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Stability analysis in genotypes of safflower (*Carthamus tinctorius* L.)

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Abstract
To study the G x E interaction and the stability of various safflower genotypes. twelve genotypes of safflower, AICRP on Safflower Parbhani, oil seeds research station in Latur, agricultural research station in Badnapur, and agricultural research station in Somnathpur were the subjects of field experiments carried out at AICRP in an RBD design with three replications. Thirteen morphological characters were used as the subjects of the observations. Analysis of variance revealed significant genotypic differences existed among all the genotypes for all the studied characters, and stability and character association analysis were conducted in accordance with the model of Eberhart and Russell (1966). The genotype PBNS-207 was the highest yielding, followed by PBNS-185 and PBNS-154, according to mean performance. Environmental indices indicated that environment E4 (Somnathpur), E2 (Latur), E1 (Parbhani), and E3 were the most favourable (Badnapur). The stability parameters showed that PBNS-185 had the highest seed yield per plant stability.

Keywords: Adaptability, G x E interaction, safflower, seed yield, stability

Introduction
One of the most significant and versatile oilseed crops for Rabi is safflower (*Carthamus tinctorius* L.), which is a member of the Asteraceae or Compositae family. Only one of the twenty-five species in the genus Carthamus, with chromosome number 2n=24, is grown commercially (Singh, 2007) [14]. It is indigenous to the Mediterranean and Asia. Safflower is a promising alternative crop in semi-arid agroecosystems and drought-affected areas because of its high drought tolerance (Sargar *et al*., 2021) [13]. Safflower oil contains oleic, linoleic, and linolenic unsaturated fatty acids as well as the saturated fatty acids palmitic and stearic. The traditional safflower seed oil contains the following fatty acids: 6-8% palmitic acid, 2-3% stearic acid, 16-20% oleic acid, and 71-75% linoleic acid.
Safflower yield is affected by a variety of factors, including location, planting date, air temperature, soil, water availability, and light intensity, particularly during the seedling and flowering stages (Hussain *et al.*, 2016) [8]. To create superior cultivars, plant breeders heavily rely on genotype-environment interactions. Interpreting G x E interactions is crucial in safflower breeding efforts for locating superior genotypes under various conditions. The G x E analysis results also show the genotypes' phenotypic stability in each examined environment. (Abdulahi *et al*., 2009) [1]. In these situations, the breeder is frequently forced to choose between selecting genotypes with high general adaptations that can perform well under a variety of conditions or developing specific genotypes for specialised adaptations. (Pourdad & Mohammadi, 2008) [11]

Material and Methods
During the 2019 *Rabi* season, the current investigation was conducted at four sites: AICRP on Safflower Parbhani, Oilseeds Research Station Latur, Agricultural Research Station Badnapur, and Agricultural Research Station Somanathpur. From the AICRP on Safflower, Parbhani, nine safflower genotypes and three check varieties—PBNS-86, PBNS-12, and Sharda—were obtained. At four different locations, genotypes were planted. The experimental material was evaluated in Randomized Block Design (RBD) with three replications at AICRP on Safflower, Parbhani (E1), Oilseeds Research Station, Latur (E2), Agricultural Research Station, Badanapur (E3), and Agricultural Research Station, Somanathpur (E4).

Name of genotypes

Sr. No.	Genotypes
1	PBNS – 86 (check)
2	PBNS – 185
3	PBNS – 200
4	PBNS – 201
5	PBNS – 12 (check)
6	PBNS – 153
7	PBNS – 154
8	PBNS – 197
9	PBNS – 198
10	Sharda (check)
11	PBNS – 207
12	PBNS – 208

Five plants were selected randomly from each treatment for recording observations. Observations were recorded on thirteen characters including Oil content (%) and Seed yield per plant (g). The data recorded for different characters were subjected to statistical analysis. The mean data collected on five competitive selected plants in each replication on each line were subjected to analysis of variance location wise as per the method described by Panse and Sukhatme (1985) [10]. The stability analysis was estimated by using model of Eberhart & Russell (1966) [4].

Result and Discussion:

The analysis of variance for all thirteen characters was significant over different environments. This indicated that material chosen for study is variable and there is scope for further study. Analysis of variances for stability by Eberhart and Russell's (1966) [4], with four environments for various traits showed in table 1. In terms of days to 50% flowering, plant height, number of seeds per capitulum, days to rosette period, seed yield per plant, and seed yield per plot, it was indicated that E1 (Parbhani) is a favourable environment. Plant height, primary branch count, capitula count, number of seeds per capitulum, days to rosette period, oil content, and hull content are all favourable in environment E2 (Latur). Plant height, the number of primary branches per plant, test weight, hull content, and seed volume weight were all favourable in the E3 (Badnapur) environment. All characters except plant height, the number of primary branches per plant, and seed volume weight were found to be favourable in environment E4 (Somnathpur). The different environmental indices indicate that it is necessary to identify genotype in accordance with environmental indices.

The variance resulting from genotypes was significant for plant height and test weight, but highly significant for oil content, hull content, and seed volume weight, according to the results of a pooled analysis of variances across environments. Hull content showed significant environmental variation, while days to 50% flowering, days to maturity, plant height, number of capitula per plant, number of seeds per capitulum, days to rosette, and seed yield per plant and per plot showed highly significant environmental variation. Days to rosette period, days to 50% flowering, days to maturity, plant height, number of capitula per plant, number of seeds per capitulum, and seed yield per plant all had highly significant variance due to Environment + (Genotype x Environment). While the Environment (linear) was highly significant for all characters except for the number of primary branches per plant and test weight, it was significant for oil content, hull content, and seed volume weight.

The fact that the mean squares due to pooled deviation were significant for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of capitula per plant, number of seeds per capitulum, days to rosette period, test weight, seed yield per plot, and seed yield per plant but non-significant for oil content, hull content, and seed volume weight shows that genotypes differed significantly in terms of stabilities, making it impossible to predict their performance under various conditions Non-linear component was highly significant for all characters, according to Badiger *et al*. (2009) [2]. Genotype, environment, and the Environment + (Genotype x Environment) component was all found to be significant by Yadav (2017) [15].

It is difficult to determine the stable genotype when environmental factors, G x E interactions, and various macro and micro-environments are present. There have been numerous attempts to define genotype behaviour in response to various environments. The statistical method developed by Finley and Wilkinson (1963) [5] has been very helpful in identifying phenotypic stability in genotype performance, and he uses the linear regression slope (bi) as a measure of stability. The analysis of Finley and Wilkinson (1963) [5] was enhanced by Eberhart and Russell. To provide genotypic performance predictability and unpredictability, they added a new parameter deviation from regression (S^2di). The most stable genotype, in accordance with Bains and Gupta (1972) [3], is one with a high mean performance, regression coefficient, and a deviation from regression close to zero. The stability parameters were computed and presented in table 2, and the results of the current study showed that there was a significant G x E interaction for all characters. A stable genotype, according to Eberhart and Russell (1966) [4], is one that satisfies the following criteria: high mean (X), regression coefficient (bi) = 1, and deviation from regression (S^2di), which is as small as possible or close to zero.

Days to rosette period revealed that genotypes PBNS-153, PBNS-197 and PBNS-185 were more stable across the environment and high mean, while, genotype PBNS-207 and PBNS-86 were stable and identified as early genotype with bi > 1 recommended for better environment. Whereas, for days to 50% flowering genotypes PBNS-201, PBNS-12, PBNS-198, PBNS-153 and PBNS-207 had observed stable genotype that deviated significantly and regression coefficient near to unity (bi = 1) is recommended for all environments. The genotype PBNS-185 and PBNS-154 had most stable with regression coefficient greater (bi > 1) than unity is recommended for fovorable environment.

Whereas, for days to maturity genotype PBNS-185 and PBNS-86 were identified as early genotype as well PBNS-207, PBNS-153 and Sharda were stable genotype across the environment. However, for primary branches PBNS-198, PBNS-185, PBNS-154 and PBNS-12 were more stable across the genotype. Sharda were significant and regression coefficient greater than unity (bi > 1) and PBNS-208 genotype had bi >1recommanded to favourable environment. Genotype PBNS-200, PBNS-201, PBNS-12 and PBNS-153 were stable for both number of capitula per plant and number of seed per capitulum. For plant height PBNS-198 and PBNS-12 were high mean with regression coefficient greater than unity (bi >1), while, genotype PBNS-154 and PBNS-200 were significant and stable across the environment with bi > 1 as well genotype PBNS-201 was most stable but non-significant

with bi > 1. For test weight genotype PBNS-185, PBNS- 154, PBNS-200 and PBNS-12 observed more stable. Whereas, for seed volume weight genotype PBNS-201 and PBNS-207 were observed highly stable. While, genotype PBNS-153 were high mean with regression coefficient near to unity (bi ≈ 1) were recommended for all environments. The genotype PBNS-208, PBNS-185, PBNS-12 and PBNS-86 were stable genotypes for oil content had bi > 1suitable to better environment, whereas, PBNS-200 was with high oil content mean, bi > 1 indicating suitability to favorable environment. Genotype PBNS-197 had high mean with bi < 1 suitable for unfavorable environment. However, for hull content genotype PBNS-12 and PBNS-86 were stable with regression coefficient greater than unity (bi > 1). The similar findings are observed by Moghaddam and Pourdad (2013) [9] and Rasale (2013) [12].

The genotype PBNS-207, PBNS-185 and PBNS-208 exhibited stable performance had high mean with regression coefficient greater then unity (bi > 1) and genotype PBNS-185 had significant S^2di indicates suitability to favorable environment. Whereas, genotype Sharda had low mean with bi < 1 and significant. S^2di indicating suitable to unfavorable environment. The genotype PBNS-154 and PBNS-197 had high mean with regression coefficient near to unity (bi ≈1) and genotype PBNS-197 had significant S^2di indicating suitable to all environment. Genotype PBNS- 185 and PBNS-153 were significant and stable with regression coefficient (bi >1), while genotype PBNS-198, PBNS-207 and PBNS-208 had stable and bi > 1 for both seed yield per plot and seed yield per plant. Some genotypes have higher mean, bi <1 or bi > 1, while others have high mean, bi = 1, but S^2di is high indicating instability regarding performance. The present findings are close agreement with Hamza (2014) [7] and Golkar *et al.*, (2020) [6].

Table 1: Analysis of variance for stability with four environments

Character	Genotype	Environment	G x E	Env + (G x E)	Env (L)	G x E (L)	Pooled deviation	Pooled error
Days to 50% flowering	3.76	202.33**	2.82	19.45**	607.01**	1.25	3.30**	0.26
Days to maturity	3.09	955.44**	4.02	83.31**	2866.32**	4.30	3.56**	1.27
Plant height (cm)	17.10*	203.75**	8.34	24.63**	611.27**	12.12	5.92**	1.99
No. of primary branches/plant	0.41	0.59	0.46	0.47	1.77	0.35	0.48**	0.14
Number of capitula/plant	5.04	316.52**	5.19	31.13**	949.57**	4.57	5.04**	1.51
Number of seeds/capitulum	7.73	365.87**	5.50	35.53**	1097.63**	7.09	4.31**	1.36
Days to rosette period	2.05	17.88**	1.42	2.79*	53.64**	1.85	1.11**	0.22
Test weight (g)	0.24*	0.12	0.09	0.09	0.36	0.04	0.10**	0.01
Oil Content (%)	6.10***	0.52	0.21	0.24	1.56*	0.18	0.21	0.24
Hull content (%)	9.83***	3.86*	1.00	1.24	11.59**	0.52	1.13	1.02
Seed volume weight (g/lit)	258.34***	12.71	7.03	7.50	38.15*	4.71	7.50	12.79
Seed yield/Plot (g)	11923.53	141607.82**	11936.95	22742.85	424823.46**	4454.38	14371.71**	3391.57
Seed yield/ plant (g)	1.58	34.97**	1.53	4.32**	104.92**	1.38	1.47**	0.48

* and ** indicates significance at 5 and 1 percent level respectively.

Table 2: Stability parameters for thirteen characters in safflower

Sr. No.	Genotype	Days to rosette period			Days to 50% flowering			Days to maturity		
		Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
1	PBNS – 86 (ch.)	28.33	1.07	0.86*	77.83	0.769	2.82**	129.8	0.89	8.6 **
2	PBNS - 185	28.58	1.75	-0.09	78.00	1.284	0.98*	128.8	0.72*	-1.2
3	PBNS - 200	29.16	0.16	0.41	79.25	1.178*	-0.25	131.3	0.98	2.6
4	PBNS - 201	27.66	0.75	-0.05	78.25	1.042	1.08*	129.8	0.92	0.5
5	PBNS – 12 (ch.)	28.75	0.70	2.13**	78.25	1.048	11.10**	130.7	0.87	-0.6
6	PBNS - 153	28.25	2.04*	-0.17	78.58	0.972	3.40**	130.8	1.16	9.6 **
7	PBNS - 154	28.16	0.51	3.66**	80.33	1.114	4.64**	132.1	1.07	-0.5
8	PBNS - 197	29.33	1.99	0.97**	78.41	0.734	3.44**	130.7	1.02	2.2
9	PBNS - 198	27.50	0.96	-0.03	78.83	1.018	2.23**	130.1	0.99	2.4
10	Sharda (ch.)	28.75	0.86	2.57**	79.08	0.879	0.44	130.6	1.11	3.9 *
11	PBNS - 207	27.66	1.07	-0.04	79.41	1.014	5.51**	130.0	1.19	0.6
12	PBNS - 208	29.83	0.10	0.23	81.08	0.949	0.76*	131.6	1.03	-1.1
	Mean	28.50			78.94			130.5		
	S.E.±	0.60			1.05			1.10		
	S.E. (b)	0.49			0.25			0.10		

Sr. No.	Genotype	Number of primary branches/plant			Number of capitula/plant			Number of seeds/capitulum		
		Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
1	PBNS – 86 (ch.)	8.66	-0.67	-0.08	21.08	0.91	4.36*	25.50	1.04	-0.83
2	PBNS - 185	8.29	2.66	0.72**	20.66	1.24	4.27*	29.66	0.88	0.01
3	PBNS - 200	8.34	0.12	0.56*	20.91	1.31*	-1.12	26.00	1.30	2.70
4	PBNS - 201	8.04	-0.85	0.80**	20.66	1.04	5.00*	29.25	1.31	1.59
5	PBNS – 12 (ch.)	8.26	2.61	-0.10	22.75	1.00	1.02	28.08	1.43	8.29**
6	PBNS - 153	8.12	-1.26	0.14	24.33	1.27	1.73	28.33	1.17	-0.68
7	PBNS - 154	7.63	2.30	0.09	21.41	0.86	9.39**	28.66	0.53	4.15*
8	PBNS - 197	7.89	0.49	-0.04	20.41	1.04	7.66**	27.83	0.74	5.27*
9	PBNS - 198	8.12	3.55*	-0.10	21.00	1.20	-0.67	29.33	0.76	3.49*

10	Sharda (ch.)	8.23	1.16	1.83**	21.50	0.87	0.06	27.16	1.13	0.73
11	PBNS - 207	7.59	0.67	0.07	22.41	0.69	7.12**	29.50	0.89*	-1.38
12	PBNS - 208	8.56	1.20	0.10	21.16	0.53	3.91*	29.41	0.76	11.35**
	Mean	8.14			21.52			28.22		
	S.E. ±	0.40			1.29			1.19		
	S.E. (b)	1.80			0.25			0.21		

Sr. No.	Genotype	Plant height (cm)			Test weight (g)			Seed volume weight (g/lit)		
		Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
1	PBNS – 86 (ch.)	68.75	1.44	0.63	6.11	1.06	0.02	563.5	0.31	-12.99
2	PBNS - 185	73.33	0.42	0.90	5.67	2.82	0.27**	573.8	0.68	-11.75
3	PBNS - 200	69.66	1.35	17.03**	5.75	1.97	0.04*	570.6	0.78	0.08
4	PBNS - 201	69.50	1.77*	-1.97	5.55	1.37	0.06*	567.5	3.25	7.77
5	PBNS – 12 (ch.)	74.66	1.08	0.28	6.22	1.79	-0.005	577.2	-1.13*	-13.11
6	PBNS - 153	71.75	1.39	3.36	5.98	1.11	0.19**	578.2	0.96	-11.75
7	PBNS - 154	71.16	1.14	18.73**	6.02	1.99	0.03	574.4	1.86	0.28
8	PBNS - 197	72.58	0.33	3.07	6.17	0.41	0.07*	556.6	0.49	-10.82
9	PBNS - 198	75.00	1.27*	-2.04	5.74	-1.53	0.01	562.9	0.27	-8.17
10	Sharda (ch.)	74.00	0.88	4.55*	6.13	-1.18	0.11**	558.1	0.36	6.58
11	PBNS - 207	73.33	0.55	1.11	5.72	1.17	-0.009	566.6	3.02	-3.393
12	PBNS - 208	71.58	0.32	0.08	5.57	0.99	0.19**	581.4	1.29	-11.11
	Mean	72.11			5.89			569.2		
	S.E. ±	1.40			0.18			1.60		
	S.E. (b)	0.34			1.86			1.50		

Sr. No.	Genotype	Hull content (%)			Oil Content (%)		
		Mean	bi	S^2di	Mean	bi	S^2di
1	PBNS – 86 (ch.)	52.16	1.43	-0.99	30.08	2.46	-0.05
2	PBNS - 185	49.33	0.26	2.02	31.71	1.82	-0.08
3	PBNS - 200	49.00	0.92	-0.35	34.52	1.64	-0.15
4	PBNS - 201	50.83	1.63	-0.83	32.14	0.46	-0.20
5	PBNS – 12 (ch.)	53.33	1.53	-0.41	31.27	2.37*	-0.23
6	PBNS - 153	52.16	0.21	0.86	30.03	0.34	0.05
7	PBNS - 154	48.83	1.63	-0.83	31.30	2.35	0.11
8	PBNS - 197	48.16	-0.28	1.29	33.24	-0.49	-0.05
9	PBNS - 198	50.00	1.22	0.43	32.06	0.47	0.18
10	Sharda (ch.)	49.50	1.55	-0.27	31.30	-0.56	0.26
11	PBNS - 207	50.66	0.07	0.27	31.63	-0.51	-0.02
12	PBNS - 208	49.66	1.80	-0.18	32.15	1.60	-0.11
	Mean	50.30			31.78		
	S.E. ±	0.61			0.26		
	S.E. (b)	1.08			1.27		

Sr. No.	Genotype	Seed yield/Plot (g)			Seed yield/ plant (g)		
		Mean	bi	S^2di	Mean	bi	S^2di
1	PBNS – 86 (ch.)	920.6	0.98	46202.9**	12.1	0.55	4.79**
2	PBNS - 185	953.2	1.42	17183.8**	12.51	1.61	1.06*
3	PBNS - 200	862.4	0.56	3685.3	11.57	0.59	0.18
4	PBNS - 201	917.0	0.69	2270.4	12.13	0.94	0.68
5	PBNS – 12 (ch.)	910.9	0.90	16132.9**	12.11	0.93	0.48
6	PBNS - 153	844.3	1.25	14666.1**	11.36	1.48	1.19*
7	PBNS - 154	940.8	0.90	-285.1	12.47	0.99	-0.10
8	PBNS - 197	905.8	0.63	9794.2*	12.07	0.96	1.57*
9	PBNS - 198	913.9	1.59	5911.6	12.03	1.51	-0.22
10	Sharda (ch.)	767.4	0.95	10975.4*	10.41	0.68	1.37*
11	PBNS - 207	958.2	1.08	8043.3*	12.75	1.03	0.77
12	PBNS - 208	943.2	1.36	-1638.7	12.37	1.22	0.22
	Mean	903.1			12.00		
	S.E.±	69.2			0.70		
	S.E. (b)	0.60			0.41		

* and ** indicates significance at 5 and 1 percent level respectively.

Conclusion

The genotypes PBNS-207 and PBNS-185 were found to have higher seed yields and wider adaptability based on mean performance and stability parameters. According to the environmental indices, the environments in Parbhani (E1) and Somnathpur (E4) are favourable, whereas those in Latur (E2) and Badnapur (E3) are unfavourable. The genotypes PBNS-200 were discovered to have a special adaptation to a poor

environment, while PBNS-198 and PBNS-185 were found to have a special adaptation to a better environment. Their high mean values for other yield components and average yield stability could be the cause of this. Multilocation trials may be used to evaluate these genotypes.

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