Original Research Article

MULTI ENVIRONMENT ANALYSIS OF SOYBEAN GENOTYPES TO DELINEATE STABILITY AND ADAPTABILITY FOR YIELD AND QUALITY PARAMETERS

Abstract

The present investigation was carried out at three locations of Gujarat under the jurisdiction of Anand Agricultural University (AAU) during *kharif*-2022. Three diverse environments were selected for conducting an experiment ~~*i.e.*, Experimental Farm, Department of Genetics & Plant Breeding, B. A. College of Agriculture, AAU, Anand considered as E_1, Agricultural Research Station, AAU, Derol as E_2 and Tribal~~

~~Research cum Training Centre, AAU, Devgadh Baria considered as E_3.~~The experimental material comprised of 40 genotypes of soybean sown in a randomized block design with three replications at all environments. Based on the AMMI analysis for seed yield per plant, E_3 was considered as the most suitable environment for seed yield per plant while, E_2 was considered as the poor environment. The genotypes G4, G16 and G40 were considered as the most stable genotypes and had general adaptation for seed yield per plant among all the genotypes since they were least affected by the environment. The genotypes G15, G22, G24, G25, G27, G29, G32 and G39 performed well in the poor environment (E_2). Genotypes G10, G20 and G33 had specific adaptability in potential environment (E_3) Based on the AMMI stability value G24, G25 and G22 were considered as stable genotypes over environment while, G33, G20 and G35 were considered as unstable genotypes.According to the AMMI 2 biplot G15, G16, G22, G24, G25, G27, G32 and G39 were considered as high yielding with general adaptability. The vertex genotypes for E_3 were G10, G12, G20 and G33. G31 was for E_2 while, vertex genotype for E_1 was G26.

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Key words: AMMI analysis, AMMI Stability Value, GGE Biplot and Stability

Introduction

Soybean [*Glycine max* (L.) Merrill, 2n=2x=40] is an important oilseed crop known as “Golden bean” which belongs to the family *Leguminosae* along with many essential food legume crops such as chickpea, peanut, alfalfa, faba bean, lentil and pea.

Soybean yield is a complex quantitative trait that is influenced by interactions between genes and the environment (Yongchun *et al*., 2008). Environmental factors, particularly day length at different latitudes, have a significant impact on soybean yield (Singh and Vatsa, 2009; Zhang *et al*., 2015; Bhartiya *et al*., 2017). According to Camara *et al*. (1997), the primary climatic element affecting soybean adaptation to various ecoregions is photoperiod. The growing region of each soybean cultivar was constrained to a relatively small range of latitudes due to photoperiodic sensitivity in order to achieve its highest yield (Cober and Morrison, 2010). When grown 2°N of their usual cultivation latitudes, some soybean cultivars had markedly lower yields (Gai and Wang, 2001). However, soybean is grown around the world at latitudes ranging from 50°N to 35°S (Mcblain *et al*., 1987).

Plant breeders frequently tried to increase yield by focusing on yield-related traits (Dao *et al*., 2017). The genotypic correlation coefficients could be effectively divided into direct and indirect impacts and their relationships with grain yield could be clearly understood with the use of correlation studies and path coefficient analyses (Debebe *et al*., 2014). The features that have a substantial impact on soybean grain yield had been identified using path analysis (Li *et al*., 2013; Yahaya and Ankrumah, 2017; Al-Ballat and Al-Araby, 2019). The interpretation of genetic tests and predictions was hampered by the genotype-environment (G X E) interaction, which is a significant issue in the study of quantitative traits like yield and yield component (Farshadfar and Sutka, 2003; Becker and Leon, 1988).

GGE biplot is an efficient method for recommending specific genotypes in specific mega-environments, evaluating the mean performance and stability of genotypes, and analysing the power of target environments to distinguish genotypes (Yan and Kang, 2003; Tiwari, 2019). It visually examines the relationships between genotypes, test environments and genotype-by-environment interactions. When genotypes are tested in a variety of environments where the interaction between genotype and environment was significant (as in the advanced stages of testing), as well as when a large number of hybrids are evaluated in fewer locations (as in the early stages of testing), where the main goal is to discard inferior genotypes, the use of GGE biplot is more prevalent. In conclusion, GGE biplot tool has become increasingly popular in cultivar evaluation and mega-environment investigation for plant breeders and agricultural researchers (Yan *et al*., 2000), and many studies on G × E interaction effect on crop growth, yield and other agronomic traits have been conducted in various plants using GGE biplot.

Keeping all these in view present study was conducted to delineate the adaptability and stability of genotypes of soybean.

Materials and Methods

Experimental materials were comprised of 40 genotypes (Table 1) of soybean sown in three different locations of Gujarat, under the jurisdiction of Anand Agricultural University (AAU)

Table 1 List of soybean genotypes and their source

Sr. No.	Name	Source	Sr. No.	Name	Source
1	Gourav	AAU, Devgadh Baria	21	GS 2	JAU, Amreli
2	Doko	AAU, Devgadh Baria	22	GS 3	JAU, Amreli
3	Birsa Soya	AAU, Devgadh Baria	23	PS 1670	JAU, Amreli
4	Lee	AAU, Devgadh Baria	24	BAUS 31-17	JAU, Amreli

5	JS 335	AAU, Devgadh Baria	25	MACS 1701	JAU, Amreli
6	JS 20-34	AAU, Devgadh Baria	26	RSC 11-35	JAU, Amreli
7	JS 20-69	AAU, Devgadh Baria	27	SL 1212	JAU, Amreli
8	NRC 131	AAU, Devgadh Baria	28	PS 1661	JAU, Amreli
9	EC 37939	AAU, Devgadh Baria	29	PS 1660	JAU, Amreli
10	EC 39045	AAU, Devgadh Baria	30	KDS 114	JAU, Amreli
11	EC 39044	AAU, Devgadh Baria	31	JS 22-14	JAU, Amreli
12	EC 100804	AAU, Devgadh Baria	32	JS 22-11	JAU, Amreli
13	NRC 193	AAU, Devgadh Baria	33	AS-15	JAU, Amreli
14	EC 109543	AAU, Devgadh Baria	34	NRC 128	JAU, Amreli
15	NRC 192	AAU, Devgadh Baria	35	PS 1659	JAU, Amreli
16	RVS 2011-4	JAU, Amreli	36	MACS NRC 1711	JAU, Amreli
17	BAUS 96-17	JAU, Amreli	37	IVT-E	JAU, Amreli
18	AUKS 203	JAU, Amreli	38	CAUM 52	JAU, Amreli
19	GS 1	JAU, Amreli	39	RVSM 2012-11	JAU, Amreli
20	DS 3152	JAU, Amreli	40	NRC 37	JAU, Amreli

during *kharif*-2022. The diverse environments selected for conducting an experiment were Experimental Farm, Department of Genetics & Plant Breeding, B. A. College of Agriculture, AAU, Anand considered as E_1, Agricultural Research Station, AAU, Derol as E_2 and Tribal Research cum Training Centre, AAU, Devgadh Baria considered as E_3. The experimental material comprised of 40 diverse genotypes of soybean sown in a randomized block design with three replications at all environments. Each genotype was grown in a single row plot of 3.0 m length spaced at 45 × 10 cm. The recommended cultural practices including plant protection-measures were followed uniformly to raise a good crop and the observations were recorded and analyzed using AMMI model of stability analysis.

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AMMI model was used in the analysis of data obtained from three different locations. The model for the analysis id given below

ANOVA: $Yij= \mu + \alpha_g + \beta_e + \alpha\beta_{ge} + \rho_{ij} + \varepsilon_{ijk}$

PCA : $Y_{ij} = \mu + \Sigma_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ij} + \varepsilon_{ijk}$

AMMI :$Y_{ij} = \mu + \alpha_g + \beta_e + \Sigma_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ij} + \varepsilon_{ijk}$

Where,

The additive parameters

μ = Grand mean

α_g= Deviation of genotype ‘g’ from grand mean

β_e = Deviation of environment ‘e’

The multiplicative parameters

λ_n= Singular value for Interaction Principal Component Axis n (IPCA)

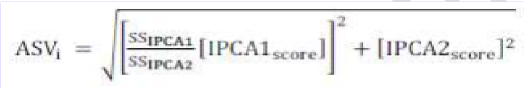
γ_{gn}= Genotype eigenvector for axis ‘n’

δ_{en}= Environment eigenvector

ρ_{ij} = Residual

ε_{ijk} = Error term

AMMI stability value (Purchase *et al*., 2000) was calculated to correlate the mean value and stability based on IPCA scores. It was calculated using following formula.



$$ASV_i = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}}[IPCA1_{score}]\right]^2 + [IPCA2_{score}]^2}$$

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Check assumptions of the models

ANOVA model assumtions:

- Normality:
- Homogeneity of variance:
- Independence:

AMMI model assumptions:

1. **Equal Weights**
2. **No Outliers**
3. **Residual Terms**

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Results and Discussion

Analysis of variance

The analysis of variance for all the individual location (Table 2) revealed highly significant mean sum of squares due to genotypes for all the characters *viz*., Days to 50% flowering, days to maturity, plant height, primary branches per plant, pods per plant, pod length, seeds per pod, seed yield per plant, 100 seed weight, protein and oil content indicating presence of high genetic variability in the experimental material.

The broad range of variability was revealed from the pooled analysis of variance (Table 3) among the tested genotypes as it was found significant at both 5% and 1% level of significance for all the characters studied. The selected environments were also found significantly different for all the characters. This indicated the environment selected for the present study were different. For all characters except days to maturity G × E interaction were found highly significant which indicated the role of environment for expression of all these characters (Table 3). AMMI stability analysis was performed for all the characters showing significant G X E interaction (Table 4).

Combined analysis of variance for yield and its attributing traits

The effect of G x E on expression of characters in soybean can be best explained with the use of AMMI model ANOVA of AMMI showed significant variations for genotypes, environments and G x E at both level of significance for all the characters studied except days to maturity. Hence the GGE biplot analysis was not possible for that character.

The findings of the pooled analysis of variance as per the AMMI model are shown in Table 4. From the ANOVA of AMMI model, the maximum per cent of variation was contributed by environment for days to flowering (64.02%), plant height (79.11%), primary branches per plant (49.26%), pods per plant (41.34%), protein content (33.80%) and grain yield per plant (48.62%) and genotypes contributed highest variation to pod length (61.47%), seeds per pod (52.71%) and oil content (70.44%). The GEI effect was significant for all the characters studied. Which explains that most of the characters were largely influenced by the environment for complete expression.

Mean value comparison among genotypes across environments (Table 5)

The mean value for all the characters across environments was significant for all the characters. The mean value for 50% flowering ranged from 52.00 to 46.78 with an average of 49.39 days. The genotypes, G6 and G5 required less days for 50% flowering. However, the mean values for seed yield per plant was ranged from 37.99g/plant to 7.79g/plant. The genotype G10 had higher seed yield per plant whereas, G6 had lower seed yield per plant. The average oil content in these genotypes was 17.61 with a range of 11.8%-23.43%. The highest oil content was found in the G17 while, G28 had lowest oil content

Table 2 Environment wise RBD analysis for all characters

Sources	df	Days to 50% flowering			Days to maturity			Plant height (cm)			Primary branches per plant		
		E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3
Replication	2	9.56	11.43	8.57	2.04*	0.88*	1.79*	10.20*	24.31	78.74	2.04*	0.88*	1.79*
Treatment	39	23.44**	11.51**	19.51**	6.04**	4.00**	11.22**	56.96**	226.76**	660.17**	6.04**	4.00**	11.22**
Error	78	6.18	4.68	3.46	0.57	0.21	0.53	2.19	11.13	38.38	0.57	0.21	0.53
Total	119												

Sources	df	Pods per plant			Pod length (cm)			Seeds per pod			Seed yield per plant (g)		
		E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3
Replication	2	252.66	120.40	450.43	0.12	0.01	0.06	0.07*	0.09*	0.12*	35.61*	28.31*	40.32
Treatment	39	2250.73**	1953.83**	5096.36**	0.30**	0.27**	0.61**	0.13**	0.30**	0.47**	238.54**	117.82**	538.15
Error	78	83.38	64.48	112.76	0.08	0.08	0.10	0.02	0.02	0.03	7.42	5.87	18.50
Total	119												

Sources	df	100 seed weight (g)			Oil content (%)			Protein content (%)		
		E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3
Replication	2	0.25	0.29	0.58	0.47	1.78*	2.88*	2.19*	1.62	4.08*
Treatment	39	8.13**	6.13**	9.19**	42.66**	33.03**	25.46**	50.87**	53.09**	64.55**
Error	78	0.38	0.22	0.26	0.50	0.48	0.66	0.63	0.83	1.04
Total	119									

Table 3 Pooled RBD analysis of all environments for all characters

Sources	df	DF	DM	PH (cm)	PB	PP	PL (cm)	SPP	SYP (g)	100 SW (g)	OC (%)	PC (%)
Rep/Env	2	2	2	2	2	2	2	2	2	2	2	2
Environment	2	1889.90**	2202.68**	69691.60**	402.60**	127849.70**	1.94**	0.01**	16506.40**	233.49**	20.81**	517.27**
Genotypes	39	33.07**	68.70**	520.89**	9.64**	5227.12**	0.79**	0.48**	417.43**	12.83**	72.00**	64.62**
G X E	78	10.70**	20.95	211.51**	5.81**	2036.89**	0.20**	0.21**	238.54**	5.31**	14.57**	51.95**
Pooled error	234	4.78	17.55	17.24	0.44	86.87	0.09	0.02	10.60	0.28	0.55	0.83
Total	359											

DF-Days to 50% flowering
DM- Days to maturity
PH-Plant height
PB-Primary branches per plant

PP- Pods per plant
PL-Pod length
SPP-Seeds per pod
SYP-Seed Yield per Plant

100SW-100 Seed Weight
OC-Oil Content
PC-Protein Content

***, ** Significant at 5% and 1% respectively**

Table 4 Pooled analysis of variance over environments as per AMMI model for various characters of soybean

Source of variation	df	Days to 50% flowering		Plant height (cm)	
		MSS	% Explained	MSS	% Explained
		1		2	
Trials	119	49.61		1480.63	
Environments	2	1889.91**	64.02	69691.61**	79.11
Genotypes	39	33.07**	21.84	520.89**	11.53
G × E	78	10.70**	14.14	211.51**	9.36
IPCA I	40	12.38**	59.40	352.24**	85.4
IPCA II	38	8.92**	40.60	63.37**	14.6
Pooled Error	234	4.78		17.23	

Source of variation	df	Primary branches per plant		Pods per plant	
		MSS	% Explained	MSS	% Explained
		3		4	
Trials	119	13.73**		5196.93	
Environments	2	402.60**	49.26	127849.70**	41.34
Genotypes	39	9.64**	23.00	5227.12**	32.96
G × E	78	5.81**	27.74	2036.89**	25.69
IPCA I	40	8.51**	75.1	3369.32**	84.8
IPCA II	38	2.97**	24.9	634.34**	15.2
Pooled Error	234	0.44		86.87	

Source of variation	df	Pod length (cm)		Seeds per pod	
		MSS	% Explained	MSS	% Explained
		5		6	
Trials	119	0.42		0.30	
Environments	2	1.94**	7.74	0.01**	0.05
Genotypes	39	0.79**	61.47	0.48**	52.71
G × E	78	0.20**	30.79	0.21**	47.23
IPCA I	40	0.31**	79.2	0.29**	70.3
IPCA II	38	0.08**	20.8	0.13**	29.7
Pooled Error	234	0.09		0.02	

Source of variation	df	Seed yield per plant (g)		100 seed weight (g)	
		MSS	% Explained	MSS	% Explained
		7		8	
Trials	119	570.80		11.61	
Environments	2	16506.39**	48.62	233.49**	33.80
Genotypes	39	417.43**	23.98	12.83**	36.21
G × E	78	238.54**	27.40	5.31**	29.99
IPCA I	40	396.70**	85.3	5.77**	55.7
IPCA II	38	72.07**	14.7	4.83**	44.3
Pooled Error	234	10.60		0.28	

Source of variation	**df**	**Oil content (%)**		**Protein content (%)**	
		MSS	**% Explained**	**MSS**	**% Explained**
		9		**10**	
Trials	119	33.50		63.92	
Environments	2	20.81**	1.04	517.27**	13.60
Genotypes	39	72.00**	70.44	64.62**	33.13
G × E	78	14.57**	28.51	51.95**	53.27
IPCA I	40	27.44**	96.6	52.78**	52.1
IPCA II	38	1.02**	3.4	51.07**	47.9
Pooled Error	234	0.55		0.83	

***, ** Significant at 5% and 1% levels, respectively**

AMMI model analysis for days to 50% flowering, seed yield per plant and oil content

According to the model of stability analysis, the genotypes, environment and G x E had significant effect on the expression of days to 50% flowering, seed yield per plant and oil content.

For 50% flowering the significantly ($p<0.05$) higher variation was contributed by the environments (64.02%) followed by genotypes (21.84%) and G x E (14.14%). It also reported that first two IPCAs explained 100% of GEI with 59.40% of variation due to PC1 and 40.60% of variation due to PC2. Amare and Tamado (2014) indicated the most accurate model for AMMI can be forecasted by using the first two IPCA. The PC1 accounted about 59.4% and PC 2 accounted 40.6% of the variation. Similar results of G x E variation was observed by Dabessa *et al.* (2016) and Silva *et al.* (2022).

In case of seed yield per plant, the significantly higher variation was explained by environment (48.62%) followed by GEI (27.40%) and genotypes (23.98%). Further the PC1 explained 85.3% and PC2 explained 14.7% of variation combined making 100% of variation of GEI. Both the above characters are majorly explained by the environmental sum of squares which indicates that the selected environments were diverse and the influence of environment on expression of these characters. Similar results were also reported by the Atnaf *et al.* (2013), Mukuze *et al.* (2020), Mwiinga *et al.* (2020) and Razmi *et al.* (2020)

Soybean being the oilseed crop, oil content is one of the most important quality parameter to be considered. For oil content, the genotypes (70.44%) contributed highest variation followed by GEI (28.51%) and environment (1.04%). This explains that environment had a least significant role in the expression of this character. Further GEI was divided into only first two IPCAs, PC1 explained 96.6%

of the variation and PC2 explained 3.4% of the variation with significant differences ($p<0.05$). Similar result was reported by Dabessa *et al.* (2016), Kocaturk *et al.* (2019) and Mukuze *et al*. (2020).

Table 5 Mean values comparison among genotypes across the locations

Sr. No.	Genotype	DF	PH	NPB	NPP	PL	SPP	SYP	100 SW	OC	PC
1	**Gourav**	46.11	38.88	7.23	108.08	3.81	3.00	27.98	8.73	12.79	36.30
2	**Doko**	50.44	37.17	6.82	98.19	4.11	3.24	31.20	7.98	15.97	43.11
3	**Birsa Soya**	45.22	34.33	6.91	102.90	3.92	2.61	24.30	10.18	18.64	34.54
4	**Lee**	48.33	28.89	5.98	123.33	4.07	2.61	33.04	9.87	17.78	36.00
5	**JS-335**	42.11	25.12	7.89	103.23	3.85	2.86	28.37	10.02	16.38	38.38
6	**JS-20-34**	46.78	22.44	3.92	30.88	4.00	2.67	7.79	9.08	19.36	38.54
7	**JS-20-69**	47.44	35.97	9.11	97.51	3.84	2.78	24.36	8.58	13.34	35.82
8	**NRC-131**	47.89	43.09	7.57	110.29	3.92	3.12	28.51	8.88	12.36	38.82
9	**EC-37939**	44.56	43.16	8.33	122.67	3.49	3.13	31.72	8.53	18.03	37.81
10	**EC 39045**	48.33	50.36	9.80	144.98	3.59	2.94	37.99	7.37	15.51	36.78
11	**EC 39044**	52.00	32.66	8.51	91.70	3.62	2.86	21.39	9.30	13.06	41.93
12	**EC 100804**	50.11	51.67	8.96	119.91	3.59	3.02	26.01	6.72	13.43	35.10
13	**NRC 193**	50.44	44.08	7.68	114.57	3.53	2.50	27.08	8.19	12.78	32.99
14	**EC109543**	48.77	31.54	7.38	106.68	3.72	3.04	33.98	9.89	15.81	36.15
15	**NRC 192**	45.00	45.83	6.38	74.23	3.96	2.93	26.09	11.03	16.40	39.98
16	**RVS-2011-4**	47.11	39.35	6.07	81.98	3.95	3.07	26.78	10.92	21.12	40.06
17	**BAUS-96-17**	49.11	31.69	7.63	120.68	3.76	2.92	36.62	10.97	23.43	37.74
18	**AUKS-203**	46.33	35.08	6.80	43.06	4.29	3.16	10.87	10.13	15.18	37.26
19	**GS 1**	48.44	39.84	7.96	124.66	3.29	2.69	29.28	8.04	14.39	35.24
20	**DS-3152**	47.44	33.97	7.69	105.84	3.89	2.91	36.46	10.40	18.12	37.21
21	**GS 2**	50.33	61.26	8.71	130.92	4.02	3.03	34.31	10.02	17.62	37.24
22	**GS 3**	47.77	33.90	7.72	64.56	3.80	2.93	18.67	8.32	17.20	31.94
23	**PS-1670**	48.00	28.64	7.04	91.91	4.06	2.69	27.19	9.92	15.56	38.13
24	**BAUS 31-17**	50.00	32.92	7.06	83.81	3.58	2.66	21.64	9.62	15.50	34.56
25	**MACS 1701**	45.55	28.55	6.93	57.39	4.58	3.60	20.02	10.03	16.11	36.45
26	**RSC-11-35**	46.11	38.48	7.28	97.84	3.88	3.16	31.01	11.20	16.46	38.62
27	**SL-1212**	46.66	29.75	7.44	80.61	3.42	2.54	17.85	7.56	17.48	35.50
28	**PS-1661**	48.44	42.17	6.91	89.24	3.46	3.13	20.74	8.40	11.80	37.20
29	**PS-1660**	47.78	34.82	7.38	67.63	3.36	2.84	18.61	7.74	14.08	41.68
30	**KDS-114**	46.77	31.23	7.61	82.72	4.10	3.11	23.95	8.80	21.36	36.31
31	**JS-22-14**	48.89	34.94	7.30	81.64	4.26	3.09	24.38	11.69	15.80	40.19
32	**JS-22-11**	46.89	40.17	7.73	85.14	3.65	3.23	21.59	8.24	20.87	41.42
33	**AS-15**	47.33	40.24	9.24	85.19	3.69	3.04	29.39	8.63	17.71	34.46
34	**NRC-128**	49.22	36.17	7.20	69.82	3.97	2.82	17.05	9.54	18.73	35.40
35	**PS-1659**	49.11	28.70	8.12	103.57	3.57	3.03	28.32	8.77	14.79	36.12
36	**MACS NRC 1711**	49.00	30.64	6.24	101.66	4.19	3.20	32.91	9.31	17.67	37.25
37	**IVT-E**	46.22	31.37	7.12	64.08	3.79	3.12	21.13	11.27	15.41	36.82
38	**CAUM-52**	45.44	39.68	7.06	91.28	3.88	3.21	29.55	9.83	13.04	44.15
39	**RVSM-2012-11**	48.78	38.37	6.21	76.76	4.36	3.08	25.52	10.84	12.79	41.34
40	**NRC-37**	48.44	27.46	6.90	118.21	4.36	3.19	35.82	9.22	21.63	36.91
	SEm	1.25	2.12	0.37	5.34	0.16	0.08	1.81	0.30	0.43	0.53
	C. V. (%)	4.60	10.22	8.75	10.32	7.63	4.79	12.50	5.69	4.50	2.42
	C. D. (5%)	3.53	5.96	1.05	15.05	0.48	0.23	5.12	0.86	1.20	1.47
	Grand mean	47.72	36.36	7.39	93.73	3.85	2.97	26.23	9.34	16.38	37.54
	Max.	52.00	61.26	9.8	144.98	4.58	3.60	37.79	11.69	23.43	44.15
	Min.	46.78	22.44	3.92	30.88	3.29	2.50	7.79	6.72	11.80	31.94

Footnote: CV-, CD-, SEm-

Table 6IPCA scores and ASV of different soybean genotypes and environments for days to 50 % flowering

Sr. No.	Genotype	IPCA I	IPCA II	ASV	Rank of ASV
1	**Gourav**	-0.31	0.29	0.54	9
2	**Doko**	-0.53	-0.69	1.04	28
3	**Birsa Soya**	-1.57	0.90	2.48	40
4	**Lee**	-0.63	0.39	1.00	27
5	**JS-335**	-0.81	0.29	1.22	33
6	**JS-20-34**	-0.04	0.84	0.84	22
7	**JS-20-69**	-0.36	-0.23	0.58	10
8	**NRC-131**	-0.59	0.68	1.10	29
9	**EC-37939**	-0.48	0.41	0.81	19
10	**EC 39045**	0.14	-0.23	0.30	3
11	**EC 39044**	-0.33	-1.10	1.20	32
12	**EC 100804**	0.05	-0.82	0.83	21
13	**NRC 193**	-0.32	-0.51	0.70	16
14	**EC109543**	0.12	-0.44	0.48	7
15	**NRC 192**	-0.07	-0.40	0.42	4
16	**RVS-2011-4**	0.02	-0.54	0.54	8
17	**BAUS-96-17**	-0.32	-0.51	0.70	15
18	**AUKS-203**	0.15	-0.37	0.43	5
19	**GS 1**	0.35	0.53	0.74	17
20	**DS-3152**	0.77	-0.06	1.12	31
21	**GS 2**	0.27	0.52	0.66	13
22	**GS 3**	0.66	0.80	1.25	34
23	**PS-1670**	0.93	-0.18	1.38	37
24	**BAUS 31-17**	0.60	-0.30	0.94	24
25	**MACS 1701**	0.39	-0.11	0.58	11
26	**RSC-11-35**	-0.89	-0.53	1.42	38
27	**SL-1212**	0.44	0.03	0.66	12
28	**PS-1661**	0.03	0.26	0.27	1
29	**PS-1660**	0.64	-0.004	0.94	25
30	**KDS-114**	1.04	0.90	1.60	39
31	**JS-22-14**	-0.35	-0.59	0.79	18
32	**JS-22-11**	0.32	-0.49	0.68	14
33	**AS-15**	0.50	0.56	0.92	23
34	**NRC-128**	-0.62	-0.34	0.96	26
35	**PS-1659**	-0.54	0.25	0.83	20
36	**MACS NRC 1711**	-0.09	-0.26	0.29	2
37	**IVT-E**	-0.45	1.07	1.26	35
38	**CAUM-52**	0.77	-0.06	1.12	30
39	**RVSM-2012-11**	0.83	0.32	1.26	36
40	**NRC-37**	0.28	0.15	0.44	6
E_1	**Anand (E_1)**	-1.11	-2.47		
E_2	**Derol (E_2)**	-1.79	2.10		
E_3	**Devgadh Baria (E_3)**	2.90	0.36		

Comment [Ma4]: Give footnote what the CV, CD and SEm stands for

Table 7 IPCA scores and ASV of different soybean genotypes and environments for seed yield per plant (g)

Sr. No.	Genotype	IPCA I	IPCA II	ASV	Rank of ASV
1	**Gourav**	-1.00	1.62	6.00	22
2	**Doko**	1.80	-0.24	10.47	31
3	**Birsa Soya**	-0.71	-1.27	4.31	18
4	**Lee**	0.25	1.24	1.89	9
5	**JS-335**	-0.60	0.66	3.54	16
6	**JS-20-34**	-1.96	-0.54	11.40	34
7	**JS-20-69**	-1.15	-0.53	6.67	24
8	**NRC-131**	1.75	0.27	10.18	30
9	**EC-37939**	1.96	-0.28	11.38	33
10	**EC 39045**	1.90	0.66	11.05	32
11	**EC 39044**	-1.05	0.73	6.12	23
12	**EC 100804**	2.04	-1.26	11.92	35
13	**NRC 193**	-0.43	-1.55	2.94	13
14	**EC109543**	-0.68	0.69	3.98	17
15	**NRC 192**	0.26	0.04	1.52	6
16	**RVS-2011-4**	-0.15	-0.77	1.15	5
17	**BAUS-96-17**	-2.16	-0.97	12.56	36
18	**AUKS-203**	-1.67	-0.99	9.73	29
19	**GS 1**	-2.16	0.61	12.57	37
20	**DS-3152**	2.79	0.26	16.19	39
21	**GS 2**	0.36	0.99	2.32	12
22	**GS 3**	0.14	-0.07	0.82	3
23	**PS-1670**	1.29	0.29	7.47	27
24	**BAUS 31-17**	0.00	0.17	0.17	1
25	**MACS 1701**	0.02	-0.14	0.18	2
26	**RSC-11-35**	-1.09	2.20	6.69	25
27	**SL-1212**	-0.33	-0.46	1.99	10
28	**PS-1661**	0.93	-0.79	5.45	20
29	**PS-1660**	-0.28	0.50	1.69	8
30	**KDS-114**	1.03	-0.17	5.97	21
31	**JS-22-14**	-1.55	-1.86	9.21	28
32	**JS-22-11**	-0.27	0.36	1.60	7
33	**AS-15**	2.94	0.03	17.04	40
34	**NRC-128**	-0.56	-0.57	3.28	14
35	**PS-1659**	-2.60	0.62	15.10	38
36	**MACS NRC 1711**	1.25	-0.01	7.26	26
37	**IVT-E**	0.59	-0.58	3.47	15
38	**CAUM-52**	-0.82	-0.11	4.76	19
39	**RVSM-2012-11**	0.16	-0.49	1.06	4
40	**NRC-37**	-0.26	1.70	2.28	11
E_1	**Anand (E_1)**	-3.80	3.76		
E_2	**Derol (E_2)**	-3.15	-4.00		
E_3	**Devgadh Baria (E_3)**	6.95	0.24		

AMMI biplot analysis and ASV rankings

The GGE refers to the genotype main effect (G) and the genotype x environment interaction (GE), which are the two most important sources of variation for cultivar evaluation in a multi environment trials (Yan *et al.*, 2007). A GGE biplot displays the genotypic main effect (G) and genotype by environment interaction (GE) of a genotype by-environment dataset (Yan *et al.*, 2000).

Table 8 IPCA scores and ASV of different soybean genotypes and environments for oil content (%)

Sr. No.	Genotype	Mean (%)	Rank	IPCA I	IPCA II	ASV	Rank of ASV
1	**Gourav**	12.79	36	-0.34	0.12	9.65	14
2	**Doko**	15.97	21	-0.50	-0.46	14.10	22
3	**Birsa Soya**	18.64	8	-1.06	-0.09	30.03	35
4	**Lee**	17.78	11	0.96	0.06	27.38	33
5	**JS-335**	16.38	19	1.47	0.87	41.83	39
6	**JS-20-34**	19.36	6	-0.11	0.30	3.08	3
7	**JS-20-69**	13.34	33	-0.34	0.48	9.72	15
8	**NRC-131**	12.36	39	-0.53	0.35	15.00	26
9	**EC-37939**	18.03	10	-0.88	0.17	25.13	32
10	**EC 39045**	15.51	25	0.26	0.04	7.39	11
11	**EC 39044**	13.06	34	-0.76	0.12	21.63	30
12	**EC 100804**	13.43	32	0.38	-0.16	10.72	18
13	**NRC 193**	12.78	38	1.00	-0.26	28.36	34
14	**EC109543**	15.81	22	1.25	-0.30	35.51	37
15	**NRC 192**	16.40	18	1.73	0.52	49.26	40
16	**RVS-2011-4**	21.12	4	-0.60	-0.11	17.09	27
17	**BAUS-96-17**	23.43	1	0.22	-0.33	6.29	8
18	**AUKS-203**	15.18	28	0.24	0.07	6.89	10
19	**GS 1**	14.39	30	-0.23	0.55	6.55	9
20	**DS-3152**	18.12	9	1.33	-0.29	37.83	38
21	**GS 2**	17.62	14	1.14	-0.28	32.52	36
22	**GS 3**	17.20	16	-0.84	0.20	23.77	31
23	**PS-1670**	15.56	24	-0.36	0.05	10.26	17
24	**BAUS 31-17**	15.50	26	0.51	-0.14	14.48	24
25	**MACS 1701**	16.11	20	0.49	-0.12	13.87	21
26	**RSC-11-35**	16.46	17	-0.14	0.01	3.92	4
27	**SL-1212**	17.48	15	-0.18	-0.03	5.20	6
28	**PS-1661**	11.80	40	-0.50	0.08	14.31	23
29	**PS-1660**	14.08	31	-0.04	-0.09	1.01	2
30	**KDS-114**	21.36	3	-0.29	-0.37	8.33	12
31	**JS-22-14**	15.80	23	-0.63	0.47	17.89	29
32	**JS-22-11**	20.87	5	-0.43	-0.32	12.35	20
33	**AS-15**	17.71	12	-0.53	0.07	14.94	25
34	**NRC-128**	18.73	7	-0.34	-0.24	9.60	13
35	**PS-1659**	14.79	29	-0.34	-0.21	9.75	16
36	**MACS NRC 1711**	17.67	13	-0.61	0.18	17.40	28
37	**IVT-E**	15.41	27	-0.39	-0.20	10.98	19
38	**CAUM-52**	13.04	35	-0.20	-0.05	5.76	7
39	**RVSM-2012-11**	12.79	37	0.01	-0.05	0.29	1
40	**NRC-37**	21.62	2	0.17	-0.59	4.79	5
Environments							
E_1	**Anand (E_1)**	16.79	1	3.56	-0.13		
E_2	**Derol (E_2)**	15.96	3	-2.05	-1.27		
E_3	**Devgadh Baria (E_3)**	16.41	2	-1.51	1.40		
	Grand mean	16.38					

Genotypes having a zero IPCA 1 score are less influenced by the environment and better adapted to all environments.According to AMMI biplot (Fig.1a) analysis for 50% flowering, G16, G18, G27 and G32 genotypes had low mean and near zero IPCA value indicated the adaptation to all environments. Genotypes G3, G5, G6 and G26 were positioned far away from the origin with lower mean value indicated that they were unstable genotypes and adapted only to favourable environment.Based on ASV values the genotypes, G28, G36 and G10 had lowest ASV values hence considered as highly stable genotypes and G3, G30 and G26 had lowest ASV values hence they were identified as highly unstable genotypes.

Whereas, biplot (Fig.2a) for seed yield per plant genotypes G4, G16 and G40 were considered as the most stable genotypes among all the genotypes since they were least affected by the environment. The genotypes G15, G22, G24, G25, G27, G29, G32 and G39 performed well in the poor environment. Genotypes G10, G20 and G33 were considered as specifically adapted to the favourable environment (E_3). Based on ASV ranking genotype G24, G25 and G22 considered as high stable genotypes. G33, G20 and G35 got highest ranking 40, 39 and 38 respectively and considered as a highly unstable genotypes.

Based on the biplot (Fig. 3a) for oil content, the genotypes G6, G17, G26 and G27 having general adaptability as it was found at the right-hand side of the grand mean level and close to IPCA=0 line. G29, G39, G10, G18, G19 and G38 genotypes had low mean and near zero IPCA value indicated their adaptation to poor environment. Genotypes G4, G5, G15, G20 and G21 were positioned far away from the origin with higher IPCA value indicated that unstable genotypes and adapted to only favourable environment (E_1). According to the ASV parameter the genotypes, G39 G29 and G6 were considered as highly stable genotypes with lowest ASV values whereas, genotypes G15, G5 and G20 were considered as unstable genotypes with highest ASV values.

Which won where polygon view of GGE biplot

GGE biplot produces best polygons to view or visualize the genotype x environment interaction pattern (Yan and Kang, 2003). Visualization of the ‘Which-won-where’ pattern in the polygon view is helpful to estimate possible existence of different mega-environments in the target environment (Yan and Rajcan, 2002; Yan *et al.*, 2000; Yan and Tinker, 2006). Figure 1b, 2b and 3b presents a polygon view of thirty two soybean genotypes tested at three environments. With this biplot, a polygon was constructed by connecting the vertex genotypes (located farthest away from the biplot origin in various directions) with straight lines and as a result, the rest of the genotypes placed inside the polygon. The polygon is formed by connecting the signs of the genotypes that are farthest away from the biplot origin, such that all other genotypes are contained in the polygon and perpendicular lines divide the polygon into sectors. Sectors help to visualize the mega-environments. This means that winning genotypes for each sector are placed at the vertex.

The AMMI model analysis of variance revealed a significant IPCA II value. This aided in the creation of the AMMI II biplot (Fig. 1b). According to Fig. 2b whole biplot was divided in to seven sectors. The genotypes in a sector were similar in performance compared to the genotypes in other sectors. First sector contained Devgadh Baria (E_3) with a vertex genotype G30 which indicated that this genotype showed highest days for 50% flowering at Devgadh Baria (E_3). Anand environment was found in the 3rd sector with a vertex genotypes of G11 and G12 which indicated that these genotypes took more days for flowering. The 5th sector contained Derol (E2) with a vertex genotypes of G3 and G37 which indicated that these genotypes showed highest days for flowering at Derol.

According to the biplot 2 (Fig.2b) of seed yield per plant, the polygon was formed with 7 sectors. The E3 was found in the 2nd sector with a vertex genotypes of G10, G12, G20 and G33. The 4th sector contained the E2 with a vertex genotype G31 and the 7th sector contained E1 with vertex genotype G26. However, genotypes within the polygon, particularly those located near the biplot origin were less responsive than the genotypes on the vertices and the ideal genotype would be one closest to the origin. The genotypes G15, G16, G22, G24, G25, G27, G32 and G39 were found near the origin which indicated that they were insensitive to the environmental conditions. Genotype G33 and G36 found on the PC2 line which indicated that these were high yielding genotypes.

Biplot 2 for oil content (Fig.3b) was drawn by considering both PC1 and PC2 values which resulted in the formation of eight sectors.1st sector contained E1 environment with a vertex genotype G5, G14, G15 and G20. E2 environment was found in 5th sector with a vertex genotypes G3, G9 and G22. The 7th sector contained E3 environment with a vertex genotype G19. In this study, genotypes G6, G26, G27, G38 and G39 were found very close to the origin and hence were unaffected by environmental interaction forces, resulting in general adaptation to all the environments.

Conclusion

The present study was conducted to delineate the stability and adaptability of genotypes of soybean by using combined ANOVA, AMMI analysis and GGE biplot technique. Based on the individual analysis of variance all the parameters *viz.,* days to 50% flowering, days to maturity, plant height, primary branches per plant, pods per plant, pod length, seeds per pod, seed yield per plant, 100 seed weight, oil content and protein content showed significant differences among the genotypes across all the locations. In pooled analysis of variance all parameters except days to maturity showed significant G X E interaction which resulted in the analysis of stability by AMMI model. Analysis of variance based on AMMI model indicated that variation due to environment and G X E played a significant role in the expression of most of the characters studied. G X E further partitioned into interaction principal component axis (IPCA I and IPCA II). As per the per cent contribution from IPCA I and IPCA II, AMMI 1 and AMMI 2 biplots were constructed. For days to flowering the genotypes G1, G7, G15, G16 and G18 took less days to flower with higher stability hence, these genotypes can be exploited for earliness character with stability in soybean.

According to the AMMI 1 model for seed yield per plant, E_3 was considered as the most suitable environment for seed yield per plant while, E_2 was considered as the poor environment. The genotypes G4, G16 and G40 were considered as the most stable genotypes and had general adaptation for seed yield per plant among all the genotypes since they were least affected by the environment. The genotypes G15, G22, G24, G25, G27, G29, G32 and G39 performed well in the poor environment (E_2). Genotypes G10, G20 and G33 had specific adaptability in potential environment (E_3) because of the similar sign of environment with their IPCA I scores. Based on the AMMI stability value G24, G25 and G22 were considered as stable genotypes over environment while, G33, G20 and G35 were considered as unstable genotypes.According to the AMMI 2 biplot G15, G16, G22, G24, G25, G27, G32 and G39 were considered as high yielding with general adaptability. The vertex genotypes for E_3 were G10, G12, G20 and G33. G31 was for E_2 while, vertex genotype for E_1 was G26. Genotypes G4, G16 and G40 were considered as best genotypes with high average seed yield per plant and general adaptability to all the locations which can be used for further breeding activities.

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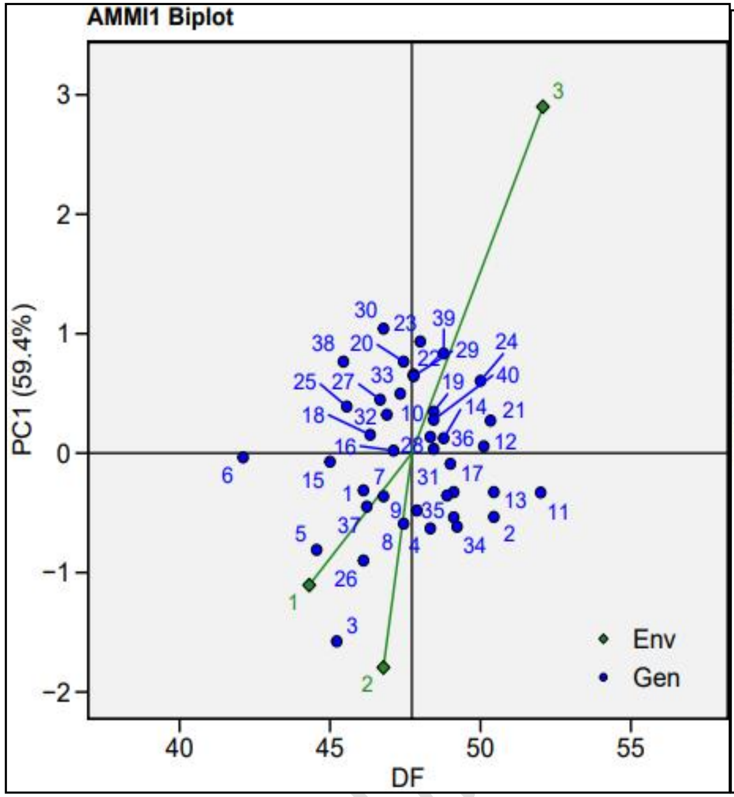

Fig. 1a AMMI 1 biplot display of all genotypes for days to 50% flowering

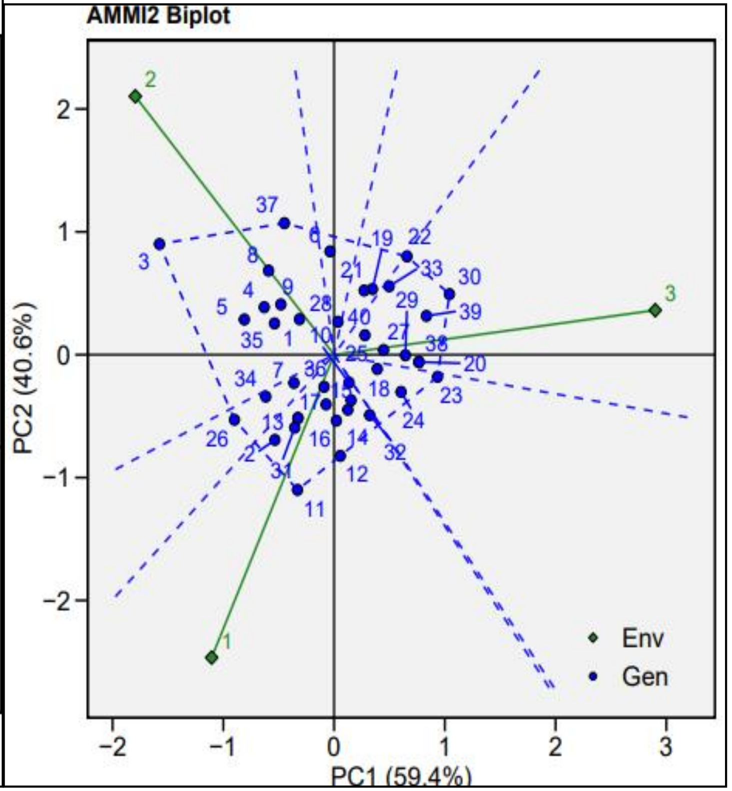

Fig. 1b AMMI 2 biplot display of all genotypes for days to 50% flowering

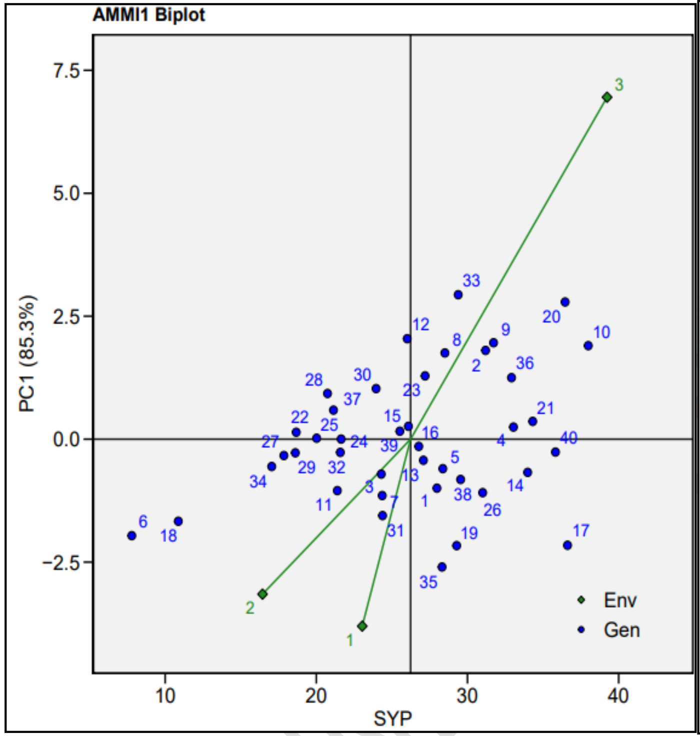

Fig. 2a AMMI 1 biplot display of all genotypes for seed yield per plant

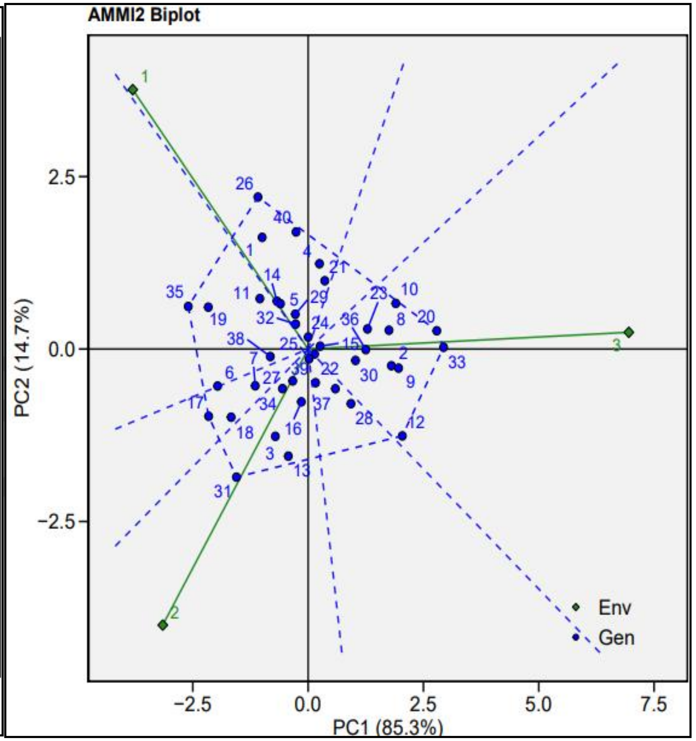

Fig. 2b AMMI 2 biplot display of all genotypes for seed yield per plant

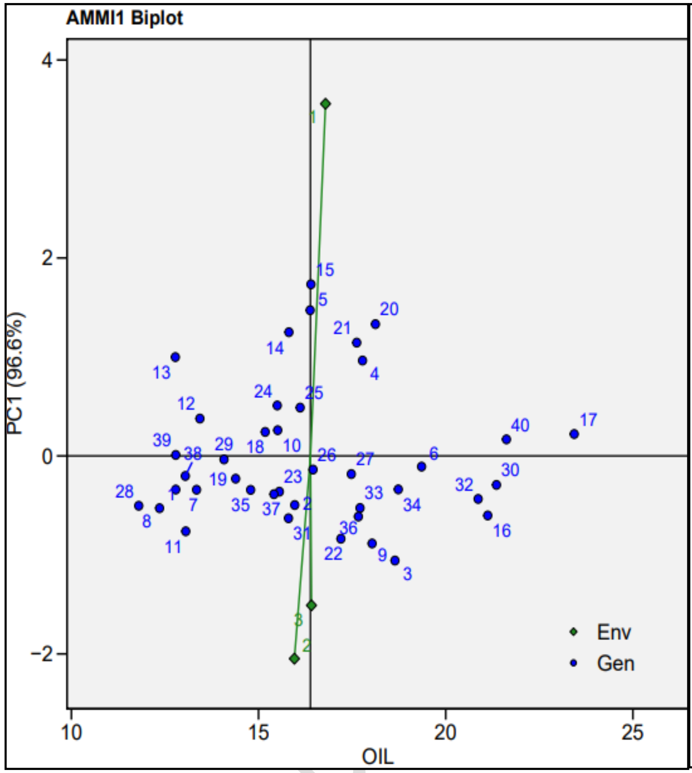

Fig. 3a AMMI 1 biplot display of all genotypes for oil content p

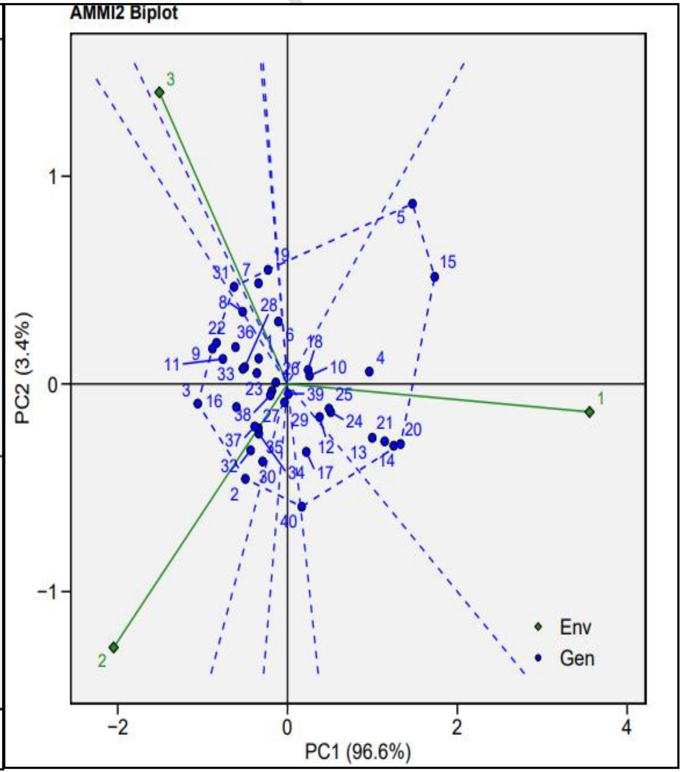

Fig. 3b AMMI 2 biplot display of all genotypes for oil content