Egypt. J. Agron. **Vol. 41,** No. 2, pp. 79 - 91 (2019)

Assessment of Variability for Drought Tolerance Indices in Some Wheat (*Triticum aestivum* L.) Genotypes

Manal Hassan Eid[#], Samah Sabry
Botany Department, Faculty of Agriculture Suez Canal University, Ismailia, Egypt.

ESTIMATION of nine yield-based drought tolerance indices was studied in ten wheat genotypes and identification of best index and best drought tolerant genotype. Nine drought tolerance indices comprising stress tolerance index (STI), tolerance index (TOL), stress susceptibility index (SSI), geometric mean productivity (GMP), mean productivity (MP), harmonic mean (HAM), yield index (YI), yield stability index (YSI) and drought resistance index (DRI) were each estimated based on yield under non-stress (Yp) and stress condition (Ys). The results of the genetic analysis for all drought tolerance indices studied demonstrated that GMP, MP and HAM had less variation between phenotypic coefficients of variability and genotypic coefficient of variability corresponded to high heritability. GMP, MP and HAM were nominated as the best useful indices that looking for drought tolerant genotypes. Also, they had positive correlation with Yp and Ys. The genotypes 1, 6 and 10 were considered drought tolerant while genotypes 3, 4, 5, 7 and 9 as drought susceptible. Genotype 8 was identified as highly drought susceptible. The studied genotypes showed considerable variation in performance and tolerated various drought conditions that could be exploited in further investigation.

Keywords: Wheat, Drought indices, Genetic analysis, Tolerant genotype.

Introduction

Bread wheat (*Triticum aestivum* L.) is annual crop, self-pollinator and contains Genome Hexoploid (AABBDD). Wheat, ranking second among cereals, supplies nutrients to more than one billion of population (Mergoum et al., 2009 and Braun et al., 2010). The demand of wheat is anticipated to increase by 40% in next ten years (FAO, 2015).

Arid and semiarid areas adversely affected by drought environment that suffered from reducing more than 50% of yield crops (Jalilvandy & Mehdi, 2013). Plant breeders detected intensively for reliable and rapid method to combat drought problems. So, the researches on wheat to develop or introduce new superior genotypes or varieties that are very valuable (Subhani et al., 2012; Khan et al., 2013; Mahmood et al., 2013 and Aktas, 2016). These genotypes can tolerate serious drought stress without considerable reduction in grain yield. However, Talebi et al. (2009), Pireivatlou et al. (2010) and Koleva & Dimitrova (2018) recommended indictors naming "drought indices" for recognition of drought tolerant genotypes. Mitra (2001) considered that these indices represent drought stress measurement from the difference between grain yield under (Ys) stress and (Yp) non-stress (Clarke et al., 1984 and Huang, 2000).

Multiple drought tolerance indices were calculated based on the potential yield (Yp) under normal and yield (Ys) under water stress conditions. Many investigators used these indices in their studies (Guttieri et al., 2001; Saba et al., 2001; Braun et al., 2010; Nazari & Pakniat, 2010; Abdi et al., 2012; Ahmadizadeh et al., 2012 and Parchin et al., 2013). Although, drought tolerance indices have been manipulated in different crops (Richard, 1996; Sio-Se Mardeh et al., 2006 and Darvishzadeh et al., 2011), the genetic properties and consistencies of these indices are in needed to more studies (Arshadi et al., 2018 and Besufikad, 2019).

Genotypic coefficient of variance supplies

[#]Corresponding author email: eid_manl@hotmail.com
DOI: 10.21608/agro.2019.10401.1153

facts on the genetic variation display in quantitative traits in base population, but it is too difficult to define the quantity which was heritage. So the heritability measurements assist it to predict the improvement in the selection (Ene et al., 2016). Thus, the heritable portion of the variation could be more useful with help of heritability estimates. However, heritability is the proportion of observed phenotypic variation in a progeny that is influences by genetic effects (i.e. heritable) (Kearsey & Pooni, 1996 and Sleper & Poehlman, 2006). Heritability of a trait is influenced by the number of genes involved, the population and the environment. Altering one of these factors results in different estimates of heritability (Acquaah, 2007 and Besufikad, 2019). High heritability is leaded the traits to improve very easy and accelerate than low heritability. The traits with high heritability, their phenotypic variations are caused by genetic divergence between the genotypes. Whereas, the traits with low heritability, are less influenced by genetics components contrarian to environmental components. So that the traits will response slowly towards selection and will have low genetic gain in breeding (Falconer, 1989).

Correlation studies have identified drought indices associated with grain yield that may be effectively used to improve grain yield (Butler et al., 2005; Farshadfar & Javadinia, 2011 and Augustina et al., 2013)

This investigation was carried out in order to enhance efficiency of drought tolerance indices for recognizing the promising tolerant genotypes. This may provide good and reliable indicators for identification between sensitive drought and drought tolerance in wheat crops.

Materials and Methods

Field experiments were conducted at the Experimental Farm, Faculty of Agriculture Suez Canal University, Ismailia; Egypt during the two successive seasons (2015-2016) and (2016-2017). October 20 was the planting date for both seasons. Genetic material comprised ten wheat genotypes were kindly provided by Field Crops Research Institute, Agricultural Research Center, Egypt and International Center for Agricultural Research in the Dry Areas (ICARDA) and were used as plant material in this study. Pedigree and description of these genotypes are presented in Table1.

Supplemental irrigation was provided by sprinklers for two water regimes during plant growth. Drought was created by withholding irrigation after 30 days from sowing and giving two supplementary irrigations, after 60 and 90 days from sowing. Control treatment was well watered throughout the growing period as needed to minimize water shortage until 10 days prior to maturity. Water application was monitored via a water meter and the Control treatment (well-watered) received 420mm, while the drought experiment (severe stress) received 140mm. The experimental plot consists of 6 rows, 3m long with 5cm row to row. All agricultural practices were carried out as recommended for wheat production in this area.

TABLE 1. Pedigree and the origin of ten wheat genotypes.

Number	Genotype	Pedigree	Origin
1	Sahel 1	NS 732/PIMA//VEERY ‘’S”	Egypt
2	Giza 168	MIL/BUC/seriCM93046-8M-OY-OM-2Y-OB	Egypt
3	Gemmiza 9	Ald”S”/Huac”S”//CMH74A.630/5x CGM4583-5GM-1GM-0GM	Egypt
4	Sakha 69	NIA/RL4220//7C/YR”s”CM15430-2S-1S-0S	Egypt
5	Gemmiza 3	Bb/7c2//4504Kal315sk8/4/Rrv/ww15/3/Bj’’S’’//on3/Bon.Gm4024-1Gm-13Gm-oGm	Egypt
6	Rufom-5	ICD 85-0988- 6AB- TR- 3AB- OTR	ICARDA
7	Kavco-8	ICW 85- 0012- 300L-300AP-300L-OAP	ICARDA
8	Giza 163	T.aestivum/Bon//Cno/7c CM33009-F-15M-4Y-2M-1M-1M-1Y-0M	Egypt
9	Giza 167	AU/UP301//511/SX/3/Pew”S”/4/Mai”S”Mai	Egypt
10	Gemmiza 10	Maya 74 “S”/On//1160-147/3/Bb/4/Chat”S” /5/ctow.	Egypt

The experimental design used here is a randomized complete block design (RCBD) with three replicates. The experimental plot consisted of 6 rows, 3m long and 5cm apart in which grains were drilled by hand. The normal recommended agricultural practices of wheat production were applied at the proper time.

Statistical analysis

In order to consider susceptibility or tolerance ratio of genotypes to water stress and evaluated main criteria for wheat genotypes, nine indices were used as described below:

1-Stress tolerance index, STI= (Yp*Ys)/ $\bar{Y}p2$ (Fernandez, 1992).

2-Stress tolerance, TOL= Yp-Ys (Rosielle & Hamblin, 1981).

3-Stress susceptibility index, SSI= (1-(Ys/Yp)/ SI (Fischer & Maurer, 1978), where, the stress intensity, SI= 1− ($\bar{Y}s/\bar{Y}p$).

4-Geometric mean productivity, GMP= $\sqrt{(Ys \times Yp)}$ (Fernandez, 1992).

5-Mean productivity Index, MPI= Ys+Yp/2 (Hamblin, 1981)

6-Harmonic Mean, HARM= 2(YpxYs/Yp+Ys) (Fernandez, 1992)

7-Yield index, YI= Ys/$\bar{Y}s$) (Gavuzzi et al., 1997).

8-Yield stability index, YSI= Ys/ Yp (Bouslama & Schapaugh, 1984).

9- Drought resistance index, DI= Ys x (Ys/Yp)/ $\bar{Y}s$ (Lan, 1998).

where, Yp and Ys present the mean yield of genotype under non-stress and the mean yield of genotype under stress, respectively. $\bar{Y}p$ and $\bar{Y}s$ were total mean of grain yield for all genotypes under non-stress and stress conditions, respectively.

Rank sum, RS= Rank mean (R) + Standard deviation of rank (SDR) (Farshadfar et al., 2012 a).

Correlation analysis among indices and both grain yields under normal and stress conditions was measure. Cluster analysis of the genotypes based on yield in the non-stress and water stress conditions and based on nine drought indices was carried out using the average linkage algorithm and Euclidean distance measure.

Genetic components include genotypic variance ($б^2$ g) and phenotypic variance ($б^2$ p), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated using the method given by Syukur et al. (2012) whereas broad sense heritability (h^2bs) was analyzed according to Allard (1960). Genetic advance (GA) and the genetic advance as percentage of the mean (GAM) were calculated according to Johnson et al. (1955), GA= i h^2bs Vp, where i= 2.06 (5% selection intensity), Vp: the phenotypic standard deviation of the character, h^2bs: heritability. The genetic advance as percentage of the mean (GAM) %= GA/x– × 100. GA= genetic advance, and x– = Great mean of a character.

Results and Discussion

Mean performance of genotypes based on the tolerance indices

This study was conducted to reveal the right tolerance indices for testing of genotypes under drought environment, nine drought tolerance indices were estimated by means of the yield in non-stress and stress conditions (Table 2). The highest yield value (Yp) was recorded in genotype 10 followed by genotype 1 under non-stress condition. Similar trends were showed by both of two genotypes for Ys under stress condition. The lowest yield value was obtained in genotype 4 followed by genotype 3 under non-stress condition and in genotype 8 and genotype 7 under stress condition. The variation in Yp and Ys suggested the occurrence of important resources for getting drought tolerant genotypes under this study. The results are similar to those of Abdi et al. (2013).

STI ranged from 0.22 to 1.39; the higher values of up to 1 indicate high stress tolerance. Menezes et al. (2014) reported a high STI rate for the genotype represents its high drought tolerance and its high yield. Genotypes 10, 1 and 6 had the largest STI rate and Yp and Ys, indicating, they might be the best promising tolerant whereas genotype 8 showed the smallest STI rate (0.22) and grain yield (101.90) under stress condition. Mevlut & Sait (2011) considered that the genotypes with high STI normally have high difference in yield in stress and non-stress environment. These findings are in adherence to Farshadfar et al. (2013).

TOL was considered an efficient measurement to increase yield under drought environment (Fernandez, 1992). The highest TOL values were related to genotype 8, 9 and 7 (373.50, 269.70 and 253.30), respectively. Therefore, high amount of TOL is a sign of genotype susceptibility to stress (Parchin et al., 2013). While, genotypes 1 and 6 with low TOL values (75.30 and 76.40) were considered as tolerant genotypes. Similar results were found in those of Prakash (2007), Mahdi (2012) and Raman et al. (2012).

Regarding to SSI, Genotype 1 recorded the lowest value of 0.35 followed by genotype 6 (0.40) and could identify as the promising tolerant genotypes. Because of they revealed minor yield reductions under drought condition. These results are in harmony with Chauhan et al. (2007) and Kumar et al. (2014). However, the development of different genotypes in relation to time of drought stress or shortage of adjustment with difficult conditions might due to the reason of variation in SSI. Nerveless, Akbarabadi et al. (2015) expressed that it is not necessity to select genotypes tolerance based on this index high yield, but these genotypes have drought tolerance mechanism, that cause low yield difference between non-stress condition and stress condition. Genotypes 8, 9 and 7 with high SSI values (1.97, 1.45 and 1.45, respectively) can be considered drought susceptible. Similar results were found in those of Abdi et al. (2013) and Raman et al. (2012).

Genotypes with highest GMP and MP values and YI were preferred under stress conditions (Farshadfar & Javadinia, 2011). Therefore, based on these current indices, genotypes 10, 1 and 6 exhibited the highest value, indicating tolerant genotypes whereas genotype 8 was the most sensitive genotype. These results are in agreement with Koleva & Dimitrova (2018).

Regarding to the highest YSI values were recorded for genotypes 1, 6 and 10 (0.86, 0.83 and 0.70), respectively. These current genotypes had the same tend to DRI. These findings are cooperated with Karimizadeh & Mohammadi (2011) and Ghobadi et al. (2012).

TABLE 2. Mean values of drought tolerance indices and grain yield under non-stress and stress conditions (over two years).

Genotypes	Yp	Ys	STI	TOL	SSI	GMP	MP	HAM	YI	YSI	DRI
G1	553.90	478.60	1.23	75.30	0.35	514.87	516.25	513.50	1.73	0.86	1.49
G2	469.80	300.40	0.65	169.40	0.90	375.66	385.10	324.35	1.09	0.63	0.68
G3	363.70	208.90	0.35	155.80	1.07	275.63	286.30	265.37	0.75	0.57	0.43
G4	348.10	205.30	0.33	142.80	1.02	267.32	276.70	258.27	0.74	0.58	0.43
G5	410.20	230.60	0.43	179.60	1.10	307.55	320.40	295.23	0.83	0.56	0.46
G6	471.40	395.00	0.86	76.40	0.40	431.51	433.20	429.83	1.43	0.83	1.19
G7	434.00	180.30	0.26	253.70	1.45	279.73	307.15	254.76	0.65	0.41	0.26
G8	477.20	101.90	0.22	375.30	1.97	220.51	289.55	167.93	0.37	0.21	0.07
G9	461.20	191.50	0.41	269.70	1.45	297.18	326.35	270.62	0.69	0.41	0.28
G10	651.50	460.30	1.39	191.20	0.75	547.61	555.90	539.45	1.67	0.70	1.17

Yp: Grain yield under non-stress environment, Ys: Grain yield under stressed, STI: Stress tolerance index, TOL: Stress tolerance, SSI: Stress susceptibility index, GMP: Geometric mean productivity, MP: Mean productivity, HAM: Harmonic mean, YI: Yield index, YSI: Yield stability index and DRI: Drought resistance index.

Ranking method

Various indices presented different genotypes as drought tolerant (Table 3). Noticeably, it is argumentative to recognize the drought tolerant genotypes based on a single criterion. According to Farshadfar et al. (2012 a) who calculated mean rank and standard deviation of ranks of all drought tolerance indexes and identified the best favorable drought tolerant genotypes based on these two criteria. With respect to all indices, genotypes 1 (RS= 1.95), 6 (RS= 3.54) and 10 (RS= 3.98) were the most drought tolerant genotypes, respectively. Whereas, genotypes 8 (RS= 11.22), 7 (RS= 9.32) and 9 (RS= 8.84) were the most susceptible to drought stress (Table 3). The data are comforted with Mohammadi et al. (2011), Farshadfar et al. (2012 a, 2014) and Khalili et al. (2012).

Phenotypic, genotypic variances and coefficient of variability

The variations in crops divide into heritable and non-heritable such as phenotypic and genotypic variances and phenotypic and genotypic coefficients of variation. Therefore, recognizing the status of variability in crop species is vitally important since it supplies the base for selection. A wide range of variance was observed for all drought tolerance indices among ten wheat genotypes (Table 4). There is the presence of inherent genetic variation among the ten wheat genotypes. The observations revealed that genetic variance was less than phenotypic variance for all indexes indicating the environment might have effects on this experiment. ∂^2P and ∂^2G were greater under stress (13039.13 and 13032.83, respectively) than ∂^2P and ∂^2G under non-stress condition (7875.86 and 7861.37, respectively) for grain yield. This may be due to the effects of environment (Besufikad, 2019).

HAM had expressed high phenotypic and genotypic variance (14842.1 and 14829.14) followed by YS (13039.13 and 13032.83). STI recorded low phenotypic and genotypic variance (0.18 and 0.17) followed by YI (0.22 and 0.21). This result is consistent with Saba et al. (2001) and Darvishzadeh et al. (2011). The PCV values were ranged from 19.12% for Yp to 74.10% for DRI. Similarly, the GCV values ranged from 19.10% for Yp to 74.10 for DRI (Table 4). GCV was less than PCV for all indexes.

In some cases, GCV was near to PCV for Yp, Ys, TOL, SSI, GMP and HAM presenting the expression of these indices was influenced by genetic effects and they having potential to improve in further selection (Naeem et al., 2015). Since, PCV and GCV values greater than 20% are considered as high and values between 10% and 20% as medium, whereas values less than 10% are considered as low (Deshmukh et al., 1986). Therefore, this study documented that high PCV and GCV for all drought indices expect Yp had low PCV and GCV. Nevertheless, high values of PCV and GCV for drought indices implied the existence of greater magnitude of genetic variability and these indices might control by genetic factor. Therefore, selection may be effective based on these indices (Arshadi et al., 2018).

TABLE 3. Genotypes ranks, ranks mean (R^-), standard deviation of ranks (SDR) and rank sum (RS) of drought tolerance indices.

Genotypes	Yp	Ys	STI	TOL	SSI	GMP	MP	HAM	YI	YSI	DRI	R^-	SDR	RS
G1	2	1	2	1	1	2	2	2	1	1	1	**1.45**	**0.50**	**1.95**
G2	5	4	4	5	4	4	4	4	3	4	4	4.10	0.51	4.61
G3	6	6	7	4	6	7	9	7	6	6	6.5	6.36	1.15	7.51
G4	8	7	8	3	5	8	10	8	7	5	6.5	6.91	1.83	8.74
G5	10	5	5	6	7	5	6	5	5	7	5	6.00	1.48	7.48
G6	4	3	3	2	2	3	3	3	4	2	2	**2.82**	**0.72**	**3.54**
G7	9	9	9	8	8.5	6	7	9	9	8.5	9	**8.36**	**0.96**	**9.32**
G8	3	10	10	10	10	10	8	10	10	10	10	**9.18**	**2.04**	**11.22**
G9	7	8	6	9	8.5	9	5	6	8	8.5	8	**7.55**	**1.29**	**8.84**
G10	1	2	1	7	3	1	1	1	2	3	3	**2.27**	**1.71**	**3.98**

TABLE 4. Estimates of mean, phenotypic variation (σ^2P), genotypic variation (σ^2G), phenotypic coefficient of variation (σ P), genotypic coefficient of variation (σ G), coefficient of variation (%CV) heritability in broad sense (h2bs), genetic advance (GA) and genetic advance as percentage of the mean (GAM) for drought indices.

	Mean	σ^2P	σ^2G	σ P	σ G	%CV	h2bs	GA	GAM
Yp	464.10	7875.86	7861.37	19.12	19.10	33.10	99.82	182.50	39.32
Ys	275.28	13039.13	13032.83	41.48	41.47	71.84	99.95	235.11	85.41
STI	0.61	0.18	0.17	69.00	67.54	117.46	95.53	0.83	135.40
TOL	188.92	8312.21	8298.34	48.26	48.23	83.55	99.83	187.49	99.25
SSI	1.05	0.25	0.24	47.90	46.67	81.90	94.86	0.98	93.62
GMP	351.76	12479.18	12461.87	31.75	31.73	54.97	99.9	229.89	65.00
MP	396.69	10087.77	10072.29	27.17	27.15	47.03	99.84	206.56	55.88
HAM	331.93	14842.10	14829.14	36.71	36.69	63.56	99.91	250.74	75.75
YI	0.99	0.22	0.21	47.20	46.20	81.41	96.40	0.93	93.50
YSI	0.58	0.042	0.039	35.60	34.20	59.72	92.90	0.39	67.71
DR	0.65	0.23	0.22	74.10	73.10	136.53	97.00	0.01	1.55

The coefficient of variation (CV %) compares the relative amount of variability between crop plant traits (Sharma, 1988). DR was recorded the highest coefficient of variation (136%) followed by SST with 117.46%. Both of indexes might have higher amounts of exploitable genetic variability among the studied drought tolerance indices. As the results indicated, there is greater potential for favorable advance in selecting these indexes compared to others. Whereas, Yp showed the lowest CV% (33.10%). Consequently, Yp, has low exploitable genetic variability and less potential for favorable advance when compared to other indices. Likewise, Ys had greater variation (CV%= 71.84) than Yp (CV%= 33.10%). The difference between the values of CV% might due to the genotypic yields are right type for particular condition and non-right for other conditions (Mohammadi et al., 2011 and Farshadfar et al., 2013).

Broad sense heritability and genetic advance

Broad sense heritability contains additive and non-additive gene actions and plays useful role in expecting a good selection (Tazeen et al., 2009). Measurement of broad sense heritability in this study showed the reliability of drought tolerance indices as a guide to its genetic importance. Ys was recorded for the highest value of heritability with 99.5% whereas the smallest value (92.9%) was for YSI. The value of heritability was considered very high when it was greater than 80% (Singh, 2001).

Furthered, drought tolerance indices showed very high heritability indicating these indices affected by less environmental elements and selected easy because of high additive effect. Moreover, these superior heritability values were recorded in Table 4, indicated the possibility of improvement in the indices (Naeem et al., 2015; Besufikad, 2019 and Sumanth et al., 2017). These results are partially constant with Darvishzadeh et al. (2011) who demonstrated that MP, GMP, STI, HAM and YI have reasonable heritability and are capable to choose the genotypes with high yield in stress conditions. As consequence, Dashti et al. (2007) and Yue et al. (2005) investigated that effect of QTL on drought indexes varied from 4.90 to 36%.

It has been emphasized that without genetic advance, the heritability values would not be of practical importance and reliable in selection based on phenotypic appearance. So, genetic advance should be considered useful along with heritability in coherent selection breeding program (Sumanth et al., 2017 and Besufikad, 2019). The highest value of genetic advance was recorded for HAM, followed by Ys (250.74 and 235.11), respectively. This suggested the selection for best high yielding genotypes, 5% genotypes as parents are only, mean HAM of the offspring might improve a large value of 250.74 that mean genotypic value of new generation for HAM index will improve from 331.93 to 582.67. Similar trends to Ys, it will improve from 275.28 to 507.39. The observations were shown, GMP, MP and HAM had high genetic advance along with high heritability. Genetic advance with heritability have high values pointing together out that these indices are regulated by additive gene action. This result is consistent with Rameeh (2012), Hamdi et al. (2013) and Tahmasebpour (2013).

Whereas, YI, YSI and DRI had low genetic advance along with high heritability indicated that the effects of environments are greater more than the effects of genetics. Because of the three indices will not useful for further selection (Ene et al., 2016 and Besufikad, 2019).

Moreover, genetic advance as percent of the mean (GAM) varied from 1.55% to 135.40% for DRI and STI, respectively. The highest value of GAM joint to high heritability was recorded for STI indicated that improvement in this index is possible through mass selection and progeny selection (Hosseini et al., 2012 and Naeem et al., 2015).

Correlation analysis

The correlation coefficients between Yp, Ys and drought tolerance indices were estimated and identified the best drought index. In addition to it could be an acceptable indicator for choosing the most promising genotypes. Table 5 presented STI, GMP, MP, HAM, YI, YSI and DRI had positive correlation with Yp and Ys. According to Blum (1988) indicated the favorable index has positive correlation with yield under stress and non–stress environments. Therefore, these results might be fruitful for choosing good drought indices. However, Yp and Ys had significantly positive correlation (0.70). Tanner & Sinclair (1983) explained the reason for positive correlation between yield under normal and stress conditions was that the efficiency of water-use remained the same and not varied with change in water availability.

Yp had positive correlation with each of STI (0.84), GMP (0.81), MP (0.89), HAM (0.76), YI (0.71), YSI (0.33) and DRI (0.63).These indices were suitable for selection genotypes in non-stress condition. Where, TOL and SSI correlated negatively with Yp, (-0.02 and -0.032, respectively).These findings are in consensus of results of Toorchi et al. (2012) and Naghavi et al. (2013). Similarly, Ys had significantly positive correlation with STI (0.97), GMP (0.98), MP (0.95), HAM (0.99), YI (0.99), YSI (0.90) and DRI (0.98). Moreover, these indices reflected greater yield performance under stress than non-stress condition. In addition to they were suitable for survey of drought tolerance and more applicable in recognizing the genotypes with high yield under stress conditions. The data is in harmony with Khalili et al. (2012). On other hand, there were significantly negative correlations between Ys with TOL (-0.72) and SSI (-0.90).

STI had positive correlation with GMP, MP and HAM and so STI could include similar information as GMP had significantly positive correlation with Yp and Ys. This correlation with Yp (0.81) was less than Ys (0.98). Exceptionally, TOL correlated positively with SII (0.95) and they could recognition the same information (Nandan et al., 2010 and Ajayi et al., 2014).

This study showed that YSI has higher positive correlation with Ys (0.90) than with Yp (0.33). These observations are disagreed with Abdi et al. (2013) who recorded negative correlation was only in YSI with Yp while positive correlation was in YSI with Ys. Nerveless, Falahi et al. (2011) recommended that choosing genotypes with high yield stress and a poor performance in normal conditions for drought breeding program. Over all, STI, GMP, MP and HAM could be better predictor of Yp and Ys. These findings were reliable with those recorded by Khakwani et al. (2011) and Farshadfar et al. (2012 b). In General, the observations showed negative correlation between sensitivity indices and tolerance indices as well as grain yield under non-stress and stress conditions. Since the genotypes with smaller amounts of sensitive indicators and tolerance to stress, known as tolerant genotypes selection based on these indices genotypes1, 6, and 10 are tolerance to drought stress condition (Abdi & Taher, 2016).

Cluster analysis

Construction of dendrogram based on 9 drought tolerance indices and yield under non-stress and drought conditions was illustrated in Fig. 1. The ten wheat genotypes split into three main clusters (Fig. 1). Cluster I contained sensitively genotypes that had high values of stress susceptibility (TOL and SSI) and low values of tolerance indices and separated into two groups. First group comprised genotypes 3, 4 and 5. Second group contained genotype 7 and 9.

TABLE 5. Correlation coefficient among grain yield under non-stress and stress conditions and nine drought tolerance indices.

	YP	Ys	STI	TOL	SSI	GMP	MP	HAM	YI	YSI	DRI
YP	1										
Ys	0.70*	1									
STI	0.84*	0.97*	1								
TOL	**-0.02**	-0.72*	**-0.54**	1							
SS1	**-0.32**	-0.90*	-0.77*	0.95*	1						
GMP	0.81*	0.98*	0.99*	-0.59*	-0.80*	1					
MP	0.89*	0.95*	0.98*	**-0.46**	-0.71*	0.98*	1				
HAM	0.76*	0.99*	0.98*	-0.65*	-0.84*	0.99*	0.96*	1			
YI	0.71*	0.99*	0.96*	-0.72*	0.89*	0.98*	0.95*	0.98*	1		
YSI	**0.33**	0.90*	0.77*	-0.94*	0.99*	0.81*	0.72*	0.85*	0.90*	1	
DRI	0.63*	0.98*	0.93*	-.0.77*	0.92*	0.94*	0.90*	0.95*	0.98*	0.92*	1

* Significance at 5% level of probability.

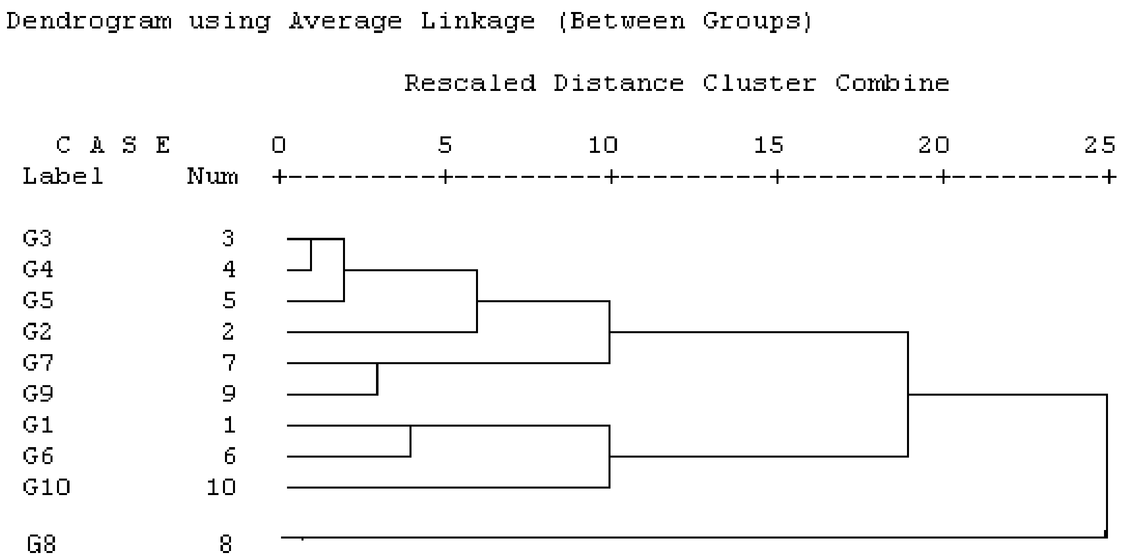

Fig. 1. Dendrogram of 10 wheat genotypes based on cluster analysis using 9 drought tolerance indices and yield under non-stress and stress conditions (Genotype codes: see Table .

Cluster II contained tolerant genotypes that had low value of stress susceptibility and high value of tolerance indices (genotype 1, 6 and 10). Where, genotype8 separated only in cluster III and considered very sensitivity genotype. Based on the result of the cluster analysis and comparison of the means, it was shown that cluster II expressed the best drought sensitive/tolerance indices. This implies that selecting for those indices will provide preference of the genotypes in this cluster over others (Ene et al., 2016). However, this classification was in paralleled with the results of Farshadfar et al. (2012 b).

Conclusion

To present the main points of drought tolerance indices concisely that GMP, MP and HAM had less variation between phenotypic coefficients of variability and genotypic coefficient of variability corresponded to high heritability. They can be used as an option for each other to choose drought tolerant genotypes with high yield performance in various environments. According to all different statistical procedures, the genotypes 1, 6 and 10 could be considered as three promising drought tolerant genotypes with high and stable yield under non-stress and stress conditions while genotypes 3, 4 5 7 and 9 could be considered drought susceptible. Genotype 8 was identified as highly drought susceptible. So this genotype is not suitable for drought stress condition. The results of this study recommended GMP, MP and HAM to make good selection and to construct genetic mapping of drought tolerance in wheat breeding program.

References

Abdi, H., Azizov, E., Bihamta, M.R. and Chogan, R. (2012) Assessment and determination of the most suitable drought resistance index for figures and advanced lines of bread wheat. *Inter. J. Agri. Sci.* **2**(1), 78-87.

Abdi, N., Darvishzadeh, R. and Maleki, H. (2013) Effective selection criteria for screening drought tolerant recombinant inbred lines of sunflower. *Genetika,* **45,** 153-166.

Abdi, H. and Taheri, M. (2016) Study of drought tolerance in bread wheat cultivars using biplot. *Int. J. Life. Sci. Scienti. Res.* **2**(6), 651-657.

Acquaah, G. (2007) "*Principles of Plant Genetics and Breeding*". Blackwell Publishing Ltd, Malden, USA.

Ahmadizadeh, M., Valizadeh, M., Shahbazi, H. and Nori, A. (2012) Behavior of durum wheat genotypes under normal irrigation and drought stress conditions in the greenhouse. *Afr. J. Biotechnol.* **11**(8), 1912-1923.

Ajayi, A.T. Adekola, M., Taiwo, B. and Azuh, V. (2014) Character expression and differences in yield potential of ten genotypes of cowpea (*Vigna unguiculata* L. Walp). *Int. J. Plant Res*. **4**(3), 63-71.

Aktas, H. (2016) Drought tolerance indices of selected landraces and bread wheat (*Triticum aestivum* L.) genotypes derived from synthetic wheat. *Appl. Ecol. Env. Res.* **14**(4), 177-189.

Akbarabadi, A., Danial, K. and Abbas, R. (2015) Study of variability of bread wheat lines based on drought resistance indices. *Biharean Biologist*, **9**(2), 88-92.

Allard, R. (1960) "*Principles of Plant Breeding*". John Wiley and Sonc Inc., New York, USA.

Arshadi, A., Ezzat, K., Asgar, S. and Mehdi, Z. (2018) Application of secondary traits in barley for identification of drought tolerant genotypes in multi-environment trials. *Aust. J. Crop Sci.* **12**(01), 157-167.

Augustina, U., Iwunor, P. and. Ijeoma, O. (2013) Heritability and character correlation among some rice genotypes for yield and yield components. *J.of Plant Breed. Genet.* **1**, 73-74.

Besufikad, E. (2019) Genetic variability, heritability and expected genetic advance as indices for selection in soybean (*Glycine max* L. Merrill) varieties. *Amer. J. Life Sci.* **6**(4), 52-56.

Blum, A. (1988) "*Plant Breeding for Stress Environments*", pp. 38-78. Boca Raton, CRC Press.

Bouslama, M. and Schapaugh, W. (1984) Stress tolerance in soybean. Part 1: Evaluation of three screening techniques for heat and drought tolerance. *Crop Sci.* **24**, 933-937.

Braun, H., Atlin, G. and Payne, T. (2010) In: "*Climate Change and Crop Production*", Reynolds, C.R.P. (Ed.). CABI, London, UK.

Butler, D., Byrne, F., Mohammadi, V. and Chapman, P. (2005) Agronomic performance of *Rht* Alleles in a spring wheat population across a range of moisture levels. *Crop Sci.* **45**, 939-947.

Chauhan, J., Tyagi, M., Kumar, A., Nashaat, N. and Singh, M. (2007) Drought effects on yield and its components in Indian mustard (*Brassica juncea* L.). *Plant Breeding,* **126**, 399-402.

Clarke, M., Towenley-Smith, T. and McCaig, T. (1984) Growth analysis of spring wheat cultivars of varying drought resistance. *Crop Sci.* **24**, 537-541.

Darvishzadeh, R., Pirzad, A., Bernousi, I., Abdollahi, B.M. (2011) Genetic properties of drought tolerance indices in sunflower. *Acta Agriculturae Scandinavica, Section B - Soil & Plant Science*, **61**(7), 593-601.

Dashti, H., Yazdi-Samadi, B., Ghannadha, M. and Quarri, S. (2007) QTL analysis for drought resistance in wheat using doubled haploid lines. *Int. J. Agric. Biol*. **9**, 98-101.

Deshmukh, S., Basu, M.S. and Reddy, P. (1986) Genetic variability, character association and path analysis of quantitative traits in Virginia bunch varieties of ground nut. *Indian J. Agr. Sci.* **56**, 816-821.

Ene, O., Peter, E. and Christian, U. (2016) Studies of phenotypic and genotypic variation in sixteen cucumber genotypes. *Chil. J. Agr. Res.* **76**(13), 307-311.

Falahi, H., Jafarbai, J.and Sayedi, F. (2011) Evaluation of drought tolerance in durum wheat (*Triticum aestivum* L.) genotypes using drought tolerance indices. *Seed and Plant Impro. J.* **271**(1), 115-22.

Falconer, D. (1989) "*Introduction to Quantitative Genetics*". 3rd ed., Longman, London.

FAO (2015) Production and Protection Series http://www.fao.org/worldfoodsituation/csdb/en/?fb_

Farshadfar, E. and Javadinia, J. (2011) Evaluation of chickpea (*Cicer arietinum* L.) genotypes for drought tolerance. *Seed and Plant Impro. J.* **27**(4), 517-537.

Farshadfar, E., Rasoli, V., Da Silva Teixeira, J.A. and Farshadfar, M. (2011) Inheritance of drought tolerance indicators in bread wheat (T*riticum aestivum* L.) using a diallel technique. *Aust. J. Crop Sci.* **5**(7), 870-878.

Farshadfar, E., Bita, J. and Mostafa, A. (2012 a) Biplot analysis of drought tolerance indicators in bread wheat lanraces of Iran. *Int. J. Agr. Crop Sci.* **4-5**, 226-233.

Farshadfar, E., Elyasi, P. and Aghaee, M. (2012 b) *In vitro* selection for drought tolerance in common wheat (*Triticum aestivum* L.) genotypes by mature embryo culture. *Amer. J. Sci. Res*. **48**, 102-115.

Farshadfar, E., Mohammad, M. and Seyed, M. (2013) Assessment of drought tolerance in land races of bread wheat based on resistance/ tolerance indices. *Inter. J. Adv. Biol. and Biom. Res.* **1**(2), 143-158.

Farshadfar, E., Azadahe, S. and Mohammad, S. (2014) Screening landraces of bread wheat genotypes for drought tolerance in the field and laboratory. *Inter. J. Farm. Allied Sci*. **3**(3), 304-311.

Fernandez, G. (1992) Effective selection criteria for assessing plant stress tolerance. In: *Proceedings of the International Symposium on Adaptation of Vegetables and other Food Crops in Temperature and Water Stress*, Taiwan 13-16 August 1992, pp. 257-270.

Fischer, R.A. and Maurer, R. (1978) Drought resistance in spring wheat cultivars. *Aust. J. Agric. Res.* **29**, 897-912.

Gavuzzi, P., Rizza, F., Palumbo, M. and Ricciardi, G.L. (1997) Evaluation of field and laboratory predictors of drought and heat stress in winter cereals. *Can. J. Plant Sci.* **77**, 523-531.

Ghobadi, M., Mohammad, E., Danial, K. and Alireza, Z. (2012) Evaluation of drought tolerance indices in dryland bread wheat genotypes under post-anthesis drought stress. *IJFSB*, **6**(7), 1257-1261.

Guttieri, M.J., Stark, J.C., Brien, K. and Souza, E. (2001) Relative sensitivity of spring wheat grain yield and quality parameters to moisture deficit. *Crop Sci.* **41**, 327-335.

Hamdi, A., El-Ghareib, S. and Shafey, A. (2013) Genetic variability, heritability and expected genetic advance for earliness and seed yield from selection in lentil. *Egypt Journal of Agriculture Research*, **81**, 125-137.

Hosseini, S., Zeiniolabedin, T. and Hemmatollah, P. (2012) Analysis of tolerance indices in some rice (*Oryza sativa* L.) genotypes at salt stress condition. *IRJABS,* **3**(1), 1-10.

Huang, B. (2000) Role of root morphological and physiological characteristics in drought resistance of plants. In: "*Plant Environment Interactions*", R.E. Wilkinson (Ed.), pp. 39-64. Marcel Dekker Inc., New York.

Jalilvandy, A. and Mehdi, R. (2013) Assessment of drought tolerance indices in wheat genotypes. *Intl. J. Agri. Crop Sci*. **6**(7), 370-374.

Johnson, H., Robinson, H. and Comstock, R. (1955) Estimates of genetic and environment variability in Soybean. *Agron. J.* **47**, 314-318.

Karimizadeh, R. and Mohammadi, M. (2011) Association of canopy temperature depression with yield of durum wheat genotypes under supplementary irrigation and rain-fed conditions. *Aust. J. Crop. Sci.* **5**, 138-146.

Kearsey, J. and Pooni, H.S. (1996) "*The Genetical*

Analysis of Quantitative Traits", p. 52. Taylor and Francis, London and New York. .

Khakwani, A., Dennett, M. and Munir, M. (2011) Drought tolerance screening of wheat varieties by inducing water stress conditions. *Songklanakarin J. Sci. Technol.* **33**(2), 135-142.

Khalili, M., Naghavi, M. and Aboughadareh, A. (2012) Evaluating of drought stress tolerance based on selection indices in spring canola cultivars (*Brassica napus* L.). *Journal of Agricultural Science*, **4**(11), 78-85.

Khan, M., Shabbir, G., Akram, Z., Shah, M. and Iqbal, M. (2013) Character association studies of seedling traits in different wheat genotypes under moisture stress conditions. *Sabrao. J. Breed Genet.* **45**(3).

Koleva, M. and Dimitrova, V. (2018) Evaluation of drought tolerance in new cotton cultivars using stress tolerance indices. *Agrofor International Journal,* **3**(1), 11-17.

Kumar, S., Dwived, S.K., Singh, S.S., Lekshmy, J.H.A. and Elanchezhian, S.R. (2014) Identification of drought tolerant rice genotypes by analyzing drought tolerance indices and morpho-physiological traits. *Sabrao J. Breed Genet.* **46**(2), 217-230.

Lan, J. (1998) Comparison of evaluating methods for agronomic drought resistance in crops. *Acta Agriculturae Boreali Sinica,* **7**, 85-87.

Mahdi, Z. (2012) Evaluation of drought tolerance indices for the selection of Iranian barley (*Hordeum vulgare*) cultivars. *Afr. J. Biotechnol.* **11**(93), 15975-15981.

Mahmood, A., Mian, M. and Iqbal, M. (2013) Chakwal-50: A high yielding and disease resistant wheat variety for rainfed region. *J. Anim. Plant Sci.* **23**(3), 833-839.

Menezes, C., Ticona-Benavente, C.A. and. Cardoso, M.J. (2014) Selection indices to identify drought-tolerant grain sorghum cultivars. *Genet. Mol. Res.* **13**(4), 9817-9827

Mergoum, M., Singh, P.K, Anderson, J.A. and Pena, R. (2009) Spring wheat breeding. In: "*Hand Book of Plant Breeding (Cereals)*". Carena, M.J. (Ed), pp. 127-156. Springer Science.

Mevlut, A. and Sait, C. (2011) Evaluation of drought tolerance indices for selection of Turkish oat (*Avena sativa* L.) landraces under various environmental conditions. *Zemdirbyste.* **98**(2), 157-166.

Mitra, J. (2001) Genetics and genetic improvement of drought resistance in crop plants. *Curr. Sci. India,* **80**, 758-763.

Mohammadi, M., Karimizadeh, R. and Abdipour, M. (2011) Association of canopy temperature depression with yield of durum wheat genotypes under supplementary irrigation and rain-fed conditions. *Aust. J. Crop Sci.* **5**(4), 487-493.

Naeem, M., Ahmed, M. Noreen, S. and Shah, M. (2015) Estimation of genetic components for plant growth and physiological traits of wheat under normal and stress conditions. *Saarc J. Agri.* **13**(1), 90-98.

Naghavi, M., Alireza, A. and Marouf, K. (2013) Evaluation of drought tolerance indices for screening some of corn (*Zea mays* L.) cultivars under environmental conditions. *Not. Sci. Biol.* **5** (3), 388-393.

Nandan, R., Sweta S. K. and Singh. (2010) Character association and path analysis in rice (O*ryza sativa* L.) genotypes. *World Journal of Agricultural Sciences*, **6**(2), 201-206.

Nazari, L. and Pakniyat, H. (2010) Assessment of drought tolerance in barley genotypes. *J. Appl. Sci.* **10**, 151-156.

Parchin, R., Abdollah, N. and Farshadfar, E. (2013) Assessment of drought tolerance in genotypes of wheat by multivariate analysis. *World Applied Sciences Journal*, **22**(4), 594-600.

Pireivatlou, A.S., Masjedlou, B.D. and Aliyev, R.T. (2010) Evaluation of yield potential and stress adaptive trait in wheat genotypes under post anthesis drought stress conditions. *Afric. J. Agric Res.* **5**, 2829-2836.

Prakash, V. (2007) Screening of wheat genotypes under limited moisture and heat stress environments. *Indian J. Genet.* **67**(1), 31-33.

Raman, A., Verulkar, S., Mandal, N.P., Varrier, M. and Shukla, V.D. (2012) Drought yield index to select high yielding rice lines under different drought stress severities. *Rice,* **5**(31), 1-12.

Rameeh, V. (2012) Genetic parameters assessment of siliquae associated with stress indices in rapeseed cultivars. *Annales Universtitatis Mariae Curie – Sklodwskalublin - Polonia*, 35-44.

Richard, R.A. (1996) Defining selection criteria to improve yield under drought. *Plant Growth Regul.* **20**, 157-166.

Rosielle, A. and Hamblin, J. (1981) Theoretical aspects of selection for yield in stress and non-stress environments. *Crop Sci*. **21**(6), 943-946.

Saba, J., Moghaddam, M. and Ghassem, K. (2001) Genetic properties of drought resistance indices. *J. Agric. Sci. Technol.* **3**, 43-49.

Sharma, J.R. (1988). "*Statistical and Biometrical Techniques in Plant Breeding*", 432p. New Age International Limited Publishers, New Delhi, India.

Singh, B. (2001) "*Plant Breeding: Principles and Methods*", 6th ed., Kalyani Publishers, New Delhi, India.

Sio-Se Mardeh, A., Ahmadi, A. and Poustini, K. (2006) Evaluation of drought resistance indices under various environmental conditions. *Field Crop Res.* **98**, 222-229.

Sleper, D.A. and Poehlman, J.M. (2006) "*Breeding Field Crops*", 5th ed. Blackwell Publishing Professional, Ames, Iowa, USA.

Subhani, A., Tariq, M., Jafar, M.S., Latif, R. and Iqbal, M.S. (2012) Role of soil moisture in fertilizer use efficiency for rainfed areas- A Review. *Journal of Biology Agriculture and Healthcare*, **2**(11), 1-9.

Sumanth, V., Suresh, B. and Jalandhar, R. (2017) Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (*Oryza sativa* L.). *J. Pharmacogn. Phytochem.* **6**(4), 1437-1439.

Syukur, M., Sujiprihati, S. and dan Yunianti, R. (2012) Teknik, Pemuliaan Tanaman. Cet.1. Jakarta. Penebar Swadaya.

Tahmasebpour, B. (2013) The genetic evaluation of drought resistance indices and valuated traits in summer safflower cultivars. *Res. J. Chem. Env. Sci.* **1**(4), 32-36.

Talebi, R., Fayaz, F. and Naji, A.M. (2009) Effective selection criteria for assessing drought stress tolerance in wheat (*Triticum durum* Desf.). *General Appl. Plant Physiol.* **35**, 64-74.

Tanner, C.B. and Sinclair, T.R. (1983) Efficient water use in crop production: research or re-search? In: "*Limitations to Efficient Water Use in Crop Production*", H.H. Taylor, W.R. Jordan, T.R. Sinclair (Ed.), pp. 1-27. American Society of Agronomy.

Tazeen, M., Nadia, K. and Farzana, N. (2009) Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. *J. Food Agric. Environ.* **7**(3-4), 278-282.

Toorchi, M., Naderi, R., Kanbar, A. and Shakiba, M.R. (2012) Response of spring canola cultivars to sodium chloride stress. *Ann. Biol. Res*. **2**(5), 312-322.

Yue, B., Xiong, L., Xue, W., Xing, Y., Luo, L. and Xu, C. (2005) Genetic analysis for drought resistance of rice at reproductive stage in field with different types of soil. *Theor. Appl. Genet.* **11**, 1127-1136.

(Received 15/3/2018)
accepted 25/4/2018*)*

تقيم التباين لمؤشرات تحمل الجفاف فى بعض التراكيب الوراثية للقمح

منال حسن عيد، سماح صبرى
قسم النبات الزراعى – كلية الزراعة – جامعة قناة السويس – اسماعيلية – مصر.

تم تقيم تسعة مؤشرات تحمل الجفاف على أساس المحصول فى عشرة تراكيب وراثية للقمح وكذلك تحديد أفضل مؤشر و أفضل تركيب وراثى مقاوم للجفاف. احتوت 9 مؤشرات الجفاف على مؤشر تحمل الاجهاد (STI)، مؤشر التحمل (TOL)، مؤشر القابلية للإجهاد (SSI)، متوسط الإنتاج الحسابى (GMP)، متوسط الأنتاجية (MP)، متوسط التوافقية (HAM)، مؤشر المحصول الناتج (YI)، مؤشر ثبات المحصول الناتج (YSI)، مؤشر مقاومة الجفاف (DRI) و قد تم قياسهم على أساس المحصول (Ys) تحت ظروف الأجهاد وكذلك المحصول (Yp) تحت الظروف الطبيعية. أظهرت نتائج التحليل الوراثي لجميع مؤشرات تحمل الجفاف التي تمت دراستها أن GMP و MP و HAM لديهم فارق قليل بين معامل الأختلاف المظهري ومعامل الأختلاف الوراثي وذلك يتوافق مع التاثير الوراثى الكبير على تلك المؤشرات. أيضا تم التوصية بأن كلا من GMP و MP و HAM كأفضل المؤشرات المفيدة فى تحديد التراكيب الوراثية المقاومة للجفاف. هذا و قد اظهرت النتائج أن التراكيب الوراثية رقم 1، 6 و 10 مقاومة للجفاف في حين أن التراكيب الوراثية 3 و 4 و 5 و 7 و 9 غير مقاومة للجفاف. بينما التركيب الوراثى 8 كان شديد الحساسية الجفاف. أظهرت التراكيب الوراثية المدروسة تباينًا كبيرًا في الأداء وتحمل ظروف الجفاف المختلفة و التي يمكن الأستفادة منها في مزيد من البحث.