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Research Article

Stability and G×E interaction study in sunflower (*Helianthus annuus* L.) for diverse environments

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Abstract

The present research was carried out to estimate the G×E interaction and stability of four CMS lines, nine testers and 39 hybrids over three locations viz., Oilseed Research Unit, Dr. PDKV, Akola, Regional Research Centre, Amravati, and Agriculture Research Station, Yavatmal during the *kharif*-2019 season in randomized block design with three replication using Eberhart and Russell's model. Pooled analysis of variance due to genotype and environments showed highly significant for all the traits revealing the existence of variability among genotypes and environments. G×E interaction was significant for all the traits except 100 seed weight indicating the differential response of genotype to different environments. Environmental indices revealed that Akola was the most favourable location for the expression of sunflower crop. The three hybrids viz., PDKVSH - 952, LSFH - 171 and AKSF -10-1-1A × Gp₉₆₁ were found to be stable for seed yield while four hybrids i.e., CMS - 302 A×AK- 1R, DRSH - 1, CMS - 302 A×Gp₉₆₁ and CMS - 302 A×PKV - 103R were found suitable for favourable environments. The current work may be helpful for determining stable genotypes in sunflower for different locations.

Keywords: Sunflower, Stability, Eberhart and Russell and G × E interaction

INTRODUCTION

After oil palm, soybean, and rapeseed, sunflower (*Helianthus annuus* L.) is the world's fourth most produced edible oilseed crop (Ghaffari *et al.*, 2019). Its seeds have a high oil content ranging from 38% to 42%, and the two most significant fatty acids in sunflower oil, linoleic acid (55–60%) and oleic acid (25–30%), are both found in high concentrations in the oil (Manalili *et al.*, 2021 and Nagrale *et al.*, 2022). These polyunsaturated fatty acids are thought to lower blood cholesterol levels and hence lower the risk of coronary heart disease (Vijayakumar *et al.*, 2016). Sunflower crop has health advantages because of the abundance of protein, minerals, vitamins, magnesium, potassium, betaine, phosphorus, and phenolic acid

(Nagraj and Anjani, 1996). It is an important commercial oilseed crop and grows in different agro-climatic regions because of its day-length neutrality, wider adaptability and responsiveness to added inputs. Due to the economic and nutritional importance of sunflower, there is need for development of high yielding hybrids/ genotypes which are adapted to wide range of environmental conditions. Seed yield is a complex trait strongly influenced by environmental fluctuations; hence, the selection of genotypes at a single location is ineffective (Shrestha *et al.*, 2012). Developing buffered hybrids/genotypes is the major aim of sunflower breeders. Thus, the evaluation of genotypic performance for stability under different

environmental conditions for yield and its components has become an important part of crop improvement program. The development of sunflower hybrid/genotypes with stable yield will be beneficial to farming community to get consistent yield. In the current investigation, 52 sunflower genotypes were evaluated under three different environments for Identification of stable genotypes with high yield based on Eberhart and Russell (1966) model.

MATERIALS AND METHODS

The goal of the present study is to develop genotypes/hybrids of sunflower with stable performance across the environments. The experimental material comprised of four CMS lines viz., AKSF -10 – 1 – 1 A, CMS – 302A, CMS – 17A and ARM – 250A) and nine testers viz., GP₆961, GP₆1075, GP₆389, GP₆2902, AK – 1R, 856 R, PKV – 103R, 298 – 1R and PKV – 106R and their thirty-six hybrids developed using L×T design along with three checks (LSFH – 171, PDKVSH – 952 and DRSH-1). The experiments were conducted in randomized block design with three replications at three locations, i.e., Oilseed Research Unit, Dr. PDKV, Akola, Regional Research Centre, Amravati, and Agriculture Research Station, Yavatmal in the *khariif*-2019 season. Each entry was sown in a row of 3.0 m length with a 60 × 30 cm spacing. All the recommended practices were followed for raising healthy crop. Observations were recorded on five randomly selected plants in each replication for five important yield contributing characters viz., days to maturity, head diameter, 100 seed weight, seed filling percentage and seed yield per plant. The mean data of five plants in each replication for each entry was utilized for statistical analysis. Eberhart and Russell (1966) method was employed to estimate the three parameters of stability namely mean, regression coefficient (b_i) and mean squared deviation (S²d_i) for each genotype.

RESULTS AND DISCUSSIONS

Pooled analysis of variance revealed that the mean squares of genotypes and environments were highly significant for all five characters (**Table 1**), suggesting the presence of variability among the genotypes and environments. Variances due to genotypes × environments interaction were significant for all the traits except 100 seed weight indicating the differential response of genotypes to different environments. Similar results were also reported by Ahmed and Abdalla (2008), Chandra *et al.* (2018) and Patel *et al.* (2019). The variances due to E + (G×E) interactions were also found to be significant for all the characters except for seed filling percentage which revealed the relatively complex type of interaction. Significant mean squares due to environments (linear) indicated the presence of linear variation among genotypes. The mean sum of squares for pooled deviation were significant for all the five important yield contributing traits (Balu *et al.*, 2007), indicating the non-predictable nature of the genotypes by significantly differing for stability.

A positive environmental index and the highest mean values reveal an environment's favourability at a particular location (Breeze 1969). Among the three environments, environments E1 (Akola-*Khariif*-2019) registered high positive environmental index (5.87) and highest mean value (28.53g) for seed yield and most of yield contributing traits followed by E2 (Amravati- *Khariif*-2019) and E3 (Yavatmal *Khariif*-2019) (**Table 2**). Akola location provided favorable conditions for expression of most phenotypic characters. Hence, Akola could be concluded as the favorable location for the studied sunflower genotypes. Similar findings were also reported by Balu *et al.* (2007) and Halaswamy *et al.* (2001).

Table 1. Analysis of variance for stability in seed yield and its contributing components in sunflower genotypes across three different environments

Source of Variation	d.f.	Mean Sum of square				
		Days to maturity	Head Diameter	100 Seed weight	Seed Filling	Seed yield
Genotypes	51	18.05**	12.38**	2.43**	117.08**	180.72**
Environments + (G× E Interaction)	104	2.41**	5.17*	1.11**	22.56	70.50**
Environments	2	26.11**	79.85**	24.18**	260.08**	1386.33**
Genotypes × Environments	102	1.95*	3.71*	0.65	17.90*	44.70
Environments (linear)	1	52.22**	159.69**	48.36**	520.16**	2772.65**
Genotypes × Environments (linear)	51	2.62**	4.05	0.80	14.01	60.35**
Pooled deviation	52	1.25**	3.31**	0.49**	21.38**	28.49**
Pooled error	306	0.42	0.20	0.01	1.72	2.48
Total	155	7.56	7.54	1.54	53.66	106.76

Table 2. Mean performance and environment indices for seed yield and its contributing traits at three different locations

S. No.	Characters	Mean			Environmental index		
		AK-2019	AMT-2019	YTL-2019	AK-2019	AMT-2019	YTL-2019
1	Days to maturity	89.39	87.98	88.57	0.74	-0.66	-0.081
2	Head diameter (cm)	15.36	13.63	12.96	1.37	-0.35	-1.024
3	100 Seed weight (g)	6.62	6.42	5.35	0.48	0.29	-0.779
4	Seed filling (%)	56.11	52.58	51.96	2.55	-0.97	-1.58
5	Seed yield/ plant (g)	28.53	20.58	18.84	5.87	-2.067	-3.810

Based on Eberhart and Russell model, a genotype is considered to be stable if it shows unit regression coefficient around unity ($b_i = 1$) with high mean performance and non-significant deviation from the regression (S^2d_i). If the regression coefficient is more than unity ($b_i \geq 1$), the genotype shows below average stability; if the b_i value is less than unity it shows above average stability and will be adapted for poor environmental conditions. The genotypes identified to be suitable for favourable un favourable and across all the environments are presented in **Table 4**.

The important result of stability parameters *i.e.* mean performance, regression coefficient (b_i) and deviation from regression (S^2d_i) for five important yield contributing traits have been presented in **Table 3**. For days to maturity, among the 52 genotypes only one parent *i.e.* GP₆389 (86.89 days) and three hybrids *viz.*, CMS - 17 A × AK- 1R (85.56 days), CMS - 17 A × 856R(86.11 days) and CMS - 302 A × PKV - 103R(86.89 days) were earliest with regression coefficient close to one and non-significant deviation from regression hence these hybrids may be considered for general adaptability to all the environments. This is in line with the findings of Rukmini Devi *et al.* (2006), Balu *et al.* (2007) and Patil *et al.* (2020).

For head diameter, the hybrids like AKSF -10-1-1A × PKV 106 R (14.92cm), CMS - 302 A × AK- 1R (16.95cm), CMS- 17 A × PKV-106 R(18.43cm), ARM – 250 A × 856R (15.29cm), AKSF -10-1-1A × Gp₆961(13.84cm) and one parents CMS-302A(13.72cm) expressed higher diameter over the population mean with respective regression coefficient values of 1.31,1.40,1.54,1.57,1.22 and 0.71 and non-significant deviation from linear regression, hence possess average stability and are widely adaptable. These results were identical to the findings of Rukmini Devi *et al.* (2006) and Balu *et al.* (2007). The hybrids CMS - 302A × Gp₆961 (16.24cm) and CMS - 302 A × Gp₆1075 (14.23cm) had b_i values more than unity ($b_i > 1$) and were found to be specifically adapted to rich environments, while the hybrid AKSF -10-1-1A × 856R(15.21cm) had b_i value less than one ($b_i < 1$) with non-significant deviation from regression and exhibited above average stability (adapted to poor environments).

Among the 52 genotypes, four hybrids *i.e.*, DRSH – 1 (8.01g), ARM – 250 A × 856R(7.24g), CMS - 302A × AK-1R(6.83g) and AKSF -10-1-1A × Gp₆961(6.24g) for 100 seed weight showed highest mean over the population mean with regression coefficient near to unity ($b_i = 1$) and non-significant deviation from regression. Hence it can be considered as ideal and highly adaptable hybrid having average stability and is expected to perform well in all the environments. In contrast, the hybrids AKSF-10-1-1A × PKV-103R(6.71g), CMS - 302 A × Gp₄2902(6.57g), ARM – 250 A × Gp₆961(6.40g) and AKSF -10-1-1A × Gp₆1075(6.20g), are expected to give good seed yields under favorable environmental conditions due to greater values of the regression coefficient ($b_i > 1.0$) with high mean over the grand mean and non-significant deviation from regression. One parent *i.e.*, GP₆1075(6.24g) and one hybrid *i.e.* CMS - 17 A × PKV-298-1R(6.58g) had regression coefficient less than unity ($b_i < 1$) exhibited above average stability *i.e.* adapted better under poor environments.

For seed filling percentage, the genotypes CMS - 302 A × AK- 1R(62.68%), LSFH – 171 (60.48%), PDKVSH – 952 (61.33), DRSH – 1 (63.01), CMS-302A(54.21%) were found to be stable and recorded high mean than the population mean (53.55%)with regression coefficient values around unity($b_i=1$) and deviation from regression coefficient (S^2d_i) non-significant to zero. On the other hand, the hybrids CMS - 302 A × 856R(52.29%), AKSF -10-1-1A × Gp₆961(51.52%) recorded stable but low mean than the population mean while, only one hybrid CMS - 302 A × Gp₆961(61.08%) showed high mean, b_i more than unity and were found to be suitable for favorable environments. Hence it shows below-average stability for seed filling percentage. On the other hand, the genotypes AKSF -10-1-1A × 298 – 1 R(54.28%), AKSF -10-1-1A × PKV 106 R (58.58%) and GP₆1075(53.09%) showed high mean with regression values less than one ($b_i < 1$) and exhibited above average stability, hence is adaptable to poor environments (Chandra *et al.*,2018).

For seed yield per plant, seven hybrids recorded highest seed yield over the population mean (22.65g) with non-significant deviation from regression (**Table 3**). Only two

Table 3. Stability parameters *i.e* Mean (x), regression coefficient (b_i), deviation from regression (S²d_i) for seed yield and its component traits in three different environments.

S. No.	Genotypes	Days to Maturity			Head Diameter (cm)			100 Seed Weight (g)		
		Mean	Bi	S ² d _i	Mean	Bi	S ² d _i	Mean	Bi	S ² d _i
01	AKSF -10-1-1A × Gp ₆ 961	86.33	-0.36	1.00	13.84	1.22	0.35	6.24	1.60	-0.01
02	AKSF -10-1-1A × Gp ₆ 1075	85.11	-0.11	0.74	13.83	2.27	19.09**	6.20	2.35	0.00
03	AKSF -10-1-1A × Gp ₆ 389	85.11	-1.90	-0.43	15.74	-1.23	3.92**	6.27	0.82	2.24**
04	AKSF -10-1-1A × Gp ₄ 2902	90.56	3.53	6.02**	15.32	-0.33	8.45**	6.66	0.86	0.51**
05	AKSF -10-1-1A × AK- 1R	88.44	1.76	1.18	12.51	0.39	-0.06	6.20	1.49	1.07**
06	AKSF -10-1-1A × 856R	88.22	0.14	0.51	15.21	-0.13	-0.09	5.92	1.81	0.02
07	AKSF -10-1-1A × PKV-103 R	89.56	3.00	2.18*	14.83	3.60	13.62**	6.71	1.92	-0.01
08	AKSF -10-1-1A × 298 – 1 R	87.67	3.55	-0.43	13.46	0.36	4.24**	6.71	1.86	0.22**
09	AKSF -10-1-1A × PKV 106 R	89.78	0.72	-0.43	14.92	1.31	-0.18	6.47	2.09	0.26**
10	CMS - 302 A × Gp ₆ 961	89.44	2.56	3.30**	16.24	3.18	0.03	6.88	2.13	0.39**
11	CMS - 302 A × Gp ₆ 1075	86.89	-0.36	0.84	14.23	2.68	-0.20	6.90	1.56	0.32**
12	CMS - 302 A × Gp ₆ 389	88.33	-1.18	5.06**	10.33	-0.33	0.54	5.51	0.04	-0.01
13	CMS - 302 A × Gp ₄ 2902	87.33	4.10	0.24	14.26	0.76	8.14**	6.57	1.95	0.01
14	CMS - 302 A × AK- 1R	90.00	1.52	1.48*	16.95	1.40	-0.03	6.83	1.38	0.00
15	CMS - 302 A × 856R	91.11	2.48	0.82	12.38	2.23	21.15**	5.87	1.65	1.45**
16	CMS - 302 A × PKV – 103R	86.89	0.69	-0.39	14.74	0.45	0.95*	6.61	1.92	1.83**
17	CMS - 302 A × PKV – 298- 1R	87.11	0.25	-0.42	11.54	1.17	0.80*	5.11	1.44	0.79**
18	CMS – 302 A × PKV-106 R	91.00	4.41	0.29	11.89	0.80	-0.18	6.63	0.06	3.17**
19	CMS - 17 A × Gp ₆ 961	90.56	-2.23	1.30*	10.90	-0.63	0.42	6.42	-0.29	0.82**
20	CMS - 17 A × Gp ₆ 1075	87.78	1.26	0.26	10.24	-0.10	0.39	5.50	0.68	0.28**
21	CMS - 17 A × Gp ₆ 389	88.67	-1.32	0.48	13.99	2.34	8.49**	6.21	2.11	0.11**
22	CMS - 17 A × Gp ₄ 2902	86.11	0.55	2.00*	14.26	0.92	11.71**	6.39	1.82	3.36**
23	CMS - 17 A × AK- 1R	85.56	0.77	-0.06	12.22	1.42	3.23**	7.02	2.39	0.10**
24	CMS - 17 A × 856R	86.11	0.91	-0.30	13.96	1.67	2.98**	6.28	2.35	1.86**
25	CMS - 17 A × PKV – 103R	85.33	0.23	5.74**	13.29	0.82	1.38**	5.98	1.97	0.01
26	CMS - 17 A × PKV – 298- 1R	85.56	3.50	-0.20	15.46	2.09	14.74**	6.58	0.65	-0.01
27	CMS- 17 A × PKV-106 R	89.56	4.71	-0.39	18.43	1.54	-0.18	6.43	-0.08	0.04*
28	ARM – 250 A × Gp ₆ 1075	89.33	2.53	0.01	14.39	2.62	1.00**	6.29	1.85	1.85**
29	ARM – 250 A × Gp ₆ 961	91.89	1.62	-0.34	14.93	3.39	4.59**	6.40	1.70	0.01
30	ARM – 250 A × Gp ₆ 389	92.22	1.51	0.46	16.09	2.33	1.93**	7.05	0.47	0.43**
31	ARM – 250 A × Gp ₄ 2902	91.11	2.48	0.82	15.38	1.11	2.03**	7.07	2.04	0.79**
32	ARM – 250 A × AK- 1R	85.11	0.25	-0.42	11.86	0.13	0.17	5.37	0.83	0.01
33	ARM – 250 A × 856R	86.89	-0.36	0.84	15.29	1.57	0.37	7.24	0.73	0.00
34	ARM – 250 A × PKV- 103 R	92.67	0.94	-0.42	17.26	2.12	4.27**	6.76	-0.71	0.24**
35	ARM – 250 A × 298 – 1 R	89.78	1.65	-0.43	16.87	2.96	0.89**	7.01	2.82	0.84**
36	ARM – 250 A × PKV 106 R	90.67	2.26	0.66	14.74	2.06	11.23**	6.75	-0.39	0.46**
37	LSFH – 171	91.11	-1.00	3.09**	16.39	1.12	1.40**	6.78	1.02	0.56**
38	PDKVSH – 952	87.33	1.99	1.61*	16.55	1.41	1.04**	7.77	0.91	0.08**
39	DRSH – 1	93.33	0.27	-0.29	18.41	0.24	1.60**	8.01	0.99	-0.01
40	AKSF-10-1-1A	89.33	-0.71	5.28**	14.389	0.31	0.89*	4.929	0.81	0.01
41	CMS-302A	85.44	-1.08	0.70	13.722	0.71	0.15	4.132	0.05	0.01
42	CMS-17A	86.11	-0.33	1.53*	13.699	-0.16	-0.12	5.292	-0.35	-0.01
43	ARM-250A	92.00	0.94	-0.42	13.754	-0.5	0.54	5.016	0.21	0.01
44	GP ₆ 961	88.00	1.29	0.78	12.889	0.79	2.4*	5.561	0.05	0.1**
45	GP ₆ 1075	89.89	0.50	-0.38	12.841	0.02	-0.16	6.024	-0.12	0.02
46	GP ₆ 389	86.89	0.77	-0.06	13.602	0.23	0.07	6.502	-0.08	0.09**
47	GP ₄ 2902	91.00	2.23	0.58	13.637	-0.06	1.37**	5.836	0.38	0.06*
48	AK- 1R	82.44	-1.35	0.03	10.783	-0.31	0.3	4.272	0.36	0.21**
49	856 R	92.33	1.40	-0.41	11.966	0.06	0.6*	4.684	-0.11	-0.01
50	PKV-103R	90.11	0.05	-0.14	10.929	0.09	-0.12	3.966	-0.09	0.09**
51	298-1R	91.11	0.72	-0.43	10.542	-0.06	0.76*	4.486	0.08	0.16**
52	PKV- 106R	89.67	0.27	-0.29	11.534	-0.08	0.46	4.749	0.02	0.12**
	Mean	88.65			13.99			6.13		

Table 3. Stability parameters i.e Mean (x), regression coefficient (bi), deviation from regression (S²di) for seed yield and its component traits in three different environments.

S. No.	Genotypes	Seed Filling (%)			Seed yield/plant(g)		
		Mean	Bi	S ² di	Mean	Bi	S ² di
01	AKSF -10-1-1A × Gp ₆ 961	51.522	1.28	2.13	21.04	0.75	-2.55
02	AKSF -10-1-1A × Gp ₆ 1075	51.098	2.04	46.17**	18.43	0.65	22.42**
03	AKSF -10-1-1A × Gp ₆ 389	56.44	-0.85	16.86**	26.11	-1.19	96.15**
04	AKSF -10-1-1A × Gp ₄ 2902	55.56	0.64	23.93**	25.43	-0.59	67.17**
05	AKSF -10-1-1A × AK- 1R	51.031	0.71	-1.74	18.23	0.20	0.30
06	AKSF -10-1-1A × 856R	59.387	1.38	49.02**	28.99	1.45	52.36**
07	AKSF -10-1-1A × PKV- 103 R	58.947	2.65	59.04**	31.75	2.83	84.41**
08	AKSF -10-1-1A × 298 – 1 R	54.282	-1.92	0.32	20.50	-0.06	3.86
09	AKSF -10-1-1A × PKV 106 R	58.582	-0.16	-1.48	23.08	0.37	-1.38
10	CMS - 302 A × Gp ₆ 961	61.083	1.65	3.33	31.19	2.92	-1.06
11	CMS - 302 A × Gp ₆ 1075	55.303	2.56	26.85**	26.06	2.67	13.89*
12	CMS - 302 A × Gp ₆ 389	51.448	0.41	15.1**	17.81	0.03	-0.59
13	CMS - 302 A × Gp ₄ 2902	55.422	0.85	109.33**	23.51	0.08	131.87**
14	CMS - 302 A × AK- 1R	62.676	0.93	0.2	36.03	1.79	1.24
15	CMS - 302 A × 856R	52.286	0.89	3.52	17.78	0.77	29.32**
16	CMS - 302 A × PKV – 103R	58.497	2.04	7.6*	27.59	2.15	-1.24
17	CMS - 302 A × PKV – 298- 1R	48.939	3.89	1.11	19.42	1.90	-0.87
18	CMS – 302 A × PKV-106 R	50.008	0	38.5**	18.44	0.16	1.72
19	CMS - 17 A × Gp ₆ 961	49.531	1.38	28.71**	17.52	0.17	6.08
20	CMS - 17 A × Gp ₆ 1075	44.207	-0.77	5.19*	14.63	0.04	5.11
21	CMS - 17 A × Gp ₆ 389	55.267	3.13	76.7*	27.77	3.03	67.25**
22	CMS - 17 A × Gp ₄ 2902	58.259	2.34	103.49**	31.01	1.69	192.19**
23	CMS - 17 A × AK- 1R	50.237	1.08	3.85	18.45	0.51	-1.65
24	CMS - 17 A × 856R	56.047	1.85	46.04**	23.37	1.72	7.48*
25	CMS - 17 A × PKV – 103R	53.118	0.79	25.43**	21.89	0.87	25.93**
26	CMS - 17 A × PKV – 298- 1R	57.793	2.23	66.8**	27.82	1.95	54.53**
27	CMS- 17 A × PKV-106 R	64.123	0.85	6.35*	38.70	1.65	14.23*
28	ARM – 250 A × Gp ₆ 1075	56.559	1.5	22.48**	24.48	1.57	11.67*
29	ARM – 250 A × Gp ₆ 961	54.318	4.76	17.79**	27.87	3.54	32.92**
30	ARM – 250 A × Gp ₆ 389	61.398	1.27	17.28**	33.39	2.11	81.01**
31	ARM – 250 A × Gp ₄ 2902	58.056	0.49	44.66**	29.68	1.15	70.10**
32	ARM – 250 A × AK- 1R	49.349	0.26	0.9	16.91	0.31	-2.52
33	ARM – 250 A × 856R	60.547	1.12	5.69***	32.50	2.30	19.01**
34	ARM – 250 A × PKV- 103 R	60.888	0.97	32.6**	34.59	2.08	140.44**
35	ARM – 250 A × 298 – 1 R	58.474	2.62	38.14**	32.98	2.98	17.50**
36	ARM – 250 A × PKV 106 R	55.08	0.4	74.45**	26.63	0.82	129.93**
37	LSFH – 171	60.481	0.97	2.96	25.42	0.84	1.14
38	PDKVSH – 952	61.339	0.68	-0.04	29.59	1.03	-1.39
39	DRSH – 1	63.019	0.98	-1.52	35.11	1.88	-1.16
40	AKSF-10-1-1A	50.46	0.97	-1.46	16.81	0.29	0.26
41	CMS-302A	54.21	0.75	-1.74	19.33	0.46	-2.38
42	CMS-17A	47.60	0.63	-1.49	14.05	0.14	-1.94
43	ARM-250A	49.82	0.59	-0.39	15.88	0.06	-1.09
44	GP ₆ 961	47.26	-1.18	6.72*	14.80	0.40	-2.51
45	GP ₆ 1075	53.09	0.35	-1.26	17.84	0.54	-1.95
46	GP ₆ 389	51.49	0.56	0.31	16.39	0.46	-1.95
47	GP ₄ 2902	43.56	0.57	-1.65	12.75	0.01	1.25
48	AK- 1R	41.00	0.47	-1.42	8.54	0.16	-0.59
49	856 R	42.12	0.48	7.27*	10.64	0.18	-1.20
50	PKV-103R	40.81	-0.38	0.99	8.79	-0.03	-2.23
51	298-1R	42.01	0.26	-1.35	10.59	0.12	-2.53
52	PKV- 106R	40.82	0.04	-1.04	9.95	0.09	-1.33
	Mean	53.55			22.65		

Table 4. Genotypes suitable for all environments, favorable/ unfavorable environment identified based on Eberhart and Russell (1966) model

S. No.	Characters	Genotypes Response to Stability		
		Average stability (suitable for all environments)	Below average stability ($b_i > 1$) (suitable for rich environment)	Above average stability ($b_i < 1$) (suitable for poor environment)
1	Days to maturity	CMS - 17 A × AK- 1R , CMS - 17 A × 856R, CMS - 302 A × PKV – 103R, and Gp ₆ 389.	CMS - 17 A × PKV – 298- 1R, CMS - 302 A × Gp ₄ 2902, GP ₆ 961 and AKSF -10-1-1A × AK- 1R.	AK- 1R, AKSF -10-1-1A × Gp ₆ 1075,, AKSF -10-1-1A × Gp ₆ 389, ARM – 250 A × AK- 1R, CMS-302A, CMS-17A, AKSF -10-1-1A × Gp ₆ 961, GP ₆ 1075, ARM – 250 A × 856R, CMS - 302 A × Gp ₆ 1075, ,AKSF -10-1-1A × 856R and CMS - 302 A × PKV – 298- 1R.
2	Head diameter	CMS- 17 A × PKV-106 R, CMS - 302 A × AK- 1R, ARM – 250 A × 856R, AKSF -10-1-1A × PKV 106 R.	CMS - 302 A × Gp ₆ 961 and CMS - 302 A × Gp ₆ 1075.	AKSF -10-1-1A × 856R.
3	100 seed weight	DRSH – 1, ARM – 250 A × 856R, CMS - 302 A × AK- 1R and AKSF -10-1-1A × Gp ₆ 961.	AKSF-10-1-1A × PKV-103 R, CMS - 302 A × Gp ₄ 2902, ARM – 250 A × Gp ₆ 961 and AKSF -10-1-1A × Gp ₆ 1075.	CMS - 17 A × PKV – 298- 1R and GP ₆ 1075.
4	Seed filling percentage	DRSH – 1, CMS - 302 A × AK- 1R, PDKVSH – 952 , LSFH – 171 and CMS- 302A.	CMS - 302 A × Gp ₆ 961.	AKSF -10-1-1A × PKV 106 R, AKSF -10-1-1A × 298 – 1 R and GP ₆ 1075.
5	Seed yield	PDKVSH – 952, LSFH – 171 and AKSF -10-1-1A × Gp ₆ 961.	CMS - 302 A × AK- 1R, DRSH – 1 C, CMS - 302 A × Gp ₆ 961 and CMS - 302 A × PKV – 103R.	AKSF -10-1-1A × PKV 106 R.

hybrids PDKVSH-952(29.59g) and LSFH-171(25.42g) were identified stable across the environments due to their higher mean overpopulation mean (22.65g) with regression coefficient values near to unity ($b_i = 1.03$ and 0.84 , respectively) and non-significant deviation from the regression (S^2_d). The hybrid AKSF -10-1-1A × Gp₆961 (21.04g) showed stable performance but mean is lower than the population mean, while the hybrids CMS - 302 A × AK- 1R (36.03g), DRSH – 1 (35.11g) CMS - 302A × Gp₆961 (31.19g) and CMS - 302 A × PKV – 103R (27.59g) exhibited below average stability due to its highest mean with greater than one regression coefficient ($b_i > 1$) values. Hence these hybrids can be adaptable to favorable environments. Only one hybrid AKSF -10-1-1A × PKV 106 R (23.08g) had higher mean value with a regression coefficient less than unity ($b_i < 1$) revealing that this is specifically adaptable to poor environments (above average stability). The results of Rukmini Devi *et al.* (2006), Balu *et al.* (2007) and Mahajan *et al.* (2009) and Chandra *et al.* (2018) were in agreement with our findings.

Based on the results of the current study, it can be inferred that the Akola location was suitable for the expression of most of phenotypic characters under investigation in the studied genotypes. Further, the sunflower hybrids *viz.*, PDKVSH-952, LSFH-171 and AKSF -10-1-1A × Gp₆961 were found to be consistent and high yielders across the locations. These hybrids can be recommended for cultivation over a wide range of environments based on their adaptability and stability.

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