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COMPARISON OF AMMI, PARAMETRIC AND NON-PARAMETRIC MODELS IN IDENTIFYING HIGH-YIELDING AND STABLE OILSEED RAPE GENOTYPES

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ABSTRACT

One of the complex issue in the way of releasing new high-yielding and stable oilseed rape cultivars is genotype by environment interaction (GEI) which reduce selection efficiency. In the current study, parametric and non-parametric statistics as well as the AMMI model have been compared to identify the best stability models to clarify GEI complexity. The experiment has been conducted in the warm regions of Iran including; Gorgan, Sari, Zabol, and Hajiabad during two cropping seasons (2016-2017 and 2017-2018) for 16 genotypes in a randomized complete block design with three replications. The AMMI analysis of variance on grain yield showed the significant effects of genotype, environment, and the interaction effects of GEI on yield. Based on the AMMI ANOVA, the major contribution of GEI was captured by the first and second interaction principal component axes (IPCA1 and IPCA2) which explained 34.29% and 29.81% of GEI sum of the square, respectively. Additionally, Different parametric and non-parametric stability methods including; bi, S^2_{di}, CV_i, W^2_i, σ^2_i, P_i, $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $S_i^{(6)}$, $Npi^{(1)}$, $Npi^{(2)}$, $Npi^{(3)}$, $Npi^{(4)}$, KR and TOP have also investigated. Based on AMMI, parametric, and non-parametric stability statistics, genotypes G2 (SRL-95-7) and G9 (SRL-95-16) were selected as the stable and high-yielding genotypes. Likewise, Principal component analysis based on rank correlation matrix enabled us to distinguish high-yielding genotypes to stable (high-yielding genotypes in various environments) and unstable (high-yielding genotypes in low-yielding environments) ones. Furthermore, a significant Spearman correlation was observed between yield mean and GSI, P_i, $S_i^{(3)}$, $S_i^{(6)}$, $Npi^{(3)}$, $Npi^{(4)}$, and KR. Therefore, different efficient strategies were identified in this study and since we looked up high-yielding and stable genotypes, G2 (SRL-95-7) and G9 (SRL-95-16) were finally selected.

Keywords: AMMI, *Brassica napus*, Genotype by environment interaction (GEI), Principal component analysis, Stability analysis

INTRODUCTION

Brassica species from the Brassicaceae family have been widely used for thousands of years to produce oil (Warwick et al., 2006, Wu et al., 2018). According to the FAO report, oilseed rape (*Brassica napus* L.; 2n = 38) is considered as the second oilseeds crop after soybean, which is cultivated in 44130191 hectares of the world (FAO, 2018). Iran is one of the major producers of oilseed rape in the middle east ranked 27th in oilseed rape cultivation in the world (FAO 2018). However, oilseed rape cultivation is facing environmental stresses such as drought and high temperatures in the warm regions of Iran. Climate change has increased environmental stresses, including heat and drought stress, which affected oilseed rape production (Lobell and Gourdji , 2012). Oilseed rape crop is adapted to the areas with high rainfall (Resketo and Szabo, 1992, Richards, 1978). But rainfall has decreased over the past four decades in the warm regions of Iran (Tabari et al., 2012). Therefore, the identification of adaptable cultivars for the warm regions would be essential in oilseed rape breeding programs.

Genotypes exhibit very different performances in the different environments, known as genotype by environment interactions (GEI). Therefore, it is necessary to evaluate the GEI to identify superior genotypes. The performance of each genotype is affected by environment, genotype, and their interaction effects (Yan et al., 2007). Several multi environmental trials have been conducted in various crops to clarify the GEI. Recently, oilseed rape genotypes were evaluated in multiple environments to identify high-yielding genotypes with the highest stability (Agahi et al., 2020). The GEI weakens the relationship between genotype and environment and thus reduces the selection efficiency (Getahun, 2017). The greater the amount of GEI, the less the correlation between genotype and environments could be expected which causes to reduce selection efficiency (Brandiej and Meverty, 1994). It has been reported that GEI is one of the complex issues in plant breeding programs to produce high-yielding and stable genotypes (Gauch Jr, 2006). Determining the GEI helps to evaluate and select high-yielding and sustainable genotypes accurately (Roy, 2000).

The GEI cannot be explained independently by genotype or environment. Therefore, several statistical methods, including parametric and non-parametric methods, have been developed to interpret the GEI (Yan et al., 2007). Among the parametric methods, several statistical models like Additive main effects and multiplicative interaction (AMMI) (Kempton, 1984; Zobel et al., 1988), regression coefficients (bi) (Eberhart and Russell, 1966), coefficient of variability (CV_i) (Francis and Kannenberg, 1978), Wrike's equivalence (W^2_i) (Wricke, 1962), Shukla's stability variance (σ^2_i) (Shukla, 1972) and superiority index (P_i) are widely used by breeders to determine the compatibility and stability of lines. The AMMI model is a combined analysis of variance for the main effects of genotype and environment and principal component analysis (PCA) which multiplicative parameters in one analysis (Zobel et al., 1988). AMMI method used as a popular statistical method by oilseed rape breeders to identify high-yielding and stable genotypes by clarifing GEI in multi environmental trials (Marjanović-Jeromela et al., 2011; Nowosad et al., 2017; Zali et al., 2016).

The purpose of this experiment is to investigate the efficiency of AMMI, parametric and non-parametric statistical models among new promising spring oilseed rape pure lines to identify high-yielding and stable genotypes for the warm regions of Iran.

In the present study 16 promising oilseed rape genotypes were investigated based on multi environmental trial experiments to compare various stability statistical models including AMMI, parametric and non-parametric in addition to their efficiency in detection high-yielding and stable oilseed rape genotypes for the warm regions of Iran.

MATERIALS AND METHODS

Location and experimental design

The compatibility and stability of the spring oilseed rape grain yield genotypes which were included nine promising lines along with five open-pollinated and two hybrid cultivars were evaluated in this study (Table 1). The multi environmental trial has been conducted in the north (Gorgan, Sari) and south (Zabol and Hajiabad) warm regions of Iran during two cropping seasons (2016-2017 and 2017-2018) in a randomized complete block design (RCBD) with three replications (Table 2). Each plot consisted of four rows with five meters long and 30 cm intervals. The amount of seed consumption was 6 kg/ha which was sown according to the instructions on the suitable dates in each region. At the time of physiological ripening, each cultivar was harvested to calculate grain yield from two midline lines by removing half a meter from the beginning and end of each line.

Table 1. Description of spring oilseed rape genotypes used in this experiment

Genotypes' code	Genotypes' name	Type	Origin
G1	SRL-95-2	Open-pollinated	Iran
G2	SRL-95-7	Open-pollinated	Iran
G3	SRL-95-8	Open-pollinated	Iran
G4	SRL-95-9	Open-pollinated	Iran
G5	SRL-95-11	Open-pollinated	Iran
G6	SRL-95-12	Open-pollinated	Iran
G7	SRL-95-13	Open-pollinated	Iran
G8	SRL-95-15	Open-pollinated	Iran
G9	SRL-95-16	Open-pollinated	Iran
G10	Zafar(check)	Open-pollinated	Iran
G11	Dalgan(check)	Open-pollinated	Iran
G12	OG-AL(check)	Open-pollinated	Iran
G13	RGS003(check)	Open-pollinated	Germany
G16	Long Pod(check)	Open-pollinated	Iran
G14	Hyola 401(check)	Hybrid	Canada
G15	Hyola 50(check)	Hybrid	Canada

ANOVA and stability methods

Combined ANOVA has been conducted based on RCBD to check the significance of the source of variations including genotype, environment, and GEI. To check the significance of partitioned components of genotype by environment interaction (IPCAs) the AMMI ANOVA has also been conducted. To interpret the GEI, the Additive main effects and multiplicative interaction (AMMI) (Kempton, 1984; Zobel, et al., 1988) was utilized. Additionally, parametric stability analysis including; regression coefficients (bi) (Eberhart and Russell, 1966), regression deviation (S^2_{di}) (Eberhart and Russell, 1966), coefficient of variability (CV_i) (Francis and Kannenberg, 1978), Wrike's equivalence (W^2_i) (Wricke, 1962), Shukla's stability variance (σ^2_i) (Shukla, 1972), superiority index (P_i) (Lin and Binns, 1988),

Table 2. Geographical, climate and soil data of the eight tested environments

Code	Location	Cropping season	Longitude (E)	Latitude (N)	Altitude (m)	Average temperature (ºC)	Accumulated rainfall (mm)	Soil texture	Soil PH	Soil Ec (ds/m)	Soil O.C (%)	Mean yield (kg ha^{-1})
Sari1	Sari	2016-2017	53º 13′	36º 46′	15	15.1	560	Loamy	7.8	0.64	1.28	3077
Sari2	Sari	2017-2018	53º 13′	36º 46′	15	16.5	490	Loamy	7.6	0.61	1.32	2785
Gorgan1	Gorgan	2016-2017	54º 24′	36º 53′	5	15.2	590.5	Silty-Clay-Loam	7.27	1.35	1.40	2826
Gorgan2	Gorgan	2017-2018	54º 24′	36º 53′	5	15.6	508.3	Silty-Clay-Loam	7.30	1.31	1.35	2793
Zabol1	Zabol	2016-2017	61º 40′	30º 54′	492	16.8	58.2	Sandy-Loam	8.2	3	0.34	3054
Zabol2	Zabol	2017-2018	61º 40′	30º 54′	492	17.2	45.8	Sandy-Loam	8	3.4	0.30	2660
Hajiabad1	Hajiabad	2016-2017	55º 52′	28º 18′	920	17.1	210	Sandy-Loam	8.1	2.4	0.47	3293
Hajiabad2	Hajiabad	2017-2018	55º 52′	28º 18′	920	16.8	243	Sandy-Loam	8	2.2	0.53	3305

Coefficients of determination (R^2) (Pinthus, 1973), environmental variance (S^2x_i) (Lin et al., 1986) and also non-parametric stability analysis including Huehn non-parametric statistics (Huehn, 1990a; Huehn, 1990b), Thennarasu's statistics (Tiiennarasu, 1995), Kang's Method (KR) (Kang, 2004), Top index (Fox et al., 1990) and Tai's environmental effects (α) and deviation from the linear regression (λ) (Tai, 1971) were calculated to interpret the stability of the genotypes across different environments.

Statistical software

To analyze the data, they were first entered into EXCEL software (ver. 2016) (EXCEL, 2016) and then composite analysis was performed based on RCBD criteria using SAS software (ver. 9.4) (SAS, 2017). Parametric and non-parametric stability statistics were calculated using SAS software (ver. 9.4) (SAS, 2017). AMMI stability analysis has been conducted using GEA-R software (Pacheco et al., 2016). Spearman correlation analysis and also principal component analysis of stability parameters have been also conducted to identify the relationship among different stability statistics applied in this study using XLSTAT software.

RESULTS

Primary results

The results of field trials demonstrated various grain yields of oilseed rape genotypes under different environments. The grain yield of the tested genotypes varied from 1921 kg ha^{-1} (genotype G12 in Zabol1) to 3878 kg ha^{-1} (genotype G14 in Hajiabad2). The highest and lowest mean grain yields across all environments were obtained by genotypes G9 and G12 with 3412 and 2507 kg ha^{-1}, respectively (Table 5). Combined ANOVA of data from multi environmental trials indicated a significant difference at the level of 1% for grain yield in the different environments. This implies a difference in the environmental conditions of the regions and years tested. The GEI was also significant at the level of 1% (Table 3). Therefore, stability analysis had to be conducted to clarify the GEI. Utilizing the AMMI model along with other parametric and non-parametric stability models provides a useful tool in clustering genotypes according to their yield and stability values across all environments that lead us to diagnose the GEI.

Table 3. Combined ANOVA of 16 oilseed rape genotypes across eight tested environments

S.O.V	Df	Sum Sq.	Mean Sq.	F value
Env.	7	20033417.22	2861916.75	6.72*
Error	16	6817796.15	426112.26	5.86
Gen.	15	11329954.33	755330.29	2.40*
Gen. x Env.	105	33000967.90	314294.93	4.32*
Error	240	17442796.53	72678.32	
Total	383	88624932.12		

S.O.V. = Source of variation. Df = Degree of freedom. Sum Sq. = Sum of square. Mean Sq. = Mean square. *, ** indicate significance at the 5% and 1% probability levels, respectively.

Combined AMMI analysis

Due to the significant GEI in this study, 8 environments (combination of 4 locations and 2 years) were examined. The AMMI analysis of variance on grain yield showed the significant effects of genotype, environment, and GEI on yield with, 31.13%, 17.60%, and 51.27% of contribution on the total sum of the square, respectively (Table 4). Based on the AMMI ANOVA, the major contribution of GEI was captured by the first and second interaction of principal component axes (IPCA1 and IPCA2) which explained 34.29% and 29.81% of GEI sum of the square, respectively (Table 4).

Table 4. AMMI ANOVA for seed yield of the 16 oilseed rape genotypes across eight tested environments

Source	df	SS	MS	F	%SS
Treatments	127	64364339	506806	6.97**	72.63
Genotypes	15	11329954	755330	10.39**	17.60
Environments	7	20033417	2861917	6.72**	31.13
Interactions	105	33000968	314295	4.32**	51.27
IPCA 1	21	11317194	538914	7.42**	34.29
IPCA 2	19	9839114	517848	7.13**	29.81
Residuals	65	11844661	182226	2.51**	35.89
Block	16	6817796	426112	5.86**	
Error	240	17442797	72678	-	
Total	383	88624932	231397	-	

To determine the relationships among genotypes and environments in oilseed rape yield trials, an AMMI biplot was designed, where IPCA1 and IPCA2 scores were plotted against each other (Fig. 1). IPCA1 and IPCA2 of AMMI biplot accounted for 64.11% of the total sum of square GEI. The highest values of IPCA1 were obtained by genotypes G5, G1, and G9. Besides, the highest values of IPCA2 were reached by genotypes G9, G6, and G2 (Figure 1 and Table

5). Genotypes on the highest point in a certain section of the biplot perform the best in environments located in the same location (Nowosad et al., 2017). According to this biplot, the genotypes G4, G6, G7, and G11 positively interacted with Zabol 1 and 2 environments but negatively with Gorgan 1 and 2. The vice versa were observed for G10 and G15 genotypes. It was also observed that genotypes G4, G6, G7, and G11 had a positive interaction with Hajiabad 1 and 2 but negatively interacted with Sari 1 and 2. The vice versa were observed for G1 and G12 genotypes. To identify the superior genotypes, it is necessary to choose stable ones with high-yielding (Carbonell et al., 2004; Yan and Kang, 2002). To this end, the stability of genotypes was also investigated based on a biplot for grain yield (Figure 2). A lower score of interaction (IPCA1) obtained by high-yielding genotypes G9 and G2 confirmed their high stability. Therefore, these two genotypes could be considered as the best ones using AMMI biplot.

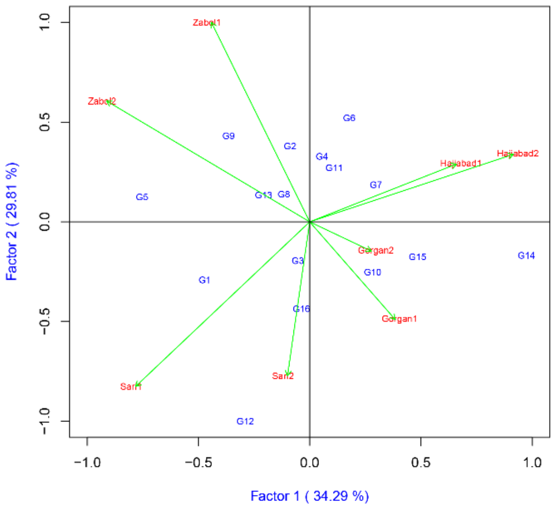

Figure 1. Biplot for genotype by environment interaction of oilseed rape genotypes, using the first and second components (IPCA1 and IPCA2)

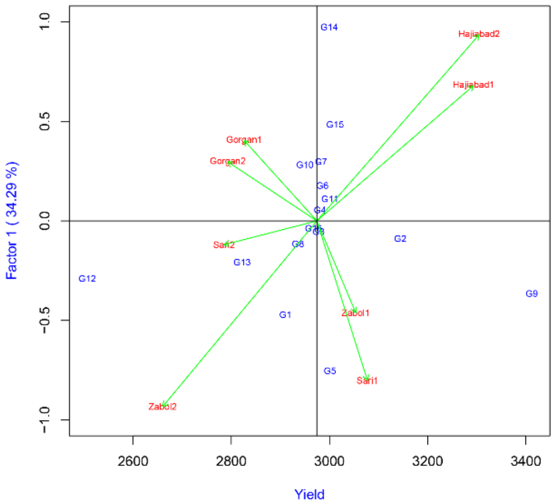

Figure 2. Biplot for the first component of interaction (IPCA 1) and oilseed rape grain yield means. The vertical line at the center of the biplot is the general grand mean.

Parametric stability statistics

The eight important stability parameters were calculated and presented in Table 5. Regression coefficient (bi) shows the sensitivity of genotypes to environmental change. So that, genotypes with bi values of less and greater than one shows lower and higher sensitivity to environmental change, respectively. Therefore, genotypes with less than one value of bi could be adaptable to low-yielding environments, while genotypes with greater than one value of bi could be adaptable to high-yielding environments (Eberhart and Russell, 1966). Based on this, genotypes like G3, G6, G7, and G8 with bi values greater than one are ideal for high-yielding environments, whereas genotypes like G2 and G9 with bi values less than one were ideal for low-yielding environments. Deviation from regression (S^2_{di}) is calculated in addition to regression coefficients. Using this method, genotypes with the lower variance of regression deviations are considered stable ones (Eberhart and Russell, 1966). Therefore, genotypes like G1, G2, G3, G4, G7, G8, and G9 with the lower variance of regression deviations were selected as the most stable genotypes.

Environmental variance (S^2x_i) (Lin et al., 1986) could be applied to show the variance of genotypes across the environments. The lower the values of S^2x_i, the higher stability would be expected (Lin et al., 1986). Accordingly, genotypes G1, G2, G4, G9, and G13 obtained the lowest values of S^2x_i indicated their stability.

Coefficients of determination (R^2) were introduced as one of the parametric stability which could identify stable genotypes (Becker and Leon, 1988). Based on this, all genotypes except G12 indicated high values of R^2 which indicated their high stability across environments.

Based on Francis and Kannenberg method, a low coefficient of variability (CV_i) and high mean yield could be considered for the selection of desirable genotypes (Francis and Kannenberg, 1978). Accordingly, genotypes G2 and G9 with the lowest values of CV_i and also with the higher mean yield than check varieties were selected as desirable genotypes.

Based on Wrike's equivalence (W^2_i) (Wricke, 1962) and Shukla's stability variance (σ^2_i) (Shukla, 1972) genotypes with the lowest values of W^2_i less affected by the environment (Shukla, 1972; Wricke, 1962). Considering these two parametric methods, genotypes G3, G8, and G2 which showed the lowest values of W^2_i and σ^2_i were identified as genotypes that presented the lowest variation by the environmental influence. Although, G8 and G3 were removed because of the low mean yield.

According to the superiority index (P_i), the genotype with the highest yield is selected as a reference for each environment and other genotypes were compared with the reference genotype. Based on this, genotypes with the lowest P_i-values are nominated as desirable genotypes (Lin and Binns, 1988). Consequently, genotypes G9 and G2 with the lowest P_i-values were considered as superior genotypes.

Table 5. Stability parameters for grain yield of 16 oilseed rape genotypes grown in eight tested environments

Genotype	Mean		AMMI Model				Parametric Stability Methods								Non Parametric Stability Methods											
	GY	GAI	IPCA1	IPCA2	ASV	GSI	bi	S^2_{di}	CV_i	S^2x_i	P_i	R^2	W^2_i	σ^2_i	$S_i^{(1)}$	$S_i^{(2)}$	$S_i^{(3)}$	$S_i^{(6)}$	$Npi^{(1)}$	$Npi^{(2)}$	$Npi^{(3)}$	$Npi^{(4)}$	KR	TOP	α	λ
G1	2910	2903	13.21	-8.14	17	27	0.30	52716	7.57	50634	14487266	0.11	519468	62361	0.90	18.29	12.80	5.05	0.63	0.06	0.42	0.10	22	50.00	-0.72	1.79
G2	3144	3133	2.49	10.65	11	9	0.68	60466	9.46	79229	4846828	0.35	406091	43851	1.21	12.29	12.29	5.58	0.50	0.08	0.52	0.14	6	12.50	-0.33	2.24
G3	2977	2959	1.50	-5.45	6	12	1.17	40455	11.43	115603	13373306	0.70	254100	19036	0.83	11.93	10.12	4.67	0.44	0.05	0.40	0.15	11	25.00	0.17	1.52
G4	2981	2966	-1.53	9.19	9	14	0.58	85066	10.27	93233	11692244	0.22	582697	72685	1.85	22.29	17.33	7.24	1.06	0.14	0.51	0.17	18	25.00	-0.43	3.14
G5	3001	2976	21.11	3.49	25	19	0.65	172850	14.01	173697	12522073	0.15	1086928	155008	2.56	37.13	31.03	10.51	0.94	0.11	0.68	0.33	19	37.50	-0.35	6.48
G6	2985	2946	-4.99	14.61	16	17	1.68	115263	17.39	267600	13964198	0.63	886048	122211	1.80	27.41	22.25	9.57	0.56	0.08	0.60	0.15	20	87.50	0.70	4.16
G7	2983	2952	-8.35	5.21	11	14	1.71	42496	15.41	209968	12960565	0.83	463044	53149	1.30	15.55	12.27	5.63	0.19	0.02	0.46	0.19	14	0.00	0.72	1.40
G8	2936	2916	3.25	3.90	5	14	1.21	50729	12.18	131314	13898646	0.67	323435	30356	1.31	9.93	7.51	4.40	0.31	0.03	0.32	0.11	15	37.50	0.22	1.90
G9	3412	3400	10.23	12.09	17	13	0.43	91444	10.06	89555	721021	0.12	682888	89042	1.38	7.07	15.23	12.17	0.13	0.05	1.42	0.48	12	62.50	-0.58	3.32
G10	2950	2933	-7.91	-7.06	12	20	0.52	111499	11.24	111814	15086728	0.15	764368	102345	0.88	18.55	15.51	4.98	0.81	0.10	0.55	0.16	24	87.50	-0.49	4.12
G11	3001	2975	-3.08	7.60	8	8	1.55	53171	14.61	188721	10588815	0.76	445033	50209	1.20	18.41	16.37	6.84	0.13	0.01	0.49	0.15	9	25.00	0.56	1.89
G12	2507	2474	8.12	-28.02	30	31	0.17	219691	14.66	190086	43072385	0.01	1603760	239389	1.54	16.79	9.22	3.79	1.13	0.08	0.50	0.14	32	12.50	-0.85	8.02
G13	2822	2808	5.80	3.78	8	18	0.79	51967	9.62	81909	16711848	0.46	329923	31415	1.28	11.14	6.78	2.92	0.19	0.02	0.31	0.08	18	25.00	-0.21	1.94
G14	2999	2943	-27.29	-4.73	32	22	1.77	211609	20.38	367349	19949525	0.51	1514606	224833	3.55	47.93	46.28	19.10	1.31	0.29	0.87	0.39	21	37.50	0.79	7.75
G15	3011	2974	-13.58	-4.89	16	14	1.80	66630	16.79	249327	15388920	0.77	663899	85942	1.76	22.98	22.58	9.39	0.13	0.02	0.66	0.21	13	50.00	0.82	2.26
G16	2967	2948	1.04	-12.24	12	20	0.98	78987	11.91	125408	15400943	0.46	474034	54944	0.87	17.71	14.59	7.39	0.75	0.08	0.45	0.11	18	25.00	-0.02	2.98

GY: Grain yield, GAI: Geometric adaptability index, IPCA: Interaction principal component axes, ASV: AMMI stability value, GSI: Genotype selection index, bi: regression coefficients, S^2d_i:, CV_i: coefficient of variability , S^2x_i: Environmental variance, P_i: superiority index , R^2: Coefficients of determination , W^2_i: Wrike's equivalence , σ^2_i: Shukla's stability variance , $S_i^{(1,2,3,4)}$: Huehn's non-parametric statistics, $Npi^{(1,2,3,4)}$: Thennarasu's statistic, KR: Kang's Method, TOP: Top index, α: Tai's environmental effects, λ: deviation from the linear regression.

Non-Parametric stability statistics

Non-parametric methods have been also utilized to identify the yield stability of oilseed rape previously (Oghan et al., 2016; Pourdad et al., 2014). In the present study, non-parametric yield stability statistics were also calculated (Table 5). Huehn's non-parametric statistics (Huehn, 1990; Huehn, 1990) including $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, and $S_i^{(6)}$ were computed and presented in table 5. Low values of these parameters determine high-yielding stable genotype (Huehn, 1990a; Huehn, 1990b; Huhn and Nassar, 1989). Among these parameters, $S_i^{(2)}$ emphasized ranking variance of genotypes across all environments (Huehn, 1990). The lowest values of $S_i^{(2)}$ observed for genotype G9 that confirmed this genotype as a high-yielding stable genotype.

Thennarasu's statistics are another non-parametric method based on mean rank across all environments (Tiiennarasu, 1995). Based on Thennarasu's statistics, specially $Npi^{(1)}$, Genotype G9 could be selected as a stable genotype. It is reported that Thennarasu's and also Huehn methods express the biological aspect of sustainability and might not be able to identify high-yielding stable genotypes (Soughi et al., 2016). Therefore, other dynamic non-parametric methods should also be considered. Kang's Method (KR) considered both mean yield and Shukla stability variance ranks (Kang, 2004). Accordingly, genotypes G2 and G9 with the lowest values of KR, selected as the superior ones considering both yield and stability. Fox et al (Fox et al., 1990) also defined a non-parametric method that categorized genotypes into Low, Middle, and Top indices. High values of Top index show high stability and desirability of genotypes (Fox et al., 1990). Considering Top index, genotypes G6 and G9 were selected as stable and desirable genotypes.

Environmental effects (α) and deviation from the linear regression (λ) were two other non-parametric methods introduced by Tai (Tai, 1971). Genotypes with (α, λ) values closer to (-1, 1) would be the most stable ones (Tai, 1971). Genotypes G2, G4, G5, G9, G10, and G12 met these criteria and were categorized as the stable ones using Tai's method. On the other hand, positive α values indicated specific adaptability of genotypes to high-yielding environments while negative α values indicated specific adaptability of genotypes to low-yielding environments. Therefore, these genotypes are suitable for the low-yielding environment in the warm regions of Iran.

AMMI-based stability statistics

AMMI could better describe the stability concept because of interpreting genotype by environment interaction (Sabaghnia et al., 2008). AMMI model parameters are shown in table 5. Various grain yield stability was observed among 16 tested genotypes using AMMI stability values (ASV). Based on the ASV parameter, the closer values to zero, are the more stable genotype (Purchase et al., 2000). Consequently, genotypes G8 and G3 with ASV values of 5 and 6 indicated the highest stability; in contrast with the genotype G14 (control cultivar Hayola 401) which showed the highest ASV value and was defined as the most unstable genotype. Additionally, based on the biplot analysis, the inclined genotypes to the origin of the biplot are more stable (Torbaghan et al., 2014). Based on this, genotypes G8 and G3 which were the closest ones to the origins of the biplot were identified as the most stable genotypes (Fig. 1). However, it should be noted that their grain yield was not suitable enough. Grain yield should also be considered along with stability (Carbonell et al., 2004; Yan and Kang, 2002). Genotype selection index (GSI), is another AMMI-based stability parameter that incorporates both ranks of mean grain yield and ASV (Bocianowski et al., 2020). The feature of this indicator is considering grain yield rank in addition to stability rank (Bocianowski et al., 2020). Therefore, lower GSI values are more desirable. Accordingly, genotypes G11 (control cultivar Dalgan), G2, and G9 were identified as the superior genotypes based on AMMI stability statistics.

Rank correlation

Spearman correlation was conducted to identify the relationship among different statistical methods (Table 6). GSI as AMMI stability parameter showed its high correlation with parametric stability statistics including S^2_{di}, P_i, W^2_i, and σ^2_i., while ASV showed a relatively high correlation with both parametric and non-parametric stability statistics. On the other hand, parametric stability statistics including S^2_{di}, $W^2_{i,}$ and σ^2_i showed a significant correlation with non-parametric statistics. Furthermore, correlation analysis showed a significant relationship between yield mean and GSI, $P_{i,}$ $S_i^{(3)}$, $S_i^{(6)}$, $Npi^{(3)}$, $Npi^{(4),}$ and KR. Therefore, these statistics were recognized as the best statistics methods in the current study to identify high-yielding stable genotypes.

To better understand, the relationship among the stability parameters demonstrated based on the rank correlation matrix using principal component analysis. The first two principal components of standard values accounted for 70.3% (44.93% and 25.37% PCA1 and PCA2, respectively) of variation (Figure 3). Similar results have been previously reported for spring oilseed rape genotypes of Iran (Oghan et al., 2016). The principal component analysis is utilized to clarify the two concepts in the story of stability; the static (biological) and dynamic (agronomic) concepts (Becker and Leon, 1988). To identify the superior genotypes, it is necessary to select the stable genotypes with the high-yielding potential (Carbonell et al., 2004, Yan and Kang, 2002) which is consistent with the concept of dynamic stability. Therefore, to produce a high-yielding and stable genotype a breeder should separate dynamic stability concepts from static ones. As shown in fig. 3, parameters are separated into dynamic and static stability. S^2x_i and mean yield are introduced as symbols of the static and dynamic stability concepts, respectively (Becker and Leon, 1988). Therefore, the right and left sides represent static and dynamic stability concepts which included S^2x_i and mean yield, respectively. Consequently, three groups were obtained from 24 statistical parameters of stability. The first group separated statistics influenced by yield in their ranking including GY, GAI, R^2, bi, α, and TOP. Dedicated selection for the low-yielding environment

Table 6. Spearman rank correlation of yield and stability parameters

Variables	GY	GAI	ASV	GSI	bi	S^2_{di}	CV_i	S^2x_i	P_i	R^2	W^2_i	σ^2_i	$S_i^{(1)}$	$S_i^{(2)}$	$S_i^{(3)}$	$S_i^{(6)}$	$Npi^{(1)}$	$Npi^{(2)}$	$Npi^{(3)}$	$Npi^{(4)}$	KR	TOP	α	λ
GY	**1.00**																							
GAI	**0.91**	**1.00**																						
ASV	0.17	-0.02	**1.00**																					
GSI	**-0.61**	**-0.71**	**0.63**	**1.00**																				
bi	0.36	0.15	-0.22	-0.32	**1.00**																			
S^2_{di}	0.14	-0.01	**0.78**	**0.52**	-0.26	**1.00**																		
CV_i	0.19	-0.05	0.29	0.13	**0.68**	0.35	**1.00**																	
S^2x_i	0.19	-0.05	0.29	0.13	**0.68**	0.35	**1.00**	**1.00**																
P_i	**-0.63**	**-0.80**	0.32	**0.78**	0.09	0.26	0.33	0.33	**1.00**															
R^2	0.29	0.20	-0.49	**-0.52**	**0.93**	**-0.53**	**0.53**	**0.53**	-0.08	**1.00**														
W^2_i	0.11	-0.07	**0.87**	**0.60**	-0.20	**0.93**	0.44	0.44	0.31	-0.46	**1.00**													
σ^2_i	0.11	-0.07	**0.87**	**0.60**	-0.20	**0.93**	0.44	0.44	0.31	-0.46	**1.00**	**1.00**												
$S_i^{(1)}$	0.31	0.12	0.48	0.17	0.19	**0.60**	**0.51**	**0.51**	0.04	-0.05	**0.63**	**0.63**	**1.00**											
$S_i^{(2)}$	0.21	0.05	**0.52**	0.37	0.27	**0.59**	**0.54**	**0.54**	0.23	0.04	**0.65**	**0.65**	**0.51**	**1.00**										
$S_i^{(3)}$	**0.60**	0.44	**0.53**	0.07	0.29	**0.59**	0.44	0.44	-0.10	0.06	**0.62**	**0.62**	**0.55**	**0.86**	**1.00**									
$S_i^{(6)}$	**0.74**	**0.59**	**0.54**	-0.06	0.31	0.49	0.40	0.40	-0.25	0.10	**0.51**	**0.51**	**0.54**	**0.56**	**0.86**	**1.00**								
$Npi^{(1)}$	-0.36	-0.36	0.48	**0.70**	-0.34	**0.63**	0.10	0.10	0.40	**-0.52**	**0.57**	**0.57**	0.30	**0.51**	0.25	0.07	**1.00**							
$Npi^{(2)}$	0.02	0.01	0.47	0.43	-0.29	**0.66**	0.01	0.01	0.08	-0.49	**0.56**	**0.56**	0.36	**0.53**	0.46	0.34	**0.89**	**1.00**						
$Npi^{(3)}$	**0.70**	**0.51**	**0.68**	0.03	0.04	**0.74**	0.35	0.35	-0.19	-0.20	**0.75**	**0.75**	**0.62**	**0.54**	**0.79**	**0.80**	0.19	0.47	**1.00**					
$Npi^{(4)}$	**0.72**	**0.62**	0.40	-0.19	0.24	0.43	0.43	0.43	-0.33	0.12	**0.51**	**0.51**	**0.55**	0.43	**0.73**	**0.77**	0.00	0.27	**0.84**	**1.00**				
KR	**-0.61**	**-0.71**	**0.55**	**0.94**	-0.36	**0.59**	0.16	0.16	**0.67**	**-0.55**	**0.68**	**0.68**	0.26	0.45	0.14	-0.07	**0.74**	0.50	0.10	-0.12	**1.00**			
TOP	0.14	-0.02	0.30	0.20	-0.02	0.32	0.05	0.05	0.06	-0.19	0.38	0.38	0.17	0.33	0.49	0.39	-0.03	0.12	0.44	0.26	0.32	**1.00**		
α	0.36	0.15	-0.22	-0.32	**1.00**	-0.26	**0.68**	**0.68**	0.09	**0.93**	-0.20	-0.20	0.19	0.27	0.29	0.31	-0.34	-0.29	0.04	0.24	-0.36	-0.02	**1.00**	
λ	0.08	-0.06	**0.69**	**0.51**	-0.24	**0.97**	0.33	0.33	0.32	**-0.51**	**0.87**	**0.87**	**0.62**	**0.50**	0.50	0.41	**0.63**	**0.66**	**0.69**	0.37	**0.58**	0.32	-0.24	**1.00**

Values in bold are different from 0 with a significance level alpha=0.05. GY: Grain yield, GAI: Geometric adaptability index, ASV: AMMI stability value, GSI: Genotype selection index, bi: regression coefficients, S^2d_i**:, ** CV_i**:** coefficient of variability , S^2x_i: Environmental variance, P_i: superiority index , R^2: Coefficients of determination , W^2_i: Wrike's equivalence , σ^2_i**:** Shukla's stability variance , $S_i^{(1,2,3,4)}$: Huehn's non-parametric statistics, $Npi^{(1,2,3,4)}$: Thennarasu's statistic, KR: Kang's Method, TOP: Top index, α: Tai's environmental effects, λ: deviation from the linear regression would be available by bi, α parameters. Therefore, selection based on group 1 parameters could lead us to identify high-yielding genotypes with general adaptability, especially for low-yielding environments in the warm regions of Iran. Group 2 includes S^2x_i, CV_i, $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $S_i^{(6)}$, $Npi^{(1)}$, $Npi^{(2)}$, $Npi^{(3)}$, $Npi^{(4)}$, ASV, λ, S^2_{di}, W^2_i and σ^2_i parameters which represent the static concept and separate genotypes with high stability. Therefore, the second group could also be considered for genotype selection by focusing on their stability in the warm regions of Iran. The third group is also contained parameters which influenced both yield and stability in genotype ranking. Distance of this group from mean yield might be due to significant negative correlation of the included parameters (which their low values indicated high-yielding stable genotypes) with the mean yield. Therefore, this group is recommended for selecting the high-yielding stable genotypes across the warm regions of Iran.

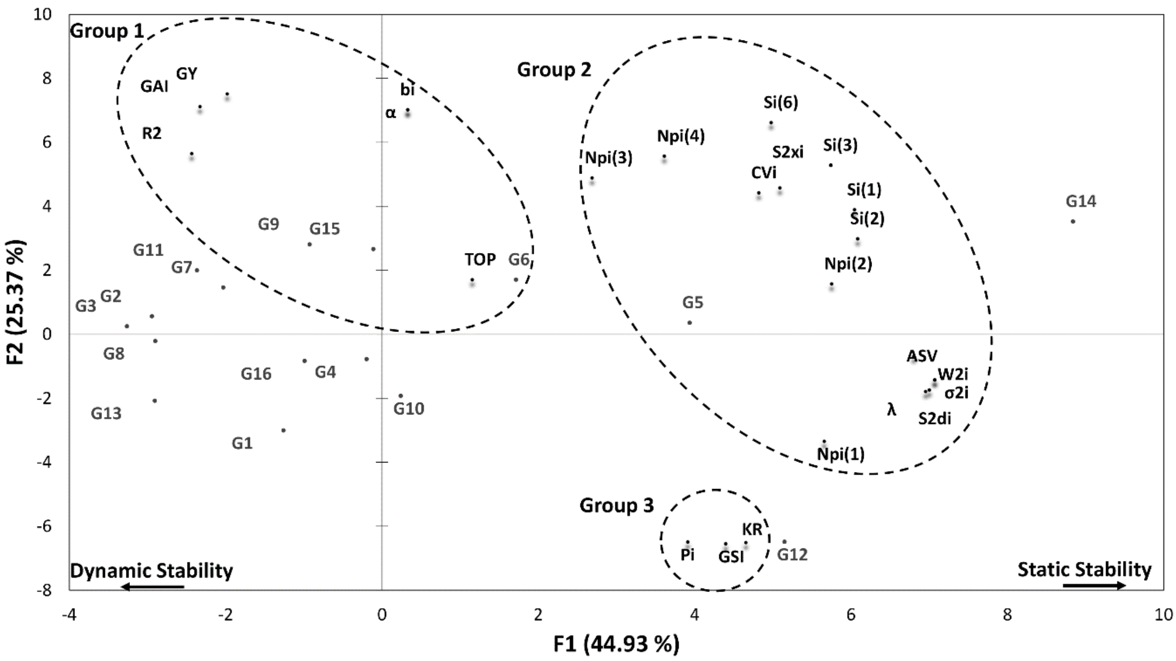

Figure 3. Biplot of the first two PCA of ranking values of 16 oilseed rape genotypes grown in eight tested environments. GY: Grain yield, GAI: Geometric adaptability index, ASV: AMMI stability value, GSI: Genotype selection index, bi: regression coefficients, S^2d_i**:**, CV_i: coefficient of variability , S^2x_i: Environmental variance, P_i: superiority index , R^2: Coefficients of determination , W^2_i: Wrike's equivalence , σ^2_i: Shukla's stability variance , $S_i^{(1,2,3,4)}$: Huehn's non-parametric statistics, $Npi^{(1,2,3,4)}$: Thennarasu's statistic, KR: Kang's Method, TOP: Top index, α: Tai's environmental effects, λ: deviation from the linear regression.

CONCLUSION

Combined AMMI analysis of 16 oilseed rape genotypes showed a high value of GEI in the present study. Therefore, various stability analyses including AMMI, parametric and non-parametric methods applied and compared to identify stable genotypes under different environments. Correlation analysis revealed a significant relationship between mean yield and some stability parameters including GSI**,** P_i, $S_i^{(3)}$, $S_i^{(6)}$, $Npi^{(3)}$, $Npi^{(4)}$, and KR. Therefore, these parameters should be considered in oilseed rape breeding in the warm regions of Iran to identify high-yielding and stable genotypes. Biplot analysis of the rank correlation separated 24 different stability methods into three main groups which could be utilized for different strategies in oilseed rape selection. The first group of parameters was suitable for achieving high-yielding genotypes in low-yielding environments. The second group was appropriate for the selection of stable genotypes. Finally, the third group was ideal to identify high-yielding and stable genotypes. Among the evaluated genotypes, G2 (SRL-95-16) and G9 (SRL-95-7) were superior using most of the stability methods and were also selected by each main group separated in the PCA biplot. Some stable genotypes were removed in continuous; like G3 and G8 due to their low-yielding. The selected genotypes (G2 and G9) were defined as high-yielding (more than all check varieties) stable genotypes. The superiority of these selected genotypes was also confirmed by AMMI biplot analysis which presented their low scores of interaction (IPCA1). Based on these results, genotypes G2 and G9 were selected as superior genotypes for the warm regions of Iran.

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