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Stability Analysis of Some Novel Cytoplasmic Male Sterile Sources of Sunflower and Their Hybrids

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Abstract: Genetic makeup along with environmental stimuli affect the expression of a trait in plants. Drought tolerance in addition to stability of characters over a wide range of environmental conditions is not well studied in sunflower. Therefore, here we have performed a stability analysis study of sunflower genotypes. The experimental material comprised of 19 lines of sunflower comprising 9 alloplasmic *cms* lines from different wild sources along with one common maintainer from *petiolaris* source, 4 *cms* lines and one maintainer from cultivated source (cytoplasm from *H. petiolaris*), 4 restorer lines and 60 F_1 hybrids (developed in line x tester design). The experiment was conducted over two years i. e. spring season 2011 and spring season 2012 over the two environments one normal irrigated and another water stress environment at Punjab Agricultural University, Ludhiana, India. The data were recorded for different morphophysiology, yield and quality trais and analysis as per standard procedures. The genotype × environment interaction was further partitioned into linear and non-linear components according to Eberhart and Russel model. Eleven sunflower hybrids were found to be stable across the environments for seed yield. While, sufficient variability was also recorded for the oil content with the highest oil percentage in the cross combination ARG-2A × P100R (34.61). Overall, this study provides useful information regarding the stability of newly developed and cytoplasmically diverse sunflower hybrids under north Indian conditions.

Keywords: stability, sunflower, sunflower and water stress, sunflower hybrid, water use efficiency, wild cytoplasmic sources

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Introduction

Sunflower (*Helianthus annuus* L.) is an important oilseed crop widely adopted and accepted for its high-quality edible oil. Its seeds contain high oil content ranging from 35–50 %. Sunflower introduced in India in seventies has acquired the status of an important commercial oilseed crop and has spread across a number of climatic and geographical regions because of its day length neutrality, wider adaptability and responsiveness to added inputs. However, the present alarming situation of depleting underground water advocates the saving of water. Thus to cope with such a situation the water use efficient genotypes need to be developed and identified so that the number of irrigations can be reduced. Water stress is one of the major causes for crop losses worldwide, reducing average yields to 50 % or even more (Wang *et al.*, 2003); furthermore, possible global climate change scenario suggests a future increase in the risk of drought (IPCC, 2001). Therefore, breeding crop varieties for improved water use efficiency is of utmost importance (Condon *et al.*, 2004).

Sunflower hybrids are object of breeding attention because of their agronomic and economic advantages over varieties (high productivity, high oil content, uniformity, *etc.*). The favourable characters of sunflower hybrids like production stability, response to high input agriculture, high self-fertility, uniform growth and maturity shifted the focus towards heterosis breeding, leading to the release of first ever sunflower hybrid BSH-1 in India (Seetharam, 1981), which provided required thrust to expand sunflower cultivation in the country. Since then, many hybrids have been released for commercial cultivation based on cytoplasmic genetic male sterility system. The synthesis of hybrids with high heterotic effect became possible after the discovery of the first *cms* source by P. Leclercq (Leclercq, 1968) and detection of fertility restoration genes by M. Kinman (Kinman, 1970) that gave the required impetus to commercial hybrid seed production.

Line by tester based genetic crosses are better choices in case of crosspollinated crops like sunflower than diallel methods used more popularly in case of self-pollinated crops (Kaushik and Dhaliwal, 2018). Since then many hybrids have been released for commercial cultivation both by public and private sectors and available variability in the parental material has been used. Consequently, there have been relatively less efforts to diversify the inbreds to get better heterosis over check hybrids.

Development of sterile *cms* analogues of lines used in sunflower breeding programmes for commercial hybrid development is one of the practical applications of *cms* investigations. At present only one *cms* source *i. e.* PET-1 is being widely used for sunflower hybrid breeding programme. Such cytoplasmic uniformity poses a potential risk for hybrid sunflower production. A number of

research institutes and international projects are concentrating on this issue (Serieys, 1999; Tavoljanskiy *et al*., 2004). The alloplasmic lines (*i. e*. different cytoplasms in common nuclear genetic background) may contain certain factors affecting some water use efficiency traits. In order to achieve the desired goal of breeding for developing water use, efficient genotypes in sunflower one must have a thorough understanding of the interaction between alien cytoplasm and nuclear genes from commercially cultivated source *i. e*. *H. petiolaris* and the impact of this interaction on heterosis for yield-related traits as well as water use efficiency traits. Utilization of alloplasmic/isonuclear lines in hybrid development will help in making valid comparison between the diverse *cms* lines/sources. Drought tolerance in addition to stability of characters over a wide range of environmental conditions is not well studied in sunflower (Tyagi *et al*., 2018). Therefore, here we have performed a stability analysis study of sunflower genotypes in the north Indian plains.

Materials and methods

The present investigation was carried out at experimental at Punjab Agricultural University, Ludhiana. Ludhiana represents the Indo-Gangetic plains and is situated at 36°54′ N latitude, 25°48′ E longitude and a mean height of 247 meters above sea level.

Experimental material

The experimental material consisted of 80 genotypes of sunflower comprising nine alloplasmic *cms* lines (cytoplasm from different wild sources) along with one common maintainer NC-41B (cytoplasm from *petiolaris* source) developed and evaluated at PAU, Ludhiana (Tyagi and Dhillon, 2016; Tyagi *et al*., 2018)., four *cms* lines and one maintainer from cultivated source (cytoplasm from *H. petiolaris*), four restorer lines, 60 F_1 hybrids (developed in line × tester design). The experiment was conducted over two years i. e. spring season 2011 and spring season 2012 by adopting following procedure.

Morphological and seed yield traits

Days to 50 % flowering was recorded by counting number of days from the date of sowing to the date when 50 % of the plants in a genotype had flowered in each environment. Maturity was recorded as total number of days from date of sowing to

the date of physiological maturity i. e. when back side of the capitulum turned yellowish - brown and brackets started drying. The plant height was measured from base to the tip of main stem at the time of maturity when plant attained maximum growth. The mean data of five plants was used for statistical analysis from each replication and environment. Head diameter was measured in centimeters from one end of head to other after seed setting from five random plants at maturity. In order to be precise, diameter of each head was measured from two cross sections and their arithmetic means was worked out. The harvested seeds from five competitive plants were weighed and average seed yield per plant was worked out. 100 seed weight was taken as weight of 100 seeds drawn at random from each genotype from each replication and environment separately. Harvest index (HI), defined as the ratio of seed yield (SY) to the total biomass [vegetative mass (VM) + Seed Yield] at maturity was calculated as suggested by (Donald, 1962).

Drought susceptible index (DSI)

Drought susceptibility index (DSI) was calculated by the formula given by Fischer and Maurer (1978).

$$S = \frac{1 - Y/Y_p}{1 - X_d/Y_p}$$

Where Y is the seed yield per plant of a given genotype under drought, Y_p is the seed yield per plant of the same genotype under irrigation, X_d is the mean seed yield of all genotypes within group (restorer or inbred and hybrids) under drought, and X_p is the seed yield per plant of all genotypes within group under irrigation.

Stay-green stem (visual observation)

Stay-green stem was observed at the time of physiological maturity of genotypes. The genotypes which showed green stem at that stage were recorded as stay-green genotypes.

Physiological traits

The total number of leaves from top to bottom of five plants from each genotype was counted in each replication. The average was worked out and expressed as number of leaves per plant.

Leaf area (m^2 per plant)

Leaf area per unit dry weight method was used to calculate leaf area. For this leaf area of one plant from one genotype was calculated using graph sheet. The total leaves from the same plant were then dried in the oven and their dry weight was recorded to calculate area per unit of dry weight (1 g dry wt. = M_1m^2). Dry weight of all the genotypes were recorded and multiplied with this common factor i. e. M_1 to obtain leaf area for all the genotypes

Specific leaf weight (SLW) (g)

SLW was calculated using the following formula

$$\text{Specific leaf weight(g)} = \frac{\text{Dry weight of total leaves per plant(g)}}{\text{Total no. of leaves per plant}}$$

Leaf area index

Leaf area index (LAI) defined as leaf area per unit soil area (m^2) was calculated as follows (Watson, 1958).

$$\text{LAI} = (\text{A} \times \text{N})/10,000$$

Where A is leaf area (cm^2) and N is plants per m^2.

Leaf water potential (MPa)

Leaf water potential Mega-Pascal's (Mpa) was recorded by leaf water potential meter (Water Potential System – WESCOR – 4,357,526,011) on three plants in each replication for all genotypes.

Relative leaf water content (RLWC) (in %)

For this 100 mg leaf discs (fresh weight) from each genotype were submerged in distilled water in test tubes till saturation. After 6 hrs the leaf discs were removed from test tubes. Surface water of the discs was blotted off without putting any pressure and then they were weighed to obtain saturated weight.

Then after drying the discs at 70 °C for 72 hr their dry weight was determined. From these data RLWC was calculated (Weatherly 1950) as follows:

$$\text{RLWC} = \frac{\text{Fresh weight} - \text{Dry weight}}{\text{Saturated weight} - \text{Dry weight}} \times 100$$

Photosynthetic efficiency (SPAD readings)

Photosynthetic efficiency in terms of chlorophyll content was recorded by SPAD in five intact plants (third-fourth leaf from top of plant) in each replication of all genotypes in both the treatments.

Proline content (mg/1 g dry weight of leaf)

The proline content was estimated using the standard protocol for proline content estimation under water stress as defined elsewhere (Bates *et al.*, 1973). The proline content was expressed in mg/g of dry weight in leaf.

Oil content (in %)

To determine oil percentage in seeds, the wide line nuclear magnetic resonance (NMR) with the Newport Analyzer was used (Newport Analyzer MK III A, Newport Instruments Ltd., Milton Keynes, England) via the protocol defined elsewhere (Robertson and Morrison, 1979).

Fatty acid composition (in %)

Gas Liquid Chromatography (GLC) was used for fatty acid estimation Fatty acids were first converted to their methyl esters by standard method of transesterification defined elsewhere (Seppanen-Laakso *et al.*, 2002).

The mean values all the traits from each genotype in each replication from each environment were used for analysis of variance Fisher (1954) and estimation of stability parameters as per Eberhart and Russell model (1966). The model of Eberhert and Russel (1966) is extensively applied to genotype × environment

interaction studies because it applies both linear and non-linear components in order to provide useful information regarding the stability of a genotype.

Results and discussion

Based on three parameters of stability *i. e*. mean performance across four environments, regression coefficients and deviations from regression line, a genotype is considered to be stable if it shows high mean value *i. e*. above average performance, unity regression coefficient (bi) with non-significant deviation from regression line (δ^2di). These stability parameters are presented in Tables 1 to 8 and character wise results are explained below

Analysis of variance studies

Analysis of variance for different characters studied in this study revealed highly significant differences among genotypes.

The G × E interactions encountered in multi-environmental experiments hinders the progress in development of cultivars with wider adaptability.

Days to 50 % flowering

The mean performance revealed that among parents P69R (73.75) and PHIR-27A (72.67) took maximum days to 50 % flowering followed by the hybrids NC-41B × P69R (73.29), NC-41B × P124R (72.96), NC-41B × P100R (72.83) and 234A × P100R (72.63). The results revealed high amount of variability in the material. The presence of high amount of variability among different genotypes in sunflower for days to flowering has also been reported by Rao *et al.* (2004).

The parameters of stability (Table 2) indicated that the ten hybrids and female parent *cms*-XA and male P124R had unity regression and significant deviation from regression line indicating that these are stable over the environments with unpredictable performance, however, the thirteen hybrids and male parent P69R also showed unity regression but non-significant deviation from regression line which indicates that these genotypes were stable over the environment with predictable performance.

The genotype P69R, 234A × P100R, NC-41B × P69R, NC-41B × P124R, NC-41B × P100R and PHIR-27A had high mean, below average stability (b > 1)

Table 1: Analysis of variance for stability of different traits.

Source of variation	d.f.	Mean Squares									
		1	2	3	4	5	6	7	8	9	10
Genotypes	78	9.45**	9.45**	9.45**	9.45**	9.45**	9.45**	9.45**	9.45**	9.45**	186.89**
Env. + (env X gen.)	237	6.68**	6.68**	6.68**	6.68**	6.68**	6.68**	6.68**	6.68**	6.68**	77.22**
Env.(linear)	1	647.89**	2003.72**	18,081.32**	980.01**	736.10**	2.58**	1.90**	74.10**	31.91**	4666.59**
Geno. X env.	78	2.97**	−14.24**	−227.94**	−7.79**	−2.20**	9.18**	4.43**	7.78**	3.96**	133.85**
Pooled deviation	158	4.45**	4.37**	8.10**	7.66**	6.45**	5.47**	7.82**	5.71**	7.86**	20.23**
Pooled error	624	0.39	0.27	4.02	1.63	0.35	0.00	0.00	0.02	0.00	0.78

Source of variation	d.f.	Mean Squares										
		11	12	13	14	15	16	17	18	19	20	21
Genotypes	78	186.89**	186.89**	186.89**	186.89**	186.89**	186.89**	186.89**	186.89**	186.89**	186.89**	186.89**
Env. + (env X gen.)	237	77.22**	77.22**	77.22**	77.22**	77.22	77.22**	77.22**	77.22**	77.22**	77.22**	77.22**
Env.(linear)	1	291.53**	91.03**	28.13**	7934.78**	1,687,209.00**	5273.95**	226.50**	11.47**	17.25**	271.14**	195.67**
Geno. X env.	78	81.29**	207.30**	118.88**	89.23**	−21,571.43**	−45.73**	75.41**	164.97**	96.19**	92.06**	122.06**
Pooled deviation	158	73.86**	12.92**	56.97**	21.57**	86.49*	105.03**	77.17**	34.33**	68.24**	68.67**	54.34**
Pooled error	624	0.50	0.00	0.05	2.94	151.46	1.34	0.06	0.06	0.03	0.14	0.20

*, ** - significant at 5% and 1% level respectively

1. Days to 50% flowering, 2. Days to maturity, 3. Plant height (cm), 4. Head diameter (cm), 5. Number of leaves per plant, 6. Leaf area (m2)/plant, 7. Specific leaf weight (g), 8. Leaf area index, 9. Leaf water potential (MPa), 10. Relative leaf water content (%), 11. Photosynthetic efficiency (SPAD readings), 12. Proline content (mg/2 g dry weight of leaf), 13. 100 Seed weight (g), 14. Seed yield per plant (g), 15. Biological yield per plant (g), 16. Harvest index (%), 17. Oil content (%), 18. Palmitic acid (%), 19. Stearic acid (%), 20. Oleic acid (%), 21. Linoleic acid (%)

Table 2: Mean performance, regression coefficient (bi) and deviation from regression (δ^2di) for days to 50% flowering, days to maturity and plant height over different environments.

S. No.	Genotypes	Days to 50 % flowering				days to maturity				Plant Height (cm)			
				± SE				± SE				± SE	
		Mean	bi	bi	σ^2 di	Mean	bi	bi	σ^2 di	Mean	bi	bi	σ^2 di
1	CMS-XA × RCR-8297	71.88	1.24**	0.25	0.53	97.46	−0.40	0.43	4.78**	153.17	0.07	0.17	6.31
2	CMS-XA × P69R	70.08	0.84**	0.21	0.35	97.17	−0.41	0.21	1.14*	123.23	0.05	0.11	3.03
3	CMS-XA × P124R	70.21	1.27**	0.24	0.47	98.54	−0.44	0.43	4.64**	129.92	0.01	0.18	7.03
4	CMS-XA × P100R	68.38	2.05*	0.68	3.84**	97.33	−1.06	0.52	6.77**	143.37	−0.15	0.28	18.38*
5	E002-91 × RCR-8297	68.04	1.33**	0.14	0.15	96.21	−0.55	0.38	3.64**	159.94	0.06	0.18	7.11
6	E002-91 × P69R	69.08	0.60	0.74	4.45**	98.25	−0.17	0.47	5.57**	136.14	0.20*	0.08	1.35
7	E002-91 × P124R	69.88	0.92	0.68	3.83**	99.21	−0.06	0.53	7.24**	148.15	0.02	0.18	7.26
8	E002-91 × P100R	69.96	1.68**	0.21	0.37	100.13	−0.70	0.48	5.81**	151.37	0.08	0.22	11.30
9	PKU-2A × RCR-8297	69.46	0.06	0.88	6.36**	101.50	0.04	0.50	6.36**	161.60	0.22**	0.05	0.65
10	PKU-2A × P69R	69.17	0.26	0.20	0.33	99.13	−0.12	0.13	0.41	134.34	0.05	0.04	0.34
11	PKU-2A × P124R	67.46	−0.82	0.38	1.19*	96.58	0.53**	0.13	0.44	129.33	0.07	0.12	3.33
12	PKU-2A × P100R	70.04	1.26	1.39	15.78**	98.54	−0.80	0.75	14.08**	142.31	0.27	0.25	14.14*
13	ARG-2A × RCR-8297	69.54	0.29	0.57	2.69**	99.58	−0.38	0.22	1.20*	148.64	−0.13	0.07	1.18
14	ARG-2A × P69R	69.75	2.04**	0.28	0.63	97.54	−1.01*	0.43	4.68**	103.77	−0.02	0.28	17.68*
15	ARG-2A × P124R	70.13	1.01	0.64	3.40**	99.46	−0.77**	0.03	0.03	127.78	−0.05	0.18	7.33
16	ARG-2A × P100R	69.21	0.94*	0.33	0.87	99.92	−0.45	0.27	1.91**	136.44	0.08	0.13	3.82
17	ARG-3A × RCR-8297	69.58	0.10	0.65	3.45**	98.71	0.30	0.31	2.36**	154.40	0.05	0.12	3.18
18	ARG-3A × P69R	70.54	1.77*	0.65	3.43**	98.92	−1.10**	0.20	1.03*	126.15	−0.07	0.26	15.72*
19	ARG-3A × P124R	69.29	1.23	0.99	8.03**	98.54	−0.86	0.44	4.84**	130.23	−0.24	0.18	7.73
20	ARG-3A × P100R	68.96	1.60**	0.29	0.70	98.00	−0.84*	0.30	2.30**	134.29	−0.02	0.22	11.12
21	ARG-6A × RCR-8297	69.25	1.27	0.87	6.22**	99.79	−0.69	0.52	6.78**	139.21	−0.21	0.18	7.67

(*continued*)

Table 2: (*continued*)

S. No.	Genotypes	Days to 50 % flowering				days to maturity				Plant Height (cm)			
		Mean	bi	± SE bi	σ^2 di	Mean	bi	± SE bi	σ^2 di	Mean	bi	± SE bi	σ^2 di
22	ARG-6A × P69R	68.96	0.91	1.16	11.01**	97.46	0.03	0.75	14.39**	97.71	−0.10	0.24	13.28*
23	ARG-6A × P124R	68.54	1.05**	0.33	0.88	96.50	−0.27	0.42	4.43**	114.54	0.06	0.15	5.03
24	ARG-6A × P100R	70.13	1.48	0.94	7.24**	98.21	−1.10**	0.18	0.78	139.73	−0.01	0.27	16.15*
25	DV-10A × RCR-8297	71.08	1.00	0.69	3.93**	98.25	−0.62	0.35	3.11**	145.07	−0.17	0.14	4.77
26	DV-10A × P69R	69.46	1.59*	0.64	3.33**	96.38	−0.98**	0.24	1.43**	98.12	−0.11	0.23	12.30*
27	DV-10A × P124R	70.21	1.37	0.66	3.62**	98.83	−0.94**	0.08	0.18	127.67	−0.05	0.22	11.05
28	DV-10A × P100R	69.04	2.35**	0.50	2.09**	97.29	−0.92	0.74	13.99**	130.42	−0.06	0.33	24.36**
29	PHIR-27A × RCR-8297	70.17	0.54	0.78	4.94**	100.71	0.11	0.49	5.98**	135.54	0.19	0.09	1.94
30	PHIR-27A × P69R	71.88	0.24	0.72	4.25**	101.33	0.12	0.41	4.30**	116.06	0.19**	0.03	0.18
31	PHIR-27A × P124R	70.79	0.86	0.88	6.36**	100.71	−0.74*	0.31	2.47**	119.98	−0.20	0.15	4.86
32	PHIR-27A × P100R	70.67	0.85	0.41	1.39*	99.17	−0.19	0.39	3.92**	137.17	−0.01	0.14	4.37
33	PRUN-29A × RCR-8297	70.96	−0.84	0.95	7.47**	99.46	−0.02	0.64	10.36**	155.77	−0.25	0.12	3.30
34	PRUN-29A × P69R	69.88	0.17	0.94	7.18**	98.00	−0.23	0.51	6.61**	138.23	−0.24**	0.04	0.45
35	PRUN-29A × P124R	69.04	0.76	0.74	4.47**	96.38	0.02	0.52	6.83**	126.88	0.00	0.17	6.83
36	PRUN-29A × P100R	69.50	0.99**	0.25	0.51	96.21	−0.35	0.34	2.91**	149.67	0.08	0.13	3.75
37	40A × RCR-8297	71.46	0.91*	0.40	1.32*	99.17	−0.46	0.28	2.01**	150.81	0.09	0.13	3.86
38	40A × P69R	70.21	0.53	0.56	2.57**	96.88	−0.24	0.35	3.02**	140.44	−0.13	0.09	1.85
39	40A × P124R	70.71	0.27	0.54	2.42**	97.67	−0.03	0.33	2.70**	144.85	0.15**	0.03	0.26
40	40A × P100R	71.58	1.63	1.63	21.72**	100.54	−1.55**	0.28	2.03**	147.23	−0.12	0.37	30.98**
41	42A × RCR-8297	71.38	−0.22	0.25	0.51	99.08	0.22**	0.06	0.08	177.73	0.04	0.05	0.52
42	42A × P69R	70.79	−0.09	0.47	1.78*	98.46	−0.05	0.27	1.79**	159.35	0.08	0.07	1.00
43	42A × P124R	71.04	1.86**	0.36	1.09	100.38	−0.96*	0.38	3.64**	158.83	−0.06	0.26	15.00*

(*continued*)

Table 2: (*continued*)

S. No.	Genotypes	Days to 50 % flowering				days to maturity				Plant Height (cm)			
				± SE				± SE				± SE	
		Mean	bi	bi	σ^2 di	Mean	bi	bi	σ^2 di	Mean	bi	bi	σ^2 di
44	42A × P100R	69.58	1.11	0.71	4.16**	101.33	−0.62	0.41	4.28**	166.13	−0.17	0.16	5.77
45	234A × RCR-8297	71.46	0.29	0.63	3.26**	100.96	−0.14	0.36	3.34**	191.06	−0.15*	0.07	1.02
46	234A × P69R	71.54	1.88**	0.15	0.18	101.25	−0.77	0.53	7.20**	166.94	0.00	0.25	14.72*
47	234A × P124R	70.50	0.71	0.77	4.89**	99.04	0.04	0.52	6.94**	159.77	−0.02	0.17	6.93
48	234A × P100R	72.63	2.31	1.63	21.82**	101.08	−1.79**	0.34	2.95**	170.12	−0.29	0.39	34.01**
49	38A × RCR-8297	70.63	0.30	0.58	2.79**	100.21	0.06	0.35	3.10**	159.48	−0.06	0.11	2.70
50	38A × P69R	69.46	0.72	0.52	2.25**	99.46	−0.45	0.27	1.79**	146.90	0.08	0.12	3.55
51	38A × P124R	70.58	1.03**	0.28	0.63	98.25	−0.57*	0.18	0.87*	137.77	−0.05	0.14	4.71
52	38A × P100R	70.71	0.43	0.94	7.32**	99.46	−0.40	0.49	6.04**	155.92	−0.25**	0.07	1.15
53	NC-41B (C) × RCR-8297	71.88	−0.11	0.20	0.32	97.04	−0.04	0.12	0.35	106.27	−0.04	0.03	0.14
54	NC-41B (C) × P69R	73.29	1.63	0.78	4.96**	96.17	−1.11**	0.11	0.30	80.14	−0.05	0.26	15.50*
55	NC-41B (C) × P124R	72.96	1.89	1.75	25.11**	98.04	−1.74**	0.25	1.62**	96.87	−0.15	0.40	37.27**
56	NC-41B (C) × P100R	72.83	1.32	0.87	6.19**	99.42	−1.02**	0.07	0.13	128.54	−0.11	0.23	11.92
57	42B × RCR-8297	71.83	−0.13	0.28	0.65	99.25	0.15	0.13	0.43	176.81	−0.03	0.05	0.60
58	42B × P69R	70.58	0.36	0.43	1.49*	99.17	−0.23	0.23	1.36**	160.83	0.08	0.07	1.18
59	42B × P124R	71.08	1.95**	0.49	1.97**	100.25	−1.09**	0.31	2.43**	157.21	−0.04	0.28	17.33*
60	42B × P100R	69.92	0.95	0.59	2.87**	100.92	−0.50	0.37	3.45**	166.29	−0.14	0.14	4.31
61	CMS-XA	69.58	−1.16	1.26	13.04**	100.17	1.16**	0.24	1.41**	86.21	0.16	0.26	15.59*
62	E002-91	69.58	0.01	0.86	6.00**	101.17	0.41	0.39	3.83**	100.58	0.17	0.11	2.54
63	PKU-2A	69.42	0.83	0.53	2.31**	98.58	−0.16	0.44	4.85**	68.44	−0.03	0.15	5.04
64	ARG-2	70.50	0.89	0.65	3.45**	98.75	−0.24	0.49	5.99**	97.57	−0.10	0.16	5.67
65	ARG-3	68.83	0.30	0.68	3.74**	100.25	0.21	0.37	3.55**	113.21	0.03	0.13	4.02

(*continued*)

Table 2: (*continued*)

S. No.	Genotypes	Days to 50 % flowering				days to maturity				Plant Height (cm)			
		Mean	bi	± SE bi	σ^2 di	Mean	bi	± SE bi	σ^2 di	Mean	bi	± SE bi	σ^2 di
66	ARG-6A	68.67	−0.52	0.55	2.51**	97.42	0.51**	0.10	0.25	89.79	0.07	0.12	3.06
67	DV-10A	71.42	3.22**	0.89	6.51**	101.00	−1.13	1.14	32.93**	93.88	0.28	0.42	39.76**
68	PHIR-27A	72.67	1.53*	0.58	2.72**	98.83	−0.55	0.58	8.50**	75.19	−0.08	0.22	11.49
69	PRUN-29A	69.08	−0.26	0.93	7.09**	102.42	0.52	0.39	3.90**	111.92	−0.03	0.18	7.24
70	40A	68.25	−0.23	0.60	2.94**	96.33	0.40	0.21	1.11*	107.71	0.11	0.09	1.83
71	42A	68.08	−0.08	0.89	6.46**	97.50	0.44	0.40	4.01**	131.48	0.20	0.09	2.01
72	234A	68.50	−0.02	0.80	5.22**	99.17	0.33	0.39	3.85**	144.02	−0.05	0.15	4.90
73	38A	69.50	−0.20	0.99	7.99**	100.50	0.44	0.47	5.69**	117.36	−0.10	0.18	7.10
74	NC-41B (C)	70.92	0.60	0.39	1.22*	97.50	−0.08	0.32	2.62**	67.23	0.00	0.11	2.70
75	42B	69.00	0.11	1.05	9.08**	98.17	0.49	0.49	6.08**	124.42	0.19	0.15	4.84
76	RCR-8297	68.33	−0.40	0.75	4.60**	95.67	0.48	0.30	2.29**	109.90	0.18	0.09	1.75
77	P69R	73.75	2.44**	0.28	0.66	95.50	−0.92	0.75	14.43**	66.44	0.10	0.32	23.93**
78	P124R	70.17	1.29	0.63	3.29**	95.92	−0.45	0.54	7.48**	80.82	−0.10	0.20	8.84
79	P100R	69.25	−0.01	0.75	4.59**	97.33	0.40	0.32	2.55**	98.35	0.10	0.12	3.46
	Mean	70.18				98.75				130.85			
	Min.	67.46				95.50				66.44			
	Max.	73.75				102.42				191.06			
	SE ±	0.15				0.18				3.16			

and significant deviations from regression line; hence they are suitable to poor environments with unpredictable performance.

Days to maturity

The mean performance for days to maturity over four environments presented in Table 2 revealed that PRUN-29A (102.42) had the maximum number of days to maturity. Among hybrids, thirty-three hybrids and among parents, *cms*-XA, E002-91A, ARG-2A, ARG-3A, DV-10A, PHIR-27A, PRUN-29A, 234A and 38A recorded above average stability ($b < 1$) for days to maturity. The "b" value for all these genotypes was non-significant except for ARG-2A × P124R, ARG-3A × P69R, PHIR-27A × P124R, 40A × P100R, 42A × RCR-8297, 42A × P124R, 234A × P100R, NC-41B × P100R, 42B × P124R and *cms*-XA whereas deviations from regression line were significant for all except PKU-2A × P69R, ARG-2A × P124R, 42A × RCR-8297, NC-41B × P100R and 42B × RCR-8297.

The stability parameters showed that the genotypes PKU-2A × P69R, PHIR-27A × P69R, 42A × P100R, 234A × P69R, E002-91A and PRUN-29A had high mean, above average stability to environments ($b < 1$) and non-significant deviation from regression line, thus, these genotypes are expected to do well under poor environments, and their performance would be predictable. While the genotype 40A × P100R, 234A × P100R, 42B × P124R and DV-10A showed high mean, below average stability ($b > 1$) and non-significant deviation from regression line, hence, these genotypes are suitable to favourable environment with predictable performance.

Plant height (cm)

The mean performance of genotypes presented in Table 2 showed that 234A × RCR-8297 (191.06 cm) recorded the maximum height followed by 42B × RCR-8297 (176.81), 42A × RCR-8297 (177.73), 234A × P100R (170.12), 234A × P69R (166.94), 42B × P100R (166.29) and 42A × P100R (166.13). All the genotypes exhibited regression coefficient less than unity, but some of them exhibited significant deviations from regression line. Similar observations have been reported by Ahmad and Adella (2009) while studying the stability of plant height.

The hybrids E002-91A × P69R, PHIR-27A × P69R, PRUN-29A × P69R and 40A × P124R had low mean, above average stability to environments ($b < 1$) with non-significant deviation from regression line, hence these genotypes are suitable to favourable environment with predictable performance. PKU-

2A × RCR-8297, 234A × RCR-8297 and 38A × P100R recorded high mean, above average stability to environments (b < 1) and non-significant deviation from regression line, thus, these genotypes are expected to do well under poor environments, and their performance would be predictable.

Head diameter (cm)

The mean performance of genotypes presented in Table 3 showed that among parental lines E002-91A (21.85) recorded the maximum head diameter followed by ARG-3A (21.05), PRUN-29A (20.97) and among crosses, NC-41B × P100R (21.09), DV-10A × P124R (20.47) and 38A × P100R (18.10). Among the total genotypes, all exhibited less than unity regression coefficient, except PKU-2A × P100R, E002-91A × P100R, PRUN-29A × RCR-8297 and P69R. Rao *et al*. (2004) also found that linear component of G × E interaction was significant whereas non-linear component of G × E interaction was not significant for head diameter.

Among parental lines, E002-91A and ARG-3A had high mean, above average stability (b < 1) with non-significant deviation from regression hence these parental line are stable over the environment with respect to head diameter with predictable performance. Among hybrids 38A × P100R, DV-10A × P124R, NC-41B × P100R and parental line PRUN-29A had high mean, above average stability (b < 1) with significant deviation from regression hence these genotypes are suitable to poor environment with predictable performance. Genotypes DV-10A exhibited high mean, below average stability (b > 1) and significant deviations from regression line which indicates its suitability to favourable environments but with unpredictable performance.

Number of leaves per plant

Sufficient variability was observed among the genotypes for number of leaves per plant. The results shown in Table 3 revealed that the hybrid 234A × P69R recorded maximum number of leaves per plant (34.99) followed by 234A × P100R (33.89) below average stability (b > 1) and 234A × P124R (31.60) and 234A × RCR-8297 (30.81) above average stability (b < 1) with significant deviation from regression line which indicates their stability for this trait over environments with unpredictable performance. The genotypes *cms*-XA × P69R, PKU-2A × P69R, ARG-2A × P100R, 40A × RCR-8297, 38A × P69R and 42B × P69R had fulfilled the two criteria *i. e*. the regression coefficient above average stability (b < 1) and non-significant deviation from regression line indicating their stability for this trait. but their mean performance was

Table 3: Mean performance, regression coefficient (bi) and deviation from regression (δ^2di) for head diameter, no. leaves per plant and leaf area over different environments.

S. No.	Genotypes	Head Diameter (cm)				No. of Leaves/Plant				Leaf area (m2)/plant			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
1	CMS-XA × RCR-8297	16.73	0.74	0.53	3.47	22.33	0.85	0.61	3.44**	0.32	19.24**	4.94	0.80**
2	CMS-XA × P69R	16.68	0.54	0.34	1.44	21.53	0.75*	0.26	0.61	0.56	13.80**	2.20	0.16**
3	CMS-XA × P124R	16.96	0.54	0.65	5.26*	22.53	0.68	0.73	4.90**	0.47	17.63*	7.76	1.97**
4	CMS-XA × P100R	17.51	0.36	1.28	20.23**	21.11	0.93	1.35	16.97**	0.34	24.60	18.49	11.16**
5	E002-91 × RCR-8297	16.82	0.76	0.56	3.83	25.05	1.00	0.55	2.77**	0.42	20.72**	3.73	0.45**
6	E002-91 × P69R	16.46	0.97**	0.08	0.08	25.10	1.00*	0.36	1.23*	0.63	15.06	8.25	2.22**
7	E002-91 × P124R	17.26	0.35	0.73	6.55*	23.04	0.20	0.87	7.10**	0.38	11.77	12.42	5.03**
8	E002-91 × P100R	17.67	1.00	0.68	5.78*	21.55	1.31	0.66	4.02**	0.48	26.52**	4.06	0.54**
9	PKU-2A × RCR-8297	18.55	0.84	0.40	2.00	24.68	0.79	0.61	3.44**	0.58	8.47	12.63	5.20**
10	PKU-2A × P69R	17.72	0.29**	0.07	0.07	24.43	0.36**	0.03	0.01	0.60	5.44*	1.91	0.12**
11	PKU-2A × P124R	17.13	−0.13	0.56	3.83	22.50	−0.46	0.56	2.94**	0.59	−9.97	8.42	2.31**
12	PKU-2A × P100R	15.99	1.61*	0.70	6.11*	22.56	2.12**	0.37	1.26*	0.76	28.72	16.44	8.82**
13	ARG-2A × RCR-8297	17.28	−0.27	0.46	2.59	22.79	0.04	0.57	3.03**	0.86	1.04	9.62	3.02**
14	ARG-2A × P69R	15.75	0.84	1.04	13.31**	20.80	1.38	0.98	8.90**	0.30	29.01*	11.05	3.98**
15	ARG-2A × P124R	15.88	0.36	0.74	6.79*	22.50	0.89	0.65	3.93**	0.38	14.48	11.31	4.17**
16	ARG-2A × P100R	17.52	0.70	0.34	1.45	20.53	0.93**	0.22	0.44	0.35	16.29**	2.26	0.17**
17	ARG-3A × RCR-8297	16.83	0.12	0.52	3.39	21.88	−0.19	0.60	3.32**	0.45	1.34	10.30	3.46**
18	ARG-3A × P69R	16.95	0.60	1.06	14.01**	25.50	1.28	0.96	8.68**	0.32	24.47	14.11	6.50**
19	ARG-3A × P124R	17.35	−0.26	1.06	13.86**	22.55	0.30	1.22	13.85**	0.34	10.86	19.46	12.36**
20	ARG-3A × P100R	16.38	0.66	0.83	8.48**	17.70	1.12	0.76	5.36**	0.38	22.77*	9.09	2.69**
21	ARG-6A × RCR-8297	16.48	−0.20	1.01	12.54**	21.54	0.18	1.17	12.65**	0.35	11.24	18.14	10.74**
22	ARG-6A × P69R	14.31	−0.12	1.07	14.31**	19.54	−0.35	1.22	13.82**	0.29	7.05	20.40	13.58**

(*continued*)

Table 3: (*continued*)

S. No.	Genotypes	Head Diameter (cm)				No. of Leaves/Plant				Leaf area (m2)/plant			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
23	ARG-6A × P124R	16.48	0.59	0.51	3.20	20.48	0.63	0.62	3.55**	0.34	15.80*	6.32	1.30**
24	ARG-6A × P100R	17.42	0.74	1.02	12.80**	22.29	1.48	0.80	5.93**	0.48	23.08	15.13	7.47**
25	DV-10A × RCR-8297	17.16	−0.14	0.80	7.92**	24.42	0.24	0.91	7.78**	0.48	9.26	14.27	6.65**
26	DV-10A × P69R	15.03	0.36	1.02	12.93**	23.00	0.96	1.01	9.42**	0.45	20.26	14.67	7.02**
27	DV-10A × P124R	20.47	0.50	0.89	9.84**	23.03	1.11	0.78	5.67**	0.25	19.50	12.59	5.17**
28	DV-10A × P100R	15.77	0.74	1.31	21.42**	20.92	1.11	1.43	19.04**	0.58	30.63	17.05	9.49**
30	PHIR-27A × P69R	15.30	0.75*	0.28	0.98	22.67	0.59	0.56	2.87**	0.33	8.97	9.84	3.16**
31	PHIR-27A × P124R	15.96	−0.26	0.85	8.97**	21.94	0.27	0.99	9.04**	0.38	7.16	16.18	8.54**
32	PHIR-27A × P100R	16.74	0.28	0.56	3.89	23.58	0.27	0.66	4.03**	0.37	10.85	8.67	2.45**
33	PRUN-29A × RCR-8297	16.41	−1.16*	0.41	2.04	23.21	−0.95	0.81	6.12**	0.70	−18.57	12.05	4.74**
34	PRUN-29A × P69R	16.56	−0.79	0.53	3.45	25.68	−0.60	0.77	5.60**	0.73	−5.35	14.47	6.83**
35	PRUN-29A × P124R	15.19	0.21	0.73	6.56*	23.13	0.02	0.86	6.83**	0.65	8.83	13.05	5.56**
36	PRUN-29A × P100R	17.26	0.70	0.35	1.49	22.02	0.82	0.38	1.35*	0.43	16.43**	1.69	0.09**
37	40A × RCR-8297	16.00	0.73	0.34	1.39	25.73	0.98**	0.16	0.23	0.22	16.34**	3.33	0.36**
38	40A × P69R	17.85	−0.25	0.52	3.34	24.46	−0.14	0.62	3.63**	0.37	3.00	10.47	3.58**
39	40A × P124R	16.95	0.63**	0.14	0.23	27.81	0.61	0.32	0.98	0.54	8.49	6.86	1.54**
40	40A × P100R	17.18	0.53	1.58	30.88**	24.10	1.68	1.45	19.51**	0.37	23.58	26.85	23.53**
41	42A × RCR-8297	16.48	0.02	0.24	0.71	29.61	−0.15	0.25	0.61	0.56	−2.38	4.35	0.62**
42	42A × P69R	16.21	0.31	0.32	1.23	29.58	0.37	0.35	1.17*	0.56	2.23	7.29	1.73**
43	42A × P124R	17.35	0.64	1.02	12.82**	26.98	1.16	0.99	9.10**	0.59	25.33	12.22	4.87**
44	42A × P100R	16.74	−0.13	0.86	9.11**	26.35	0.23	0.98	8.97**	0.60	10.39	15.11	7.45**
45	234A × RCR-8297	15.41	−0.43	0.44	2.45	30.81	−0.36	0.57	3.00**	0.37	−1.13	10.48	3.58**
46	234A × P69R	16.46	0.80	0.93	10.80**	34.99	1.13	0.97	8.82**	0.72	26.53*	9.96	3.24**

(*continued*)

Table 3: (*continued*)

S. No.	Genotypes	Head Diameter (cm)				No. of Leaves/Plant				Leaf area (m2)/plant			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
47	234A × P124R	15.67	0.13	0.74	6.85*	31.60	−0.06	0.86	6.94**	0.46	7.60	13.57	6.01**
48	234A × P100R	14.89	0.16	1.87	43.51**	33.89	1.39	1.93	34.72**	1.01	26.83	31.27	31.91**
49	38A × RCR-8297	15.99	−0.17	0.49	2.97	29.34	−0.30	0.54	2.73**	0.73	0.89	9.81	3.14**
50	38A × P69R	14.11	0.67	0.36	1.60	23.81	0.95**	0.14	0.17	0.53	13.98*	6.02	1.18**
51	38A × P124R	16.04	0.30	0.59	4.37	24.62	0.63	0.58	3.11**	0.38	13.60	7.69	1.93**
52	38A × P100R	18.10	−0.67	0.65	5.32*	26.87	−0.38	0.89	7.41**	0.69	−1.47	15.68	8.03**
53	NC-41B (C) × RCR-8297	14.74	−0.19	0.11	0.16	19.86	−0.12	0.18	0.31	0.43	−2.68	2.81	0.26**
54	NC-41B (C) × P69R	16.20	0.62	1.04	13.46**	23.81	1.34	0.90	7.53**	0.43	23.38	14.56	6.92**
55	NC-41B (C) × P124R	17.54	0.55	1.75	37.98**	20.08	1.82	1.62	24.48**	0.34	26.64	29.42	28.26**
56	NC-41B (C) × P100R	21.09	0.29	1.02	12.86**	22.76	0.99	0.97	8.81**	0.66	17.26	16.15	8.51**
57	42B × RCR-8297	17.42	−0.21	0.19	0.45	30.18	−0.32	0.16	0.23	0.51	−3.48	3.99	0.52**
58	42B × P69R	16.63	0.49*	0.20	0.51	29.54	0.63**	0.12	0.14	0.51	8.43	5.09	0.84**
59	42B × P124R	17.71	0.77	1.06	13.86**	27.10	1.39	0.95	8.44**	0.64	27.60	12.46	5.07**
60	42B × P100R	17.18	−0.09	0.73	6.55*	26.28	0.18	0.83	6.46**	0.58	9.00	12.72	5.28**
61	CMS-XA	15.17	−0.11	1.22	18.51**	18.88	−0.98	1.23	14.10**	1.68	−14.43	21.57	15.19**
62	E002-91	21.85	0.52	0.59	4.34	16.56	0.11	0.80	5.94**	1.01	3.99	13.26	5.74**
63	PKU-2A	16.95	0.17	0.63	4.98*	15.06	0.13	0.74	5.08**	0.46	9.54	10.61	3.67**
64	ARG-2	15.01	−0.03	0.74	6.71*	18.19	0.01	0.85	6.71**	0.50	8.44	13.04	5.55**
65	ARG-3	21.05	0.13	0.57	4.01	20.04	−0.15	0.66	4.01**	0.84	3.42	10.96	3.92**
66	ARG-6A	16.80	−0.06	0.54	3.60	18.90	−0.44	0.54	2.71**	0.47	−6.52	9.46	2.92**
67	DV-10A	16.30	2.34	1.10	15.01**	19.19	2.73	1.24	14.38**	0.59	54.19**	5.74	1.08**
68	PHIR-27A	15.68	0.30	0.97	11.71**	18.33	0.49	1.09	11.15**	0.45	18.08	14.59	6.95**
69	PRUN-29A	20.97	−0.37	0.73	6.53*	24.75	−0.82	0.67	4.22**	0.70	−7.13	14.16	6.54**

(*continued*)

Table 3: (*continued*)

S. No.	Genotypes	Head Diameter (cm)				No. of Leaves/Plant				Leaf area (m2)/plant			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
70	40A	16.97	0.21	0.48	2.90	20.94	−0.13	0.57	3.08**	0.41	−1.14	9.81	3.14**
71	42A	11.25	0.57	0.60	4.47	26.73	0.16	0.83	6.36**	0.63	3.60	13.86	6.27**
72	234A	11.86	−0.31	0.61	4.61	28.25	−0.63	0.60	3.37**	0.56	−3.99	12.33	4.97**
73	38A	10.99	−0.56	0.71	6.22*	22.50	−0.95	0.65	3.98**	0.44	−8.19	14.71	7.06**
74	NC-41B (C)	8.83	0.20	0.45	2.46	16.17	0.14	0.53	2.61**	0.31	7.52	7.39	1.78**
75	42B	10.59	0.59	0.75	6.95*	25.79	0.09	0.99	9.09**	0.67	5.40	16.29	8.66**
76	RCR-8297	7.90	0.38	0.59	4.35	22.21	0.00	0.75	5.25**	0.29	−1.20	12.66	5.23**
77	P69R	10.31	1.37	1.04	13.41**	24.33	1.73	1.10	11.24**	0.59	37.46**	8.25	2.22**
78	P124R	9.91	0.12	0.90	10.00**	20.52	0.28	1.02	9.74**	0.47	13.98	14.55	6.91**
79	P100R	9.52	0.24	0.59	4.25	19.88	−0.15	0.69	4.49**	0.32	1.17	11.84	4.57**
	Mean	16.10				23.54				0.52			
	Min.	7.90				15.06				0.22			
	Max.	21.85				34.99				1.68			
	SE ±	0.29				0.43				0.02			

below average hence cannot be considered ideal genotypes, however, PKU-2A x P69R, 40A × RCR-8297, 38A × P69R and 42B × P69R had above average mean performance.

Leaf area (m^2)

The mean performance of genotypes presented in Table 3 showed that among the parental lines *cms*- × A (1.68) recorded the maximum leaf area followed by E002-91A (1.01) and among crosses 234A × P100R (1.01). Except 38A × RCR-8297, all the genotypes exhibited regression coefficient more than unity with significant deviations from regression line.

The hybrids *cms*-XA × RCR-8297, *cms*-XA × P69R, *cms*-XA × P124R, E002-91A × RCR-8297, E002-91A × P100R, PKU-2A × P69R, ARG-2A × P69R, ARG-2A × P100R, ARG-3A × P100R, ARG-6A × P124R, PRUN-29A × P100R, 40A × RCR-8297, 234A × P69R, 38A × P69R, female parent DV-10A and male parent P69R recorded below average stability (b > 1) with significant deviation from regression line hence will perform better over favourable environment, but their performance will be unpredictable.

Specific leaf weight (g)

The mean performance of genotypes presented in Table 4 showed that among the parental lines *cms*-XA (4.33) recorded the maximum leaf area followed by E002-91A (2.88) and ARG-2A × RCR-8297 (1.99). Except PKU-2A × P100R, ARG-6A × RCR-8297, 42A × P100R, 234A × RCR-8297, 38A × P69R and 42B × P69R all the studied genotypes exhibited regression coefficient more than unity with significant deviations from regression line.

The genotypes E002-91A × P124R, ARG-3A × RCR-8297, PHIR-27A × RCR-8297, NC-41B × RCR-8297, E002-91A, ARG-3A, 42B and P100R showed below average significant stability to environments (b > 1) with significant deviation from regression line hence will perform better over favourable environments with unpredictable performance.

Leaf area index

Sufficient variability was observed among the genotypes for leaf area index. The results shown in Table 4 revealed that leaf area index was highest in *cms*-XA

Table 4: Mean performance, regression coefficient (bi) and deviation from regression (δ^2di) for specific leaf weight, leaf area index and leaf water potential over different environments.

S. No.	Genotypes	Specific Leaf Weight (g)				Leaf Area Index				Leaf Water Potential (MPa)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
1	CMS-XA × RCR-8297	0.76	14.79	13.20	4.20**	1.75	3.66**	0.77	0.56**	−2.49	2.45	3.73	5.62**
2	CMS-XA × P69R	1.40	4.23	11.25	3.05**	3.07	2.51**	0.57	0.31**	−2.89	0.88	2.77	3.11**
3	CMS-XA × P124R	1.08	13.50	14.17	4.84**	2.56	3.35*	1.37	1.77**	−2.52	1.40	4.06	6.65**
4	CMS-XA × P100R	0.84	5.05	29.32	20.73**	1.85	4.44	3.55	11.79**	−2.61	−2.47	7.00	19.80**
5	E002-91 × RCR-8297	0.85	10.81	15.84	6.05**	2.29	3.85**	0.74	0.51**	−2.55	1.69	4.13	6.88**
6	E002-91 × P69R	1.26	9.83	14.05	4.76**	3.45	2.83	1.52	2.17**	−2.58	4.02	2.57	2.66**
7	E002-91 × P124R	0.89	20.73*	9.36	2.11**	2.11	2.44	2.19	4.49**	−2.21	2.64	3.82	5.88**
8	E002-91 × P100R	1.21	13.43	20.20	9.84**	2.62	4.92**	0.84	0.66**	−2.54	2.25	5.22	10.99**
9	PKU-2A × RCR-8297	1.19	5.25	15.83	6.04**	3.19	1.58	2.36	5.20**	−2.83	3.99	2.80	3.16**
10	PKU-2A × P69R	1.29	1.68	4.86	0.57**	3.31	0.99*	0.39	0.14**	−2.77	0.82	1.07	0.47**
11	PKU-2A × P124R	1.44	2.43	12.66	3.86**	3.26	−1.72	1.65	2.55**	−2.24	1.76	2.86	3.31**
12	PKU-2A × P100R	1.78	−0.19	30.40	22.28**	4.16	5.06	3.31	10.27**	−2.43	3.38	7.03	19.97**
13	ARG-2A × RCR-8297	1.99	−10.08	8.67	1.81**	4.74	0.01	1.80	3.04**	−2.45	−3.37*	1.36	0.75**
14	ARG-2A × P69R	0.77	8.09	26.50	16.92**	1.67	5.27*	2.24	4.70**	−2.76	−0.07	6.62	17.71**
15	ARG-2A × P124R	0.91	−7.94	16.84	6.83**	2.08	2.42	2.27	4.85**	−2.22	−2.22	4.04	6.60**
16	ARG-2A × P100R	0.88	5.16	13.16	4.18**	1.90	2.97**	0.63	0.37**	−2.30	1.42	3.18	4.09**
17	ARG-3A × RCR-8297	1.14	15.76**	4.54	0.50**	2.48	0.51	1.89	3.37**	−2.27	2.84	2.15	1.86**
18	ARG-3A × P69R	0.64	−2.79	25.90	16.17**	1.74	4.27	2.86	7.69**	−2.64	−2.17	6.16	15.32**
19	ARG-3A × P124R	0.78	−7.89	23.69	13.53**	1.89	1.79	3.69	12.78**	−2.62	−5.14	4.71	8.94**
20	ARG-3A × P100R	1.17	4.46	21.28	10.92**	2.10	4.10	1.87	3.26**	−2.56	−0.37	5.25	11.13**
21	ARG-6A × RCR-8297	0.86	0.64	23.04	12.80**	1.92	2.00	3.41	10.92**	−2.74	−3.60	5.02	10.18**
22	ARG-6A × P69R	0.78	23.26	18.07	7.87*	1.59	1.66	3.74	13.10**	−2.65	1.26	5.90	14.07**

(*continued*)

Table 4: (*continued*)

S. No.	Genotypes	Specific Leaf Weight (g)				Leaf Area Index				Leaf Water Potential (MPa)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
23	ARG-6A × P124R	0.89	15.36	10.25	2.53**	1.88	3.06*	1.02	0.98**	−3.00	2.42	3.22	4.19**
24	ARG-6A × P100R	1.21	−9.96	24.92	14.97**	2.63	3.90	3.10	9.03**	−2.38	−2.15	6.14	15.23**
25	DV-10A × RCR-8297	1.02	−2.90	18.15	7.95**	2.64	1.59	2.70	6.86**	−2.79	−3.33	3.79	5.80**
26	DV-10A × P69R	1.04	−2.87	23.77	13.62**	2.48	3.53	2.90	7.87**	−3.09	−2.73	5.50	12.22**
27	DV-10A × P124R	0.56	−5.95	21.31	10.95**	1.36	3.34	2.56	6.14**	−2.45	−2.19	5.08	10.40**
28	DV-10A × P100R	1.48	19.54	28.95	20.20**	3.20	5.76	3.14	9.25**	−2.73	0.68	7.82	24.71**
29	PHIR-27A × RCR-8297	1.02	19.93*	7.43	1.33**	2.58	2.55	1.81	3.06**	−2.41	5.28**	1.11	0.50**
30	PHIR-27A × P69R	0.74	12.77	10.20	2.51**	1.83	1.80	1.77	2.95**	−2.85	4.48**	1.01	0.41**
31	PHIR-27A × P124R	0.90	−11.72	17.89	7.72**	2.11	1.06	3.07	8.85**	−2.55	−4.89	3.35	4.54**
32	PHIR-27A × P100R	0.79	13.50	9.50	2.18**	2.01	2.16	1.53	2.19**	−2.52	1.34	3.15	4.01**
33	PRUN-29A × RCR-8297	1.59	−24.52	11.38	3.12**	3.84	−3.71	2.05	3.92**	−2.39	−6.61**	1.95	1.54**
34	PRUN-29A × P69R	1.48	−7.83	16.50	6.56**	4.02	−1.07	2.68	6.76**	−2.54	−4.75	2.60	2.74**
35	PRUN-29A × P124R	1.46	19.97	9.17	2.03**	3.58	1.91	2.34	5.12**	−2.75	2.35	3.76	5.72**
36	PRUN-29A × P100R	0.98	10.60	11.42	3.14**	2.34	3.09**	0.18	0.03**	−3.13	2.19	2.96	3.53**
37	40A × RCR-8297	0.46	4.02	13.69	4.52**	1.22	2.95**	0.82	0.62**	−2.61	1.43	3.26	4.30**
38	40A × P69R	0.84	2.18	12.33	3.67**	2.02	0.57	1.95	3.57**	−2.59	−1.83	2.74	3.04**
39	40A × P124R	0.99	6.56	9.54	2.19**	2.95	1.61	1.26	1.49**	−2.81	2.93	1.55	0.97**
40	40A × P100R	0.82	−26.43	31.67	24.18**	2.03	3.70	5.28	26.18**	−2.56	−6.02	7.91	25.28**
41	42A × RCR-8297	0.97	4.34	4.48	0.48**	2.84	−0.35	0.84	0.66**	−2.66	1.28	0.97	0.38**
42	42A × P69R	1.04	−3.48	8.32	1.67**	2.75	0.33	1.37	1.76**	−2.67	0.82	2.04	1.68**
43	42A × P124R	1.29	5.57	24.92	14.97**	2.97	4.58	2.43	5.53**	−2.86	−0.88	6.13	15.19**
44	42A × P100R	1.31	−0.17	19.55	9.21**	3.41	1.84	2.85	7.63**	−2.65	−3.08	4.25	7.30**
45	234A × RCR-8297	0.64	−0.17	12.23	3.60**	2.04	−0.20	1.96	3.59**	−2.49	−2.38	2.47	2.46**

(*continued*)

Table 4: (*continued*)

S. No.	Genotypes	Specific Leaf Weight (g)				Leaf Area Index				Leaf Water Potential (MPa)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
46	234A × P69R	1.16	14.75	22.41	12.10**	3.96	4.95*	1.86	3.25**	−2.26	1.20	5.98	14.43**
47	234A × P124R	0.79	19.51	9.91	2.37**	2.55	1.69	2.45	5.62**	−2.34	2.08	3.88	6.08**
48	234A × P100R	1.60	−20.99	39.89	38.35**	5.57	4.38	6.08	34.68**	−2.41	−8.12	8.66	30.33**
49	38A × RCR-8297	1.31	9.66	9.17	2.03**	4.02	0.33	1.82	3.10**	−2.19	0.23	2.79	3.14**
50	38A × P69R	1.15	−0.35	13.47	4.37**	2.94	2.46	1.28	1.53**	−2.85	0.90	3.23	4.21**
51	38A × P124R	0.84	1.26	14.30	4.93**	2.08	2.43	1.53	2.19**	−2.31	−0.96	3.43	4.76**
52	38A × P100R	1.35	−8.57	17.25	7.18**	3.82	−0.40	2.92	7.99**	−2.65	−4.98	2.75	3.06**
53	NC-41B (C) × RCR-8297	1.16	−5.20**	1.42	0.05**	2.37	−0.56	0.49	0.23**	−2.83	−1.32**	0.25	0.02**
54	NC-41B (C) × P69R	1.11	−6.70	25.19	15.30**	2.39	4.01	2.97	8.29**	−2.69	−2.42	6.02	14.66**
55	NC-41B (C) × P124R	0.94	−27.83	35.57	30.50**	1.85	4.22	5.79	31.49**	−2.47	−6.78	8.70	30.55**
56	NC-41B (C) × P100R	1.48	−11.33	22.15	11.83**	3.60	2.85	3.19	9.56**	−2.10	−3.76	5.10	10.51**
57	42B × RCR-8297	0.98	2.88	5.06	0.62**	2.64	−0.56	0.78	0.57**	−2.70	−0.04	1.33	0.72**
58	42B × P69R	1.06	0.11	9.12	2.00**	2.78	1.49	1.01	0.97**	−2.38	1.12	2.08	1.75**
59	42B × P124R	1.21	2.22	26.90	17.44**	3.36	4.92	2.56	6.17**	−2.88	−1.11	6.53	17.25**
60	42B × P100R	1.22	1.54	16.52	6.58**	3.19	1.62	2.39	5.37**	−2.72	−2.31	3.70	5.53**
61	CMS-XA	4.33	21.91	23.04	12.80**	9.27	−2.17	4.18	16.38**	−2.31	5.84	5.38	11.69**
62	E002-91	2.88	19.64*	7.49	1.35**	5.55	1.05	2.42	5.49**	−2.24	5.21**	1.13	0.52**
63	PKU-2A	1.47	14.17	10.66	2.74**	2.51	1.94	1.90	3.40**	−2.15	1.06	3.49	4.93**
64	ARG-2	1.35	11.56	14.55	5.10**	2.76	1.70	2.39	5.36**	−2.24	−0.25	4.07	6.70**
65	ARG-3	1.97	16.99**	5.12	0.63**	4.61	0.90	1.99	3.73**	−2.26	2.58	2.62	2.77**
66	ARG-6A	1.28	9.53	10.23	2.52**	2.60	−0.99	1.84	3.16**	−2.25	2.54	2.39	2.32**
67	DV-10A	1.45	35.93	37.24	33.43**	3.24	10.20**	0.47	0.21**	−2.40	7.64	9.60	37.21**
68	PHIR-27A	1.22	14.58	20.07	9.71**	2.46	3.45	2.67	6.68**	−2.45	0.07	5.51	12.28**

(*continued*)

Table 4: (*continued*)

S. No.	Genotypes	Specific Leaf Weight (g)				Leaf Area Index				Leaf Water Potential (MPa)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
69	PRUN-29A	1.44	15.59	13.57	4.44**	3.83	−0.98	2.72	6.92**	−2.58	1.72	4.09	6.77**
70	40A	0.97	12.38	7.39	1.32**	2.25	0.01	1.84	3.16**	−3.02	3.36*	1.47	0.88**
71	42A	1.01	18.69	9.72	2.28**	2.55	0.96	2.54	6.05**	−2.87	5.47**	1.04	0.43**
72	234A	0.96	13.08	11.45	3.16**	3.07	−0.47	2.34	5.12**	−2.58	0.97	3.53	5.03**
73	38A	0.96	13.00	15.93	6.12**	2.40	−1.21	2.82	7.47**	−2.94	0.41	4.48	8.12**
74	NC-41B (C)	0.94	11.76	6.56	1.04**	1.70	1.54	1.30	1.60**	−2.77	1.32	2.41	2.35**
75	42B	1.11	25.55**	7.23	1.26**	2.85	1.40	2.96	8.21**	−2.84	6.25**	1.75	1.23**
76	RCR-8297	0.74	12.21	11.98	3.46**	1.60	0.00	2.37	5.25**	−2.86	4.41*	1.82	1.33**
77	P69R	1.30	23.49	27.68	18.47**	3.26	7.03**	1.44	1.94**	−2.82	3.61	7.46	22.49**
78	P124R	1.15	12.25	18.54	8.29**	2.57	2.69	2.67	6.70**	−2.88	−0.47	4.99	10.05**
79	P100R	0.85	17.89**	5.52	0.74**	1.74	0.52	2.18	4.47**	−3.13	3.88	1.96	1.56**
	Mean	1.17				2.82				−2.59			
	Min.	0.46				1.22				−3.13			
	Max.	4.33				9.27				−2.10			
	SE ±	0.06				0.13				0.03			

(9.27) followed by 234A × P100R (5.57), E002-91A (5.55), ARG-2A × RCR-8297 (4.74) and ARG-3A (4.61).

The genotypes *cms*-XA × RCR-8297, *cms*-XA × P69R, *cms*-XA × P124R, E002-91A × RCR-8297, E002-91A × P100R, PKU-2A × P69R, ARG-2A × P100R, ARG-6A × P124R, PRUN-29A × P124R, PRUN-29A × P100R, 234A × P69R, DV-10A and P69R exhibited (b > 1) regression coefficient with significant deviations from regression line hence will perform better over favorable environment but their performance will be unpredictable.

It was further observed that genotypes 234A × P100R and *cms*-XA showed high mean, below average stability (b > 1) and significant deviations from regression line hence are suitable to poor environments with unpredictable performance. However, the genotypes ARG-3A and ARG-2A × RCR-8297 exhibited high mean, above average stability (b < 1) and non-significant deviation from regression line therefore suitable for favorable environments and their performance would be predictable.

Leaf water potential (MPa)

The mean performance of genotypes over the environments (Table 4) revealed that the genotype NC-41B (−2.10) had the highest, whereas P100R (−3.13) had the lowest mean value for leaf water potential. Stability parameters presented in Table 4 revealed that genotypes, twenty nine hybrids and nine parents viz; 40A (−3.02), 234A (−2.87), 38A (−2.94), NC-41B (−2.77), 42B (−2.84), RCR-8297 (−2.86), P69R (−2.82), P124R (−2.88) and P100R (−3.13) exhibited above average mean performance. Except *cms*-XA × P69R, PKU-2A × P69R, ARG-2A × P69R, ARG-3A × P100R and DV-10A × P100R, all genotypes expressed above unity regression (b > 1) with significant deviations from regression line hence these all are stable with unpredictable performance.

Among the hybrids, ARG-6A × P124R, DV-10A × P69R, PRUN-29A × P100R and among parental lines, P100R and 40A had high mean, below average stability to environmental changes (b > 1) with significant deviations from regression line hence, they are suitable for poor environments with unpredictable performance. While the genotypes *cms*-XA × P69R, PKU-2A × P69R, ARG-2A × P69R, DV-10A × P100R, 42A × P69R, 38A × P69R and 38A can be suitable for favourable environments as they possessed high mean (above average) and above average stability to environmental changes (b < 1) with predictable performance.

Relative leaf water content (%)

The mean performance of genotypes over the environments (Table 5) revealed that the female parent PKU-2A (81.54) had the maximum, whereas among crosses ARG-6A × P100R (47.53) had the lowest mean value for relative leaf water content. Stability parameters revealed that among the hybrids, CMS-XA × RCR-8297, E002-91A × P124R, E002-91A × P100R, ARG-3A × RCR-8297, ARG-6A × RCR-8297, PHIR-27A × P100R, 40A × P100R, and among the parental lines, ARG-2A, ARG-3A, PHIR-27A, 38A, P124R and P100R had above average mean, below average stability to environmental changes ($b > 1$) with non-significant deviations from regression line hence, they are suitable for poor environments. The crosses ARG-6A × P100R, PHIR-27A × P69R, PRUN-29A × RCR-8297, 40A × RCR-8297, 40A × P69R and parental line 40A can be suitable for favourable environments as they possessed high mean (above average) and above average stability to environmental changes ($b < 1$) with significant deviations from regression line hence these genotype are stable over the environments with unpredictable performance.

Photosynthetic efficiency (SPAD readings)

The perusal of the data indicated that among the crosses 38A × RCR-8297 (42.69) recorded the highest photosynthetic efficiency followed by 234A × P69R (42.46), PRUN-29A × RCR-8297 (42.00), RCR-8297 (41.79), 234A × P100R (40.51), 234A × RCR-8297 (40.12) and parental line ARG-3A (40.20). Except CMS-XA × P100R, ARG-3A × P124R, ARG-6A × P124R, DV-10A × P100R, PRUN-29A × P124R, 42A × RCR-8297, 234A × P124R and 42B × RCR-8297, all genotypes showed regression more than unity with significant deviations from regression line.

The stability parameters (Table 5) indicated that among the crosses CMS-XA × P100R, ARG-3A × P124R, ARG-6A × P124R, DV-10A × P100R and PRUN-29A × P124R recorded below average mean performance and above average stability to environments ($b < 1$) with significant deviation from regression line thus they are suitable for unfavourable environments but their performance is unpredictable. The genotypes 42A × RCR-8297, 234A × P124R and 42B × RCR-8297 recorded above average mean performance and above average stability to environments ($b < 1$) with significant deviation from regression line thus they are suitable for unfavourable environments but their performance is unpredictable.

While the crosses PRUN-29A × RCR-8297, 40A × RCR-8297, 234A × P69R, 38A × RCR-8297 and parental lines CMS-XA, ARG-6A, 38A, RCR-8297 and P69R exhibited high mean or above average mean, below average stability ($b > 1$) with significant deviations from regression line hence are suitable to favourable

Table 5: Mean performance, regression coefficient (bi) and deviation from regression (δ^2di) for relative leaf water content and photo synthetic efficiency and proline content over different environments.

S. No.	Genotypes	Relative Leaf Water Content (%)				Photo Synthetic efficiency (SPAD reading)				Proline content (mg/2 g dry weight of leaf)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
1	CMS-XA × RCR-8297	70.08	1.13**	0.10	0.62	36.45	3.71	1.90	13.27**	0.98	−7.58**	2.18	5.47**
2	CMS-XA × P69R	67.57	0.34	0.31	5.77**	36.33	1.70	1.02	3.81**	1.64	−1.60	2.58	7.65**
3	CMS-XA × P124R	68.30	−1.44	0.92	49.62**	33.14	−1.89	5.32	104.46**	0.86	12.43*	4.38	22.08**
4	CMS-XA × P100R	58.98	−0.08	0.30	5.42**	33.82	0.62	1.15	4.90**	1.29	1.41	1.97	4.47**
5	E002-91 × RCR-8297	54.21	3.98**	0.88	45.45**	35.06	9.78	9.55	336.56**	1.31	−29.78**	1.36	2.12**
6	E002-91 × P69R	68.38	2.63**	0.71	29.38**	34.69	6.03	6.73	167.23**	0.93	−20.10**	1.18	1.62**
7	E002-91 × P124R	64.10	1.02**	0.04	0.11	32.43	3.35	1.64	9.95**	1.04	−6.83**	1.80	3.72**
8	E002-91 × P100R	61.71	1.63**	0.18	1.92	36.42	4.60	3.35	41.50**	1.27	−11.68**	1.31	1.99**
9	PKU-2A× RCR-8297	63.07	2.73**	0.52	15.93**	35.22	6.97	6.29	146.13**	0.73	−20.18**	1.01	1.18**
10	PKU-2A× P69R	70.94	2.53**	0.51	15.40**	32.73	6.18	6.02	133.83**	0.81	−18.81**	0.71	0.58**
11	PKU-2A× P124R	65.73	−1.71*	0.77	34.77**	30.54	−2.92	5.33	105.02**	0.96	13.92**	2.80	9.06**
12	PKU-2A× P100R	67.19	−1.28*	0.57	19.25**	35.74	−2.24	3.97	58.07**	0.84	10.38**	2.12	5.20**
13	ARG-2A × RCR-8297	74.23	−0.88	0.59	20.30**	34.17	−1.12	3.32	40.65**	1.02	7.60*	2.90	9.69**
14	ARG-2A × P69R	64.41	−1.59	0.88	45.68**	36.15	−2.32	5.47	110.48**	0.96	13.41**	3.82	16.82**
15	ARG-2A × P124R	60.35	1.84**	0.20	2.37*	32.10	5.14	3.80	53.16**	1.26	−13.03**	1.88	4.05**
16	ARG-2A × P100R	69.38	2.37**	0.46	12.73**	33.61	5.95	5.53	113.05**	0.87	−17.57**	0.59	0.39**
17	ARG-3A × RCR-8297	63.08	1.24**	0.04	0.11	31.90	4.01	2.07	15.75**	1.10	−8.36**	2.10	5.10**
18	ARG-3A × P69R	59.74	4.75**	1.21	86.73**	34.64	11.01	11.98	529.78**	1.10	−36.09**	1.61	3.00**
19	ARG-3A × P124R	65.12	−0.69	0.55	17.56**	30.60	−0.65	2.89	30.92**	0.71	6.23*	2.85	9.35**
20	ARG-3A × P100R	74.38	2.57**	0.36	7.56**	26.97	6.85	5.62	116.51**	0.85	−18.66**	1.49	2.57**

(*continued*)

Table 5: (*continued*)

S. No.	Genotypes	Relative Leaf Water Content (%)				Photo Synthetic efficiency (SPAD reading)				Proline content (mg/2 g dry weight of leaf)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
21	ARG-6A × RCR-8297	60.76	1.43**	0.13	1.01	37.07	4.52	2.53	23.59**	1.27	−9.86**	2.16	5.36**
22	ARG-6A × P69R	63.97	3.99**	0.89	46.74**	34.76	9.61	9.69	346.83**	0.94	−29.96**	0.50	0.29**
23	ARG-6A × P124R	72.11	−0.28	0.41	10.15**	31.18	0.34	1.82	12.21**	1.14	3.06	2.47	7.02**
24	ARG-6A × P100R	47.53	0.51*	0.17	1.78	34.72	1.03	1.44	7.65**	0.90	−4.04**	0.43	0.21**
25	DV-10A × RCR-8297	62.69	−1.84*	0.79	37.24**	35.02	−3.61	5.55	113.67**	0.75	14.78**	3.20	11.78**
26	DV-10A × P69R	55.62	1.58**	0.21	2.65*	31.98	4.45	3.30	40.20**	0.90	−11.39**	1.33	2.04**
27	DV-10A × P124R	53.90	3.62**	0.83	40.86**	31.73	8.52	8.93	294.02**	0.72	−27.24**	0.63	0.45**
28	DV-10A × P100R	59.29	−0.03	0.30	5.35**	32.45	0.32	1.19	5.20**	0.80	0.75	2.09	5.06**
29	PHIR-27A × RCR-8297	62.16	−0.98	0.62	22.84**	34.68	−1.19	3.63	48.55**	0.83	8.48*	2.90	9.70**
30	PHIR-27A × P69R	66.44	0.45**	0.02	0.03	35.30	1.50	0.71	1.88*	1.04	−3.01**	0.83	0.79**
31	PHIR-27A × P124R	75.08	3.12**	0.62	22.65**	31.73	7.93	7.27	194.95**	0.92	−23.16**	1.21	1.68**
32	PHIR-27A × P100R	65.51	1.72**	0.15	1.28	36.65	4.97	3.41	42.86**	1.01	−12.06**	1.99	4.58**
33	PRUN-29A × RCR-8297	62.76	0.81	0.19	2.22	42.00	3.24**	0.81	2.44**	0.94	−5.01	2.53	7.36**
34	PRUN-29A × P69R	56.72	2.77**	0.65	25.31**	39.33	6.44	6.90	175.44**	1.14	−20.88**	0.85	0.84**
35	PRUN-29A × P124R	57.13	−0.90	0.69	28.45**	30.53	−0.54	3.74	51.67**	1.40	8.19*	3.43	13.56**
36	PRUN-29A × P100R	64.84	−1.91*	0.76	34.01**	34.75	−3.64	5.64	117.56**	1.15	15.29**	2.51	7.28**
37	40A × RCR-8297	49.47	0.79**	0.19	2.03	35.44	2.94*	1.12	4.64**	1.00	−4.96	2.36	6.40**
38	40A × P69R	64.61	0.61*	0.20	2.38*	33.51	2.10	1.20	5.32**	0.88	−3.92	2.01	4.65**
39	40A × P124R	60.11	0.27	0.50	14.57**	33.01	2.27	1.41	7.30**	1.19	−0.51	3.80	16.64**
40	40A × P100R	65.31	1.28**	0.12	0.81	38.24	3.63	2.59	24.70**	0.89	−9.04**	1.27	1.86**
41	42A × RCR-8297	64.17	1.20	0.99	58.32**	38.57	0.30	5.22	100.49**	0.88	−11.03	5.15	30.52**

(*continued*)

Table 5: (*continued*)

S. No.	Genotypes	Relative Leaf Water Content (%)				Photo Synthetic efficiency (SPAD reading)				Proline content (mg/2 g dry weight of leaf)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
42	42A × P69R	60.02	1.92**	0.41	9.73**	35.96	4.74	4.57	76.95**	0.89	−14.32**	0.50	0.28**
43	42A × P124R	62.14	1.11	0.96	54.42**	33.98	3.96	4.10	61.96**	0.78	−7.90	6.90	54.85**
44	42A × P100R	63.79	−0.34	0.88	45.93**	32.66	−1.22	3.56	46.66**	0.91	1.60	6.45	47.92**
45	234A × RCR-8297	70.24	−1.55	0.89	47.24**	40.12	−2.28	5.42	108.46**	0.81	13.10**	4.09	19.24**
46	234A × P69R	58.72	1.41	1.24	90.48**	42.46	8.03*	2.86	30.29**	1.24	−7.19	10.18	119.48**
47	234A × P124R	51.92	−0.77	0.68	27.06**	37.06	−0.23	3.47	44.48**	1.09	7.26	3.51	14.20**
48	234A × P100R	50.98	1.14**	0.28	4.61**	40.51	2.71	2.84	29.75**	0.89	−8.65**	0.38	0.17**
49	38A × RCR-8297	55.83	0.67**	0.22	2.94*	42.69	2.68*	0.87	2.82**	0.95	−3.97	2.46	6.95**
50	38A × P69R	61.03	0.56	0.28	4.57**	32.92	2.38*	0.97	3.49**	1.23	−3.20	2.64	8.06**
51	38A × P124R	62.19	−2.77*	1.17	81.12**	36.47	−5.46	8.28	253.28**	0.90	22.18**	4.63	24.68**
52	38A × P100R	63.11	0.56*	0.21	2.55*	33.26	2.13	0.96	3.43**	1.27	−3.40	2.11	5.14**
53	NC-41B (C) × RCR-8297	77.11	−0.79	0.57	19.36**	37.94	−1.05	3.11	35.78**	0.74	6.88*	3.02	10.53**
54	NC-41B (C) × P69R	64.67	−0.05	0.39	9.01**	36.84	1.03	1.39	7.12**	1.08	1.47	2.61	7.84**
55	NC-41B (C) × P124R	68.36	1.47**	0.30	5.45**	35.69	3.70	3.43	43.54**	1.10	−10.89**	0.67	0.52**
56	NC-41B (C) × P100R	77.31	−0.79	0.48	13.61**	34.90	−1.08	2.84	29.66**	0.90	6.71*	2.25	5.85**
57	42B × RCR-8297	66.78	1.29	1.08	68.80**	37.38	0.38	5.65	117.63**	0.87	−11.69	5.83	39.15**
58	42B × P69R	61.53	1.41*	0.62	22.86**	34.96	2.50	4.35	69.72**	0.86	−11.42**	2.30	6.10**
59	42B × P124R	64.40	0.93	0.79	37.12**	34.77	3.22	3.43	43.43**	0.78	−6.68	5.66	36.92**
60	42B × P100R	64.75	−0.84	0.94	52.02**	32.68	−3.59	3.65	49.07**	0.88	4.33	7.34	62.10**
61	CMS-XA	71.80	1.94**	0.30	5.27**	37.88	6.99*	2.68	26.41**	0.69	−12.45*	4.87	27.32**
62	E002-91	58.43	2.21**	0.30	5.43**	38.09	5.90	4.81	85.55**	0.93	−16.02**	1.31	1.97**

(*continued*)

Table 5: (*continued*)

S. No.	Genotypes	Relative Leaf Water Content (%)				Photo Synthetic efficiency (SPAD reading)				Proline content (mg/2 g dry weight of leaf)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
63	PKU-2A	81.54	2.01**	0.42	10.40**	34.90	7.13*	3.11	35.80**	0.88	−13.34*	4.85	27.11**
64	ARG-2	65.39	1.76**	0.07	0.33	37.81	5.29	3.29	39.99**	0.97	−12.25**	2.10	5.09**
65	ARG-3	66.77	1.68**	0.09	0.51	40.20	5.61	2.64	25.74**	1.34	−11.23**	3.11	11.18**
66	ARG-6A	71.25	1.88**	0.42	10.43**	38.05	7.27**	2.19	17.64**	1.32	−11.91	5.39	33.53**
67	DV-10A	55.96	1.84**	0.31	5.80**	39.07	4.72	4.18	64.39**	1.54	−13.51**	0.58	0.39**
68	PHIR-27A	53.01	1.61**	0.06	0.18	39.27	5.21	2.67	26.25**	0.74	−10.88**	2.64	8.03**
69	PRUN-29A	56.50	2.51**	0.37	8.19**	37.60	6.61	5.56	114.00**	1.05	−18.28**	1.34	2.08**
70	40A	50.09	0.81**	0.13	1.00	35.47	2.43	1.60	9.47**	1.07	−5.55**	1.51	2.62**
71	42A	54.98	1.98**	0.59	20.80**	31.98	4.23	5.31	104.03**	0.87	−15.34**	1.12	1.44**
72	234A	55.65	1.98	1.13	75.35**	38.90	2.30	7.00	180.95**	1.24	−16.67**	5.15	30.61**
73	38A	62.46	1.94**	0.14	1.17	38.58	6.60*	2.95	32.22**	1.28	−12.91**	3.80	16.60**
74	NC-41B (C)	73.17	1.88**	0.20	2.41*	31.85	6.28	3.02	33.74**	1.23	−12.67**	3.49	14.04**
75	42B	57.30	2.14*	0.78	36.32**	32.74	4.02	6.21	142.38**	0.93	−16.97**	2.33	6.26**
76	RCR-8297	59.76	1.43**	0.37	7.96**	41.79	5.79**	1.36	6.80**	0.91	−8.79	4.59	24.27**
77	P69R	61.63	2.00*	0.71	29.36**	36.93	8.72**	1.33	6.56**	0.77	−11.71	7.68	67.97**
78	P124R	54.49	1.62**	0.10	0.63	29.89	5.04	2.89	30.92**	0.90	−11.18**	2.25	5.84**
79	P100R	64.31	1.90**	0.05	0.13	32.55	6.10	3.23	38.48**	0.90	−12.97**	2.99	10.31**
	Mean	63.04				35.34				1.00			
	Min.	47.53				26.97				0.69			
	Max.	81.54				42.69				1.64			
	SE ±	0.77				0.35				0.02			

environments but their performance is unpredictable. The female parent PKU-2A and cross 38A × P69R had below average mean performance and below average stability (b > 1) with significant deviations from regression line hence are suitable to favourable environments.

Proline content (mg/2 g dry weight of leaf)

The results shown in Table 5 revealed that proline content was highest in the cross *cms*-XA × P69R (1.64). The genotypes *cms*-XA × P69R, *cms*-XA × P100R, E002-91A × RCR-8297, E002-91A × P124R, E002-91A × P100R, ARG-2A × RCR-8297, ARG-2A × P124R, ARG-3A × RCR-8297, ARG-3A × P69R, ARG-6A × RCR-8297, ARG-6A × P124R, PHIR-27A × P69R, PHIR-27A × P100R, PRUN-29A × P69R, PRUN-29A × P124R, PRUN-29A × P100R, 234A × P69R, 234A × P124R, 38A × P69R, 38A × P100R, NC-41B × P124R, ARG-3A, ARG-6A, DV-10A, PRUN-29A, 40A, 234A, 38A and NC-41B showed above average mean performance. Except DV-10A × P100R and 40A × P124R, all the genotypes recorded regression coefficient more than unity with significant regression coefficient.

100 seed weight (g)

The genotypes *viz*. NC-41B × P69R (6.71) were recorded with the highest mean performance, followed by 234A × P69R (6.64), 42A × RCR-8297 (6.49), ARG-6A × P100R (6.46), 42A × P69R (6.42), 42B × P69R (6.36), PRUN-29A (6.29), PRUN-29A × P69R (6.24), 42B × RCR-8297 (6.19) and 38A × P100R (6.01) presented in Table 6. Ahmad and Abdella (2009) also found that linear, as well as non-linear components of G × E interaction, were significant for 100 seed weight.

Three genotypes namely *cms*-XA × P100R and NC-41B × P69R exhibited higher mean than the average and above average stability to environments (b < 1) but exhibited significant deviation from regression line, thus, they are suitable for unfavourable environments but their performance is unpredictable. However, all the other genotypes exhibited below average stability (b > 1) and significant deviations from regression line hence are suitable to favourable environments.

Seed yield per plant (g)

The mean seed yield per plant is presented in Table 6. A total of 48 hybrids out of 60 hybrids) were recorded above average for their mean values over the environments.

Table 6: Mean performance, regression coefficient (bi) and deviation from regression (δ^2di) for 100 seed weight and seed yield per plant and biological yield per plant over different environments.

S. No.	Genotypes	100 Seed Weight (g)				Seed Yield/Plant (g)				Biological Yield/plant (g)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
1	CMS-XA × RCR-8297	4.92	12.93*	4.98	8.83**	53.64	0.84**	0.19	3.44	295.71	0.05	0.03	15.59
2	CMS-XA × P69R	5.64	5.96	2.80	2.80**	33.86	0.25	0.24	5.99	265.43	0.03**	0.01	0.56
3	CMS-XA × P124R	5.57	−10.91	15.88	89.84**	50.54	−1.15	0.67	44.92**	362.88	0.00	0.07	110.82
4	CMS-XA × P100R	5.58	0.56	3.95	5.56**	56.18	−0.09	0.23	5.19	340.41	0.01	0.01	3.80
5	E002-91 × RCR-8297	5.50	39.07	26.03	241.21**	56.20	3.03**	0.72	51.64**	228.08	0.10	0.14	404.83
6	E002-91 × P69R	5.65	25.81	18.03	115.73**	44.07	2.04**	0.51	26.14**	394.13	0.06	0.10	195.08
7	E002-91 × P124R	5.21	10.76	5.30	10.00**	49.37	0.73**	0.19	3.73	300.92	0.04	0.03	14.11
8	E002-91 × P100R	5.23	16.49	9.51	32.22**	41.11	1.21**	0.26	6.84	325.50	0.05	0.05	53.37
9	PKU-2A × RCR-8297	5.45	27.04	17.21	105.54**	44.15	2.07**	0.46	21.54**	234.04	0.07	0.09	178.40
10	PKU-2A × P69R	5.62	27.05	14.42	74.09**	38.22	1.97**	0.30	8.85*	288.42	0.07	0.08	151.22
11	PKU-2A × P124R	5.14	−15.73	14.67	76.68**	51.88	−1.37*	0.52	26.96**	261.79	−0.02	0.07	114.99
12	PKU-2A × P100R	5.35	−11.46	11.11	43.94**	48.08	−1.01*	0.40	15.90**	286.21	−0.02	0.05	64.19
13	ARG-2A × RCR-8297	5.18	−6.23	10.06	36.04**	52.30	−0.69	0.43	18.97**	249.13	0.00	0.04	42.94
14	ARG-2A × P69R	5.12	−13.39	15.77	88.53**	28.65	−1.28	0.62	38.64**	245.83	−0.01	0.07	118.81
15	ARG-2A × P124R	5.33	20.52*	8.71	27.00**	34.93	1.40**	0.17	2.81	213.48	0.06	0.05	60.12
16	ARG-2A × P100R	5.12	23.82	14.73	77.28**	54.31	1.81**	0.38	14.46**	311.54	0.06	0.08	135.42

(*continued*)

Table 6: (*continued*)

S. No.	Genotypes	100 Seed Weight (g)				Seed Yield/Plant (g)				Biological Yield/plant (g)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
17	ARG-3A × RCR-8297	5.24	13.38	6.16	13.49**	53.42	0.90**	0.21	4.57	343.46	0.05	0.03	20.92
18	ARG-3A × P69R	5.32	47.16	31.69	357.54**	45.33	3.68**	0.87	75.22**	416.18	0.11	0.17	617.08*
19	ARG-3A × P124R	5.30	−4.50	8.88	28.10**	52.77	−0.55	0.40	16.33**	248.47	0.00	0.04	31.57
20	ARG-3A × P100R	5.68	27.48	13.89	68.68**	52.03	1.97**	0.29	8.62	287.86	0.08	0.08	136.46
21	ARG-6A × RCR-8297	5.57	13.77	8.79	27.53**	52.43	1.01**	0.31	9.64*	196.88	0.05	0.04	36.11
22	ARG-6A × P69R	4.55	40.43	25.21	226.28**	31.94	3.08**	0.64	41.29**	170.43	0.10	0.14	405.61
23	ARG-6A × P124R	4.71	−1.04	5.86	12.23**	37.55	−0.25	0.30	9.34*	248.42	0.01	0.02	10.95
24	ARG-6A × P100R	6.46	5.26	3.62	4.68**	50.05	0.41**	0.10	1.07	313.71	0.01	0.02	8.41
25	DV-10A × RCR-8297	5.72	−15.31	16.41	95.94**	57.44	−1.41*	0.61	37.46**	229.18	−0.03	0.08	130.65
26	DV-10A × P69R	5.25	15.45	9.81	34.28**	40.41	1.17**	0.29	8.44	278.51	0.05	0.05	53.12
27	DV-10A × P124R	5.13	38.06	21.86	170.11**	43.64	2.83**	0.50	24.82**	234.75	0.09	0.12	332.49
28	DV-10A × P100R	5.49	2.38	3.50	4.37**	52.96	0.00	0.23	5.38	316.56	0.01	0.01	3.62
29	PHIR-27A × RCR-8297	4.84	−7.89	10.61	40.05**	48.19	−0.79	0.44	19.41**	212.17	0.00	0.05	51.03
30	PHIR-27A × P69R	5.04	4.77	2.36	1.98**	42.34	0.32**	0.09	0.78	277.92	0.02	0.01	2.71
31	PHIR-27A × P124R	4.86	30.73	20.01	142.64**	41.82	2.36**	0.55	30.20**	283.83	0.08	0.11	238.22
32	PHIR-27A × P100R	4.37	19.14*	8.08	23.23**	51.68	1.30**	0.18	3.24	339.83	0.06	0.05	49.41
33	PRUN-29A × RCR-8297	5.30	8.48	5.03	9.02**	58.12	0.55	0.26	6.89	371.25	0.04*	0.02	6.09
34	PRUN-29A × P69R	6.24	29.64	16.37	95.47**	51.48	2.18**	0.35	12.42*	543.63	0.07	0.10	195.09

(*continued*)

Table 6: (*continued*)

S. No.	Genotypes	100 Seed Weight (g)				Seed Yield/Plant (g)				Biological Yield/plant (g)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
35	PRUN-29A× P124R	4.35	−7.91	10.74	41.06**	45.03	−0.78	0.46	21.70**	194.50	0.00	0.05	52.16
36	PRUN-29A× P100R	5.50	−17.64	15.59	86.54**	49.09	−1.51*	0.53	27.97**	266.44	−0.03	0.08	131.81
37	40A× RCR-8297	5.80	9.62*	3.38	4.08**	46.80	0.57*	0.20	4.12	310.25	0.04*	0.01	4.42
38	40A× P69R	5.87	8.43**	1.52	0.82**	47.92	0.47**	0.15	2.19	306.54	0.03*	0.01	3.24
39	40A× P124R	5.42	5.42	5.70	11.57**	54.30	0.15	0.39	15.60**	388.13	0.04**	0.01	2.58
40	40A× P100R	5.51	13.99*	6.30	14.14**	58.67	0.97**	0.14	1.90	307.75	0.04	0.04	28.95
41	42A× RCR-8297	6.49	14.24	13.46	64.56**	54.35	1.14	0.59	35.16**	313.38	0.00	0.07	100.53
42	42A× P69R	6.42	19.09	12.25	53.46**	52.70	1.46**	0.33	10.64*	397.58	0.05	0.07	92.04
43	42A× P124R	5.38	1.81	15.92	90.26**	46.12	0.58	0.86	73.83**	276.63	0.02	0.06	88.32
44	42A× P100R	5.50	−12.65	7.66	20.91**	46.94	−0.42	0.64	40.57**	287.46	−0.04	0.04	29.64
45	234A× RCR-8297	5.58	−12.18	16.04	91.65**	47.59	−1.22	0.65	42.82**	295.50	−0.01	0.07	117.07
46	234A× P69R	6.64	6.57	19.94	141.61**	57.54	0.62	1.14	130.08**	718.17	0.07	0.07	93.15
47	234A× P124R	5.86	−6.30	10.26	37.50**	36.71	−0.68	0.46	21.68**	235.00	0.01	0.05	44.15
48	234A× P100R	5.59	11.27	7.61	20.65**	55.43	0.88**	0.21	4.43	377.68	0.03	0.04	35.09
49	38A× RCR-8297	5.54	8.38*	3.15	3.54**	45.63	0.47	0.22	4.82	288.00	0.04**	0.01	1.95
50	38A× P69R	4.75	7.99*	2.70	2.59**	36.27	0.41	0.23	5.52	185.33	0.04**	0.01	0.79
51	38A× P124R	5.98	−23.26	24.39	211.91**	45.93	−2.13*	0.90	81.10**	254.00	−0.04	0.12	291.36

(*continued*)

Table 6: (*continued*)

S. No.	Genotypes	100 Seed Weight (g)				Seed Yield/Plant (g)				Biological Yield/plant (g)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
52	38A × P100R	6.01	7.64**	1.99	1.41**	48.70	0.42*	0.17	3.06	339.92	0.03**	0.01	1.64
53	NC-41B (C) × RCR-8297	4.68	−4.78	9.74	33.75**	35.82	−0.60	0.44	19.49**	262.42	0.00	0.04	37.81
54	NC-41B (C) × P69R	6.71	0.98	5.00	8.92**	33.18	−0.09	0.29	8.69	181.92	0.02	0.02	5.39
55	NC-41B (C) × P124R	4.90	14.21	9.61	32.88**	36.62	1.11**	0.27	7.45	327.54	0.04	0.05	53.54
56	NC-41B (C) × P100R	5.39	−6.04	8.43	25.32**	36.54	−0.62	0.35	12.32*	472.00	0.00	0.04	31.69
57	42B × RCR-8297	6.19	17.37	13.42	64.16**	49.08	1.27	0.61	37.36**	327.25	0.01	0.07	116.62
58	42B × P69R	6.36	12.61	12.19	52.93**	49.59	1.11*	0.44	19.04**	404.83	0.02	0.06	77.29
59	42B × P124R	5.29	1.61	13.21	62.13**	47.23	0.49	0.71	50.31**	281.00	0.01	0.05	61.04
60	42B × P100R	5.64	−17.82*	6.78	16.36**	46.79	−0.73	0.68	46.47**	297.25	−0.07*	0.03	18.12
61	CMS-XA	4.40	21.90*	9.37	31.25**	25.17	1.38**	0.45	20.51**	292.00	0.09	0.04	35.37
62	E002-91	5.57	23.61	11.91	50.55**	26.18	1.69**	0.25	6.38	490.33	0.07	0.07	100.31
63	PKU-2A	4.73	17.38	14.59	75.83**	18.57	1.33	0.63	40.23**	268.68	0.07	0.06	74.00
64	ARG-2	4.37	18.44	9.32	30.96**	26.69	1.30**	0.27	7.16	399.33	0.06	0.05	51.93
65	ARG-3	5.34	17.67	8.90	28.22**	36.79	1.20**	0.34	11.33*	507.92	0.07	0.04	37.75
66	ARG-6A	5.18	17.72	12.90	59.27**	25.06	1.24	0.62	38.13**	198.33	0.08	0.05	47.05
67	DV-10A	4.67	19.03	10.74	41.07**	29.57	1.41**	0.25	6.37	353.93	0.05	0.06	76.33
68	PHIR-27A	3.92	16.59	8.75	27.26**	31.23	1.15**	0.31	9.52*	154.67	0.06	0.04	38.09

(*continued*)

Table 6: (*continued*)

S. No.	Genotypes	100 Seed Weight (g)				Seed Yield/Plant (g)				Biological Yield/plant (g)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
69	PRUN-29A	6.26	26.89	13.59	65.82**	27.53	1.93**	0.28	7.88	552.00	0.08	0.08	132.42
70	40A	4.67	9.91**	2.85	2.88**	23.08	0.63**	0.08	0.71	118.05	0.03	0.02	9.12
71	42A	5.42	20.30	13.37	63.62**	27.28	1.57**	0.36	12.94*	204.58	0.04	0.07	116.06
72	234A	4.82	23.63	16.01	91.32**	33.53	1.76*	0.59	34.43**	289.75	0.03	0.09	181.23
73	38A	5.63	20.18	10.62	40.16**	22.53	1.38**	0.42	17.45**	297.17	0.08	0.05	49.96
74	NC-41B (C)	4.04	17.97	11.73	48.98**	19.31	1.31*	0.45	20.70**	75.90	0.07	0.05	57.28
75	42B	5.55	23.18	14.65	76.43**	27.85	1.76**	0.40	16.29**	197.08	0.04	0.08	150.97
76	RCR-8297	4.29	14.45	9.41	31.56**	22.66	0.94	0.49	23.90**	129.17	0.07	0.03	20.50
77	P69R	5.12	19.33	15.03	80.44**	15.98	1.25	0.82	68.04**	91.87	0.10*	0.04	40.67
78	P124R	4.63	16.09	9.45	31.79**	21.34	1.16**	0.31	9.95*	127.58	0.06	0.05	44.86
79	P100R	5.13	19.76	10.29	37.68**	23.82	1.37**	0.35	12.36*	140.58	0.07	0.05	54.55
	Mean	5.34				41.72				292.43			
	Min.	3.92				15.98				75.90			
	Max.	6.71				58.67				718.17			
	SE ±	0.07				1.29				11.94			

The genotypes *cms*-XA × RCR-8297, E002-91A × P124R, ARG-3A × RCR-8297, ARG-6A × P100R, DV-10A × P100R, PHIR-27A × P69R, PRUN-29A × RCR-8297, 40A × RCR-8297, 40A × P69R, 40A × P100R, 234A × P100R and 38A × RCR-8297 exhibited high mean (> 42.34 g per plant), above average stability to environmental changes (b < 1) with non-significant deviation from regression line, hence, these could be considered as stable over environments. The genotypes *cms*-XA × P69R, 38A × P69R, NC-41B × P69R and 40A recorded above average stability to environmental changes (b < 1) with non-significant deviation from regression line, however, because of their below average mean performance these should not be recommended. The crosses E002-91A × P100R, ARG-2A × P124R, ARG-3A × P100R, ARG-6A × RCR-8297, DV-10A × P69R and the parental lines E002-91A, ARG-2A, DV-10A, PRUN-29A, P124R and P100R exhibited below average stability to environmental changes (b > 1) with non-significant deviations from regression line hence could be considered as stable, however, because of below average mean performance these cannot be recommended.

The hybrids *cms*-XA × RCR-8297, ARG-3A × RCR-8297, ARG-6A × RCR-8297, 40A × P100R and 234A × P100R had high mean values, regression coefficients near to unity with non-significant deviation from regression line indicating their suitability for poor environments (stress) with predictable performance. Similar results for seed yield per plant have been reported by Ghafoor *et al.* (2005).

Biological yield per plant (g)

The mean performance of genotypes presented in Table 6 showed that among hybrids 234A × P69R (718.17) recorded the maximum biological yield per plant followed by PRUN-29A × P69R (543.63) and *cms* analogues PRUN-29A (552.00). All the genotypes exhibited regression coefficient less than unity with non-significant deviations from regression line.

None of the genotypes fulfilled all the three requirements for a stable variety, therefore it can be concluded that all the genotypes under investigation were significantly influenced by the environments and none of the genotype was found to be stable across these environments for biological yield.

Harvest index (%)

The mean performance of genotypes presented in Table 7 showed that among the hybrids PHIR-27A × RCR-8297 (28.47) recorded the maximum harvest index followed by ARG-6A × RCR-8297 (27.68), E002-91A × RCR-8297 (27.57), *cms*-

XA × RCR-8297 (26.34) and parental line NC-41B (26.62). Except the cross 42B × P100R, female parent *cms*-XA, ARG-6A and male parent P69R, all the genotypes exhibited regression coefficient less than unity. Significant deviations from regression line were recorded for all the genotypes except *cms*-XA × P69R, *cms*-XA × P100R, DV-10A × P100R, 40A × P124R and NC-10B × P69R.

None of the genotypes fulfilled all the three requirements for a stable variety, which indicates that all the genotypes under investigation were significantly influenced by the environments and none of the genotype was found to be stable across these environments. However, the genotypes *cms*-XA × P69R, *cms*-XA × P100R, DV-10A × P100R, 40A × P124R and NC-10B × P69R had below average mean performance, above average stability to environmental changes ($b < 1$) with non-significant deviation from regression line, hence, indicating their suitability for favourable environments only.

Oil content (%)

Sufficient variability was observed among the genotypes for oil content (Table 7). The results shown in Table 7 revealed that oil content was highest in ARG-2A × P100R (34.61). The 49 genotypes out of 79 showed above average mean performance. All the genotypes except *cms*-XA × P100R, ARG-6A × P124R, DV-10A × P100R and NC-41B × P69R had regression coefficient more than unity with significant deviation from regression line. The genotypes DV-10A × P100R, 40A × P124R had high mean above average stability, (near unity regression) with significant deviation from regression line indicating stability over the environments with unpredictable performance. Significant genotypes × environment interaction for oil content has earlier been reported by Rao *et al.* (2004) and Ghafoor *et al.* (2005).

Palmitic acid (%)

The results shown in Table 7 revealed that palmitic acid was the highest in parental line 42B (7.35). Except NC-41B × P69R, all the genotypes exhibited regression coefficient more than unity and all the genotypes exhibited significant deviation from regression line.

Stearic acid (%)

The results shown in Table 8 revealed that palmitic acid was the highest in parental line DV-10A (7.05). Except 40A × P69R, 38A × RCR-8297 and 38A × P100R

Table 7: Mean performance, regression coefficient (bi) and deviation from regression (δ^2di) for harvest index, oil content and palmitic acid plant over different environments.

S. No.	Genotypes	Harvest Index (%)				Oil content (%)				Palmitic acid (%)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
1	CMS-XA × RCR-8297	26.34	−0.55	0.65	28.48**	31.27	3.44	2.74	21.59**	4.57	21.38**	6.10	5.41**
2	CMS-XA × P69R	16.57	−0.46*	0.18	2.13	33.69	1.66	1.34	5.18**	4.59	6.02	6.69	6.50**
3	CMS-XA × P124R	17.62	−0.49	1.24	103.07**	30.08	−3.37	5.75	94.75**	5.17	−26.04	20.63	61.79**
4	CMS-XA × P100R	17.76	−0.32	0.18	2.13	31.60	−0.04	1.40	5.61**	4.16	−1.04	6.17	5.54**
5	E002-91 × RCR-8297	27.57	−0.58	2.74	501.93**	27.92	10.94	10.91	341.50**	4.96	73.70*	28.58	118.59**
6	E002-91 × P69R	13.55	−0.23	1.87	232.52**	29.80	7.44	7.35	154.91**	4.61	48.12*	21.35	66.18**
7	E002-91 × P124R	19.93	−0.46	0.59	23.42**	31.86	2.71	2.65	20.11**	5.41	19.71**	4.07	2.41**
8	E002-91 × P100R	12.54	−0.45	1.05	73.74**	31.66	4.39	4.30	53.01**	4.45	30.90**	8.81	11.26**
9	PKU-2A × RCR-8297	21.59	−0.49	1.85	227.56**	30.43	7.48	7.37	155.57**	5.16	50.80*	18.24	48.34**
10	PKU-2A × P69R	16.60	−0.46	1.72	197.40**	32.22	7.95	6.30	113.74**	5.61	45.45*	19.34	54.35**
11	PKU-2A × P124R	25.87	−0.22	1.34	119.09**	30.43	−4.89	5.49	86.50**	4.44	−30.19	19.38	54.56**
12	PKU-2A × P100R	20.56	−0.16	1.00	66.46**	33.64	−3.49	4.17	49.85**	4.63	−22.85	14.23	29.40**
13	ARG-2A × RCR-8297	23.24	−0.32	0.77	39.45**	31.82	−1.89	3.63	37.85**	5.42	−16.01	12.95	24.34**
14	ARG-2A × P69R	11.75	−0.40	1.31	115.16**	30.68	−4.19	5.76	95.23**	5.96	−28.29	20.71	62.30**
15	ARG-2A × P124R	17.84	−0.59	1.16	90.39**	32.04	5.83	4.31	53.25**	6.16	33.50*	11.86	20.45**
16	ARG-2A × P100R	19.73	−0.41	1.61	172.66**	34.61	6.70	6.31	114.03**	3.62	43.72*	16.50	39.54**
17	ARG-3A × RCR-8297	17.15	−0.56	0.73	35.09**	33.17	3.45	3.14	28.27**	3.75	23.73**	5.57	4.50**
18	ARG-3A × P69R	13.32	−0.49	3.34	745.51**	31.79	13.63	13.04	487.43**	6.52	86.64*	37.88	208.41**
19	ARG-3A × P124R	25.01	−0.35	0.64	27.57**	31.57	−1.42	3.17	28.81**	5.83	−12.54	11.82	20.29**
20	ARG-3A × P100R	22.26	−0.65	1.68	189.08**	32.86	7.79	6.37	116.25**	5.06	47.16*	16.93	41.63**
21	ARG-6A × RCR-8297	27.68	−0.53	0.88	51.93**	29.93	3.30	3.99	45.71**	3.16	28.24**	4.85	3.41**

(*continued*)

Table 7: (*continued*)

S. No.	Genotypes	Harvest Index (%)				Oil content (%)				Palmitic acid (%)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
22	ARG-6A × P69R	20.06	−0.57	2.75	506.52**	30.78	11.62	10.63	323.73**	5.25	72.87*	30.12	131.74**
23	ARG-6A × P124R	17.76	−0.38	0.34	7.71**	29.88	−0.54	2.05	12.01**	4.92	−4.53	8.68	10.93**
24	ARG-6A × P100R	17.74	−0.01	0.38	9.60**	31.15	1.63	1.42	5.80**	4.65	9.02	5.04	3.69**
25	DV-10A × RCR-8297	26.11	−0.17	1.43	136.73**	31.11	−4.30	6.23	111.14**	5.38	−34.38	18.89	51.83**
26	DV-10A × P69R	21.58	−0.41	1.03	71.18**	31.92	4.02	4.32	53.59**	4.30	30.31**	8.34	10.09**
27	DV-10A × P124R	22.07	−0.52	2.51	419.24**	29.61	11.26	9.27	246.44**	3.96	64.94*	28.96	121.83**
28	DV-10A × P100R	17.77	−0.25	0.22	3.33	30.86	0.90	1.21	4.21**	5.13	−1.58	5.98	5.20**
29	PHIR-27A × RCR-8297	28.47	−0.34	0.84	47.28**	30.94	−2.55	3.82	41.82**	3.73	−17.23	14.27	29.58**
30	PHIR-27A × P69R	17.61	−0.21	0.26	4.54*	29.61	1.19	1.18	3.99**	5.63	8.76**	1.77	0.45**
31	PHIR-27A × P124R	18.35	−0.54	2.12	301.18**	28.44	8.49	8.51	207.54**	5.13	58.22*	21.11	64.71**
32	PHIR-27A × P100R	15.47	−0.60	1.07	76.40**	30.38	5.35	4.07	47.47**	4.75	31.63**	10.42	15.77**
33	PRUN-29A × RCR-8297	21.89	−0.55	0.42	11.71**	31.94	1.82	2.44	17.08**	4.88	16.78**	3.09	1.38**
34	PRUN-29A × P69R	15.38	−0.39	1.92	246.82**	31.20	8.89	6.96	138.73**	5.45	49.23	22.87	75.94**
35	PRUN-29A × P124R	24.11	−0.46	0.82	45.04**	31.97	−2.92	3.73	39.99**	5.74	−14.49	15.95	36.95**
36	PRUN-29A × P100R	18.46	−0.13	1.46	141.44**	34.49	−5.30	5.96	101.75**	4.09	−34.41	19.64	56.01**
37	40A × RCR-8297	20.91	−0.53	0.41	11.27**	32.28	2.49	2.02	11.68**	4.14	15.13*	5.21	3.94**
38	40A × P69R	21.10	−0.40	0.35	8.23**	31.42	2.45	1.30	4.87**	5.59	10.84	5.84	4.95**
39	40A × P124R	22.97	−0.69**	0.11	0.79	32.24	1.15	2.28	14.91**	6.25	5.98	9.89	14.20**
40	40A × P100R	23.11	−0.41	0.81	43.28**	30.95	3.90	3.08	27.14**	6.66	23.55*	7.73	8.68**
41	42A × RCR-8297	18.46	0.59	1.16	89.06**	30.18	5.74	4.32	53.44**	4.76	16.44	23.62	81.03**
42	42A × P69R	15.23	−0.30	1.31	115.40**	31.78	5.38	5.18	76.94**	4.28	35.40	13.72	27.34**
43	42A × P124R	17.06	−0.15	1.16	90.07**	29.89	−1.60	5.51	87.16**	5.45	28.08	15.21	33.60**

(*continued*)

Table 7: (*continued*)

S. No.	Genotypes	Harvest Index (%)				Oil content (%)				Palmitic acid (%)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
44	42A × P100R	16.68	0.60	0.75	37.45**	30.89	−4.86	2.32	15.50**	6.62	−1.28	18.42	49.28**
45	234A × RCR-8297	20.84	−0.42	1.30	112.17**	31.77	−3.69	5.86	98.49**	4.67	−28.09	20.45	60.76**
46	234A × P69R	8.31	−1.38	1.13	85.32**	32.07	−1.68	7.12	145.28**	5.49	37.87	17.63	45.15**
47	234A × P124R	17.40	−0.50	0.74	36.37**	29.65	−2.41	3.56	36.27**	4.92	−12.38	15.18	33.45**
48	234A × P100R	15.70	−0.13	0.80	42.69**	31.45	3.22	3.15	28.46**	5.39	21.01*	8.80	11.24**
49	38A × RCR-8297	16.24	−0.53	0.32	6.83**	30.79	2.12	1.83	9.62**	5.18	12.88*	5.25	4.00**
50	38A × P69R	19.99	−0.52	0.27	4.79*	29.41	2.13	1.61	7.47**	5.69	10.55	6.37	5.89**
51	38A × P124R	19.62	−0.23	2.14	306.45**	30.75	−6.56	9.27	246.58**	4.18	−51.61	28.11	114.78**
52	38A × P100R	15.29	−0.43	0.29	5.67*	31.51	2.10	1.38	5.47**	3.73	10.28	5.34	4.14**
53	NC-41B (C) × RCR-8297	15.07	−0.32	0.72	34.46**	30.31	−1.31	3.51	35.37**	3.01	−15.04	12.14	21.40**
54	NC-41B (C) × P69R	21.64	−0.44*	0.19	2.49	29.02	−0.08	1.78	9.08**	3.68	0.00	7.91	9.09**
55	NC-41B (C) × P124R	14.51	−0.24	1.00	66.95**	28.47	3.90	4.05	47.06**	4.69	27.41*	9.92	14.30**
56	NC-41B (C) × P100R	7.86	−0.24	0.67	29.83**	22.51	−1.85	3.06	26.90**	4.18	−14.20	10.87	17.17**
57	42B × RCR-8297	16.13	0.52	1.28	108.78**	29.87	7.06	4.03	46.54**	4.82	16.55	25.98	98.00**
58	42B × P69R	14.08	0.17	1.10	80.28**	30.87	3.82	4.58	60.27**	4.76	25.24	15.52	34.97**
59	42B × P124R	17.32	−0.10	0.97	62.23**	28.86	−1.25	4.59	60.35**	5.92	23.28	12.65	23.24**
60	42B × P100R	16.42	1.07	0.72	35.02**	31.02	−5.77	2.97	25.21**	6.21	−12.18	20.68	62.11**
61	CMS-XA	9.17	−1.15	1.04	72.73**	27.82	5.46	5.08	73.91**	5.94	37.79**	9.43	12.92**
62	E002-91	5.62	−0.56	1.44	139.25**	28.43	6.68	5.47	85.80**	5.86	40.54*	14.48	30.45**
63	PKU-2A	7.99	−0.91	1.24	101.91**	29.44	3.36	6.29	113.37**	4.49	42.15**	2.03	0.60**
64	ARG-2	7.68	−0.63	1.08	78.31**	29.75	4.86	4.48	57.61**	4.90	33.37**	8.57	10.67**
65	ARG-3	8.05	−0.79	0.97	63.06**	30.16	4.38	4.43	56.28**	4.42	32.76**	6.37	5.89**

(*continued*)

Table 7: (*continued*)

S. No.	Genotypes	Harvest Index (%)				Oil content (%)				Palmitic acid (%)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
66	ARG-6A	14.12	−1.11	1.05	73.79**	26.41	3.49	5.84	97.76**	7.10	39.58**	3.14	1.43**
67	DV-10A	9.16	−0.38	1.23	100.75**	31.12	5.38	4.73	64.02**	6.24	33.77*	12.51	22.74**
68	PHIR-27A	26.94	−0.69	0.95	60.43**	26.88	4.14	4.25	51.75**	6.84	31.24**	6.09	5.39**
69	PRUN-29A	5.24	−0.61	1.65	182.15**	31.77	7.67	6.20	110.23**	3.80	45.87*	16.96	41.78**
70	40A	20.90	−0.35	0.49	16.22**	29.38	2.87	1.73	8.57**	6.01	14.51*	5.92	5.08**
71	42A	13.41	−0.11	1.43	136.57**	31.16	6.15	5.37	82.79**	7.00	35.20	17.99	47.01**
72	234A	11.59	0.37	1.67	186.20**	27.08	8.61	5.43	84.52**	7.04	29.95	29.40	125.57**
73	38A	7.11	−0.94	1.12	83.29**	29.21	4.90	5.23	78.28**	5.19	38.23**	6.68	6.48**
74	NC-41B (C)	26.62	−0.80	1.13	84.97**	26.47	4.11	5.36	82.32**	5.39	37.72**	4.70	3.20**
75	42B	14.33	0.01	1.61	172.12**	30.74	7.48	5.66	91.97**	7.35	36.42	22.85	75.82**
76	RCR-8297	19.27	−0.98	0.74	36.91**	26.99	2.95	4.43	56.28**	6.37	29.98**	4.90	3.48**
77	P69R	20.55	−1.54	1.01	67.47**	19.71	3.42	6.74	130.20**	6.27	43.23**	8.81	11.28**
78	P124R	23.14	−0.60	0.99	65.92**	26.77	3.99	4.38	55.03**	5.95	31.54**	6.23	5.64**
79	P100R	19.87	−0.80	1.14	86.02**	29.18	4.98	5.00	71.64**	6.84	36.89**	7.58	8.35**
	Mean	17.72				30.30				5.18			
	Min.	5.24				19.71				3.01			
	Max.	28.47				34.61				7.35			
	SE ±	0.62				0.26				0.11			

Table 8: Mean performance, regression coefficient (bi) and deviation from regression (δ^2di) for stearic acid, oleic acid and linoleic acid over different environments.

S. No.	Genotypes	Stearic acid (%)				Oleic acid (%)				Linoleic acid (%)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
1	CMS-XA × RCR-8297	2.23	−6.83	12.39	33.51**	43.25	−4.02*	1.78	10.82**	49.94	4.93*	1.85	8.44**
2	CMS-XA × P69R	2.04	3.70	5.91	7.64**	41.93	−2.11**	0.66	1.51**	51.43	2.21	1.12	3.08**
3	CMS-XA × P124R	2.98	28.00*	10.80	25.45**	42.81	2.40	5.43	101.12**	49.04	−4.41	5.92	86.91**
4	CMS-XA × P100R	4.11	6.14*	2.62	1.50**	47.24	−0.48	1.23	5.23**	44.49	0.14	1.50	5.59**
5	E002-91 × RCR-8297	3.42	−45.96	35.97	282.46**	44.63	−11.03	9.42	304.34**	46.99	15.20	9.58	227.09**
6	E002-91 × P69R	2.59	−32.06	23.65	122.12**	42.40	−7.16	6.53	146.25**	50.40	10.06	6.63	108.87**
7	E002-91 × P124R	5.38	−7.48	10.59	24.51**	38.72	−3.32	1.85	11.72**	50.48	4.12	1.97	9.63**
8	E002-91 × P100R	2.28	−16.03	15.52	52.56**	53.32	−4.84	3.43	40.36**	39.95	6.37	3.51	30.43**
9	PKU-2A× RCR-8297	3.56	−30.17	24.99	136.33**	52.26	−7.72	6.24	133.45**	39.02	10.49	6.33	99.33**
10	PKU-2A× P69R	2.82	−25.49	24.72	133.41**	46.48	−7.79	5.41	100.29**	45.09	10.47	5.26	68.51**
11	PKU-2A× P124R	2.87	25.86	14.78	47.71**	40.20	4.03	5.20	92.90**	52.49	−6.22	5.42	72.88**
12	PKU-2A× P100R	5.46	19.67	10.71	25.07**	38.07	2.92	3.92	52.71**	51.84	−4.53	4.11	41.87**
13	ARG-2A × RCR-8297	3.23	17.79*	6.20	8.40**	49.57	1.31	3.41	40.00**	41.78	−2.54	3.76	34.98**
14	ARG-2A × P69R	4.04	27.71	12.94	36.57**	46.58	3.20	5.48	102.92**	43.42	−5.35	5.86	84.99**
15	ARG-2A × P124R	2.54	−14.73	18.93	78.27**	39.98	−6.14	3.30	37.28**	51.31	7.89*	3.17	24.91**
16	ARG-2A × P100R	2.56	−25.92	21.92	104.97**	47.26	−6.80	5.37	98.98**	46.56	9.24	5.41	72.50**
17	ARG-3A × RCR-8297	4.94	−8.86	12.98	36.81**	46.08	−4.12	2.17	16.23**	45.23	5.12*	2.28	12.92**
18	ARG-3A × P69R	3.31	−56.30	43.20	407.50**	38.12	−13.17	11.52	455.82**	52.05	18.37	11.64	335.63**
19	ARG-3A × P124R	4.64	15.58**	4.88	5.20**	38.48	0.83	2.98	30.54**	51.05	−1.86	3.33	27.40**
20	ARG-3A × P100R	2.66	−24.07	25.31	139.89**	42.67	−8.06	5.17	91.74**	49.61	10.61	5.08	63.80**
21	ARG-6A × RCR-8297	2.35	−13.49	13.78	41.46**	41.68	−4.14	3.05	31.97**	52.82	5.30	3.27	26.51**

(*continued*)

Table 8: (*continued*)

S. No.	Genotypes	Stearic acid (%)				Oleic acid (%)				Linoleic acid (%)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
22	ARG-6A × P69R	3.81	−44.64	37.05	299.79**	26.38	−11.45	9.23	292.37**	64.57	15.71	9.25	211.73**
23	ARG-6A × P124R	2.38	9.65*	3.22	2.26**	46.02	−0.10	1.90	12.40**	46.68	−0.50	2.21	12.11**
24	ARG-6A × P100R	3.33	−6.40	4.85	5.14**	53.00	−1.44	1.33	6.05**	39.02	2.06	1.33	4.37**
25	DV-10A × RCR-8297	1.80	29.35	14.14	43.63**	37.67	3.87	5.71	111.96**	55.15	−6.07	6.10	92.04**
26	DV-10A × P69R	2.97	−16.57	14.64	46.83**	38.79	−4.50	3.50	42.03**	53.94	5.98	3.62	32.54**
27	DV-10A × P124R	4.09	−38.75	34.78	264.16**	35.72	−10.83	8.13	226.90**	56.23	14.77	7.98	157.87**
28	DV-10A × P100R	2.92	6.36*	2.10	0.96**	42.97	−0.97	1.05	3.76**	48.99	0.84	1.35	4.50**
29	PHIR-27A × RCR-8297	4.27	18.48*	7.96	13.85**	48.02	1.78	3.65	45.71**	43.98	−3.18	3.95	38.62**
30	PHIR-27A × P69R	2.50	−3.26	4.72	4.86**	42.40	−1.47	0.82	2.29**	49.46	1.82	0.88	1.91**
31	PHIR-27A × P124R	2.66	−35.13	28.40	176.13**	37.82	−8.75	7.23	179.60**	54.39	11.94	7.37	134.38**
32	PHIR-27A × P100R	2.05	−13.33	17.78	69.03**	41.59	−5.76	3.03	31.41**	51.62	7.35*	2.95	21.57**
33	PRUN-29A × RCR-8297	2.92	−4.32	9.52	19.80**	43.45	−2.76	1.60	8.79**	48.75	3.21	1.91	9.04**
34	PRUN-29A × P69R	4.47	−29.02	27.07	159.98**	39.73	−8.45	6.14	129.45**	50.35	11.50	5.97	88.21**
35	PRUN-29A × P124R	3.10	17.64	9.14	18.24**	38.49	1.73	3.70	47.08**	52.67	−3.20	4.00	39.55**
36	PRUN-29A × P100R	1.83	27.70	16.33	58.22**	38.06	4.62	5.54	105.41**	56.02	−6.95	5.76	82.15**
37	40A × RCR-8297	2.04	−2.54	9.53	19.85**	44.44	−3.11*	1.07	3.94**	49.38	3.64*	1.29	4.13**
38	40A × P69R	2.88	−0.84	7.84	13.41**	42.85	−2.71**	0.49	0.84**	48.68	3.19**	0.59	0.87*
39	40A × P124R	4.23	7.03	7.23	11.41**	36.64	−2.15	1.61	8.88**	52.88	1.95	2.21	12.08**
40	40A × P100R	3.51	−10.56	12.98	36.80**	43.09	−4.18	2.35	18.95**	46.74	5.38*	2.30	13.15**
41	42A × RCR-8297	2.44	−18.58	16.98	62.94**	47.08	−3.51	4.81	79.57**	45.72	5.64	4.97	61.22**
42	42A × P69R	4.01	−21.62	17.56	67.32**	45.27	−5.41	4.45	68.05**	46.44	7.42	4.50	50.22**
43	42A × P124R	2.42	−24.45	10.82	25.58**	45.48	−0.17	5.14	90.79**	46.65	0.83	6.03	90.00**

(*continued*)

Table 8: (*continued*)

S. No.	Genotypes	Stearic acid (%)				Oleic acid (%)				Linoleic acid (%)			
		Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di	Mean	bi	± SE bi	σ² di
44	42A × P100R	4.12	−13.48	11.63	29.55**	43.05	4.34	2.23	17.00**	46.21	−4.70	2.99	22.09**
45	234A × RCR-8297	3.10	28.39	11.73	30.03**	47.82	2.81	5.52	104.48**	44.41	−4.89	5.97	88.40**
46	234A × P69R	2.34	−13.31	24.39	129.95**	51.06	−2.52	6.35	138.37**	41.12	2.44	7.57	141.94**
47	234A × P124R	2.25	16.78	7.96	13.83**	40.35	1.25	3.49	41.90**	52.49	−2.58	3.83	36.34**
48	234A × P100R	2.74	−13.51	10.34	23.36**	48.53	−3.16	2.76	26.16**	43.35	4.39	2.80	19.41**
49	38A × RCR-8297	3.83	−0.92	8.55	15.95**	43.98	−2.77*	0.91	2.83**	47.02	3.16*	1.22	3.70**
50	38A × P69R	3.00	1.18	7.96	13.82**	31.53	−2.70**	0.65	1.47**	59.79	3.00*	1.07	2.86**
51	38A × P124R	2.26	43.61	21.46	100.61**	46.67	5.91	8.50	248.20**	46.90	−9.21	9.06	203.11**
52	38A × P100R	4.24	−0.15	7.36	11.81**	45.80	−2.51**	0.53	0.97**	46.23	2.88**	0.79	1.54**
53	NC-41B (C) × RCR-8297	2.12	17.39**	4.69	4.81**	48.70	0.89	3.26	36.45**	46.17	−1.98	3.65	32.98**
54	NC-41B (C) × P69R	3.81	7.15	4.01	3.51**	47.05	−0.69	1.55	8.27**	45.46	0.28	1.91	8.99**
55	NC-41B (C) × P124R	2.72	−16.87	13.15	37.77**	47.53	−4.03	3.46	41.02**	45.05	5.53	3.54	31.04**
56	NC-41B (C) × P100R	1.85	14.89*	5.91	7.61**	52.29	1.36	2.89	28.65**	41.68	−2.44	3.14	24.46**
57	42B × RCR-8297	2.35	−16.27	20.19	89.00**	47.21	−4.51	4.92	82.92**	45.80	6.82	4.93	60.25**
58	42B × P69R	3.74	−21.61	11.77	30.24**	44.27	−3.22	4.30	63.43**	47.15	4.99	4.51	50.43**
59	42B × P124R	2.99	−20.56*	8.68	16.43**	46.37	−0.16	4.27	62.55**	44.88	0.73	5.00	61.93**
60	42B × P100R	3.75	−12.17	16.12	56.73**	44.31	6.13**	1.57	8.47**	45.82	−6.63*	2.73	18.45**
61	CMS-XA	5.61	−9.89	22.03	105.97**	49.53	−6.97*	3.11	33.21**	38.92	8.32*	3.53	30.89**
62	E002-91	2.32	−20.63	21.75	103.33**	58.96	−6.93	4.43	67.48**	32.86	9.11	4.35	46.96**
63	PKU-2A	4.88	−19.77	19.95	86.91**	49.60	−5.31	4.86	81.19**	41.02	6.68	5.48	74.39**
64	ARG-2	5.21	−14.92	17.55	67.24**	48.81	−5.55	3.36	38.72**	41.08	7.09	3.44	29.30**
65	ARG-3	4.98	−12.26	17.57	67.43**	55.55	−5.47	3.08	32.57**	35.06	6.76	3.32	27.27**

(*continued*)

Table 8: (*continued*)

S. No.	Genotypes	Stearic acid (%)				Oleic acid (%)				Linoleic acid (%)			
				± SE				± SE				± SE	
		Mean	bi	bi	σ² di	Mean	bi	bi	σ² di	Mean	bi	bi	σ² di
66	ARG-6A	5.00	−14.03	20.72	93.72**	47.96	−5.64	4.20	60.57**	39.94	6.75	4.87	58.78**
67	DV-10A	7.05	−18.81	17.51	66.96**	51.29	−5.50	3.95	53.68**	35.42	7.37	3.93	38.34**
68	PHIR-27A	4.30	−12.77	16.37	58.48**	39.00	−5.08	3.06	32.06**	49.59	6.36	3.25	26.21**
69	PRUN-29A	3.64	−23.66	24.72	133.40**	56.65	−7.87	5.07	88.37**	35.91	10.38	4.96	61.05**
70	40A	3.94	−4.44	9.14	18.22**	42.49	−3.06*	1.12	4.34**	47.56	3.79**	1.03	2.63**
71	42A	2.88	−23.71	18.61	75.62**	45.13	−5.62	4.91	82.80**	44.98	7.92	4.90	59.39**
72	234A	5.38	−24.26	24.06	126.44**	50.94	−6.31	5.97	122.50**	36.64	9.25	5.85	84.72**
73	38A	5.01	−14.26	20.35	90.45**	51.92	−6.26	3.64	45.47**	37.89	7.71	3.97	38.98**
74	NC-41B (C)	3.70	−16.77	18.63	75.80**	45.44	−5.48	4.00	54.99**	45.72	6.90	4.38	47.55**
75	42B	3.03	−25.38	21.59	101.81**	45.62	−6.37	5.47	102.51**	45.08	9.05	5.35	70.79**
76	RCR-8297	5.54	−8.16	16.78	61.48**	38.37	−4.70	3.00	30.79**	49.72	5.47	3.57	31.62**
77	P69R	4.55	−10.40	24.88	135.15**	52.16	−6.44	4.70	75.77**	37.02	7.29	5.72	81.11**
78	P124R	3.79	−14.65	15.79	54.43**	39.12	−4.84	3.31	37.71**	51.15	6.19	3.51	30.46**
79	P100R	6.04	−15.26	19.35	81.76**	51.25	−6.03	3.61	44.80**	36.11	7.58	3.82	36.12**
	Mean	3.48				44.72				46.64			
	Min.	1.80				26.38				32.86			
	Max.	7.05				58.96				64.57			
	SE ±	0.13				0.64				0.67			

all the genotypes exhibited regression coefficient more than unity with significant deviation from regression line.

Oleic acid (%)

The results shown in of Table 8 revealed that oleic acid was the highest in parental line E002-91A (58.96). Except *cms*-XA × P100R, ARG-3A × P124R, ARG-6A × P124R, DV-10A × P100R, 42A × P100R, NC-41A × RCR-8297, NC-41B × P69R and 42B × P124R, all the genotypes exhibited regression coefficient more than unity with significant deviation from regression line.

Linoleic acid (%)

The results shown in Table 8 revealed that linoleic acid was the highest among the crosses ARG-6A × P69R (64.57). Except *cms*-XA × P100R, ARG-6A × P124R, DV-10A × P100R, 42A × P124R, NC-41B × P69R and 42B × P124R, all the genotypes exhibited regression coefficient more than unity with significant deviation from regression line.

For oil content and fatty acid none of the genotypes fulfilled all the three requirements for a stable variety, therefore, it can be concluded that all the genotypes under investigation were significantly influenced by the environments for quality parameter and none of the genotype was found to be stable across these environments.

Conclusions

We have applied the Eberhart and Russel (1966) stability model to our new developed sunflower germplasm and the results of stability revealed for seed yield the hybrids *cms*-XA × RCR-8297, E002-91A × P124R, ARG-3A × RCR-8297, ARG-6A × P100R, DV-10A × P100R, PHIR-27A × P69R, PRUN-29A × RCR-8297, 40A × RCR-8297, 40A × P69R, 40A × P100R, 234A × P100R and 38A × RCR-8297 were recorded as stable over environments. The hybrids *cms*-XA × RCR-8297, ARG-3A × RCR-8297, ARG-6A × RCR-8297, 40A × P100R and 234A × P100R were recorded suitable for poor environments (stress) with predictable performance. Sufficient variability was observed among the genotypes for oil content. Oil content was highest for ARG-2A × P100R (34.61). A total of 49 genotypes recorded above average mean performance for oil content. The hybrids DV-10A × P100R

and 40A × P124R had stability over the environments with unpredictable performance. The data provides a useful information regarding the stability of diverse sunflower genotypes under the north Indian conditions.

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