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Water use Efficient Sunflower Hybrids having Diverse Cytoplasmic Background

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Abstract: A set of fifty two hybrids developed through line×tester breeding design were sown in randomized block design with three replications to evaluate their performance for seed yield under two environments (normal irrigation and water stress). Drought resistant indices and multivariate statistical analysis from the pooled data obtained from water stress and normal irrigated environments over the two years. Hybrid PRUN-29A × RCR-8297 (1.55) and 40A × P100R (1.55) had the largest stress tolerance index (STI) rate and hybrid ARG-2A × P69R the smallest rate (a high STI rate for the genotype represents its high drought resistance and its high yielding potential). Hybrid ARG-6A × P69R (2.41) had the largest extent (susceptible) of Stress susceptibility index (SSI), while hybrid E002-91 × RCR-8297 (0.13) had the least (resistant) extent a large extent of this index indicates the genotype susceptibility to drought. In terms of yield stability index (YSI), hybrid 40A × RCR-8297 (0.51) and ARG-6A × P69R (0.51) and hybrid ARG-2A × P69R (1.18) had the smallest and the largest rate respectively (genotypes with high YSI are expected to yield highly in stress conditions. Hybrid 40A × RCR-8297 (30.36) and PRUN-29A × P69R (–10.07) displayed the least and the most amount of tolerance index (TOL) index, a high amount of TOL is a sign of genotype susceptibility to stress. Hybrid PRUN-29A × P69R (1.53) displayed the least extent of yield index (YI), while hybrid ARG-6A × P69R (0.51) and 40A × RCR-8297 (0.51) displayed the highest extent.

Keywords: sunflower hybrids, cytoplasmic sources, water use efficancy, drought tolerance indices, multivariate analysis

Introduction

Sunflower introduced in India in seventies, has acquired the status of an important commercial oilseed crop and the area under its cultivation has increased across the

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India because of its day length neutrality, wider adaptability and responsiveness to added inputs. Sunflower is moderately tolerance to water stress but in north India it is being cultivated during spring season i. e. Feb-Jun, so the water requirement of the crop increases because of high temperatures at the time of anthesis and maturity and there is requirement of irrigation every week and sometimes in the light soils twice a week. Thus water use efficient genotypes need to be developed and identified so that the number of irrigations can be reduced. Crop water use efficiency is one of the most important agronomic traits, which is under the control of multi-genes and is not easily measurable. Direct selection for yield in dry environments is inefficient due to large seasonal variation in weather and generally a large genotype x environment interaction and their by results in low heritability for yield. Therefore, many selection indices based on a mathematical relation between seed yield in water stressed and non-stressed environment have been proposed mention in Table 1. Drought susceptibility index (DSI) is estimated though seed yield under drought stress and normal water regimes the ration between seed yield of both regimes give an idea about performance of genotypes (Fischer and Maurer, 1978) and seed yield potential under both the environments (Vannozi *et al.*, 1999). High value of susceptibility index indicates higher susceptibility of a particular genotype to the stress environment. Application of these drought tolerance indices in the selection of drought tolerant genotypes has been reported in several. Wild *Helianthus* species serve as potential sources of novel genetic variability and several desirable traits like biotic and abiotic stresses resistance, cytoplasmic male sterility, genes for fertility restoration and oil quality have been effectively introgressed into cultivated sunflower (Seiler, 1992; Thompson *et al.*, 1981). Commercial sunflower hybrids are generally obtained using a single source of *cms*, PET-1, *Helianthus petiolaris* (Leclercq, 1969). Recently, several cms backgrounds have been developed by intraspecific and interspecific crosses, which resulted in several cms sources being available (Serieys, 2002). Since these cms sources were known, several experiments to estimate the impact of alien cytoplasm on important yield traits have been planned before their introgression into commercial sunflower breeding programs. The alloplasmic lines 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 elite restorers lines 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 by eliminating the effect of nuclear genes. A total of nine alloplasmic CMS lines developed and evaluated for their agronomic and seed yield performance and level of diversity for different morphological, physiological, yield and quality traits under normal irrigated environment (Tyagi et al., 2013, 2015a), under water stress environment (Dhillon and Tyagi, 2016; Tyagi and Dhillon, 2016a, 2016b; Tyagi *et al.*, 2015b), characterization for drought tolerance and physiological efficiency for both normal and water stress environments (Tyagi *et al.*, 2018b) and stability (Tyagi *et al.*, 2018c) at PAU, Ludhiana. These alloplasmic lines and four euplasmic lines crossed with four restorers to develop a set of fifty two sunflower hybrids to evaluate for seed yield under two different the environments i. e. normal irrigated and water stress. The objective of present study was to identify the water use efficient sunflower hybrids having divers CMS bases.

Methods and materials

In the present study nine alloplasmic lines from diverse cytoplasmic sources viz; ARG-2, ARG-3 *(H. argophyllus)*, CMS-XA (Unknown), PRUN-29A *(H. praecox spp. runyonic)*, DV-10A (*H. debilis spp. vestitus)* and E002-91A, PKUZ-A (*H. annuus*) having one common maintainer NC-41B and four euplasmic CMS lines from conventional source (*H. petiolaris*) 40A, 42A, 238A and 38A were crossed with four restores lines RCR-8297, P69R, P124R and P100R in line×tester breeding design to develop a set of 52 sunflower hybrids which were having different cytoplasmic background. The experiment was carried out during spring season 2011 and 2012 in the experimental area of oilseed section, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, Punjab, India. The experiment was sown at an optimum time, during first week of February on a well-prepared field in randomized plot deign having three replications. The plots consisted of two row with 11 plants in each raw. The row-to-row spacing was 70 cm and the plants were spaced at 30 cm intervals within the rows. The seed yield was analyzed on a sample consisting of 15 plants (5 per replicate) to calculate the average seed yield/plant. The experiment was conducted over the two different environments (normal irrigation and water stress). In stress environment the irrigation was stopped after the anthesis was complete. The data was recorded on seed yield under both the environments and the different stress indexes values were calculated using following methods (Table 1).

Statistical analysis

The seed yield data were subjected to calculate the different drought tolerance indices through the formulas listed in Table 1 and to estimate the correlation between them using standard method. Multivariate statistical analysis was done by SAS software (SAS Institute Inc., Cary, NC, USA).

Table 1: Calculation of drought tolerance indices used for evaluation of sunflower hybrid from different cytoplasm sources.

S. No.	Drought tolerance indices	Formula	Reference
1	Drought susceptibility index	$DSI = \frac{1-\left(\frac{Y_S}{Y_P}\right)}{1-\left(\frac{\bar{Y}_S}{\bar{Y}_P}\right)}$	Fischer and Maurer (1978)
2	Geometric mean productivity	$GMP = \sqrt{(Y_S)(Y_P)}$	Fernandez (1992) and Kristin *et al.* (1997)
3	Mean productivity	$MP = \frac{Y_S + Y_P}{2}$	Rosielle and Hamblin (1981)
4	Harmonic mean	$HM = \frac{2(Y_P.Y_S)}{Y_P + Y_S}$	Jafari *et al.* (2009)
5	Tolerance index	$TOL = Y_P - Y_S$	Rosielle and Hambling (1981)
6	Stress tolerance index	$STI = \frac{(Y_S)(Y_P)}{(\bar{Y}_P)^2}$	Fernandez (1992)
7	Yield index	$YI = \frac{Y_S}{\bar{Y}_S}$	Gavuzzi *et al.* (1997)
8	Yield stability index	$YSI = \frac{Y_S}{Y_P}$	Bouslama and Schapaugh (1984)

Y_S and Y_P are stress and normal irrigated environment yield of a given hybrids. $\overline{Y}_S$ and $\overline{Y}_P$ are average yield of all hybrids under stress and normal irrigated environment, respectively.

Results and discussion

Analysis of variance revealed significant differences among sunflower hybrids for all of the studied indices. The highest yield value was obtained from the hybrids 40A × P100R (68.38 g) followed by 234A × P69R (68.13 g), 40A × 124R (68.08 g), DV10A × RCR8297 (66.27 g) and ARG2A × RCR8297 (64.97 g) under normal irrigated condition, and in PRUN29A × P69R (56.52 g) followed by CMSXA × RCR8297 (56.13 g), E002-91A × RCR8297 (55.42 g), PRUN29A × RCR8297 (53.88 g) and CMSXA × P100R (53.32 g) under water stressed condition (Table 2). However, CMSXA × P69R followed by ARG2A × P69R and ARG2A × P124R had the lower seed yield values and PRUN29A × RCR8297 and 40A × P100R had the higher seed yield in both water stressed and normal irrigated environments, hence depicted the non-responsiveness of these hybrids to different water regimes in the contribution to the final seed yield. Similar studies were carried out by Darvishzadeh *et al.* (2010), genetic variability of seed yield in both water stressed and normal irrigated stressed environments can involve the way of useful resource for selection of drought tolerant hybrids which derived from divers cytoplasmic sources through classical breeding methods.

According to Fischer and Maurer index (SSI) (1978), the hybrids ARG6A × P69R, 40A × RCR8297, E002-91A × P100R, 40A × P124R and ARG2A × RCR8297 with high SSI values were found to be the most water stress susceptible hybrids

Table 2: Mean seed yield and calculation of drought tolerance index among 52 sunflower hybrids.

Code No.	Genotypes	YP	YS	DSI (SSI)	GMP	MP	HM	TI	STI	YI	YSI
1	CMS-XA × RCR-8297	51.15	56.13	−0.48	53.58	53.64	53.52	−4.98	1.33	1.52	1.10
2	CMS-XA × P69R	37.54	30.18	0.96	33.66	33.86	33.46	7.36	0.52	0.82	0.80
3	CMS-XA × P124R	52.80	48.28	0.42	50.49	50.54	50.44	4.52	1.18	1.30	0.91
4	CMS-XA × P100R	59.05	53.32	0.47	56.11	56.19	56.04	5.73	1.46	1.44	0.90
5	E002-91 × RCR-8297	56.99	55.42	0.13	56.20	56.21	56.19	1.57	1.46	1.50	0.97
6	E002-91 × P69R	51.71	36.43	1.45	43.40	44.07	42.75	15.28	0.87	0.98	0.70
7	E002-91 × P124R	51.72	47.02	0.44	49.31	49.37	49.26	4.70	1.12	1.27	0.91
8	E002-91 × P100R	52.30	29.92	2.09	39.56	41.11	38.06	22.38	0.72	0.81	0.57
9	PKU-2A × RCR-8297	47.67	40.63	0.72	44.01	44.15	43.87	7.04	0.90	1.10	0.85
10	PKU-2A × P69R	42.32	34.12	0.95	38.00	38.22	37.78	8.20	0.67	0.92	0.81
11	PKU-2A × P124R	57.80	45.97	1.00	51.55	51.89	51.21	11.83	1.23	1.24	0.80
12	PKU-2A × P100R	58.58	37.58	1.75	46.92	48.08	45.79	21.00	1.02	1.02	0.64
13	ARG-2A × RCR-8297	64.97	39.63	1.91	50.74	52.30	49.23	25.34	1.19	1.07	0.61
14	ARG-2A × P69R	26.29	31.00	−0.88	28.55	28.65	28.45	−4.71	0.38	0.84	1.18
15	ARG-2A × P124R	41.93	27.92	1.64	34.22	34.93	33.52	14.01	0.54	0.75	0.67
16	ARG-2A × P100R	60.95	47.67	1.07	53.90	54.31	53.50	13.28	1.34	1.29	0.78
17	ARG-3A × RCR-8297	55.51	51.33	0.37	53.38	53.42	53.34	4.18	1.32	1.39	0.92
18	ARG-3A × P69R	51.90	38.77	1.24	44.86	45.34	44.38	13.13	0.93	1.05	0.75
19	ARG-3A × P124R	57.90	47.63	0.87	52.51	52.77	52.27	10.27	1.27	1.29	0.82
20	ARG-3A × P100R	61.10	42.97	1.45	51.24	52.04	50.46	18.13	1.21	1.16	0.70
21	ARG-6A × RCR-8297	62.17	42.70	1.53	51.52	52.44	50.63	19.47	1.23	1.15	0.69
22	ARG-6A × P69R	42.34	21.53	2.41	30.19	31.94	28.54	20.81	0.42	0.58	0.51

(*continued*)

Table 2: (*continued*)

Code No.	Genotypes	YP	YS	DSI (SSI)	GMP	MP	HM	TI	STI	YI	YSI
23	ARG-6A × P124R	44.02	31.08	1.44	36.99	37.55	36.44	12.94	0.63	0.84	0.71
24	ARG-6A × P100R	51.91	48.18	0.35	50.01	50.05	49.98	3.73	1.16	1.30	0.93
25	DV-10A × RCR-8297	66.27	48.62	1.30	56.76	57.45	56.09	17.65	1.49	1.31	0.73
26	DV-10A × P69R	43.52	37.30	0.70	40.29	40.41	40.17	6.22	0.75	1.01	0.86
27	DV-10A × P124R	49.30	37.98	1.12	43.27	43.64	42.91	11.32	0.87	1.03	0.77
28	DV-10A × P100R	57.28	48.64	0.74	52.78	52.96	52.61	8.64	1.29	1.31	0.85
29	PHIR-27A × RCR-8297	57.29	39.08	1.56	47.32	48.19	46.46	18.21	1.03	1.06	0.68
30	PHIR-27A × P69R	47.08	37.60	0.99	42.07	42.34	41.81	9.48	0.82	1.02	0.80
31	PHIR-27A × P124R	50.63	33.00	1.70	40.88	41.82	39.96	17.63	0.77	0.89	0.65
32	PHIR-27A × P100R	54.72	48.65	0.54	51.60	51.69	51.51	6.07	1.23	1.31	0.89
33	PRUN-29A × RCR-8297	62.36	53.88	0.67	57.97	58.12	57.81	8.48	1.55	1.46	0.86
34	PRUN-29A × P69R	46.45	56.52	−1.06	51.24	51.49	50.99	−10.07	1.21	1.53	1.22
35	PRUN-29A × P124R	48.72	41.35	0.74	44.88	45.04	44.73	7.37	0.93	1.12	0.85
36	PRUN-29A × P100R	52.49	45.68	0.63	48.97	49.09	48.85	6.81	1.11	1.23	0.87
37	40A × RCR-8297	61.98	31.62	2.40	44.27	46.80	41.88	30.36	0.91	0.85	0.51
38	40A × P69R	55.75	40.08	1.38	47.27	47.92	46.63	15.67	1.03	1.08	0.72
39	40A × P124R	68.08	40.52	1.98	52.52	54.30	50.80	27.56	1.28	1.10	0.60
40	40A × P100R	68.38	48.95	1.39	57.85	58.67	57.06	19.43	1.55	1.32	0.72
41	42A × RCR-8297	60.60	48.11	1.01	54.00	54.36	53.64	12.49	1.35	1.30	0.79
42	42A × P69R	57.53	47.87	0.82	52.48	52.70	52.26	9.66	1.27	1.29	0.83
43	42A × P124R	54.27	37.97	1.47	45.39	46.12	44.68	16.30	0.95	1.03	0.70
44	42A × P100R	56.47	37.42	1.65	45.97	46.95	45.01	19.05	0.98	1.01	0.66

45	234A × RCR-8297	52.12	43.07	0.85	47.38	47.60	47.16	9.05	1.04	1.16	0.83
46	234A × P69R	68.13	46.94	1.52	56.55	57.54	55.58	21.19	1.48	1.27	0.69
47	234A × P124R	40.28	33.15	0.87	36.54	36.72	36.37	7.13	0.62	0.90	0.82
48	234A × P100R	58.76	52.10	0.55	55.33	55.43	55.23	6.66	1.42	1.41	0.89
49	38A × RCR-8297	55.13	36.13	1.69	44.63	45.63	43.65	19.00	0.92	0.98	0.66
50	38A × P69R	40.13	32.40	0.94	36.06	36.27	35.85	7.73	0.60	0.88	0.81
51	38A × P124R	53.80	38.07	1.43	45.26	45.94	44.59	15.73	0.95	1.03	0.71
52	38A × P100R	50.72	46.68	0.39	48.66	48.70	48.62	4.04	1.09	1.26	0.92

YP = Seed yield/plant under normal irrigated environment; YS = Seed yield/plant under water stress environment; DSI = Drought susceptibility index; GMP = Geometric mean productivity; MP = Mean productivity; HP = Harmonic mean; TI = Tolerance index; STI = Stress tolerance index; YI = Yield index; YSI = Yield stability index whereas hybrids PRUN29A × P69R, ARG2A × P69R, CMSXA × RCR8297, E002-91A × RCR8297 and ARG6A × P100R with low value were found to be tolerant to water stress (Table 2). The less numerical rate of SSI indicates more water stress tolerance of a genotype. Yadav and Bhatnagar (2001) suggested the use of SSI in combination with yield value under stressed condition for identifying drought tolerant/susceptible genotypes.

Considering TOL index, a genotype would be more tolerant if it has less TOL value. Based on TOL, the hybrids PRUN29A × P69R, CMSXA × RCR8297, ARG2A × P69R, E002-91A × RCR8297 and ARG6A × P100R with low values were considered as tolerant genotypes, whereas the hybrids 40A × RCR8297, 40A × P124R, ARG2A × RCR8297, E002-91A × P100R and 234A × P69R with the high TOL values were considered as susceptible to water stress (Table 2). Fernández (1992) has suggested that TOL index was efficient in improving yield under stressed condition and the selected genotypes performed poorly under non-stressed condition. Yield stability index (YSI) also was calculated for a given sunflower hybrids using seed yield under stressed and non-stressed conditions. The genotypes with high YSI is expected to have high yield under stressed and low yield under non-stressed conditions. The lowest YSI was observed for 40A × RCR8297, ARG6A × P69R, E002-91A × P100R, 40A × P124R and ARG2A × RCR8297 and the highest YSI was observed for PRUN19A × P69R, ARG2A × P69R, CMSXA × RCR8297, E002-91A × RCR8297 and ARG6A × P100R hybrids (Table 2).

Fernandez (1992) proposed STI index which discriminates genotypes with high yield and stress tolerance potentials. A high STI demonstrates a high tolerance and the best advantage of STI is its ability to separate group A genotypes from other genotypes. Based on the STI index, the hybrids including PRUN19A × RCR8297, 40A × P100R, DV10A × RCR8297, 234A × P69R CMSXA × P100R and E002-91A × RCR8297 had the high values and considered as tolerant hybrids with high yield stability in the both conditions (Table 2). In this study, the results of GMP, MP, HM and YI indices in selection of genotypes were similar to STI index. This result is not unexpected regarding to reported significant relation between STI with GMP, MP, HM and YI indices in sunflower (Darvishzadeh *et al.*, 2010).

Correlation coefficient between seed yield and drought tolerance indices were used to identify the best criterion for selecting drought tolerant genotypes. According to literature (Darvishzadeh *et al.*, 2010; Farshadfar and Sutka, 2002), a suitable index must to have a significant relation with yield in both stressed and non-stressed states. As shown in Table 3, indices including GMP, MP, HM, YI and STI were highly correlated with each other as well as with Ys and Yp. The observed relations were consistent with those reported by Fernandez (1992) in mungbean, Farshadfar and Sutka (2002) in maize, Golabadi *et al.* (2006) in durum wheat and Darvishzadeh *et al.* (2010) in

Table 3: Correlation among drought tolerance index with other yield index.

	YP	YS	DSI (SSI)	GMP	MP	HM	TI	STI	YI	YSI
YP		0.527**	0.356**	0.846**	0.880**	0.810**	0.522**	0.834**	0.524**	−0.359**
YS			−0.585**	0.897**	0.867**	0.921**	−0.450**	0.901**	0.999**	0.581**
DSI (SSI)				−0.179	−0.119	−0.234	0.961**	−0.198	−0.587**	−0.999**
GMP					0.997**	0.998**	−0.011	0.996**	0.896**	0.175
MP						0.990**	0.054	0.992**	0.866**	0.115
HM							−0.073	0.994**	0.920**	0.230
TI								−0.027	−0.452**	−0.961**
STI									0.900**	0.194
YI										0.584**
YSI										

YP = Seed yield/plant under normal irrigated environment; YS = Seed yield/plant under water stress environment; DSI = Drought susceptibility index; GMP = Geometric mean productivity; MP = Mean productivity; HP = Harmonic mean; TI = Tolerance index; STI = Stress tolerance index; YI = Yield index; YSI = Yield stability index sunflower. However, TOL and SSI were not strongly correlated with the above mentioned indices. On the other hand, TOL and SSI show rankings different from the other indices. The positive correlation between TOL and Yp and the negative correlation between TOL and Ys was found (Table 3) which suggested selection based on TOL will lead to reduction of yield under well-watered conditions. Similar results were reported by Clarke *et al.* (1992) and Sio-Se Mardeh *et al.* (2006). SSI showed a negative correlation with Ys. No significant correlation was found between YP and SSI.

Thus SSI index is suitable factor for the identification of water stress tolerant genotypes. SSI has been widely used by researchers for discriminating drought tolerant/susceptible genotypes (Clarke *et al.*, 1984, 1992; Fischer and Maurer, 1978; Winter *et al.*, 1988). TOL and SSI indices were employed by Gavuzzi *et al.* (1993) to identify genotypes with superior drought adaptation in trials conducted in several locations of southern Italy. The correlation coefficients of YSI with Yp were negative while it had positive correlation with Ys. These results are disagreed with Bouslama and Schapaugh (1984) who stated that cultivars with a high YSI were expected to have high yield under both stressed and non-stressed conditions. However, Sio-Se Mardeh *et al.* (2006) found that cultivars with the highest YSI exhibit the low yield under non-stressed and the high yield under stressed conditions. In this research, there was significant positive correlation between TOL and SSI while there was significant negative correlation between YI and YSI.

Interrelationship among selected indices and seed yield

It is evident from correlation coefficients (Table 3) that GMP, MP, HM, YI and STI are better predictors of Yp and Ys. Results indicated that seed yield was significantly positive associated with SSI (0.356**), TOL (0.522**), STI (0.834**) and YI (0.524**), while significant negative correlation was observed with YSI (–0.359**) under normal environment. But, under stress environment significant positive correlations was recorded between seed yield and STI (0.901**), YI (1.000**) and YSI (0.581**), while significant negative association with SSI (–0.585**) and TI (–0.450**). All these indices were also observed positive and negative related to each other. According to literature, a suitable index must have a significant relation with yield in both stressed and non-stressed conditions. Indices SSI, TOL, STI and YI were highly significantly correlated with each other as well as with seed yield under both stress and normal environments.

Multivariate analysis

Principal component analysis (PCA) revealed that the first PCA (PC1) explained 65.43 % of the variation and had positive correlation with Yp, Ys, GMP, MP, HM, STI, YI and YSI (Table 4). Thus, the first dimension can be named as the yield potential and water stress tolerance. Genotypes possessed high values of PC1, could be high yielding under stressed and non-stressed environments. The second PCA (PC2) explained 34.00 % of the total variability and correlated positively with TI and DSI (Table 4). Therefore, the second component can be named as a stress-tolerant dimension and it separates the stress-tolerant genotypes from non-stress tolerant ones. Selection of genotypes that have high PC1 and low PC2 are suitable for both stressed and non-stressed environments. Considering high value of PC1 and low value of PC2, hybrids with code number of 1, 3, 4, 5, 7, 17, 24, 28, 32, 34, 36, 42, 45, 48 and 52 were superior genotypes for both stressed and non stressed environments. Hybrids with code numbers 11, 13, 16, 19, 20, 21, 25, 33, 39, 40, 41 and 46 exhibited high values of PC2 can be considered more suitable for normal irrigated environment than for water stress environment. Moreover, in agreement with Darvishzadeh *et al.* (2010), the proximity of genotypes to important drought tolerant indices in the biplot presentation (Figure 1) could depict water use efficient genotypes. Considering to Figure 1, there was high genetic variability for water stress tolerance among the hybrids. Farshadfar and Sutka (2002), Sio-Se Mardeh *et al.* (2006), Golabadi *et al.* (2006) and Tyagi and Dhillon (2018a) also obtained similar results in multivariate analysis of drought tolerance in different crops.

Table 4: Eigen value and vectors of principal component analysis for potential yield (YP), stress yield (YS) and drought tolerance indices.

S. No.	Parameters	Principal component 1	Principal component 2
1	Eigen value	6.54	3.40
2	Percentage of variance	65.43	34.00
3	Cumulative percentage	65.43	99.43
4	YP	0.27	0.38
5	YS	0.38	−0.12
6	DSI	−0.16	0.49
7	GMP	0.38	0.13
8	MP	0.37	0.16
9	HM	0.38	0.10
10	TI	−0.09	0.52
11	STI	0.38	0.12
12	YI	0.38	−0.12
13	YSI	0.16	−0.49

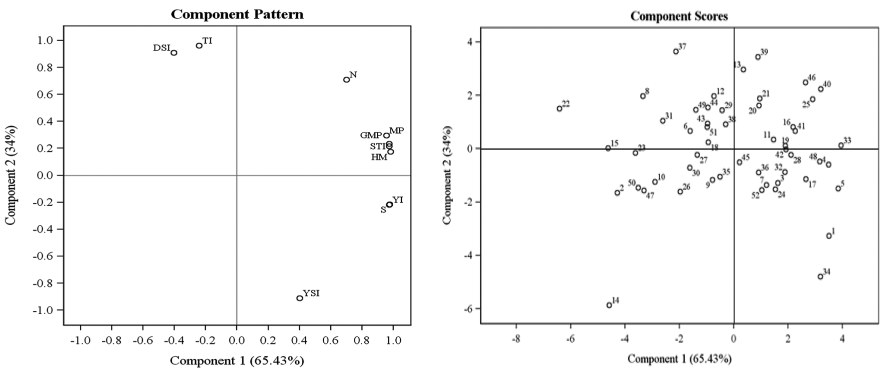

Figure 1: Screening drought tolerance indicators using biplot analysis (a and b).

The cluster analysis was done to study the variation between genotypes based on drought tolerance indices. Cluster analysis based on drought tolerance indices (Figure 2), grouped the hybrids into five separate clusters which involved twenty, seven, seventeen, seven, and one hybrids in each group respectively (Table 5). Cluster II and cluster V were comprised genotypes that had low yield in water stress environment. Hence, genotypes distributed to these groups could be stable in normal irrigated environment and clubbed as group B. Clustering results revealed that the cluster III and IV genotypes (low Ys and Yp) have high TOL and SSI values in the most cases, therefore,

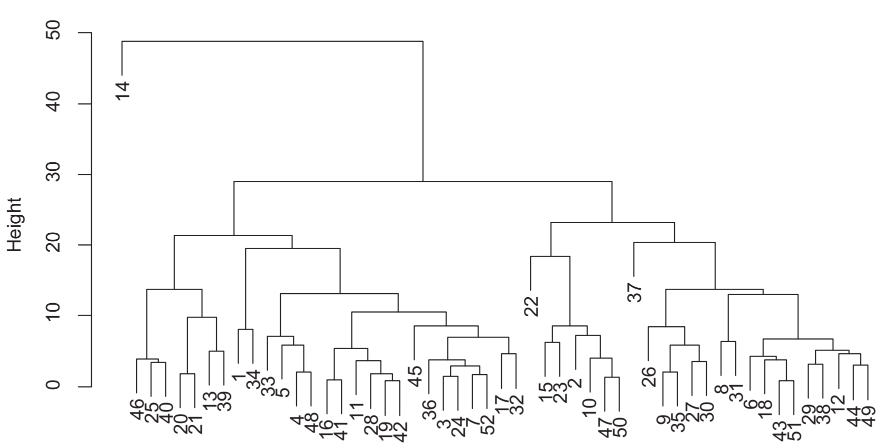

Figure 2: Dendrogram from cluster analysis based on drought tolerance indices and seed yield of sunflower hybrids in both normal and stress environment.

Table 5: Cluster composition with hybrids.

Clusters	No. of Hybrids	Code No.
Cluster-I	20	1,3,4,5,7,11,16,17,19,24,28,32,33,34,36, 41,42,45,48 and 52
Cluster-II	7	2,10,15,22,23,47 and 50
Cluster-III	17	6,8,9,12,18,26,27,29,30,31,35,37,38,43,44, 49 and 51
Cluster-IV	7	13,20,21,25,39,40 and 46
Cluster-V	1	14

these clusters clubbed as group D. The cluster I included genotypes that had highest value of STI, HM and GMP indices accompanied with higher seed yield (Table 2) thus named as group A according to Fernandez's (1992). The classification based on cluster analysis was paralleled with biplot analysis and consistent with findings of Darvishzadeh *et al*. (2010).

The results of this study indicated, sunflower hybrids can be classified into three groups, the top five hybrids which showed yield stability over both the environments viz. E002-91A × RCR-8297, 42A × P69R, ARG-6A × P100R, ARG-3A × RCR-8297 and 38A × P100R indicating resistance or stability of these hybrids to water stress environment. Hybrids ARG-6A × P69R, 40A × RCR-8297, E002-91 × P100R, 40A × P124R and ARG-2A × RCR-8297 showed medium tolerance to water stress. The hybrids PRUN-29A × P69R, ARG-2A × P69R, CMS-XA × RCR-8297, ARG-6A × P100R and E002-91 × RCR-8297 all having diversified cytoplasmic background are better seed yielders under water stress environment thus well adapted to water stress conditions.

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