ARTICLE

Genotype x environment interaction analysis of multi-environment wheat trials in India using AMMI and GGE biplot models

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Abstract: *Fifty wheat genotypes were evaluated at nine diverse locations in India to identify high-yielding and stable genotypes. The analysis of variance based on additive main effects and multiplicative interaction (AMMI) indicated significant genotype, environment and genotype - environment (GE) interactions, with a total variation of 5.99, 20.23 and 73.77%, respectively. A biplot-AMMI analysis and yield stability index incorporating the AMMI stability value and yield in a single non-parametric index were used to discriminate the genotypes with highest and stable yield; the genotypes G135, G125, G104, G112 and G144 were found to be promising. Two mega environments (ME) were identified based on GGE (genotype and GE interaction) biplot analysis and the genotypes G119 and G120 and G107, G148 and G146 performed best in the mega-environments ME I and ME II, respectively. Both approaches allowed the identification of stable genotypes (G112 and G135), which can be included in the national testing program, with a view to release a new variety.*

Keywords: *AMMI, biplot, GGE, stability, wheat.*

INTRODUCTION

Worldwide as well as in India, bread wheat (*Triticum aestivum* L.) is the second most important food grain crop after rice. The importance of a sustained increase in wheat production and productivity for food security is well recognized in India, where wheat is a major staple food crop for the ever-increasing human population. The development of high-yielding genotypes coupled with resistance/tolerance to diverse biotic and abiotic stresses will be decisive to meet the demand for food grain. Multilocation trials are a key component of selection for stable and best-performing genotypes in different environments (Ahmadi et al. 2012, Oral et al. 2018, Tekdal and Kendal 2018). The grain yield, the final product of any crop, is determined by the genotypic potential (G), environmental effect (E) and the genotype x environment (GE) interaction (Yan and Kang 2002). In case of an effect of the GE interaction, the selection of genotypes based on the mean yield is inadequate (Sharifi et al. 2017).

A wide variety of methods to detect genotypes with a stable performance across environments were described in the literature. Most of them use regression analysis, sum of squared deviations from regression, Principal Component Analysis (PCA), cluster analysis and Additive Main effects and Multiplicative Interaction

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models (AMMI). The AMMI model uses ANOVA (analysis of variance) to test the main effects of both genotypes and environments and PCA to analyse the residual interaction component. The GGE biplot is a powerful model, with a graphical representation of identification of the best performing cultivars across the environments (Yan and Kang 2002). These graphical options facilitate the identification of high-yielding, stable genotypes, particularly in multi-environment trials. Moreover, yield stability and wide adaptation are increasingly important as the climate at specific locations is becoming more variable over the years. The AMMI biplot approach has been used for the identification of stable genotypes in multi-environment trials of wheat and barley (Oral et al. 2018, Tekdal and Kendal 2018). Both GGE and AMMI models have also been used to study the interaction component in multi-environment trials to identify stable wheat genotypes (Ahmadi et al. 2012, Kendal and Sener 2015, Vaezi et al. 2017, Oral and Kendal 2018). In this study, genotypes derived from the CIMMYT Elite Spring Wheat Yield Trial (ESWYT) were evaluated for grain yield across different environments to stratify the wheat genotypes according to the environmental conditions, for specific recommendations. The objectives of this study were to: i) analyse the G×E interaction on the grain yield of 50 wheat genotypes using AMMI and GGE biplot models; ii) identify high yielding and stable wheat genotype(s) across environments and to; iii) identify suitable genotype(s) for each environment.

MATERIAL AND METHODS

Experimental material and multi-environment wheat trials

Elite Spring Wheat Yield Trials (ESWYT) consisting of 50 genotypes including one local check were planted at nine test locations (Tables 1 and 2) in India in the winter (Rabi) growing season of 2016/17. The trial was arranged in a randomized complete block design, with two replications per location. The code and pedigree of all genotypes are listed in Table 3. Each genotype was planted in a plot with six 6-m rows, with a row-to-row and plant-to-plant distance of 20 cm and 10 cm, respectively. The recommended management practices were followed for aising strong and healthy crops. The grain yield data were recorded as total grain weight per plot after harvesting and the values extrapolated to kg ha^{-1}.

Table 1. Details of the different locations of evaluation of wheat genotypes

Code	**Location**	**Latitude**	**Longitude**	**Mean sea level** (m)	**Annual rainfall** (mm)	**Mean grain yield** (kg ha^{-1})
E1	Karnal	29^0 4’ N	76^0 59’ E	253	654.3	7193
E2	Hisar	29^0 10’ N	75^0 46’ E	215	287.4	5507
E3	Pantnagar	29^0 30’ N	79^0 31’ E	243	991.6	6014
E4	Gurdaspur	32^0 30’ N	75^0 21’ E	264	1282.5	6709
E5	Delhi	28^0 39’ N	77^0 13’ E	227	815.4	4651
E6	Ludhiana	30^0 54’ N	75^0 51’ E	252	576.8	6037
E7	Indore	22^0 43’ N	75^0 51’ E	550	776.8	4889
E8	Pune	18^0 31’ N	73^0 51’ E	562	1458.1	6010
E9	Dharwad	15^0 27’ N	75^0 0’ E	724	580.7	3509

Table 2. Monthly temperature pattern during the growing season at the different locations

Location	**Temperature (^{0}C) during growing season**													
	Oct.		**Nov.**		**Dec.**		**Jan.**		**Feb**		**March**		**April**	
	Max	**Min**	**Max**	**Min**	**Max**	**Min**	**Max**	**Min**	**Max**	**Min**	**Max**	**Min**	**Max**	**Min**
Karnal	34.0	15.0	28.1	7.8	25.0	6.1	21.5	3.9	24.7	5.3	29.6	11.0	37.9	17.2
Hisar	36.7	15.5	31.0	6.4	26.8	4.5	22.9	2.6	27.9	4.6	31.8	10.5	39.2	18.0
Pantnagar	33.5	14.5	28.6	8.5	23.2	7.2	20.5	4.2	27.4	5.9	32.2	10.7	37.1	16.2
Gurdaspur	33.5	14.8	27.2	8.5	24.0	7.7	16.0	4.6	24.0	6.3	31.7	11.0	36.2	16.1
Delhi	35.3	14.8	29.8	7.4	23.9	6.1	21.4	3.0	28.3	4.6	31.8	11.5	38.2	15.4
Ludhiana	34.9	16.2	28.0	7.4	22.7	7.3	22.0	5.3	25.5	5.6	29.9	12.2	39.6	18.0
Indore	35.1	20.3	32.9	12.4	27.9	7.5	29.7	7.8	34.5	9.9	36.9	13.9	41.5	18.2
Pune	31.9	20.3	32.1	12.4	30.2	8.0	31.1	9.6	33.6	10.0	36.4	14.0	37.5	17.5
Dharwad	29.8	19.1	30.1	15.0	29.6	10.7	30.3	13.3	33.3	16.1	35.3	16.4	36.4	20.6

Table 3. Pedigree details of 50 wheat genotypes

SN	Pedigree details
G101	LOCAL CHECK
G102	KACHU #1
G103	KUTZ
G104	CHIPAK
G105	MUCUY
G106	MUTUS/DANPHE #1/4/C80.1/3*BATAVIA//2*WBLL1/3/C80.1/3*QT4522//2*PASTOR
G107	CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/5/TRCH/SRTU//KACHU
G108	BAV92//IRENA/KAUZ/3/HUITES/4/DOLL/5/SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI
G109	KACHU/SAUAL/3/TACUPETO F2001/BRAMBLING//KIRITATI
G110	KACHU/SAUAL/5/SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI
G111	KACHU/SAUAL/3/TRCH/SRTU//KACHU
G112	TRCH/SRTU//KACHU/5/SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI
G113	TRCH/SRTU//KACHU/3/TRCH/SRTU//KACHU
G114	HUW234+LR34/PRINIA*2//SNLG/3/KINGBIRD #1/4/BAJ #1
G115	WHEAR//2*PRL/2*PASTOR/4/2*WBLL1/KUKUNA//TACUPETO F2001/3/UP2338*2/VIVITSI
G116	BOKOTA/3/UP2338*2/KKTS*2//YANAC
G117	UP2338*2/SHAMA/3/MILAN/KAUZ//CHIL/CHUM18/4/UP2338*2/SHAMA/5/COPIO
G118	SAUAL/WHEAR//SAUAL/3/PBW343*2/KUKUNA*2//FRTL/PIFED
G119	UP2338*2/VIVITSI/3/FRET2/TUKURU//FRET2/4/MISR 1/5/TUKURU//BAV92/RAYON*2/3/PVN
G120	CAL/NH//H567.71/3/SERI/4/CAL/NH//H567.71/5/2*KAUZ/6/WH576/7/WH 542/8/WAXWING/9/ATTILA*2/PBW65//PIHA/3/ ATTILA/2*PASTOR/10/UP2338*2/KKTS*2//YANAC
G121	NELOKI/5/FRET2/KUKUNA//FRET2/3/TNMU/4/FRET2*2/SHAMA/6/KINGBIRD #1//INQALAB 91*2/TUKURU
G122	SHA7//PRL/VEE#6/3/FASAN/4/HAAS8446/2*FASAN/5/CBRD/KAUZ/6/MILAN/AMSEL/7/FRET2*2/KUKUNA/8/TRAP#1/BOW/3/VEE/ PJN//2*TUI/4/BAV92/RAYON/5/KACHU #1/9/COPIO
G123	ELVIRA/CHIBIA//DIAMONDBIRD/4/2*MARCHOUCH*4/SAADA/3/2*FRET2/KUKUNA//FRET2
G124	ATTILA*2/PBW65/5/CNO79//PF70354/MUS/3/PASTOR/4/BAV92/6/TRCH/SRTU//KACHU/7/UP2338*2/KKTS*2//YANAC
G125	ROLF07/SAUAL/3/TRCH/SRTU//KACHU/4/ROLF07/SAUAL
G126	ROLF07/SAUAL/3/TRCH/SRTU//KACHU/4/ROLF07/SAUAL
G127	TACUPETO F2001/BRAMBLING/5/NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR*2/6/TRCH/SRTU//KACHU
G128	TACUPETO F2001/BRAMBLING/5/NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR*2/6/WAXWING/SRTU//WAXWING/KIRITATI
G129	TACUPETO F2001/BRAMBLING/5/NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR*2/6/WAXWING/SRTU//WAXWING/KIRITATI
G130	TACUPETO F2001/BRAMBLING/5/NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR*2/6/WAXWING/SRTU//WAXWING/KIRITATI
G131	KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/SAUAL/5/SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI/6/KACHU/SAUAL
G132	KACHU/SAUAL*2/3/TACUPETO F2001/BRAMBLING//KIRITATI
G133	KACHU/SAUAL*2/3/TACUPETO F2001/BRAMBLING//KIRITATI
G134	KACHU/SAUAL*2/5/SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI
G135	KACHU/SAUAL*2/4/ATTILA*2/PBW65//PIHA/3/ATTILA/2*PASTOR
G136	KACHU/SAUAL/4/VARIS/MISR 2/3/FRET2/KUKUNA//FRET2/5/KACHU/SAUAL
G137	KACHU/SAUAL/4/VARIS/MISR 2/3/FRET2/KUKUNA//FRET2/5/KACHU/SAUAL
G138	AMUR*2/3/HUW234+LR34/PRINIA//UP2338*2/VIVITSI
G139	C80.1/3*BATAVIA//2*WBLL1/5/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213)//PGO/4/HUITES*2/6/TRCH/SRTU//KACHU
G140	FRET2*2/SHAMA//PARUS/3/FRET2*2/KUKUNA*2/4/TRCH/SRTU//KACHU
G141	TRCH/SRTU//KACHU/3/WAXWING/PARUS//WAXWING/KIRITATI/4/TRCH/SRTU//KACHU
G142	TRCH/SRTU//KACHU*2/4/WBLL1/KUKUNA//TACUPETO F2001/3/UP2338*2/VIVITSI
G143	CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/6/MTRWA92.161/PRINIA/5/SERI*3//RL6010/4*YR/3/PAS-TOR/4/BAV92
G144	QUAIU #2/BAVIS #1
G145	BECARD #1/4/SOKOLL/3/PASTOR//HXL7573/2*BAU
G146	WBLL1*2/BRAMBLING/3/SOKOLL//SUNCO/2*PASTOR
G147	SOKOLL/92.001E7.32.5//SOKOLL/EXCALIBUR
G148	BAVIS #1*2/4/PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1
G149	CROC_1/AE.SQUARROSA (224)//OPATA/3/PASTOR/4/2*SOKOLL/3/PASTOR//HXL7573/2*BAU
G150	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1/4/SUNCO/2*PASTOR//EXCALIBUR/5/W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1

Statistical analysis

The AMMI analysis was carried out with the adjusted mean grain yield to assess the relationships among genotypes, locations and G×E interaction, based on the model described by Zobel et al. (1988) and Crossa (1990). The AMMI and GGE biplot package in R software (R Core Team 2013) were used for the analyses. The AMMI stability indices; AMMI distance (Di) and AMMI Stability Value (ASV) were calculated by the procedure proposed by Zhang et al. (1998) and Purchase et al. (2000), respectively. Stability per se might not be the only selection parameter because the most stable genotypes do not necessarily have the best yield performance (Mohammadi and Amri 2007). We decided to incorporate both yield and stability in a single index to classify stable genotypes. The genotype stability index (GSI) considered the ranks of the genotype yields across environments and AMMI stability values. This index incorporates the yield mean and stability index in a single criteria and is calculated as:

GSI = RASV+RY

where RASV is the rank of ASV and RY the rank of mean genotype yield of all environments.

The data were graphically analysed to interpret the GxE interaction to identify stable and adaptive genotypes by the GGE biplot, as described by Yan and Tinker (2006). The biplots were generated from the first two PCAs, without scaling, centering (2) or singular value partitioning (SVP) (2). The lines that connect the test environment to the biplot origin are called environment vectors and the cosine of the angle between the vectors of two environments approximates the correlation between them (Yan et al. 2007).

RESULTS AND DISCUSSION

GE analysis by AMMI model

The average grain yield of the genotypes over locations ranged from 4936 kg ha^{-1} (115) to 6279 kg ha^{-1} (107). Genotype G106 yielded highest at two locations (Karnal and Hisar); G119 at three (Karnal, Pantnagar and Gurdaspur) and G107 at two locations (Indore and Pune) (Table 4). The AMMI model is widely used in stability analysis as it provides an initial diagnosis of the model to be fit into multi environmental evaluation, allows a partitioning of the GxE interaction and explains patterns and relationships between genotypes and environments (Zobel et al. 1988, Crossa et al.1990). The AMMI analysis of variance for grain yield showed that 73.77% of the total sum of squares was attributable to environmental, only 5.99% to genotypic and 20.23% to GxE effects (Table 5). A large sum of squares for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield, indicating that environment has a strong influence on grain yield (Tonk et al. 2011, Munaro et al. 2014, Alam et al. 2015). The magnitude of the GxE interaction sum of squares was 3.37 times higher than that for genotypes, indicating that there were substantial differences in genotypic response across environments, in agreement with previous reports (Tonk et al. 2011, Alam et al. 2015, Vaezi et al. 2017). The multiplicative variance of the treatment sum of squares due to interaction was partitioned into seven significant interaction principal components. The first two PCs explained 46.62% of the total variation, in which the contribution of PC1 was 27.94% and that of PC2 18.68. Therefore, AMMI1 (IPCA1 vs additive main effects) and AMMI2 (IPCA2 vs IPCA1) biplots were generated to illustrate the genotype and environment effects simultaneously (Figure 1). The AMMI 1 biplot indicated that the environments E1, E4, E6, E9 and E3 were high yielding locations with high additive genotypic main effects, while the yields in the other environments were below the environmental mean. The scatter plot of the genotypes in this biplot indicated that genotype G107, followed by G119, G120, G130, G106, G104, G117, G136, G150, G101, G125 were the 10 highest yielding genotypes. The AMMI2 biplot indicated that the environments E2, E4 and E6 were discriminatory and located far away from the biplot origin. The genotypes G111, G135, G137, G134 and G130 were located close to the origin and proved highly stable, although their mean yields were on the lower side and should therefore not be recommended. Similar results regarding the stability of genotypes due to low IPCA1 values were recorded elsewhere (Mohammadi et al. 2013, Oral et al. 2018). The genotypes G128, G146, G148, G105, G141, G103, G124, G108, G127, located far away from the origin, were highly unstable and expressed a higher GE interaction (positive or negative).

Eight sectors were observed and genotype G143 clustered with E9 and E3, indicating repeatable performance. Genotype 110 clustered with E3, 144 with E5 and 146 with E2, indicating that these genotypes are stable in the respective

Table 4. Mean grain yield (kg ha^{-1}) of 50 wheat genotypes at nine locations in India

Genotypes	Karnal	Hisar	Pantnagar	Gurdaspur	Delhi	Ludhiana	Indore	Pune	Dharwad	Mean	CV
G101	6409	6389	6772	6488	4987	6610	4864	7578	2709	5867	2485
G102	6934	4132	5305	6013	4986	5032	4674	6332	3442	5205	2098
G103	7865	5000	6867	6504	3688	5488	4779	6385	4114	5632	2437
G104	7523	6563	6957	6357	4862	6062	4747	6932	3683	5965	2119
G105	7788	5764	6415	5713	4111	6289	4742	6463	3718	5667	2264
G106	8173	6875	6592	7369	4362	6132	4964	6313	3089	5985	2645
G107	7475	6597	5447	7125	5243	6995	5831	7910	3887	6279	2039
G108	6265	4132	5875	7000	4612	5549	4288	5169	4472	5262	1872
G109	7507	4688	6142	6688	4361	5059	4979	6497	3873	5532	2205
G110	6431	4271	5919	6225	4459	5555	5267	6616	3913	5406	1839
G111	7453	5174	5640	6788	4681	6080	4768	6075	3353	5557	2209
G112	8292	5695	6005	6313	4584	5847	4709	5822	3483	5639	2374
G113	6675	4722	6360	6319	3278	4785	4874	6566	3258	5204	2597
G114	7246	6771	6288	6688	4306	6887	5013	5582	3701	5831	2147
G115	6363	4688	5232	5913	3653	3892	5282	5900	3500	4936	2147
G116	6283	5278	6212	5107	4702	6159	4475	6450	4069	5415	1643
G117	7384	6042	6439	7194	5049	6662	5013	6294	3663	5971	1999
G118	7165	4306	5744	6707	5056	5332	5322	5041	2878	5283	2379
G119	8057	6181	7109	8188	3952	6919	5183	6538	3764	6210	2601
G120	7644	6597	6544	7500	5612	7019	4820	6707	3145	6176	2329
G121	6694	5834	6770	7732	4993	6684	4708	5416	3337	5796	2308
G122	7534	5764	5367	6557	6361	6038	5354	5372	2828	5686	2262
G123	7204	4931	5715	6188	3785	4023	4448	5335	3403	5003	2467
G124	7935	5347	6012	6788	3820	3980	4982	4779	4011	5294	2640
G125	7532	6598	6385	6657	4910	5723	4945	5851	3860	5829	1918
G126	6790	5174	5670	7375	4667	6082	5207	5794	4264	5669	1741
G127	6650	5035	5240	8269	4674	6640	5139	5510	3894	5672	2307
G128	6607	6841	5750	7250	5181	6679	5157	5469	3439	5819	2023
G129	6577	5417	5270	7151	4848	6580	5650	5719	3467	5631	1944
G130	7890	5868	6157	7907	5132	6515	5324	7204	2633	6070	2699
G131	6667	5451	6397	6600	4771	6327	4774	4985	2388	5373	2542
G132	7486	4931	5819	7250	4299	6452	4749	6203	3715	5656	2323
G133	6646	4479	6429	7563	5104	5967	4733	5760	3181	5540	2377
G134	7357	4306	5258	6107	4868	6130	4482	5957	2669	5237	2591
G135	7430	5591	6657	7000	5014	6302	4671	5991	3649	5811	2079
G136	7782	5486	6704	7750	4660	6235	4699	6075	4129	5946	2226
G137	7228	5451	6135	6569	5083	5464	5275	5822	3100	5570	2065
G138	7131	4549	6297	6801	4472	5390	4811	5900	3147	5388	2368
G139	6367	4861	6218	6450	4403	4819	5102	5457	3182	5206	2038
G140	7032	5695	4884	6575	4354	7034	4891	6103	3243	5534	2339
G141	7282	4375	6548	6363	4410	5525	4369	6991	3539	5489	2479
G142	6582	5729	6454	5544	4563	6410	4705	6060	3407	5495	1948
G143	7263	3854	5912	6013	4188	5729	4483	5429	4338	5245	2113
G144	7127	6250	5513	6432	5104	6353	5080	5619	4094	5730	1591
G145	5896	6771	6220	7419	4514	6667	4679	5300	4690	5795	1819
G146	7291	5695	4715	4957	5278	7292	3820	5463	2883	5266	2735
G147	7544	6042	5565	6676	4528	6974	4696	5913	3446	5709	2285
G148	7921	6875	5500	5207	4931	6182	5104	6291	3113	5680	2396
G149	7767	6597	5060	6113	4702	6363	4896	5597	3558	5628	2202
G150	7511	5695	6217	8000	4417	6960	4951	5969	3149	5874	2619
Mean	7193.1	5507.1	6014.0	6709.2	4651.6	6037.4	4889.6	6010.1	3509.4		
Min	5896	3854	4715	4957	3278	3892	3820	4779	2388		
Max	8292	6875	7109	8269	6361	7292	5831	7910	4690		

Table 5. AMMI analysis of grain yield for 50 wheat genotypes grown in nine environments in India

Source of variation	df	SS	MS	%TSS
Environments	8	100810.13	12601.27*	73.77
Genotypes	49	8190.60	167.16*	5.99
G x E	392	27645.86	70.53*	20.23
PC1	56	7724.79	137.94*	27.94
PC2	54	5165.13	95.65*	18.68
PC3	52	3670.32	70.58*	13.28
PC4	50	3261.15	65.22*	11.80
PC5	48	2962.25	61.71*	10.71
PC6	46	2228.09	48.44*	8.06
PC7	44	2000.27	45.46*	7.24
Error	450	9154.99	20.34	

* Significant at 0.001% probability

environments. The genotypes 111 and 137 were relatively closer to the biplot origin and could be good enough for E7 while 117, 130 and 144 were relatively closer to the biplot origin and could be good enough for E5, with average adaptation. Environment (E7) contributed most to the phenotypic stability of these genotypes (Figure1b), whereas E5, E9 and E3 contributed most to the GxE interactions. Tekdal and Kendal (2016) reported 10 sectors with respect to the mega environments and few lines were recommended for each environment.

The AMMI-based stability parameter, the AMMI stability value (ASV), was calculated based on the first two PCAs to produce a balanced measurement between them, and can be useful in situations where the two first IPCs explain a considerable part of the GxE interactions (Table 5). According to ASV, genotypes G111, G131, G112, G129, G137, G132, G105, G126, G135 and G142 were identified as stable for having lower ASV values, whereas genotypes G115, G123, G120, G107 and G119 were identified as being more unstable (Table 6). According to parameter Di, the values of G137, G111, G135, G132 and G112 were the lowest, whereas that of G146 was highest, followed by G124, G115, G119 and G123. The genotypes G125, G135, G104, G112, G136, G144, G105, G132, G126 and G129 were the most stable and high-yielding genotypes based on the genotype stability index, which takes both the overall mean yield and ASV into consideration (Table 6). The AMMI based AMMI stability parameters were used to screen durum wheat for identification of stable lines and were found to be adequate for the identification of stable genotypes (Mohammadi and Amri 2013, Alam et al. 2015). Similarly, AMMI stability parameters were also used to identify stably performing barley lines in Iran and were found to be promising in the identification of stable barley lines (Vaezi et al. 2017).

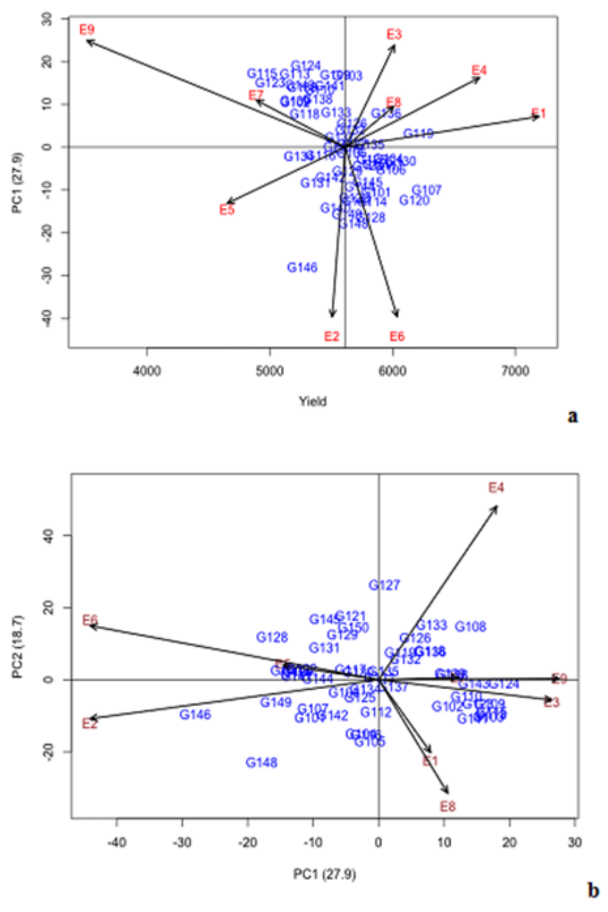

Figure 1. AMMI bi-plot model showing relationship among: a) test environments and genotypes based on grain yield; and b) among IPC-1 and grain yield.

GGE biplot analysis

The GGE biplot analysis was used to identify the best line of each environment and assess the stability of the lines. The most attractive feature of GGE biplots is the 'which-won-where' analysis, in which crossover GE interaction, mega-environment differentiation and specific genotype adaptation are graphically represented (Rakshit et al. 2014, Oral et al. 2018). The visualization of a 'which-won-where' pattern in multi-environment trials is essential to study the possible existence of different mega-environments in a region (Yan and Tinker 2006). The vertex genotypes were the most responsive for being located at the greatest distance from the biplot origin. The genotypes with either the best or poorest performance in one or all environments were considered responsive (Yan and Tinker 2006), falling within the sectors. In the biplot, the equality l.ine divides the graph into six sectors and nine environments were retained in two sectors (Figure 2), probably due to latitudinal and longitudinal differences. The test locations could be partitioned into two mega environments, one with E1, E8, E3, E4 and E7 and the second with E5, E2 and E6. In the first mega environment, the genotypes G119 and G120 were the winning genotypes and genotypes G112, G107, G148 and G146 in the second. There were strong correlations between environments located within the same sector, and variation in the genotype performance within environments indicated strong environmental influence and the existence of mega environment (Oral et al. 2018). The GGE biplot is a tool of data visualization that allows an evaluation of environments due to the discriminative ability and representativeness of the GGE view, which is an advantage over the AMMI biplot analysis (Yan et al. 2007, Aktas 2016).

Identification of ideal genotype based on GGE biplot analysis

The relationship among test environments was studied based on environment-centered (centering, 2) and environment-metric preserving (SVP, 2) without scaling option. Regarding grain yield, E2 and E6 were the most discriminating environments, whereas E5, E1 and E8 were the most representative environments, indicating their adequacy as test environments for multi-environmental trials (Fig. 2b). Environment E8 was closest to the mean environment, followed by E1 and E5. The genotype ranking in the closest to average, i.e., the most representative environments (E1 and E8), showed that genotype G107 yielded highest, followed by G120, G106 and G130. For selection of generally adapted genotypes, E2 was found

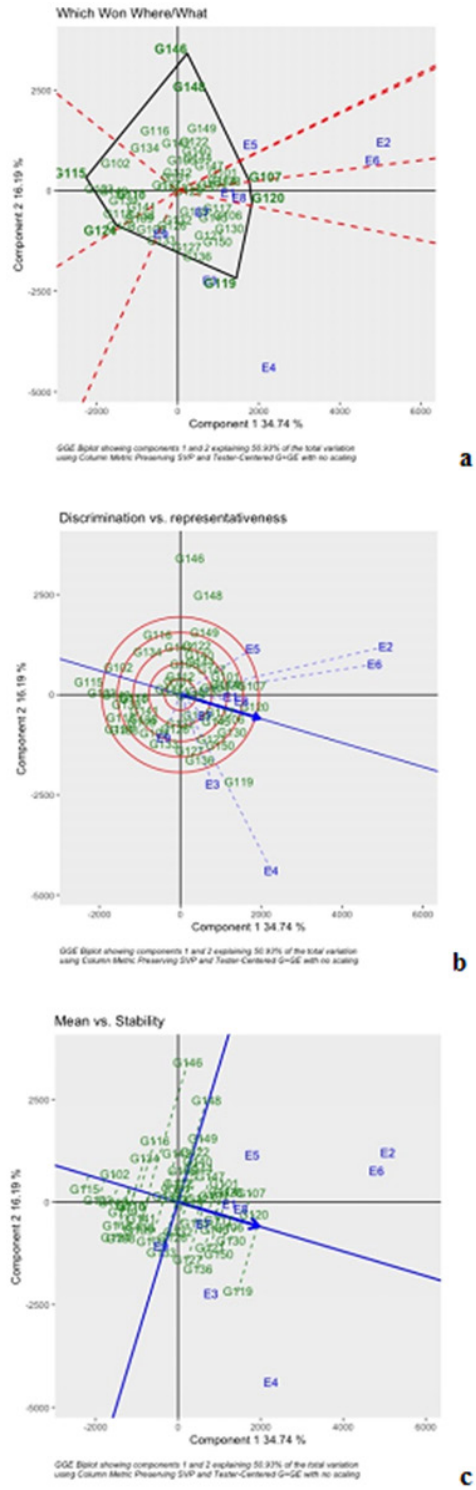

Figure 2. GGE bi-plot showing: a) "which-won-where" pattern for genotypes and environments; b) discriminating ability and representativeness of environments for grain yield; c) the relationship between mean grain yield and wheat stability.

Table 6. Mean grain yield (kg ha^{-1}) of 50 genotypes in nine environments and estimates of AMMI stability parameters

Genotypes	Gm	R_{Gm}	PC 1	PC 2	SIPCA	Di	ASV	R_{ASV}	GSI
G101	58.67	10	12.25	-3.39	367.75	19.18	18.56	31	41
G102	52.05	47	-16.84	-5.11	375.93	19.39	25.61	43	90
G103	56.32	26	-7.15	7.09	265.54	16.30	12.79	17	43
G104	59.65	7	9.47	-1.32	268.11	16.37	14.17	19	26
G105	56.67	23	1.11	-5.77	161.31	12.70	6.00	7	30
G106	59.85	5	13.60	4.60	337.79	18.38	20.78	36	41
G107	62.79	1	19.44	-1.72	507.44	22.53	29.02	47	48
G108	52.62	43	-15.28	6.63	396.49	19.91	23.71	40	83
G109	55.32	33	-10.52	5.16	191.37	13.83	16.51	29	62
G110	54.06	37	-12.77	0.82	250.15	15.82	19.05	34	71
G111	55.57	30	-1.45	-0.67	10.77	3.28	2.26	1	31
G112	56.39	25	0.00	-3.47	67.52	8.22	3.47	3	28
G113	52.04	48	-16.20	4.32	393.93	19.85	24.53	41	89
G114	58.31	11	12.00	-1.94	222.81	14.93	17.98	30	41
G115	49.36	50	-24.90	-2.46	653.41	25.56	37.18	50	100
G116	54.15	36	-6.19	-11.25	204.80	14.31	14.54	20	56
G117	59.71	6	10.83	3.31	129.74	11.39	16.47	28	34
G118	52.83	41	-12.64	0.55	238.49	15.44	18.85	33	74
G119	62.10	2	15.91	16.35	573.16	23.94	28.80	46	48
G120	61.76	3	20.17	2.20	430.53	20.75	30.13	48	51
G121	57.96	15	8.52	8.33	206.72	14.38	15.19	23	38
G122	56.86	19	4.48	-9.21	198.69	14.10	11.38	16	35
G123	50.03	49	-21.31	-0.36	561.80	23.70	31.76	49	98
G124	52.95	40	-16.63	6.45	671.59	25.92	25.60	42	82
G125	58.29	12	6.01	-0.71	141.31	11.89	8.98	11	23
G126	56.69	22	-1.49	6.38	92.39	9.61	6.75	8	30
G127	56.72	21	2.52	10.50	374.97	19.36	11.15	14	35
G128	58.19	13	13.25	-1.78	299.89	17.32	19.83	35	48
G129	56.31	27	2.76	0.08	135.20	11.63	4.11	4	31
G130	60.70	4	14.08	6.93	352.04	18.76	22.09	39	43
G131	53.73	39	-0.56	-2.55	70.33	8.39	2.68	2	41
G132	56.56	24	-0.02	5.42	48.18	6.94	5.42	6	30
G133	55.40	31	-4.46	9.15	215.79	14.69	11.31	15	46
G134	52.37	45	-8.88	-8.02	247.68	15.74	15.47	26	71
G135	58.11	14	4.55	3.76	35.56	5.96	7.75	9	23
G136	59.47	8	5.34	12.19	181.87	13.49	14.56	21	29
G137	55.70	29	-2.95	-1.12	10.59	3.25	4.53	5	34
G138	53.88	38	-10.16	4.51	133.61	11.56	15.79	27	65
G139	52.06	46	-14.72	1.74	227.33	15.08	22.00	38	84
G140	55.34	32	5.14	-7.45	129.47	11.38	10.69	13	45
G141	54.89	35	-9.80	2.99	296.90	17.23	14.90	22	57
G142	54.95	34	-0.34	-8.93	90.61	9.52	8.94	10	44
G143	52.45	44	-17.42	0.11	309.95	17.61	25.96	45	89
G144	57.30	17	5.43	-6.17	121.70	11.03	10.17	12	29
G145	57.95	16	9.71	5.04	309.91	17.60	15.32	25	41
G146	52.66	42	2.58	-25.63	735.85	27.13	25.91	44	86
G147	57.09	18	8.57	-4.69	102.82	10.14	13.60	18	36
G148	56.80	20	7.58	-18.65	505.04	22.47	21.80	37	57
G149	56.28	28	6.55	-11.76	259.10	16.10	15.28	24	52
G150	58.74	9	10.84	9.50	227.25	15.07	18.74	32	41

Gm-Genotype mean yield, ASV-AMMI stability value, Di- AMMI Distance, GSI -Genotype stability Index most suitable based on both descriptiveness and representativeness, while E1 and E8 were found to be most suitable based on representativeness for grain yield.

According to Yan and Tinker (2006), an ideal genotype should have both high mean yield and high stability within a mega-environment. In fact, an ideal genotype should have the highest PC1 score (high yielding ability) and lowest (absolute) PC2 score (high stability) (Rakshit et al. 2014, Yan and Tinker 2006). The genotypes were ranked for ideal grain yield performance, in other words, with high yield performance and stability across the nine locations (Figure 2c). The biplot defined genotypes with longest vectors coupled with zero G×E, represented by dots and arrows, as stable and high yielding. The ideal genotype 129 was stable as its projection on the AEA was close to zero. Other promising genotypes near the ideal genotype were G111, G131, G135 and G112. The low yielding genotypes (G115, G123, G143, G102, G139 and G113) were located far away from the ideal genotype. Kendal and Sener (2015) also identified mega environments for durum wheat in Turkey and identified suitable stable and ideal genotypes for grain yield and quality traits. Both the AMMI and GGE Biplot approaches proved equally effective in the identification of stable and high yielding genotypes (G129, G111, G131, G135 and G112), as also reported by Aktas (2016). On the other hand, the GGE biplot has the advantage of a higher discriminative ability and representativeness of the GGE plot than the AMMI biplot.

CONCLUSION

The GE interaction along with the genotype and environment main effects among 50 genotypes evaluated at nine locations were found to be significant.

Both approaches, AMMI and GGE biplot, allowed the identification of common genotypes (G129, G111, G131, G135 and G112) that are stable and high yielding across all locations.

The genotypes G112 and G135 were identified as high yielding and stable across all nine locations. Therefore, these lines can be included in the national testing program, to be released as a variety.

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