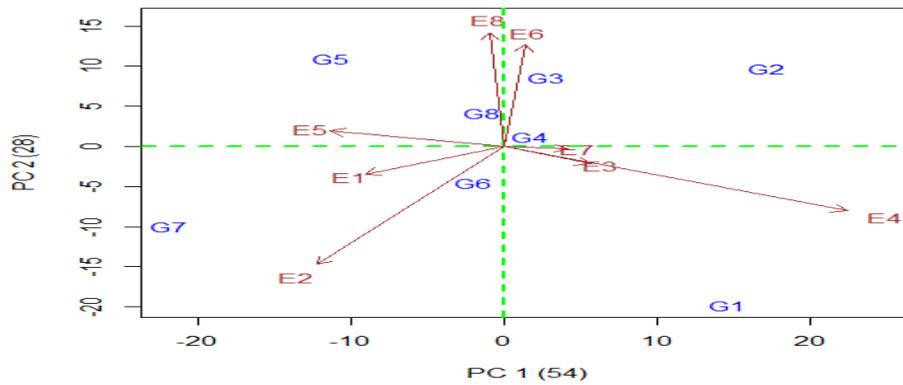


Figure 1. Bi-plot of interaction principal components analysis (PCA) axis-1 versus axis-2 for seed yield (kgha^{-1}) for 8 brassica genotypes tested in 8 environments.

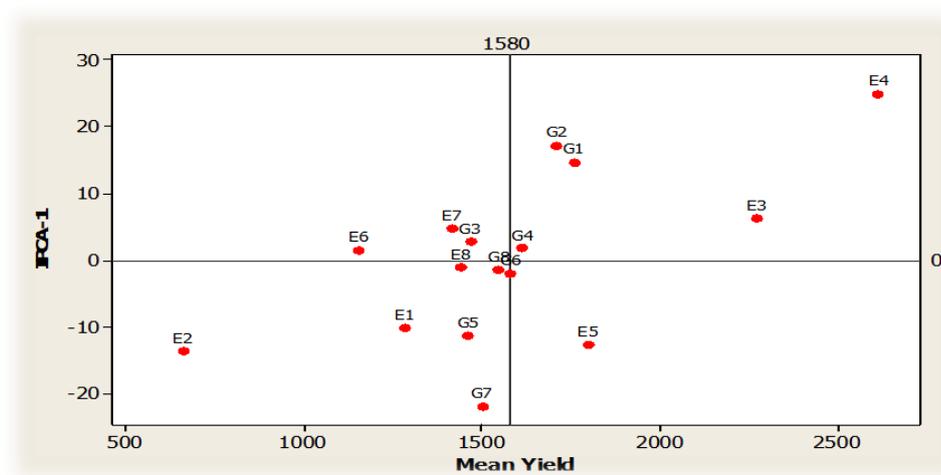


Figure 2. Biplot of interaction principal components analysis (PCA) axis-1 versus mean yield (kgha^{-1}) for 8 brassica genotypes tested in 8 environments. The vertical line represents the grand mean of the experiment while the horizontal line is for PCA axis-1=0.

Table 4. AMMI Stability Value (ASV) and Genotype Selection Index (GSI) for 8 oilseed genotypes

Name	Line/Variety	Mean Yield	IPCA-1	IPCA-2	ASV	Rank (ASV)	Rank(Mean)	GSI
G1	KN-253	1760.5	14.68	-19.86	34.6	6	1	7
G2	KN-256	1710.4	17.27	9.69	34.7	7	2	9
G3	RBN-04047	1468.3	2.82	8.52	10.1	4	7	11
G4	RBN-08004	1615.0	1.80	1.13	3.6	1	3	4
G5	Faisal Canola	1461.6	-11.29	10.87	24.3	5	8	13
G6	11CBN006	1579.9	-1.98	-4.58	6.0	3	4	7
G7	RBN-08003	1502.9	-21.86	-9.96	43.3	8	6	14
G8	RBN-04021	1547.3	-1.44	4.19	5.0	2	5	7

AMMI Stability Value (ASV) and Genotype Selection Index (GSI):

It is not necessary that the most stable genotypes give the best yield performance; hence there is a need for an approach which incorporates both average seed yield and stability in one. So we consider ASV which takes into account both IPCA 1 and IPCA 2 to justify most of the differences for GEI. Therefore the rank of ASV and mean yield are incorporated in a single selection index namely genotype selection index (GSI).

The analysis using AMMI stability value indicated that RBN-08004 (3.6), RBN-04021 (5), 11CBN006 (6) and RBN-04047 (10.1) were among genotypes with lower ASV values, in order of importance. This revealed that these genotypes are relatively more stable than others. However, RBN-08003 (43.3), KN-256 (34.7) and KN-253 (34.6) were classified under the least stable genotypes (Table 3). Stability is not the only parameter for selection of high yielding genotypes because it is not necessarily that the most stable genotypes give maximum yield. As such, the genotype selection index revealed that RBN-08004 is the best and top-ranking genotypes integrating both stability and grain yield performance parameters followed by KN-253, 11CBN006 and RBN-04021 (Table 3). This result is in agreement with that of IPCA biplot (Fig. 1). Therefore, all the above four genotypes could be potential candidates for variety verification as revealed using AMMI model and as observed in the actual field condition (FARSHADFAR, 2008).

Genotype \times environment interactions (GEI) are of leading concern in breeding programmes because it helps to understand the superiority of a genotype in diversified environments and facilitate the selection of improved genotypes (MAGARI and KANG, 1993; EBDON and GAUCH, 2002; MUNIR *et al.*, 2016). A genotype which performs well across the range of environments is considered as commercially successful. Moreover, the stability refers to its consistent performance across environments and is affected by the presence of GEI (HABEKOTTÉ, 1997; NTAWURUHUNGA *et al.*, 2001; SIDLAUSKAS and BERNOTAS, 2003; AHMAD and TAHIR, 2017). The GE interactions decrease the association between phenotypic and genotypic values because environment plays a significant role in their genotypic performance (SHARMA *et al.*, 1987; ALGHAMDI, 2004; ALI *et al.*, 2016). According to the breeder's point of view, location is fixed factor, and yield consistency over time is the only related factor of yield stability (ANNICCHIARICO, 2002). It is always endeavored to evaluate the stability of each genotype in diversified environments.

CONCLUSION

The results of studies concluded that additive main effects and multiplicative interactions (AMMI) analysis showed that the environments (86.65%) had more influence to

treatment sum of squares as compare to the interaction of genotype with environment (9.4%) and genotypes (2.65%) respectively. It indicated the presence of adequate genetic variation for useful selection to identify stable genotypes and portion of environment interaction has more influence on overall yield performance of these genotypes. The first four multiplicative axis terms (IPCA1, IPCA2, IPCA3 and IPCA4) gave detailed 54.0%, 28.0%, 9.9% and 5.6% of GEI sum of squares (SS), respectively, while IPCA1 represented more than 50% of the total variation. The results further showed that genotypes RBN-08004, RBN-04021 and 11-CBN006 were more stable with the lowest interaction and have general adaptability with yield near about their mean yield. Genotype RBN-08004 has more than average yield, IPCA value closer to zero (1.8), genotype selection index (GSI) is 4 and least AMMI stability value (ASV) of 3.6 therefore considered the most stable. According to AMMI analysis, KN-253, KN-256 and RBN-08004 (adaptive group 1) exhibited specific adaptability for Bhakar and Khanpur with yield greater than mean and positive interaction. Genotype RBN-04047 (adaptive group 2) which has yield less than mean yield and positive interaction showed specific adaptability for Chakwal and Karore.

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MULTIVARIJACIJSKA ANALIZA ZA ADAPTABILNOST I STABILNOST PRINOSA SOJEVA ULJANE REPICE (*Brassica napus* L.) U RAZLIČITIM AGRO-KLIMATSKIM ZONAMA

Tahira BIBI¹, Hafiz Saad Bin MUSTAFA^{1*}, Tariq MAHMOOD¹, Amir HAMEED²
i Qurban ALI^{3,4}

¹Direktorat za uljanu repicu, Ayub, Faisalabad, Pakistan

²Statistička Sekcija, Ayub Poljoprivredni istraživački institut, Faisalabad, Pakistan

³Centar izvrsnosti za molekularnu biologiju, Univerzitet u Pendžabu, Lahor, Pakistan

⁴Institut za molekularnu biologiju i biotehnologiju, Univerzitet u Lahoru, Lahor, Pakistan

SAŽETAK

Oplemenjivači biljaka uvek traže genotipove visokog prinosa na bazi genotipa i $G \times E$ (interakcija genotipa sa okolinom) za stabilnost i adaptabilnost u raznovrsnim uslovima životne sredine. U ovom radu je proučavano osam *Brassica napus* L. genotipova, korišćenjem RCBD dizajna sa tri ponavljanja, na osam lokacija u provinciji Pendžab, Pakistan, u 2014-2015, kako bi se utvrdila opšta i specifična adaptabilnost. Istraživanje glavnih efekata i multiplikativnih interakcija (AMMI) pokazalo je da okruženje (86,65%) ima veći uticaj na sumu kvadrata tretmana u odnosu na interakciju genotipa sa okolinom (9,4%) i genotipove (2,65%), što ukazuje na prisustvo adekvatne genetičke varijacije za odabir stabilnih genotipova. $G \times E$ interakcija je dalje podeljena analizom glavnih komponenata (PCA). Prve četiri ose (IPCA1, IPCA2, IPCA3 i IPCA4) daju detaljnije 54.0%, 28.0%, 9.9% i 5.6% sumu kvadrata (SS) za GE . AMMI metod je korišćen za prepoznavanje odgovarajućih genotipova / genotipova na određenim lokacijama / spoljašnjim sredinama. Rezultati pokazuju da su genotipovi RBN-08004, RBN-04021 i 11-CBN 006 stabilniji sa najnižim interakcijama i imaju opštu adaptabilnost sa prinosom blizu njihovog prosečnog prinosa. Genotip RBN-08004 imao je viši prinos od prosečnog, IPCA vrednost bliže nuli (1.8), selekcionni indeks genotipa (GSI) je 4, a najmanje AMMI vrednost stabilnosti (ASV) od 3.6 smatra se najstabilnijom. Prema AMMI analizi, KN-253, KN-256 i RBN-08004 (adaptivna grupa 1) su pokazali specifičnu adaptabilnost za Bhakar i Khanpur sa prinosom većim od prosečnog i pozitivnom interakcijom. Genotip RBN-04047 (adaptivna grupa 2) koji ima prinos manji od prosečnog i pozitivnu interakciju pokazao je specifičnu adaptabilnost za Chakval i Karore. Uočeno je da se procena stabilnosti pomoću AMMI analize može koristiti za selekciju genotipova iz eksperimenata koji su izvedeni u različitim uslovima spoljašnje sredine.

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