DE GRUYTER HELIA 2018; 41(68): 129–140

Vikrant Tyagi* and S. K. Dhillon

Performance and Water-Use Efficiency of Wild Cytoplasmic Sources in Sunflower

https://doi.org/10.1515/helia-2017-0015
Received August 14, 2017; accepted December 16, 2017;

Abstract: Wild *Helianthus* species should have be a main interest sunflower breeding for the introgressing elite genes for biotic and abiotic stress. The future use of wild sunflower in development of drought resistance cytoplasmic sources should be expanded to the wide range of wild species as compared to conventional sources. The objective of this study was to evaluate different parental lines for their water-use efficiency and seed yield performance under two environments for two years. ARG-2A received from *H. argophyllus*, 234A and 38A from *H. petiolaris* were found to be the most susceptible genotypes, whereas, 42A, 42B from *H. petiolaris* and ARG-6A (*H. argophyllus)* were found to be tolerant to drought stress. CMS-XA, RCR-8297, E002-91A, NC-41B and P124R were observed to be well adapted to stress environments. ARG-3A from *H. argophyllus* had a stable performance over the environments, which may be useful to develop water use efficient hybrids having diversified cytoplasmic backgrounds in sunflower breeding.

Keywords: Cytoplamic male sterile lines, drought stress, sunflower, stress tolerance index and wild sources

Introduction

Sunflower (*Helianthus annuus* L.) is one of the most important oil crops due to its high content of unsaturated fatty acids and a lack of cholesterol. It is the second largest hybrid crop, second only to maize, and the fifth largest oilseed crop, after soybean, rapeseed, cottonseed and groundnut. A major breakthrough in sunflower history was the discovery of cytoplasmic male sterility (CMS) in a wild sunflower, *Helianthus petiolaris* Nutt. (Leclercq, 1969), and restorer genes with recessive branching found in wild *H. annuus* populations (Kinman, 1970) and *H. petiolaris* (Leclercq, 1971) that led to the production of commercial sunflower hybrids.

***Corresponding author: Vikrant Tyagi,** Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, Punjab, India, E-mail: vikranttyagi97@gmail.com
S. K. Dhillon, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, Punjab, India, E-mail: sklb-pbg@pau.edu

Hybrids had higher seed yield, high oil content and quality, uniformity and enhanced resistance to biotic and abiotic stresses compared to open-pollinated varieties. In general, most cytoplasm of wild annual *Helianthus* species can accommodate cultivated nuclear genes without significant unfavorable interactions and are potential sources of cytoplasmic diversity for sunflower breeding (Seiler *et al.*, 2017). Cytoplasmic and nuclear genome interaction had a negative effects on chlorophyll, photosynthetic rate (Jan, 1990) and positive effects on oil content and quality (Serieys, 1992; Tyagi and Dhillon, 2014). The genus *Helianthus* is composed of 52 species and 19 subspecies, with 14 annual and 38 perennial (Schilling and Heiser, 1981; Schilling, 1993). The cultivated species is diploid ($2n = 2x = 34$; Schilling and Heiser, 1981), as well as all annual wild species. Tetraploid ($2n = 4x = 68$) and hexaploid ($2n = 6x = 102$) species are generally perennials. Abundant genetic variation exists in the sunflower crop wild relatives with details of the related species as potential sources of genetic improvement of sunflower reported by Warburton *et al.* (2017). Discovery of cytoplasmic male sterility (CMS) source and restorer genes from *H. petiolaris* paved the way for the development of single-cross hybrids, but also resulted in a genetic bottleneck in cultivated germplasm, by incorporating the same source of male sterility and restorer genes. Diversifying the sources of male sterility is one objective of modern sunflower breeders. Water availability for agriculture is becoming limited, and climate-change scenarios predict increased aridity in certain regions. Development of new hybrids and cultivars with more efficient water use and greater drought resistance is considered a sustainable and economically viable approach (Condon *et al.*, 2004). Nine CMS analogues were developed from different wild sunflower *spp.* and evaluated under normal irrigation (Tyagi *et al.*, 2013; 2015a; Tyagi and Dhillon, 2015), as well as under water stress conditions (Tyagi *et al.*, 2015b; Tyagi and Dhillon, 2016a) at Punjab Agricultural University, Ludhiana. These sources were used for a hybrid breeding program to develop sunflower hybrids and study the effects of different wild sources on combining ability for seed yield and component traits under different irrigation environments (Dhillon and Tyagi, 2016; Tyagi and Dhillon, 2016b; Tyagi and Dhillon, 2017). The objectives of present research was to study the different drought stress indices, to help breeders design efficient breeding strategies to improve seed yield and under varied moisture environments and diversification of *cms* sources for modern sunflower hybrid breeding.

Materials and methods

This study was carried out at the Department of Plant Breeding and Genetics, College of Agriculture, Punjab Agricultural University, Ludhiana, India.

Ludhiana represents the Indo-Gangetic plains and is situated at 36° – 54′ N latitude, 25° – 48′E longitude with a mean elevation of 247 meters above sea level. The 19 parental lines were composed of nine alloplasmic lines, four euplasmic lines, two maintainer lines and four restorer lines (Table 1) field evaluated for seed yield at two different environments (normal irrigated and water stress). Water stress was created by stopping water after anthesis for two seasons, spring of 2011 and 2012. A randomized complete block design with 3 replications was used at each location. The plot consisted of six rows 3 meter long with row to row and plant to plant distances of 0.60 m and 0.30 m, respectively. Sowing was done by dibbling three seeds per hill to ensure uniform stand which was later thinned to one plant per hill at the V_2 stage (Schneiter and Miller, 1981). Seed yield data was recorded from five randomly selected plants in each replication for both environments over the years separately. The mean data was used to calculate the different stress indices for each genotype using the corresponding normal irrigated and water stressed plots in each block. Stress-tolerance indices were calculated using the following relationships (Table 2).

Table 1: Sunflower Parental lines used in the current study.

S. No.	Parental line designation	Genotype Type	Origin
1	ARG-2A	CMS Line	*Helianthus argophyllus*
2	ARG-3A	CMS Line	*H. argophyllus*
3	ARG-6A	CMS Line	*H. argophyllus*
4	PKU-2A	CMS Line	*H. annuus*
5	E002-91A	CMS Line	*H. annuus*
6	PRUN-29A	CMS Line	*H. praecox ssp. runyonii*
7	DV-10A	CMS Line	*H. debilis ssp. vestitus*
8	PHIR-27A	CMS Line	*H. praecox ssp. hirtus*
9	CMS-XA	CMS Line	*Unknown*
10	NC-41B (C)	Maintainer line of All 9 cms	*H. petiolaris* (conventional)
11	40A	CMS Line	*H. petiolaris*
12	42A	CMS Line	*H. petiolaris*
13	42B	Maintainer line of 42A cms	*H. petiolaris*
14	234A	CMS Line	*H. petiolaris*
15	38A	CMS Line	*H. petiolaris*
16	RCR-8297	Restorer lines	*H. petiolaris*
17	P69R	Restorer lines	*H. petiolaris*
18	P124R	Restorer lines	*H. petiolaris*
19	P100R	Restorer lines	*H. petiolaris*

Statistical analysis

The data obtained from a randomized complete block design was analyzed. Stress tolerance indices were calculated using the equations cited in Table 2. Also, correlations between grain yield and stress tolerance indices, principle component analysis (PCA), biplot display and cluster analysis were determined using SAS (SAS Institute, 1999).

Table 2: Drought tolerance indices used for evaluation of sunflower parental lines.

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

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

Results and discussion

There were significant differences in yield between parental line under normal irrigated (yp) and water stressed (ys) conditions. Significant differences between sources were observed for all drought tolerance indices. The highest yield values were obtained in CMS-XA (37.48 g) followed by PHIR-27A (34.03), ARG-3A (32.17), E002-91A (32.07), RCR-8297 (30.98) and PRUN-29A (30.42) under stressed environments, and in 234A (46.43 g) followed by ARG-3A (41.42 g), DV-10A (36,38 g), ARG-2A (35.92 g) and 38A (35.05 g) under non-stressed conditions (Table 3). The lowest yield value was observed in 38A (10.00 g) followed by P69R (13.67 g) and ARG-2A (17.47 g) under stressed conditions, and CMS-XA (12.84 g), RCR-8297 (14.33 g), PKU-2A (16.33 g) and P124R (16.81 g) under non-stressed conditions. The inbred lines ARG-2A (2.51), 234A (2.72) and 38A (3.50)

Table 3: Mean seed yield under normal and stress environment and drought tolerance indices values of sunflower parental lines.

S. No.	Genotypes	Yp	Ys	DSI	GMP	MP	HM	TOL	STI	YI	YSI
1	ARG-2A	35.92	17.47	2.51	25.05	26.7	23.51	18.45	0.29	0.47	0.49
2	ARG-3A	41.42	32.17	1.09	36.5	36.8	36.21	9.25	0.62	0.87	0.78
3	ARG-6A	25.92	24.2	0.32	25.05	25.06	25.03	1.72	0.29	0.65	0.93
4	PKU-2A	16.33	20.8	−1.34	18.43	18.57	18.3	−4.47	0.16	0.56	1.27
5	E002-91A	20.29	32.07	−2.84	25.51	26.18	24.85	−11.78	0.3	0.87	1.58
6	PRUN-29A	24.65	30.42	−1.15	27.38	27.54	27.23	−5.77	0.35	0.82	1.23
7	DV-10A	36.38	22.75	1.83	28.77	29.57	27.99	13.63	0.38	0.61	0.63
8	PHIR-27A	28.42	34.03	−0.97	31.1	31.23	30.97	−5.61	0.45	0.92	1.2
9	CMS-XA	12.85	37.48	−9.38	21.95	25.17	19.14	−24.63	0.22	1.01	2.92
10	NC-41B (C)	15.08	23.53	−2.74	18.84	19.31	18.38	−8.45	0.16	0.64	1.56
11	40A	27.57	18.58	1.6	22.63	23.08	22.2	8.99	0.24	0.5	0.67
12	42A	28.13	26.42	0.3	27.26	27.28	27.25	1.71	0.34	0.71	0.94
13	42B	27.33	28.37	−0.19	27.85	27.85	27.84	−1.04	0.36	0.77	1.04
14	234A	46.43	20.62	2.72	30.94	33.53	28.56	25.81	0.44	0.56	0.44
15	38A	35.05	10.00	3.5	18.72	22.53	15.56	25.05	0.16	0.27	0.29
16	RCR-8297	14.33	30.98	−5.69	21.07	22.66	19.6	−16.65	0.21	0.84	2.16
17	P69R	18.28	13.67	1.23	15.81	15.98	15.64	4.61	0.12	0.37	0.75
18	P124R	16.81	25.87	−2.64	20.85	21.34	20.38	−9.06	0.2	0.7	1.54
19	P100R	20.68	26.95	−1.48	23.61	23.82	23.4	−6.27	0.26	0.73	1.3

had the highest stress susceptibility index (SSI) values and were found to be the most susceptible genotypes, whereas inbred lines 42B (−0.19), 42A (0.30) and ARG-6A (0.32) had low values (near to zero) and were tolerant to drought stress. The inbred lines CMS-XA (−9.38), RCR-8297 (−5.69), E002-91A (−2.84), NC-41B (−2.74) and P124R (−2.64) with negative SSI values were observed to be well adapted (better performers under stress) to stress environments. The lower the numerical number of the SSI indicates the less stress susceptibility and more water stress tolerance the genotype. Stress tolerance index, considering (TOL index), a genotype would be more tolerant if it has lower TOL values. Based on TOL, the inbred lines ARG-6A (1.72) and 42A (1.71) with low values were considered as tolerant genotypes, whereas the inbred lines 234A (25.81), 38A (25.05) and ARG-2A (18.45) with the high TOL values were considered as susceptible. The inbred lines CMS-XA (−24.63), RCR-8297 (−16.65) and E002-91A (−11.78) with negative TOL values were considered good performing inbreds under stress. Yield stability index (YSI) was also calculated for a given inbred lines using grain yield under stressed and non-stressed conditions. The genotypes with high YSI are expected to have high yield under stressed and low yield under non-stressed conditions. The lowest YSI was observed for 38A (0.29), 234A (0.44) and ARG-2A (0.49) while the highest YSI was observed for CMS-XA (2.92), RCR-8297 (2.16) and E002-91A (1.58) inbred lines (Table 3). Drought tolerance indices appear to be useful for selection of drought tolerant sunflower genotypes with high yield performance under both water stressed and non-stressed states.

Correlation between grain yield and drought tolerance indices

A correlation coefficient matrix (Table 4) revealed that TOL, MP, GMP, STI and YI indices could effectively be used for screening drought-resistant sunflower cultivars. Correlation coefficients were used to identify the best criterion for selecting drought tolerant genotypes. Stress indices and seed yield were highly significantly and positively associated with DSI (0.774**), GMP (0.691**), MP (0.746**), HM (0.621**), TOL (0.863**) and STI (0.697**), while a highly significant negative correlation was observed with YSI (−0.773**) under the normal environment. But, under a stress environment, significant positive correlations were observed between seed yield and GMP (0.470*), HM (0.484*), and highly significant positive with YI (1.000**) and YSI (0.712**), while highly significant negative association with DSI (−0.712**) and TI (−0.728**). All the indices were positive and negative relative to each other. According to the literature, a suitable index must have a significant relationship with yield in both stressed and non-stressed states. Indices DSI, TOL, STI and YI were highly and significantly correlated with each other, as well as with seed yield under stress and normal environment. There were significant positive correlations between Yp and stress-tolerance indices (DSI, GMP, MP, HM, TOL and STI). Likewise, there were positive significant correlations between Ys and the stress-tolerance indices. The positive correlations among STI, GMP and MP also exhibited the same trends. The study revealed that STI, GMP, MP and HM were better predictors of Yp and Ys than TOL and SSI. Our

Table 4: Association between different drought tolerance indices and mean yield of sunflower parental lines under normal and stress environment.

	Yp	Ys	DSI	GMP	MP	HM	TOL	STI	YI	YSI
Yp										
Ys	−0.281									
DSI	0.774**	−0.712**								
GMP	0.691**	0.470*	0.25							
MP	0.746**	0.430	0.234	0.975**						
HM	0.621**	0.484*	0.255	0.984**	0.920**					
TOL	0.863**	−0.728**	0.929**	0.246	0.306	0.189				
STI	0.697**	0.444	0.271	0.991**	0.964**	0.978**	0.264			
YI	−0.282	1.000**	−0.713**	0.468*	0.428	0.482*	−0.729**	0.443		
YSI	−0.773**	0.712**	−1.000**	−0.249	−0.234	−0.255	−0.928**	−0.271	0.713**	

*, ** significant at 5 and 1% probability level, respectively.

results are consistent with those reported by Fernandez (1992) in mungbean; Shirinzadeh *et al.* (2010) in corn; Mahajan *et al.* (2012) in Rice; Darvishzadeh *et al.* (2010) and Safavi *et al.* (2015) in Sunflower. The present study confirmed that stress tolerance index (STI), mean productivity (MP), Geometric mean productivity (GMP), harmonic mean (HM) and yield index (YI) exhibited a high correlation with seed yield in either environment. These indices were recognized as the best for selecting cultivars with high yield potential in either of the stress or non-stress environments.

Multivariate analysis

Principal Component Analysis (PCA) is one way to compress data sets of high dimensional vectors into lower dimensional ones. PCA revealed that the first PC (PCA1) explained 52.76 % of the total data variation and was positively correlated with performance under both stressed and non-stressed environments (Table 5). Thus, the first dimension represents yield potential and drought tolerance. In other words, this component was able to separate the cultivars with higher yield under both stressed and non-stressed conditions. The second PC (PCA2), which explained 44.60 % of total data variation, had a positive and high correlation with SSI but a negative correlation with yield under stressed conditions (Table 5). Therefore, the stress susceptibility dimension was able to separate the drought-

Table 5: 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	5.27	4.46
2	Percentage of variance	52.76	44.60
3	Cumulative percentage	52.76	97.36
4	Yp	0.41	−0.07
5	Ys	−0.05	0.46
6	DSI	0.32	−0.30
7	GMP	0.35	0.26
8	MP	0.35	0.25
9	HM	0.34	0.27
10	TOL	0.32	−0.30
11	STI	0.36	0.25
12	YI	−0.05	0.46
13	YSI	−0.32	0.30

Yp: yield in normal environment, Ys: yield in stress environment and drought stress indicators.

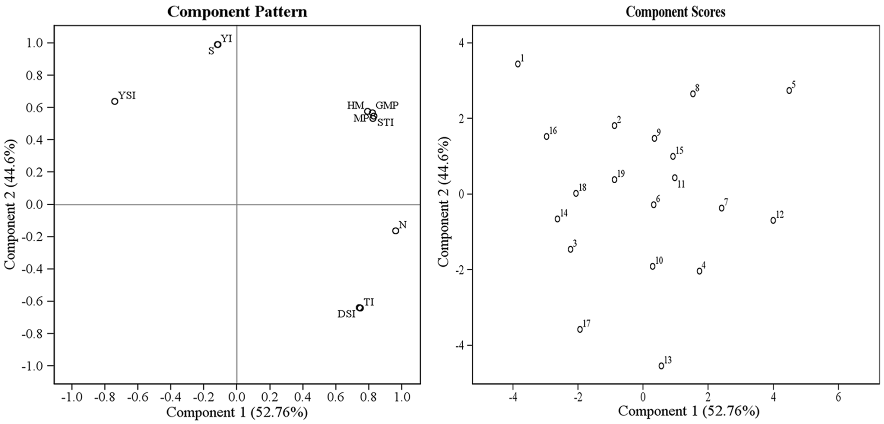

Figure 1: Screening drought tolerance indicators using biplot analysis (a and b).

susceptible genotypes. Hence, selection of genotypes that have high PCA1 and low PCA2 are suitable for both stressed and non-stressed conditions. Khodarahmpour *et al.* (2011) revealed that genotypes with larger PCA1 and lower PCA2 scores gave high yields (stable genotypes), and genotypes with lower PCA1 and larger PCA2 scores had low yields (unstable genotypes). The use of a biplot show in selecting drought-tolerant genotypes has already been used by Khodarahmpour *et al.* (2011) in maize and Mohammadi *et al.* (2010) in wheat.

Biplot indicated that the genotypes E002-91A, PRUN-29A, PHIR-27A and CMS-XA are very close in the vicinity of the vectors of drought tolerance indices, namely GMP, STI, MP and HM very close. These genotypes had the highest seed yield in drought stress conditions, and the highest yield stress of genotypes CMS-XA, respectively. On the other hand, there was genetic variability among the parental lines based on their drought resistance indices. Using important resistance indices comprising MP, GMP, TOL, YI and STI, genotypes were clustered using the unweighted pair group method with arithmetic mean classification and four clusters were established that paralleled the results of the biplot analysis (Figure 1a to 1b). It might not be possible to introduce a genotype which has high seed yield into a non-stress environment while maintaining high tolerance to drought stress. However, it is possible to introduce relatively ideal genotypes using these criteria. Following this line of thought, cluster analysis grouped the sunflower cultivars into groups based on their important resistance indices comprising MP, GMP, TOL, YI and STI (Figure 2).

Dendrogram of genotypes based on ranks of drought resistance indices and seed yield of stress and non-stress conditions according to a hierarchical

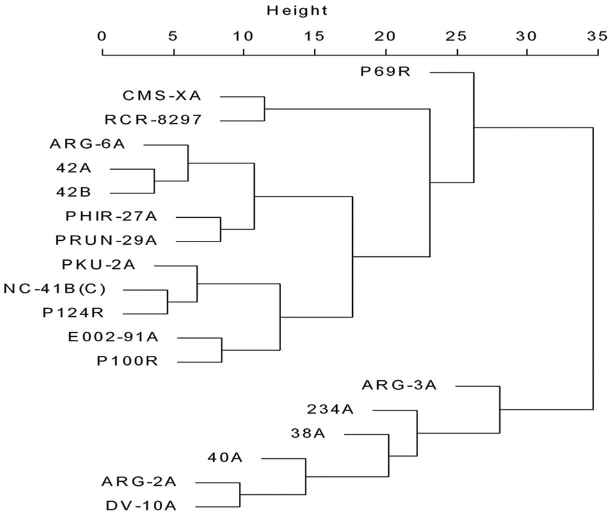

Figure 2: Dendrogram from cluster analysis based on drought tolerance indices and seed yield of sunflower parental lines in both normal and stress environment.

clustering method (Figure 2), grouped the 19 sunflower parental lines within 4 clusters, each of which having 12, 5, 1 and 1 of inbred lines, respectively. Group I was comprised of genotypes that had low yield in normal state and had high seed yield under stress environments. Hence, genotypes in to these groups could be stable in stressed state and considered as group C (Table 3). Group II comprised genotypes that had low yield in stressed states. Hence, genotypes in to these groups could be stable in non-stressed state and considered as group B. Clustering results revealed that the Group IV genotype P69R locate in group D (low Ys and Yp) among all studied genotypes. Group III was included genotype ARG-3A from *H. argophyllus* that had highest value of STI, HM and GMP indices accompany by higher seed yield under both the environments respectively (Table 2) and located in Group A of Fernandez’s (1992). The classification based on cluster analysis and the similarity with biplot analysis was consistent with the findings of Darvishzadeh *et al.* (2010).

Conclusion

Conventional cms source *H. petiolaris* (PET-1) of sunflower has a narrow genetic background and is deficient in genes for water use efficiency and other abiotic stress. The diversity of wild sunflower species should be utilized to develop new elite cms sources, which offers breeders a diverse cytoplasmic gene pool from which to discover unique genes for resistance and tolerance to drought stress and water use efficiency. It can be further use in hybrid breeding programmes to develop a high yielding water use efficient hybrids.

Acknowledgements: This study is a part of Ph. D. thesis, ("Effect of Alien Cytoplasms on Heterosis and Combining Ability of Yield, Quality and Water Use Efficiency Traits in Sunflower (*Helianthus annuus* L.)"). Vikrant Tyagi thanks the Department of Science and Technology (DST), New Delhi, India for providing INSPIRE fellowship during this study. The authors are grateful to the Indian Institute of Oilseed Research, Hyderabad, India for providing the source material.

References

Bouslama, M., Schapaugh, W.T., 1984. Stress tolerance in soybean. Part 1: Evaluation of three screening techniques for heat and drought tolerance. Crop Science 24: 933–937.

Condon, A.G., Richards, R.A., Rebetzke, G.J., Farquhar, G.D., 2004. Breeding for high water- use efficiency. Journal of Experimental Botany 55: 2447–2460.

Darvishzadeh, R., Pirzad, A., Hatami Maleki, H., Poormohammad, K.S., Sarrafi, A., 2010. Evaluation of the reaction of sunflower inbred lines and their F1 hybrids to drought conditions using various stress tolerance indices. Spanish Journal of Agricultural Researcher 8: 1037–1046.

Dhillon, S.K., Tyagi, V., 2016. Combining ability studies for development of new sunflower hybrids based on diverse cytoplasmic sources. Helia 39(64): 71–80.

Fernandez, G.C.J., 1992. Effective selection criteria for assessing stress tolerance. In: proceedings of the international symposium on adaptation of vegetables and other food crops in temperature and water stress tolerance, Asian Vegetable Research and Development Centre, Taiwan, Pp. 257–270.

Fischer, R.A., Maurer, R., 1978. Drought resistance in spring wheat cultivars: I. Grain yield responses. Australian Journal Agricultural Researcher 29: 897–912.

Gavuzzi, P., Rizza, F., Palumbo, M., Campaline, R.G., Ricciardi, G.L., Borghi, B., 1997. Evaluation of field and laboratory predictors of drought and heat tolerance in winter and its components in wheat cultivars and landraces under near optimal and drought conditions. Euphytica 113: 43–52.

Jafari, A., Paknejad, F., Jami Al-Ahmadi, M., 2009. Evaluation of selection indices for drought tolerance of corn (*Zea mays* L.) hybrids. International Journal Plant Protection 3: 33–38.

Jan, C.C., 1990. In search of cytoplasmic male-sterility and fertility restoration genes in wild Helianthus species. p. 3–5. *In Proc. Sunflower Research Workshop, Fargo*, ND. 8–9 Jan. 1990. Natl. Sunflower Assoc., Bismarck, ND.

Khodarahmpour, Z., Choukan, R., Bihamta, M.R., Majidi Hervan, E., 2011. Determination of the best heat stress tolerance indices in maize (*Zea mays* L.) inbred lines and hybrids under Khuzestan province conditions. Journal Agricultural Sciences Technical 13: 111–121.

Kinman, M., 1970. New development in the USDA and State Experiment Station sunflower breeding programmes. Proc 4th Int Sunf Conf Memphis, Tennessee, USA, 181–183.

Leclercq, P., 1969. Une sterilite cytoplasmique chez tournesol. Annales Del Amelioration Des Plantes 19: 99–106.

Leclercq, P., 1971. La sterilite cytoplasmique du tournesol-1. premieres etudes sur la restoration de law fertile. Annales Del Amelioration Des Plantes 21: 45–54.

Mahajan, G., Timsina, J., Singh, K., 2012. Performance and water-use efficiency of rice relative to establishment methods in northwestern indo-gangetic plains. Journal of Crop Improvement 25: 597–617.

Mohammadi, R., Armion, M., Kahrizi, D., Amri, A., 2010. Efficiency of screening techniques for evaluating durum wheat genotypes under mild drought conditions. Journal Plant Products 4(1): 11–24.

Rosielle, A.A., Hamblin, J., 1981. Theoretical aspects of selection for yield in stress and non-stress environments. Crop Science 21: 943–946.

Safavi, S.M., Safavi, A.S., Safavi, S.A., 2015. Evaluation of drought tolerance in sunflower (*Helianthus annuus* l.) inbred lines and synthetic varieties under non stress and drought stress conditions. Biological Forum – An International Journal 7(1): 1849–1854.

SAS Institute, 1999. SAS Online Doc. v. 8. SAS Inst., Cary, NC.

Schilling, E.E., 1993. *Helianthus* verticillatus. *In:* Flora of North America Editorial Committee (editors) Flora of North America North of Mexico. Vol. 21. Oxford Univ. Press, New York and Oxford, pp. 51, 142.

Schilling, E.E., Heiser, C.B., 1981. Infrageneric classification of *Helianthus* (Compositae). Taxon 30: 393–403.

Schneiter, A.A., Miller, J.F., 1981. Description of sunflower growth stages. Crop Science 21: 901–903.

Seiler, G.J., Qi, L.L., Marek, L.F., 2017. Utilization of sunflower crop wild relatives for cultivated sunflower improvement. Crop Science 57: 1083–1101.

Serieys, H., 1992. Cytoplasmic effects on some agronomical characters in sunflower. Proceedings of the 13th International Sunflower Conference 2: 1245–1250.

Shirinzadeh, A., Zarghami, R., Azghandi, A.V., Shiri, M.R., Mirabdulbaghi, M., 2010. Evaluation of drought tolerance in mid and late mature corn hybrids using stress tolerance indices. Asian Journal Plant Sciences 9: 67–73.

Tyagi, V., Dhillon, S.K., 2014. Effect of different CMS sources on oil content and quality of sunflower hybrids under different irrigation regimes. Agriculture: Towards a New Paradigm of Sustainability 1: 285–289. Publishing by, Excellent Publishing House, Kishangarh, Vasant Kunj, New Delhi

Tyagi, V., Dhillon, S.K., 2015. Relationship between crop growth parameters and seed yield in *CMS* analogues in sunflower. Helia 38(62): 109–120.

Tyagi, V., Dhillon, S.K., 2016a. Water-use-efficient cytoplasmic male sterility analogs in sunflower. Journal of Crop Improvement 30(5): 516–525.

Tyagi, V., Dhillon, S.K., 2016b. Cytoplasmic effects on combining ability for agronomic traits in sunflower under different irrigation regimes. SABRAO Journal of Breeding and Genetics 48(3): 295–308.

Tyagi, V., Dhillon, S.K., 2017. Effect of alien cytoplasm on combining ability for earliness and seed yield in sunflower under irrigation and drought stress. Helia 40(66): 71–83.

Tyagi, V., Dhillon, S.K., Bajaj, R.K., Gupta, S., 2015a. Phenotyping and genetic evaluation of sterile cytoplasmic male sterile analogues in sunflower (*Helianthus annuus* L.). Bangladesh Journal of Botany 44(1): 23–30.

Tyagi, V., Dhillon, S.K., Bajaj, R.K., Kaur, J., 2013. Divergence and association studies in sunflower (*Helianthus annuus* L.). Helia 36(58): 77–94.

Tyagi, V., Dhillon, S.K., Gill, B.S., 2015b. Morphophysiological expression in *cms* analogues of sunflower (*Helianthus annuus* L.) under water stress environment. Electronic Journal of Plant Breeding 6(4): 1150–1156.

Warburton, M.L., Rauf, S., Marek, L., Hussain, M., Ogunola, O., Gonzalez, J.D.J.S., 2017. The use of crop wild relatives in maize and sunflower breeding. Crop Science 57: 1227–1240.