



AMMI ANALYSIS OF WHEAT GENOTYPES UNDER RESTRICTED-IRRIGATED TIMELY SOWN CONDITIONS FOR PENINSULAR ZONE OF INDIA

Ajay Verma and G.P. Singh

ICAR-Indian Institute of Wheat and Barley Research, Karnal - 132 001, Haryana (India)

*e-mail: ajay.verma1@icar.gov.in

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ABSTRACT

Variable yield performances of cereal crops have been reported across the environments while prior to the release of cultivars in wheat genotype x environment (G x E) effects are estimated. Crossover G x E interaction decreases the efficiency of cultivar selection by reducing the correlation between phenotype- and genotype-values. In present study a number of AMMI based measures were compared for the wheat genotypes evaluated under Peninsular zone of India. Genotypes 'MPO 1336', 'HI 8805' and 'NIAW 3170' identified by the values of EV1, D1, ASTAB1 and SIPC1 favored 'MACS 4058', 'DBW 93' and 'GW 1346'. Measures based on two IPS's (ASV & ASV1) recommended 'MACS 4059', 'UAS 446' and 'NIAW 3170' genotypes. Analytic measures MASV and MASV1 selected 'MACS 4059', 'UAS 446' and 'MACS 6696' wheat genotypes for stable performance. HM, PRVG and MHPRVG identified 'UAS 446', 'MACS 6695' and 'HI 1605' consistent yield. Biplot analysis showed larger cluster of D2, EV2, ASV, ASV1 and ASTAB2. ASV expressed choice for 'HI1605', 'MACS 6695' and 'HI 8805' while ASV1 recommended 'MACS 6695', 'HI1605' and 'HI 8805' genotypes for the 2nd year (2018-19). MASV measure found 'HI1605', 'NIDW 1149', HI 8802 of choice and MASV1 settled for 'HI1 605', 'HI 8805' and 'NIDW 1149' genotypes. Wheat genotypes 'NIAW 3170', 'MACS 6695' and 'MACS 6696' were identified by HM, PRVG and MHPRVG measures. Larger cluster consisted of EV1, D1, D2, EV2, ASV, ASV1, MASV, MASV1, ASTAB1 and ASTAB2 in biplot analysis. Mean, HM, PRVG, MHPRVG and GAI along with SIPC2 and SIPC3 clubbed in 4th cluster. Analytic measures of adaptability exhibited affiliation with measure-based values of IPC scores.

Keywords: AMMI model, ASV, ASTAB, biplot analysis, MASV, SIPC

INTRODUCTION

Research trials are conducted across the environments to estimate yield along with adaptability of genotypes (Agahi *et al.*, 2020) so as to identify and recommend the genotypes possessing high yield attributes showing less fluctuations under multi-environment trials (MET) setup (Guilly *et al.*, 2017). Generally, genotype by environment (G x E) interaction has been observed in research trials on wheat across the environments (Bocianowsk *et al.*, 2019). These interactions are evaluated prior to the release of newly developed or introduced cultivars. The crossover G x E interaction decreases the efficiency of selection by diluting the association between phenotype and genotype (Tekdal and Kendal, 2018). Besides, G x E interaction cannot be explained independently by genotypes or environmental effects. Quite a number of statistical procedures (i.e. parametric and nonparametric) have been developed to analyze G x E interactions efficiently (Yang *et al.*, 2009). Additive main effects and multiplicative interaction (AMMI), parametric method, is an effective multivariate model

that is frequently used to estimate the adaptability and stability as well as to detect mega-environments (Shahriari *et al.*, 2018). AMMI analysis first uses the analysis of variance to partition the total variation into genotypes (G), environments (E) and G x E interaction effects, then applies principal component analysis (PCA) to G x E interactions. Now, this procedure has been established as an effective tool to provide accurate estimation and separate the pattern from the noise in the residuals (Gauch, 2013, Haider *et al.*, 2017). In Peninsular zone of India 3 major species of wheat viz., *Triticum aestivum*, *T. durum* and *T. dicoccum* are widely cultivated. This zone comprises mainly of the states of Maharashtra and Karnataka. The cultivation of *T. durum* and *T. dicoccum* wheat is generally restricted to rainfed/restricted irrigation situations. The present study was aimed to study AMMI in relation to yield and assess the association among AMMI and yield based analytic measures.

MATERIALS AND METHODS

Thirteen advanced wheat genotypes were evaluated at 8 locations of Peninsular zone in 2017-18 and 12 genotypes at 8 locations of the zone in 2018-19 to interpret complex genotype by environment (G x E) interactions by AMMI model. The field trials were conducted in 2017-18 and 2018-19 cropping seasons at various research centers in a randomized complete block designs with three replications. Recommended agronomic practices were followed to harvest a good yield. Details of genotype, their parentage and environmental conditions are given in Table 1. AMMI first calculates genotype and environment additive effect using ANOVA and then analyses residual I using the principal component analysis (PCA). AMMI stability value (ASV) was initially proposed by Purchase (1997) to quantify the stability measure by considering relative weight of $IPCA_1$ and $IPCA_2$ scores. In certain cases where > 2 IPCAs were significant, ASV failed to encompass all the variability explained by G x E interaction. To overcome this difficulty, Zali *et al.* (2012) presented modified ASV which covered all available IPCAs. But in doing so, Zali *et al.* (2012) interpreted the formula of ASV incorrectly in comparison to the original formula of Purchase (1997) and Purchase *et al.* (2000). In present study, the original MASV formula of Zali *et al.* (2012) and a revised version of MASV (Ajay *et al.*, 2019) were compared with other AMMI based measures of interaction effects. The description of widely used measures based on AMMI analysis, used in the present study for completeness, are as under:

EV1	EVF	$EV = \sum_{n=1}^N \lambda_{in}^2 / n$	(Zobel, 1994)
SIPC1	SIPCF	$SIPC = \sum_{n=1}^N \lambda_n^{0.5} \gamma_{in}$	(Sneller <i>et al.</i> , 1997)
ASV		$ASV = [(\frac{SSIPC_1}{SSIPC_2} PCI)^2 + (PC2)^2]^{1/2}$	(Purchase <i>et al.</i> , 2000)
D		$D = \sqrt{\sum_{n=1}^N (\lambda_n \gamma_{in})^2}$	(Annicchiarico, 1997)
ASTAB		$ASTAB = \sum_{n=1}^n \lambda_n \gamma_{ni}^2$	(Rao and Prabhakaran, 2005)
ASV1		$ASV = [(\frac{SSIPC_1}{SSIPC_2} (PCI)^2 + (PC2)^2)]^{1/2}$	(Zali <i>et al.</i> , 2012)
MASV		$MASV = \sqrt{\sum_{n=1}^{N-1} \frac{SSIPC_n}{SSIPC_{n+1}} (PC_n)^2 + (PC_{n+1})^2}$	(Zali <i>et al.</i> , 2012)
MASV1		$MASV1 = \sqrt{\sum_{n=1}^{N-1} (\frac{SSIPC_n}{SSIPC_{n+1}} PC_n)^2 + (PC_{n+1})^2}$	(Ajay <i>et al.</i> , 2019)

(EV = Eigenvector, SIPC = Sum of the value of the IPC scores, D = Parameter of Annicchiarico, IPCA, principal component of interaction, ASV = AMMI stability value; MASV = Modified AMMI stability value; ASTAB = AMMI stability)

AMMI analysis was performed using AMMISOFT version 1.0, available at <https://scs.cals.cornell.edu/people/hugh-gauch/> and SAS software version 9.3. AMMI based measures were compared with recent analytic measures of adaptability calculated as the relative performance of genetic values (PRVG) and MHVG (harmonic mean of genetic values), based on the harmonic mean of genotypic values across different environments. Another harmonic mean-based measure of relative performance of genotypic values (MHPRVG) for the simultaneous analysis of stability, adaptability and yield (Resende and Durate, 2007).

$$PRVG_{ij} = VG_{ij} / VG_i$$

$$MHVG_i = \text{Number of environments} / \sum_{i=1}^k \frac{1}{\bar{x}_i}$$

$$MHPRVG_i = \text{Number of environments} / \sum_{j=1}^k \frac{1}{PRVG_{ij}}$$

VG_{ij} is the genotypic value of the i genotype, in the j environment, expressed as a proportion of the average in this environment. Geometric adaptability index (GAI) (Mohammadi and Amri, 2008) was calculated as $\sqrt[n]{\prod_{k=1}^n \bar{X}_k}$; in which $\bar{X}_1, \bar{X}_2, \bar{X}_3, \dots, \bar{X}_m$ were the mean yields of 1st, 2nd and m^{th} genotype across the environments and n is number of environments. Genotypes with higher values of GAI are desirable.

RESULTS AND DISCUSSION

Additive main effect and multiplicative interaction (AMMI) is a statistical tool which leads to the identification of stable genotypes with their adaptation behaviour in an easy manner. AMMI constitutes a model family because 0, 1, 2 or more interaction principal components (IPC) can be retained in the model before relegating higher components to a discarded residual, with these successive models being denoted by AMMI0 having no IPC, AMMI1 having 1 IPC, AMMI2 having 2 IPC, and so on, up to the full model.

First year of study (2017-18)

In present study, the estimated sum of squares for $G \times E$ signal and $G \times E$ noise were 56.9 and 43.1%, respectively. The sum of squares for $G \times E$ signal was 0.66 times than that for genotypic main effects. Hence, narrow adaptations were found important for this dataset. Even just IPC1 alone was 1.56 times than the genotypic main effects. Also, the $G \times E$ noise was 0.5 times than the genotypic main effect. Discarding noise improves the accuracy, increases repeatability, simplifies conclusions and accelerates progress (Gauch, 2013). Highly significant environments (43.8), $G \times E$ interaction (16.2) and genotypes (13.9) were observed by ANOVA analysis. Diversity of considered locations had justified the selection of environments (Akbarpour *et al.*, 2014). The explained variation of $G \times E$ interaction accounted by each of the highly significant IPCA's, as type-1 measures benefited 34.8%, type-2 measures utilized 59.9%, type-3 measures used up to 82.5%, though IPCA4, IPCA5 and IPCA6 contributed to the tune of 7.7, 6.3 and 2.0%, respectively (Table 2). This justifies the use of AMMI derived measures based on first three IPCAs (Kendal and Tekdal, 2016).

Genotypes 'MPO1336', 'HI 8805' and 'NIAW 3170' showed least values of EV1, ASTAB1 and D1; while SIPC1 found 'MACS 4058', 'DBW 93' and 'GW1346' as genotypes of choice. The values of EV2, ASTAB2 and D2 favoured 'MACS4058', 'UAS446' and 'NIAW3170' while for SIPC2 genotypes 'MACS4058', 'HI8802' and 'MPO1336' expressed stable yield (Table 3). ASV1 and ASV measures settled for 'MACS4059', 'UAS446' and 'NIAW3170' genotypes. Approximately 82.5% of $G \times E$ interaction sum of squares was utilized by type-3 measures and EV3, ASTAB3 and D3 values preferred 'MPO1336', 'HI8805' and 'NIAW3170' genotypes; whereas SIPC3 pointed

Table 1: Wheat genotypes evaluated, their parentage and environmental conditions

Genotypes	Parentage	Environ- ments	Latitude	Longitude	Mean above sea level (m)
Year 2017-2018					
GW 1346	GW1236/AR06-3	Bagalkot	16°10'N	75°42' E	524
MPO1336	GW1189/NIDW79	Bailhongal	15°48' N	74°51' E	696
HI 8805	IWP5070/HI8638//HI8663	Dharwad	15° 27' N	75° 0' E	724
MACS 4058	MACS3125/AKDW2997-16//MACS3125	Nasik	19° 59' N	73° 47' E	583
MACS 6696	NI5439/HD2934	Niphad	20° 4' N	74° 6' E	551
MACS 4059	MACS3603/HD4502	Pune	18° 31' N	73° 51' E	562
NIAW 3170	SKOLL/ROLF07	Savalihih	19°48' N	74°27' E	519
MACS 6695	NI5439*2/HD2934	Parbhani	19° 15' N	76° 46' E	413
HI 8802	HI8627/HI8653				
HI 1605	BOW/VEE/5/ND/VG9144//KAL//BB/3/YA CO/4/CHIL/6/CASKOR/3/CROC_1/A.SQU ARROSA(224)//OPATA/7/PASTOR// MILAN/ KAUZ/3/ BAV92				
AKDW 2997-16	CPAN6140/RAJ1555				
UAS 446	DWR185/DWR2006//UAS419				
DBW 93	WHEAR/TUKURU//WHEAR				
Year 2018-2019					
NIAW 3170	SKOLL/ROLF07	Niphad	20° 4' N	74° 6' E	551
GW 1346	GW1236/AR06-3	Pune	18° 31' N	73° 51' E	562
MACS 4058	MACS3125/AKDW2997-16//MACS3125	Parbhani	19° 15' N	76° 46' E	413
DBW93	WHEAR/TUKURU//WHEAR	Savalihih	19°48' N	74°27' E	519
HI 8805	IWP5070/HI8638//HI8663	Dharwad	15° 27' N	75° 0' E	724
AKDW2997-16	CPAN6140/RAJ1555	Bailahongal	15°48' N	74°51' E	696
MACS 6695	NI5439*2/HD2934	Nippani	16° 23 ' N	74° 22' E	606
UAS446	DWR185/DWR2006//UAS419 BOW/VEE/5/ND/VG9144//KAL//BB/3/YA CO/4/CHIL/6/CASKOR/3/CROC_1/A.SQU ARROSA(224)//OPATA/7/PASTOR//MILA	Bagalkot	16°10'N	75°42' E	524
HI1605	N/KAUZ/3/BAV92				
MACS 6696	NI 5439/HD2934				
NIDW 1149	NIDW295 /NIDW15				
HI 8802(d)	HI8627/HI8653				

for 'HI 8802', 'MPO1336' and 'NIAW3170' wheat genotypes. Composite measures MASV and MASV1 selected 'MACS4059', 'UAS446' and 'MACS6696' genotypes for stable performance.

The genotypes studied exhibited highly significant yield differences. The average yield is considered an important measure to assess the potential of genotypes in this zone. The genotypes 'MACS6695', 'UAS446' and 'HI1605' appeared suitable for general and 'MACS4058' and 'HI8802' for specific cultivations. GAI pointed that genotypes 'UAS446', 'MACS6695' and 'HI 1605' had stable adaptations whereas 'MACS 4058' and 'HI 8802' were of unstable nature. HM, PRVG and MHPRVG measures identified genotypes 'UAS446', 'MACS6695' and 'HI1605', and 'MACS 4058' and 'HI 8802' suitable for general and specific adaptations, respectively. Lower standard values were observed in genotypes 'MACS4058', 'MACS6696' and 'UAS446' for consistent yield performance as far as the considered locations were concerned.

Biplot analysis based on first two significant principal components help to visualize the relationships among AMMI based and other measures (Yang *et al.*, 2009). In total, PC1 and PC2 accounted for >77% of the total variation among the measures (Fig. 1). Largest cluster consisted of

Table 2: AMMI analysis of wheat genotypes evaluated in Peninsular zone of India

Source	Degrees of freedom	Mean sum of squares	Level of significance	% of total SS	% of G x E SS	Cumulative % SS by PCA's
Year 2017-18						
Treatments	103	108.77	***	73.99		
Genotypes (G)	12	175.64	***	13.92		
Environments (E)	7	948.30	***	43.84		
G x E interactions	84	29.25	***	16.23		
IPC1	18	47.50	***		34.79	34.79
IPC2	16	38.56	***		25.11	59.90
IPC3	14	39.66	*		22.60	82.50
IPC4	12	15.74			7.69	90.19
IPC5	10	15.45			6.29	96.48
IPC6	8	6.28			2.04	98.52
Residual	6	6.06				
Error	312	12.62				
Total	415	36.48				
Year 2018-19						
Treatments	95	100.44	***	61.25		
Genotypes (G)	11	255.87	***	18.07		
Environments (E)	7	486.04	***	21.84		
G x E interactions	77	43.18	***	21.34		
IPC1	17	90.97	***		46.51	46.51
IPC2	15	40.86	*		18.43	64.95
IPC3	13	37.36			14.61	79.56
IPC4	11	29.42			9.74	89.29
IPC5	9	29.70			8.04	97.33
IPC6	7	9.88			2.08	99.41
Residual	5	3.92				
Error	288	20.96				
Total	383	40.68				

Table 3: AMMI based estimates of genotypes (2017-18)

Genotypes	EV1	EV2	EV3	D1	D2	D3	IPC1	IPC2	IPC3	ASV	ASV1	MASV	MASV1	SIPC1
GW 1346	0.023	0.084	0.075	1.89	4.63	5.28	-0.814	1.894	-1.152	2.12	2.20	3.13	3.26	-0.814
MPO 1336	0.000	0.044	0.041	0.21	3.29	3.84	0.091	-1.471	-0.897	1.48	1.48	2.32	2.38	0.091
HI 8805	0.001	0.046	0.055	0.31	3.37	4.45	-0.134	1.504	1.318	1.51	1.52	2.56	2.61	-0.134
MACS 4058	0.081	0.077	0.096	3.57	4.66	6.10	-1.536	-1.344	1.782	2.25	2.52	3.20	3.43	-1.536
MACS 6696	0.017	0.014	0.018	1.65	1.99	2.64	-0.710	0.499	0.788	0.97	1.10	1.36	1.46	-0.710
MACS 4059	0.002	0.001	0.001	0.61	0.61	0.63	-0.261	-0.047	-0.062	0.31	0.36	0.32	0.37	-0.261
NIAW 3170	0.001	0.007	0.035	0.47	1.29	3.51	0.200	-0.540	-1.481	0.59	0.61	1.69	1.71	0.200
MACS 6695	0.101	0.054	0.036	4.00	4.10	4.10	1.721	0.404	-0.041	2.07	2.42	2.11	2.46	1.721
HI 8802	0.019	0.025	0.031	1.74	2.62	3.43	-0.750	-0.876	-1.002	1.24	1.36	1.85	1.95	-0.750
HI 1605	0.136	0.070	0.048	4.63	4.70	4.75	1.993	0.344	0.333	2.37	2.78	2.42	2.83	1.993
AKDW 2997-16	0.052	0.041	0.036	2.87	3.44	3.86	1.232	-0.857	0.793	1.68	1.91	2.07	2.28	1.232
UAS 446	0.004	0.002	0.001	0.75	0.76	0.76	0.324	-0.032	0.038	0.38	0.45	0.39	0.45	0.324
DBW 93	0.063	0.037	0.027	3.16	3.36	3.49	-1.357	0.523	-0.417	1.68	1.95	1.82	2.08	-1.357

Genotypes	SIPC2	SIPC3	ASTAB1	ASTAB2	ASTAB3	Mean	S.D.	GAI	PRVG	MHPRVG	HM
GW 1346	1.080	-0.071	3.58	21.46	27.90	27.84	6.00	27.29	0.988	0.975	26.74
MPO 1336	-1.380	-2.278	0.04	10.83	14.74	28.48	5.22	28.07	1.012	1.006	27.67
HI 8805	1.370	2.688	0.10	11.37	19.80	25.71	4.95	25.31	0.914	0.906	24.93
MACS 4058	-2.880	-1.097	12.75	21.75	37.17	24.75	2.80	24.61	0.892	0.878	24.46
MACS 6696	-0.212	0.576	2.73	3.97	6.98	25.94	3.78	25.69	0.926	0.922	25.44
MACS 4059	-0.308	-0.369	0.37	0.38	0.40	28.73	4.43	28.43	1.023	1.022	28.14
NIAW 3170	-0.339	-1.820	0.22	1.67	12.31	29.27	5.22	28.86	1.041	1.034	28.44
MACS 6695	2.125	2.084	16.01	16.82	16.83	31.61	6.44	31.03	1.119	1.113	30.46
HI 8802	-1.627	-2.629	3.04	6.87	11.74	25.27	4.30	24.96	0.900	0.895	24.65
HI 1605	2.337	2.670	21.48	22.07	22.61	31.13	6.71	30.47	1.101	1.090	29.78
AKDW 2997-16	0.376	1.168	8.21	11.87	14.92	27.26	5.17	26.85	0.970	0.961	26.46
UAS 446	0.292	0.330	0.57	0.57	0.58	31.43	4.15	31.20	1.123	1.120	30.96
DBW 93	-0.834	-1.251	9.96	11.32	12.16	27.74	4.35	27.45	0.991	0.984	27.16

EV = Eigenvector, SIPC = Sum of the value of the IPC scores, D = Parameter of Annicchiarico; SIPC1 = SIPC for first IPCA, SIPC 2 = SIPC for first two IPCAs, IPCA, principal component of interaction, ASV = AMMI stability value; MASV = Modified AMMI stability value; ASTAB = AMMI stability; SD = Standard deviation

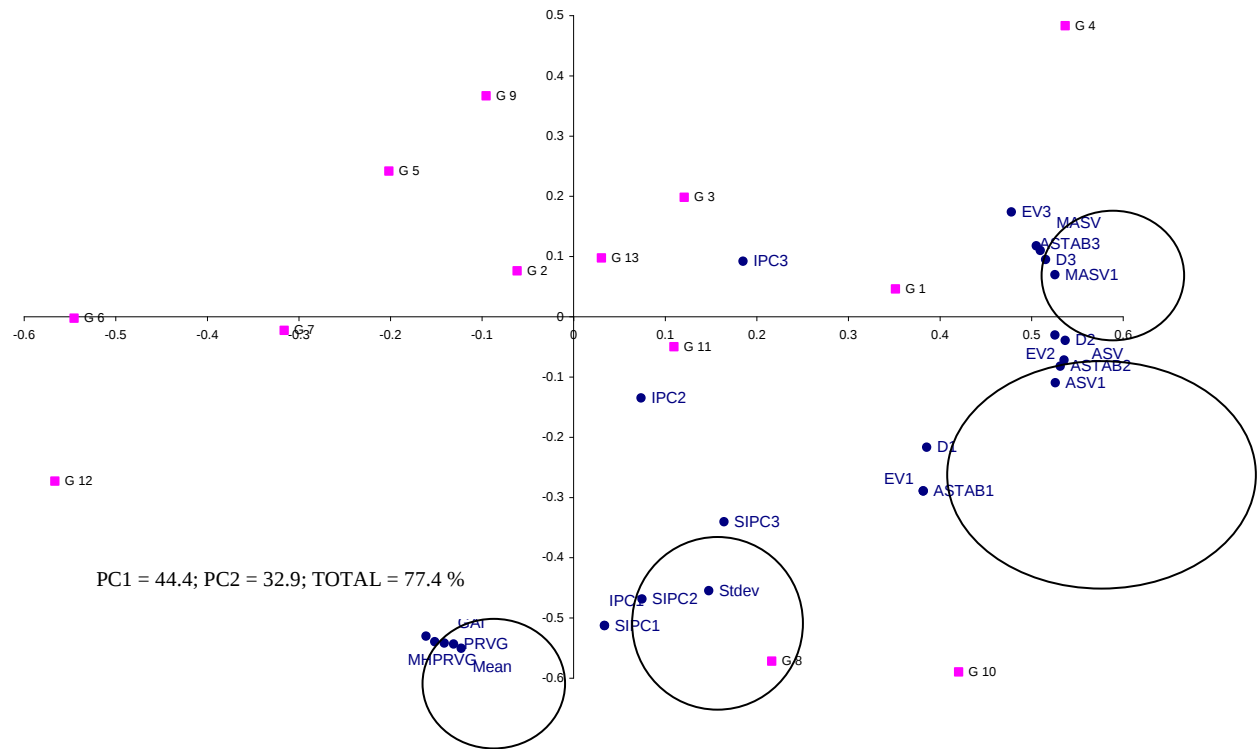


Fig. 1: Biplot analysis of genotypes and AMMI based estimates (2017-18); G1 = GW 1346, G2 = MPO 1336; G3 = HI 8805; G4 = MACS 4058; G5 = MACS 6696; G6 = MACS 4059; G7 = NIAW 3170, G8 = MACS 6695; G9 = HI 8802; G10 = HI 1605, G11 = AKDW 2997-16; G12 = UAS 446; & G13 = DBW 93

Table 4: AMMI based estimates of genotypes (2018-19)

Genotypes	EV1	EV2	EV3	D1	D2	D3	IPC1	IPC2	IPC3	ASV	ASV1	MASV	MASV1	SIPC1
NIAW 3170	0.073	0.070	0.082	4.25	5.12	6.09	1.696	1.281	-1.527	2.98	4.47	3.65	4.99	1.70
GW 1346	0.112	0.086	0.064	5.24	5.92	6.09	-2.094	-1.232	-0.659	3.55	5.43	3.86	5.68	-2.09
MACS 4058	0.119	0.080	0.053	5.42	5.86	5.87	-2.166	0.993	-0.157	3.58	5.55	3.75	5.70	-2.17
DBW93	0.004	0.040	0.027	1.04	3.23	3.24	0.413	-1.370	0.142	1.52	1.72	2.17	2.44	0.41
HI 8805	0.002	0.021	0.015	0.67	2.31	2.36	0.267	0.992	-0.225	1.08	1.20	1.57	1.75	0.27
AKDW2997-16	0.037	0.033	0.029	3.00	3.55	3.85	-1.199	0.853	-0.679	2.09	3.14	2.39	3.39	-1.20
MACS 6695	0.000	0.019	0.128	0.33	2.19	6.35	0.131	0.972	2.753	0.99	1.03	3.12	3.18	0.13
UAS446	0.012	0.064	0.043	1.74	4.16	4.17	0.696	-1.694	0.090	2.02	2.44	2.78	3.25	0.70
HI1605	0.003	0.011	0.008	0.83	1.74	1.80	0.333	-0.684	0.222	0.86	1.08	1.18	1.40	0.33
MACS 6696	0.103	0.053	0.036	5.03	5.08	5.08	2.010	-0.295	-0.088	3.21	5.08	3.22	5.09	2.01
NIDW 1149	0.016	0.012	0.008	1.97	2.21	2.22	0.787	0.454	-0.091	1.33	2.04	1.43	2.12	0.79
HI 8802	0.019	0.011	0.008	2.19	2.27	2.32	-0.874	-0.270	0.218	1.41	2.22	1.46	2.26	-0.87

Genotypes	SIPC2	SIPC3	ASTAB1	ASTAB2	ASTAB3	Mean	SD	GAI	PRVG	MHPRVG	HM
NIAW 3170	2.98	1.45	18.03	26.20	37.14	35.01	4.02	34.81	1.14	1.12	34.62
GW 1346	-3.33	-3.98	27.50	35.05	37.08	27.35	5.57	26.81	0.88	0.86	26.23
MACS 4058	-1.17	-1.33	29.41	34.31	34.43	28.98	3.89	28.74	0.94	0.92	28.48
DBW93	-0.96	-0.81	1.07	10.40	10.50	30.53	5.09	30.12	0.98	0.97	29.68
HI 8805	1.26	1.03	0.45	5.35	5.59	30.94	2.62	30.84	1.00	1.00	30.74
AKDW2997-16	-0.35	-1.02	9.01	12.63	14.79	28.59	3.36	28.40	0.93	0.92	28.19
MACS 6695	1.10	3.85	0.11	4.80	40.37	34.97	4.61	34.72	1.13	1.12	34.47
UAS446	-1.00	-0.91	3.04	17.32	17.36	26.91	5.62	26.32	0.86	0.85	25.66
HI1605	-0.35	-0.13	0.69	3.02	3.25	33.05	4.15	32.80	1.07	1.06	32.54
MACS 6696	1.72	1.63	25.33	25.76	25.80	33.97	5.44	33.58	1.10	1.08	33.19
NIDW 1149	1.24	1.15	3.88	4.91	4.94	31.79	4.03	31.56	1.03	1.02	31.34
HI 8802	-1.14	-0.93	4.79	5.15	5.38	30.83	4.25	29.16	0.95	0.94	28.78

EV = Eigenvector, SIPC = Sum of the value of the IPC scores, D = Parameter of Annicchiarico; SIPC1 = SIPC for first IPCA, SIPC 2 = SIPC for first two IPCAs, IPCA, principal component of interaction, ASV = AMMI stability value; MASV = Modified AMMI stability value; ASTAB = AMMI stability; SD = Standard deviation

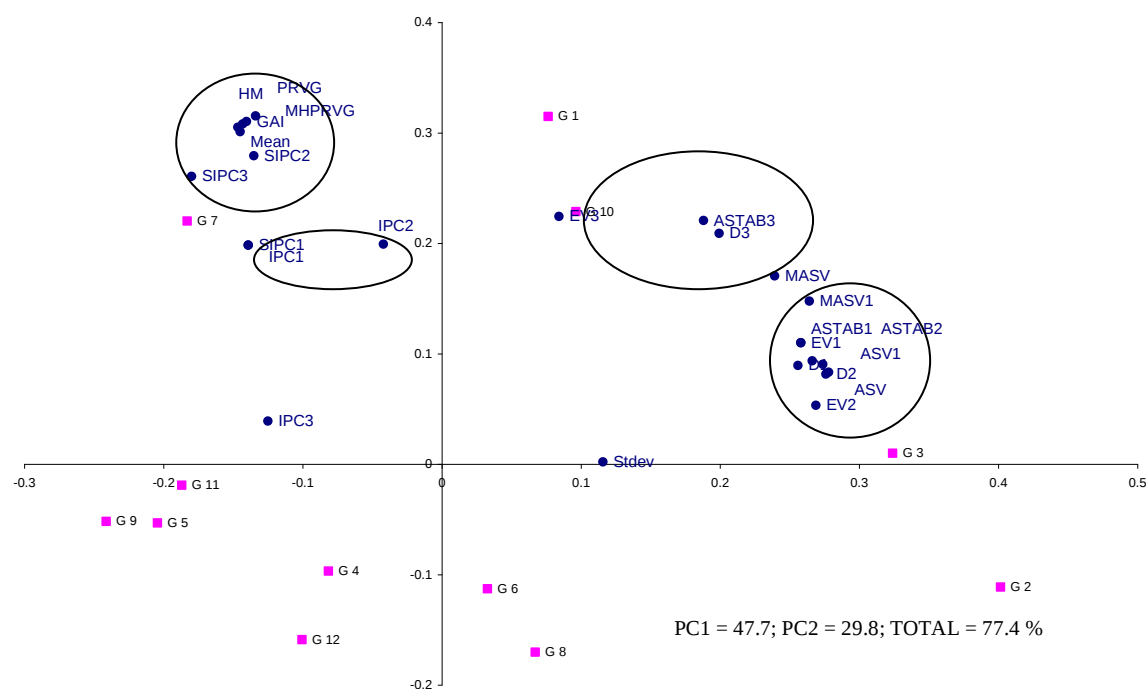


Fig. 2: Biplot analysis of genotypes and AMMI based estimates (2018-19); G 1 = NIAW 3170; G 2 = GW 1346; G 3 = MACS 4058; G 4 = DBW93; G 5 = HI 8805; G 6 = AKDW2997-16; G 7 = MACS 6695; G 8 = UAS446 G 9 = HI1605; G 10 = MACS 6696; G 11 = NIDW 1149; G 12 = HI 8802

D2, EV2, ASV, ASV1 and ASTAB2. Second nearby cluster consisted of SIPC3, SIPC1, SIPC2, IPC1 and SD measures. Third close cluster clubbed EV3, MASV1, MASV, ASTAB3 and D3 measures. Fourth cluster included all mean based measures, mean, HM, PRVG, MHPRVG and GAI. Two measures IPC2 and IPC3, observed as outliers', maintained good distance from studied measures.

Second year of study (2018-19)

The estimated sum of squares for signal and noise were 51.5 and 48.6% of G x E interaction, respectively. Highly significant environments (21.8), G x E interaction (21.3) and genotypic (18.1) were observed by ANOVA analysis (Table 2). Lower values of EV1, D1 and ASTAB1 were for 'MACS 6695', 'HI8805' and 'HI1605' genotypes. Measure EV2 pointed towards 'HI1605', 'HI 8802' and 'NIDW1149' as desirable; D2 values selected 'HI1605', 'MACS 6695' and 'NIDW 1149' while for SIPC2 were 'GW1346', 'MACS4058' and 'HI8802' and ASTAB2 values favoured 'HI1605', 'MACS6695' and 'NIDW1149' genotypes. ASV expressed choice for 'HI1605', 'MACS 6695' and 'HI 8805'; and ASV1 recommended 'MACS 6695', 'HI1605' and 'HI 8805' genotypes (Table 4). Values of EV3, D3 and ASTAB3 pointed towards 'HI1605', 'NIDW1149' and 'HI 8802' genotypes whereas SIPC3 values favoured 'GW1346', 'MACS4058' and 'AKDW2997-16' genotypes. Measure MASV found 'HI1605', 'NIDW1149' and 'HI 8802' as suitable genotypes; whereas MASV1 selected 'HI1605', 'HI8805' and 'NIDW1149' for stable performance. GAI pointed towards 'NIAW 3170', 'MACS6695' and 'MACS6696' as genotypes of stable adaptations. Values of HM, PRVG and MHPRVG identified 'NIAW3170', 'MACS6695' and 'MACS6696' genotypes for general and 'UAS446' and 'GW1346' for specific adaptations. Lower standard error values observed for 'HI 8805', 'AKDW2997-16' and 'MACS4058' genotypes as per their consistent yield performance.

Four clusters were observed for measures in Biplot analysis. First two significant principal components accounted for more than 77% total variation among measures (Fig. 2). Larger cluster consisted of EV1, D1, D2, EV2, ASV, ASV1, MASV, MASV1, ASTAB1 and ASTAB2. Second nearby cluster consisted of EV3, D3 and ASTAB3. Third cluster clubbed SIPC1, IPC1 and IPC2 measures. Last group of mean-based measures, Mean, HM, PRVG, MHPRVG and GAI along with SIPC2 and SIPC3. Measures IPC3 and standard deviation were observed as outliers.

Every AMMI based measure relates to a different concept of stability and may be useful to the select genotypes with high, stable and predictable yield across environments (Bocianowsk *et al.*, 2019). AMMI analysis has been found useful for exploring complex G x E interaction, improving selections and increasing the experimental efficiency (Agahi *et al.*, 2020). The scientific information obtained could be of considerable importance in developing location specific breeding strategies and selecting stable genotypes in breeding programme. The analytic adaptability measures exhibited affiliation with measures based on sum of the values of IPC scores.

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