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Genetic Properties of Drought Tolerance Indices in Durum Wheat

Ismail Hussain Ali [1]

ABSTRACT

A full-diallel cross of five durum wheat genotypes was made and grains of 20 F1s and their five parents was planted in two separate experiments, rainfall (stress) and irrigated (non-stress) in order to study the genetic properties of drought tolerance indices in durum wheat. The results revealed that some parents exhibited positive and high general combining ability, while some hybrids showed specific combining ability for the majority of these indices. There is uni-directional dominant effect for all traits excluding grain yield under stress conditions (Ys), yield index (YI) and yield reduction ratio (Yr). Scattering in dominant allels distribution in parents were found for all traits. There is dominant case in some single hybrids barring others for (Ys), (YI), geometric mean productivity (GMP) and stress tolerance index (STI). The estimates of gene effects revealed the significant role of additive genetic component ($\hat{D}$) for Yr and STI. The non-additive component ($\hat{H}_1$) was higher as compared to ($\hat{D}$) and the dominant genetic component ($\hat{H}_2$) was recorded with low magnitude than ($\hat{H}_1$) for all the traits. The average degree of dominance ($\sqrt{H_1/D}$) has been >1 for all traits. The ratio of the symmetry of the frequency of dominant and recessive alleles in all gene location controlling traits ($H_2/4H_1$) is less than 0.25 for all traits except Ys. All traits have shown above unity value for the proportion of dominant and recessive genes among the parents (*KD/KR*). The narrow sense heritability ($H_{n.s.}$) was moderate for Yp (0.449), Ys (0.281) and MP (0.421), while high for remaining traits. Mid-parent heterosis was found to be positive for some hybrids in all traits. Mean productivity (MP), GMP, and STI were highly positive genetically correlated with each other as well as with Ys and grain yield under non-stress conditions (Yp).

Keywords: Durum wheat, Full-diallel cross, Drought tolerance indices, Genetic properties.

INTRODUCTION

Drought, is the most significant factor restricting plant production in majority of agricultural fields of the world. Several indices have been utilized to evaluate genotypes for drought tolerance based on grain yield such as geometric mean productivity (Fernandez, 1992), mean productivity (Rosielle and Hamblin, 1981), stress susceptibility index (Fischer and Maurer, 1978), stress tolerance index (Fernandez, 1992). According to Richards (1996), selection for yield automatically integrates all the known and unknown factors that contribute to drought resistance. These indices have been compared by some researchers (Fernandez, 1992, and Richard, 1996). The studies that were done on genetic properties to study drought tolerance indices on wheat in northern part of Iraq including Kurdistan region less than wanted, so reflected negatively on the development or derived new varieties of wheat in semi-arid areas which the rainfall is limited factor for the growth of wheat.

[1] College of Agriculture/Salahaddin University, Erbil, Iraq.
✉Dr.ismail@ymail.com
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Diallel analysis is useful in intersecting the suspect of the general combining ability (GCA) and the specific combining ability (SCA). The combining ability analysis can be conducted using the Griffing Method (Griffing 1956), whereas the Hayman method can be used to study the gene action, genetic components and heritability (Hayman 1954). On the other hand graphic analysis based on Jinks and Hayman (1953a) makes it possible to have access to the information such as average dominant degree, the ratio of distribution and dispersion of dominant and recessive alleles in parents, and the direction of dominance (Gilbert, 1958). Heritability of a quantitative trait serves as reliable estimate of the magnitude of variability and hence determines the efficiency of selection for that trait. Traits with high heritability are easier to be improved than those with lower heritability. Most cultivars in self-pollinated crops, such as wheat, are pure lines produced by selection methods following hybridization. Thus, selection is mainly based on the presence of additive genetic variance in these methods (Falconer and Mackay, 1996). In spring wheat landraces, Moghaddam *et al.,* (2000) showed that indices such as stress suscibtibily index (SSI) and tolerance index (TOL) were not efficient to be used in selecting genotypes with high yield in either potential stressed or nonstressed environments.

Understanding of genetic mechanism of drought tolerance is imperative to develop suitable wheat genotypes for the arid and semi-arid areas. This study aims at studing the genetic properties of drought tolerance indices in durum wheat.

MATERIALS AND METHODES

A full- diallel cross of 5 durum wheat (*Triticum durum* Desf.) genotypes (Table, 1) was made in the growing season 2010-2011 at the station of Directorate of Agricultural Researches / Erbil, Iraq located on 36^{o} 10' N Latitude, 43^{o} E longitude and 415 m above sea level. Grains of 20 F1s and their five parents were planted on 15 November 2011 in two independent experiments: under rainfall condition (stress) (173 mm precipitation) and under irrigated condition (non-stress) during the growing season 2011-2012 using Randomized Complete Block Design with three replications. Each experimental unit consisted of one single 2m rows (one per entry) spaced 20 cm apart and 10 cm between plants. Irrigation was performed in the non-stressed plots were irrigated at tillering, jointing, flowering and grain filing stage of irrigated water equivalent to 40 mm of fresh water. After harvest the grain yield was recorded for every plot.

Table 1. Name and pedigree of durum wheat varieties were used as parents in the study.

No.	Name	Pedigree
1	Simeto	Capeiti 8 / Valnova
2	Ofanto	Appulo / Adamello
3	Acsad 65	STORK CM 470-1M-2y-CMXGDAV2 490-AA'SS"
4	MIMAN	9/LDTUS-1 CDSS928207-1M-0Y-0M-0Y-2B-0Y
5	CRAKE	10 RISSA CDSS93 Y20-1Y-2Y-0B-0Y-2B-0B

The drought tolerance indices were calculated for every genotype using the corresponding non-stressed and stressed subplots in each block as follows:

1. Mean Productivity (MP) (Rosielle and Hamblin, 1981): $MP = \frac{Ys + Yp}{2}$
2. Geometric Mean Productivity (GMP) (Fernandez, 1992): $GMP = (Yp \times Ys)^{0.5}$
3. Yield Index (YI) (Gavuzzi *et al.,* 1997): $YI = Yp / \overline{Y}s$
4. Yield Reduction Ratio (Yr) (Golestani and Assad,

1998): $(Yr) = 1 - (Ys/Yp)$

5. Tolerance Index (TOL) (Rosielle and Hamblin, 1981): $TOL = Yp\_Ys$

6. Stress Tolerance Index (STI) (Fernandez, 1992):

$$STI = \frac{(Ys)(Yp)}{(\bar{Y}p)^2}$$

7. Yield Stability Index (YSI) (Bouslama and Schapaugh, 1984): $YSI = Ys/Yp$

8. Stress Susceptibility Index (SSI) (Fischer and Maurer, 1978):

$$SSI = \frac{1 - Ys/Yp}{SI};$$ where: SI = stress intensity = $1 - \bar{Y}s/\bar{Y}p$

Yp = yield of a genotype in a non-stressed environment, Ys = yield of a genotype in drought stressed environment, $\bar{Y}_p$ = mean yield in non-stressed environment and $\bar{Y}_s$ = mean yield in drought stressed environment.

Genetic statistical analysis: An ordinary analysis of variance was performed to determine whether the genotypic differences were significant for the characters under consideration or not. Then estimates of combining ability were computed by using the method as described by Griffing (1956) method I, random model. According this approach, the linear model equation is as follows:

$$y_{ijk} = M + g_i + g_j + S_{ij} + r_{ij} + 1/b\Sigma \Sigma e_{ijk} \quad \{i, j = 1,2,\ldots n; k = 1,2,\ldots b; l = 1,2\ldots c\}$$

Where, y_{ijk}=mean of $i \times j$th genotypes over k and i, g_i= general combining ability (*gca*) effect of *i*th parent, g_j= *gca* effect of *j*th parent, s_{ij}=specific combining ability effect, r_{ij}=reciprocal effect, $1/b\Sigma\Sigma e_{ijk}$ = mean error effect.

The GCA effects for the parents, SCA effects for the F_1 hybrids and reciprocal effects were calculated. Also estimations of variance for general and specific combining ability effects of the parents, heritability in narrow senses ($H_{n.s.}$) and heterosis over mid parents were computed according to equations that have been mentioned by Singh and Chaudhary (1985). Heterosis significant was tested using the following statistical t-test for each hybrid: $t(H) = H/\sqrt{V(H)}$. The variance of heterosis were calculated from the following equation: $V(H) = (3/2)(Mse/r)$.

The data also analyzed according to Hayman's approach (Hayman, 1954) (Table, 2). The underlying model in this analysis is:

$$y_{rs} = \mu + Jr + Js + Jrs + \int + \int r + \int s + \int rs + 2Kr + 2Ks + 2Krs$$

Where, y_{rs}=entry in *r*th row and s^{th} column, μ=grand mean, *Jr*=mean deviation of r^{th} parents from grand mean, *Jrs*=remaining discrepancy due to rs^{th} reciprocal sum, ∫=mean dominance deviation, ∫*r*=dominance deviation (additional) due to r^{th} parent, ∫*s*=dominance deviation (additional) due to s^{th} parent, ∫*rs*=remaining discrepancy in rs^{th} reciprocal sum, *2Kr*=difference when r^{th} line (row) is used as male and female, *2Ks*=difference when s^{th} line (column) is used as male and female, and *2Krs*= discrepancy in rs^{th} reciprocal differences.

In Hayman's approach, the total sum of squares is partitioned into various components, namely, a (additive), b non-additive (dominant), which is further subdivided into b_1, b_2 and b_3, *c* (maternal) and d (reciprocal differences other than *c*). Significance of test of item *a,* suggests the significance of additive effects of genes and of item *b*, the dominance effects. Significance of b_1 indicates that the dominance is unidirectional. It is in fact a comparison of mean of F_1 and the mid-parental value. Asymmetry of gene distribution is indicated by the item b_2, whereas item b_3 tests that part of dominance deviation which are not attributable to b_1 and b_2. Item c tests the presence of maternal effects whereas item *d* tests the reciprocal differences other than *c*. (Singh and Chaudhary, 1985).

Table 2. Analysis of variance according to Hayman's approach (Hayman, 1954).

SOV	df	SS	Constants
a	$n-1$	$\frac{\sum (y_{r.}+y_{.r})^2}{} - \frac{2y_{..}^2}{}$	$\int Ti$
b	$\frac{1}{2}n(n-1)$	$\frac{\sum (y_{rs}+y_{sr})^2}{} - \frac{\sum (y_{r.}+y_{.r})^2}{} + \frac{y_{..}^2}{}$	$\int Jrs$
b_1	1	$\frac{(y_{..}-ny_{.})^2}{}$	$\int$
b_2	$n-1$	$\frac{\sum (y_{r.}+y_{.r}-ny_{r})^2}{} - \frac{(2y_{..}-ny_{.})^2}{}$	r
b_3	$\frac{1}{2}n(n-3)$	$b-b_1-b_2$	rs
c	$n-1$	$\frac{\sum (y_{r.}-y_{.r})^2}{}$	Kr
d	$\frac{1}{2}(n-1)(n-2)$	$\frac{\sum (y_{rs}-y_{sr})^2}{2} - \frac{\sum (y_{r.}-y_{.r})^2}{2n}$	Krs
Total	n^2-1	$\sum y_{rs}^2 - \frac{y_{..}^2}{n^2}$	

Diallel cross analysis method developed by Hayman (1954), Jinks (1954), Jinks and Hayman (1953b) and applied by Singh and Chaudary (1985) was also used to determination gene action and genetic components of variation. Parameters used in this analysis were: $\hat{D}$, variation attributed to additive genetics effects: $\hat{F}$, determine the relative frequency of dominant to recessive alleles in the parental populations and the variation level over loci, which is positive displaying the important role of the frequency of dominant genes: $\hat{H}_1$, variation due to dominance genetics effects: $\hat{H}_2$, variation due to dominance genetics effects corrected for gene distribution: $\hat{h}^2$, indicated the dominance effects due to heterozygous loci: The value of $\sqrt{H_1/D}$, is the measure of average degree of dominance, which is equal to one when the dominance is complete: $\overline{p}\overline{q}=H_2/4H_1$, is the frequency product at loci exhibited dominance: *KD/KR* is the ratio of dominant to recessive alleles in all parents: h^2/H_2, measures the number of groups of genes which control the trait and exhibited dominance and $\hat{E}$, is expected environmental component of variation. Information about gene action was inferred by plotting the covariance (Wr) of each array against its variance (Vr). The slope and position of the regression line fitted to the array points within the limiting parabola indicated the degree of dominance and the presence or absence of gene interaction. Array variances and co-variances were used to draw a regression line within the limiting parabola. The distance between the origin and the point where the regression line cut the Wr-axis provides a measure of average degree of dominance are: Partial dominance, when the intercept is positive;

complete dominance, when the line passed through the origin; over dominance, when the intercept is negative and no dominance, when the regression line touched parabola limits (Adel and Ali, 2013). Finally, genetic correlation (*rG*) between studied characters was calculated according to the following equation that has been mentioned by Walter (1975). $rG = \sigma G_x G_y / \sqrt{\sigma^2 G_x . \sigma^2 G_y}$. Where, $\sigma G_x G_y$ is the genetic covariance between x and y traits; $\sigma^2 G_x$, $\sigma^2 G_y$ is the genetic variance of x and y trait, respectively.

RESULTS AND DISCUSSION

1. Parents, F1 and reciprocals performance: Means for drought tolerance indices were significantly varied among genotypes and their crosses for grain yield (Yp and Ys) and all drought tolerance indices. According to the mean values, Yp, Ys, MP, GMP, YI, Yr, TOL, STI, YSI and SSI were 18.279, 6.821, 12.550, 11.045, 1.000, 0.612, 11.457, 6.790, 0.388, and 0.976, respectively (Table, 3). Comparison of means showed that under non-stressed conditions genotypes [5×3, 5×4, and 2×5] with averages 23.530, 23.000 and 22.500, respectively and parent [3] with average 12.833 g/plant have the maximum and the minimum grain yield per plant among genotypes. Also, under drought stress conditions genotypes [3×4, and 1×4] with average 10.000 and 9.300, respectively have the maximum grain yield and genotype [2×3] with average 4.787 g/plant have the minimum among the genotypes. Genotypes [5×3, 5×4, and 3×4] had the highest mean production (MP) and geometric performances mean (GMP), and parents [3, and 4], respectively had the least amount of these indices. The highest YI (1.464) were observed for genotype [3×4]. Genotypes [4×2, 2×5 and 3×2] had the high values of SSI and TOL. Genotypes with higher SSI and TOL values showed the great variation of a grain yield under non-stress compared with grain yield under stress conditions, while the genotypes which have less amount of these drought indices such as genotypes [1×5, 4×1, and parent 3] shows the less variation of a grain yield under non-stress and stress conditions; this result reflected positively on the value of yield reduction ratio (Y_r). So, in this case the genotypes will have less yield decrease in stress condition compared to non-stress condition (Rosielle and Hamblin, 1981). The highest stress tolerance index STI (10.598, 9.930, and 9.860) were observed for Genotypes [3×4, 5×4, and 5×3], respectively. Fernandez (1992) declared that STI is able to separate the genotypes which have a high yield and are tolerated against drought stress. The highest YSI (0.608 and 0.531) were observed for genotypes [1×5 and parent 5], respectively. It is depicted from these results that highest value of TOL, larger the yield reduction under stress conditions and more drought susceptible. The genotypes which have a little value of TOL give more yields under stress condition compared with other genotypes than non-stress conditions. The ranks of the genotypes for MP, HM, GMP and STI were almost identical (Anwar *et al.,* 2011).

Table 3. Mean performance of parents and hybrids for (Yp), (Ys) and drought tolerance indices.

	Yp	Ys	MP	GMP	YI
Parents					
1	15.9	5.913	10.907	9.668	0.867
2	14.633	6.973	10.803	10.057	1.019
3	12.833	6.477	9.655	9.115	0.951
4	16.067	5.127	10.597	9.044	0.751
5	15.333	8.133	11.733	11.162	1.193
F1 hybrids					
1 × 2	15.267	6.767	11.017	10.147	0.994
1 × 3	16.833	6.567	11.700	10.506	0.965
1 × 4	17.800	9.300	13.500	12.800	1.400
1 × 5	14.533	8.800	11.667	11.282	1.286
2 × 3	19.567	4.787	12.177	9.612	0.700
2 × 4	20.033	6.500	13.267	11.410	0.955
2 × 5	22.500	6.067	14.283	11.654	0.887
3 × 4	19.600	10.000	14.800	13.907	1.464
3 × 5	18.167	8.333	13.250	12.277	1.220
4 × 5	15.200	7.433	11.317	10.605	1.090
Reciprocals					
2 × 1	22.233	6.250	14.242	11.777	0.917
3 × 1	18.467	6.200	12.333	10.699	0.910
4 × 1	14.867	5.873	10.370	9.341	0.862
5 × 1	19.400	5.100	12.250	9.932	0.748
3 × 2	21.933	5.747	13.840	11.216	0.841
4 × 2	22.433	5.540	13.987	11.143	0.812
5 × 2	17.033	7.247	12.140	11.109	1.063
4 × 3	19.800	5.937	12.868	10.827	0.876
5 × 3	23.533	7.633	15.583	13.402	1.120
5 × 4	23.000	7.867	15.433	13.448	1.154
Grand mean	18.279	6.821	12.550	11.045	1.000
L.S.D 1%	3.056	1.386	1.586	1.359	0.196

Yp=Grain yield ander non-stress conditions; Ys=Grain yield under stress conditions; MP=mean prductivity; GMP= Geometric Mean Productivity; YI= Yield Index.

(Continued)

	Yr	**TOL**	**STI**	**YSI**	**SSI**
Parents					
1	0.622	9.987	5.127	0.378	0.991
2	0.518	7.660	5.561	0.482	0.826
3	0.494	6.357	4.549	0.506	0.788
4	0.678	10.940	4.520	0.322	1.082
5	0.469	7.200	6.825	0.531	0.748
F1 hybrids					
1 × 2	0.553	8.500	5.636	0.447	0.882
1 × 3	0.609	10.267	6.056	0.391	0.971
1 × 4	0.500	8.500	9.000	0.500	0.700
1 × 5	0.392	5.733	7.042	0.608	0.626
2 × 3	0.749	14.780	5.064	0.251	1.194
2 × 4	0.675	13.533	7.127	0.325	1.076
2 × 5	0.729	16.433	7.460	0.271	1.162
3 × 4	0.471	9.600	10.598	0.529	0.752
3 × 5	0.539	9.833	8.272	0.461	0.859
4 × 5	0.505	7.767	6.154	0.495	0.806
Reciprocals					
2 × 1	0.717	15.983	7.593	0.283	1.144
3 × 1	0.664	12.267	6.277	0.336	1.059
4 × 1	0.604	8.993	4.782	0.396	0.964
5 × 1	0.736	14.300	5.420	0.264	1.173
3 × 2	0.738	16.187	6.930	0.262	1.177
4 × 2	0.753	16.893	6.798	0.247	1.200
5 × 2	0.574	9.787	6.754	0.426	0.916
4 × 3	0.701	13.863	6.445	0.299	1.118
5 × 3	0.675	15.900	9.860	0.325	1.077
5 × 4	0.657	15.133	9.930	0.343	1.048
Grand mean	0.612	11.457	6.790	0.388	0.976
L.S.D 1%	0.124	3.531	1.705	0.124	0.197

Yr= Yield Reduction Ratio; TOL=Tolerance Index; STI=Stress Tolerance Index;YSI= Yield Stability Index; SSI=Stress Susceptibility Index.

2. Combining ability: Combining ability analysis for Yp, Ys and different drought tolerance indices in durum wheat exhibited significant differences for GCA (Table, 4). Parent [1] showed desirable GCA effects for grain yield under drought (Ys) and for GMP, YI, STI and YSI susceptibility indices, while parent [2] had desirable effects for grain yield under non-stress condition (Yp) and for Yr, TOL and SSI indices. Parent [3] didn't show desirable effect for grain yield and susceptibility indices. Parent [4] showed desirable GCA effects for Yp and MP, GMP, Yr, TOL, STI, SSI indices while parent [5] showed positive effect for Ys and desirable effect for YI and YSI indices. The comparison of values revealed that parents with desirable GCA effect can be used as gene sources in plant breeding programs. The data regarding SCA effects presented in Table (5) showed that the crosses [1×3, 2×4 and 3×4] had desirable SCA effects for the (Yp, Mp, GMP, Yr, TOL, STI, SSI), (Yp, Mp, GMP, YI, Yr, TOL, SSI) and (Yp, Ys, Mp, GMP, YI, TOL and SSI), respectively, followed by crosses [1×2] and [1×4] which showed desirable

Table 4. Estimates of GCA effects for Yp, Ys and drought tolerance indices in a 5 × 5 diallel cross of durum wheat.

parents	Yp	Ys	MP	GMP	YI
1	-0.359*	0.286*	-0.036	0.150*	0.042*
2	0.395*	-0.493*	-0.049	-0.275*	-0.072
3	0.078	-0.006	0.036	0.023	-0.0003
4	0.561*	0.002	0.282*	0.159*	0.000
5	-0.675*	0.211*	-0.232*	-0.056	0.031*
$S.E.(g_i - g_{i'})$	0.162	0.074	0.084	0.072	0.010

Yp=Grain yield ander non-stress conditions; Ys=Grain yield under stress conditions; MP=mean prductivity; GMP= Geometric Mean Productivity; YI= Yield Index.

(Continued)

parents	Yr	TOL	STI	YSI	SSI
1	-0.021*	-0.645*	0.203*	0.021*	-0.033*
2	0.034*	0.888*	-0.354*	-0.034*	0.054*
3	0.002	0.084	0.070	-0.002	0.003
4	0.014*	0.559*	0.207*	-0.014*	0.023*
5	-0.029*	-0.886*	-0.125	0.029*	-0.047*
$S.E.(g_i - g_{i'})$	0.007	0.188	0.091	0.007	0.010

Yr= Yield Reduction Ratio; TOL=Tolerance Index; STI=Stress Tolerance Index;YSI= Yield Stability Index; SSI=Stress Susceptibility Index.

Table 5. Estimates of SCA effects for Yp, Ys and drought tolerance indices in a 5 × 5 diallel cross of durum wheat.

Crosses	Yp	Ys	MP	GMP	YI
1 × 2	0.819*	0.702*	0.761*	0.878*	0.104*
1 × 3	2.185*	-0.002	1.092*	0.737*	0.001
1 × 4	-1.065*	1.147*	0.041	0.594*	0.168*
1 × 5	-0.278	-0.368*	-0.323	-0.532*	-0.056
2 × 3	0.932*	-0.961*	-0.014	-0.5728	-0.140*
2 × 4	1.999*	-0.311*	0.844*	0.348*	-0.044
2 × 5	0.685*	-0.569*	0.058	-0.216	-0.084
3 × 4	1.849*	1.055*	1.452*	1.335*	0.153*
3 × 5	0.635	0.240	0.438*	0.476*	0.035
4 × 5	0.552	-0.193	0.180	0.043	-0.027
$S.E.(g_i - g'_j)$	0.398	0.181	0.207	0.177	0.026

Yp=Grain yield ander non-stress conditions; Ys=Grain yield under stress conditions; MP=mean prductivity; GMP= Geometric Mean Productivity; YI= Yield Index.

(Continued)

Crosses	**Yr**	**TOL**	**STI**	**YSI**	**SSI**
1 × 2	-0.020	0.116	1.1448	0.020	-0.032
1 × 3	0.049*	2.187*	0.895*	-0.049*	0.079*
1 × 4	-0.083*	-2.212*	0.667*	0.083*	-0.133*
1 × 5	0.003	0.090	-0.640*	-0.003	0.004
2 × 3	0.078*	1.893*	-0.751*	-0.078*	0.124*
2 × 4	0.054*	2.309*	0.319	-0.054*	0.086*
2 × 5	0.050*	1.255*	-0.190	-0.050*	0.080*
3 × 4	-0.023	0.793*	1.697*	0.023	-0.037
3 × 5	0.017	0.395	0.540*	-0.017	0.027
4 × 5	0.014	0.745*	0.001	-0.014	0.023
$S.E.(g_i - g'_j)$	0.016	0.460	0.222	0.016	0.026

Yr= Yield Reduction Ratio; TOL=Tolerance Index; STI=Stress Tolerance Index;YSI= Yield Stability Index; SSI=Stress Susceptibility Index.

SCA effects for (Yp, Ys, Mp, GMP, YI) and (Ys, GMP, YI, STI, YSI), respectively. Also crosses [2×3] and [2×5] showed desirable SCA effects for (Yp, Yr, TOl, SSI) and (Yp, Yr, TOL, SSI), respectively, followed by cross [3×5] for (Mp, GMP and STI), then a cross [1×5] for TOL only. The data in Table (6) showed that the cross [5×2] had a desirable reciprocal effects for (Yp, Mp, GMP, YI, Yr, TOL and SSI), and a crosses [4×1], [5×1] and [5×3] for (Ys, Mp, GMP, YI, STI, YSI), (Ys, GMP, YI, STI, YSI) and (Mp, GMP, YI, STI, YSI), respectively, then a cross (5×4) for Ys, YI, YSI and SSI and a cross [4×2] for Ys and YI. The significant result of GCA and SCA suggests that both additive and non-additive gene effects were involved in the expression of these indices. The results of combining ability revealed that the parents [1 and 4] proved as a best general combiner for a maximum number of traits (7 and 5 traits, respectively). These two parents can be used in hybridization program for obtaining desirable combinations, while in case of hybrids the results of SCA revealed that the hybrids [1×3, 2×4 and 5×2] had a best specific combiner in desirable direction for seven traits. Other researchers also obtained parents which showed desirable GCA and SCA or reciprocal effects of hybrids for different traits using different genotypes (Saba *et al.,* 2001 and Farshadfar *et al.,* 2011).

Table 6. Estimates of reciprocal effects for Yp, Ys and drought tolerance indices in a 5 × 5 diallel cross of durum wheat.

Reciprocals	Yp	Ys	MP	GMP	YI
2 × 1	-3.867*	-0.550*	-2.208*	-1.651*	-0.080*
3 × 1	-3.350*	-0.533*	-1.942*	-1.448*	-0.077*
4 × 1	0.383	1.010*	0.698*	0.839*	0.147*
5 × 1	-2.4338	1.850*	-0.292	0.675*	0.269*
3 × 2	-0.117	-0.575*	-0.346*	-0.607*	-0.088*
4 × 2	-1.200*	0.481*	-0.360*	0.133	0.071*
5 × 2	3.817*	0.097	1.957*	1.156*	0.013
4 × 3	-1.167*	2.127	0.480*	1.345*	0.311*
5 × 3	-0.15	1.067	0.458*	0.789*	0.155*
5 × 4	-3.517*	0.592*	-1.463*	-0.586*	0.087*
$S.E.(r_{ij}-r_{ij}')$	0.363	0.165	0.189	0.162	0.023

Yp=Grain yield ander non-stress conditions; Ys=Grain yield under stress conditions; MP=mean prductivity; GMP= Geometric Mean Productivity; YI= Yield Index.

(Continued)

Reciprocals	Yr	TOL	STI	YSI	SSI
2 × 1	-0.052*	-3.317*	-2.147*	0.052*	-0.083*
3 × 1	-0.033*	-2.817*	-1.902*	0.033*	-0.053*
4 × 1	-0.052*	-0.627	1.113*	0.052*	-0.083*
5 × 1	-0.172*	-4.283*	0.812*	0.172*	-0.274*
3 × 2	0.024	0.458	-0.691*	-0.024	0.038
4 × 2	-0.039*	-1.680*	0.164	0.0398	-0.062*
5 × 2	0.062*	3.720*	1.339*	-0.062*	0.099*

4 × 3	-0.134*	-3.293*	1.834*	0.134*	-0.213*
5 × 3	-0.063*	-1.2178	0.997*	0.063*	-0.100*
5 × 4	-0.106*	-4.108*	-0.719*	0.106*	-0.169*
$S.E.(r_{ij}-r_{ij}')$	0.015	0.420	0.203	0.015	0.023

Yr= Yield Reduction Ratio; TOL=Tolerance Index; STI=Stress Tolerance Index;YSI= Yield Stability Index; SSI=Stress Susceptibility Index.

3. Gene action:

A. Hayman analysis: Mean square values of the Hayman genetic analysis for Yp, Ys and drought tolerance indices are presented in Table (7). Component *a*, which is an estimation of additive variance and *b* which is non-additive (dominant) were significant (p=0.01) for all studied traits. Based on the method proposed by Hayman (1954), this component of variance was divided into *b1*, *b2*, *b3*. Component *b1* means the comparison of parents with crosses. Component *b1* has been significant for all traits excluding Ys, YI and Yr, which means that highly significant of this item displaying the importance of dominance effects (Uni-directional) while non- significant indicated the absence of directional dominance of the genes. Component *b2* shows the special heterosis of each parent. The significance of this component determines if the deviation of F_1 from the average parents changes from one parent to other parent. This happens when the frequency of dominant allele are different (Aghamiri *et al.,* 2012). This component was significant (p=0.05) for all traits, which means scattering in dominant allele's distribution for all traits. Important role of specific dominant deviation of genes was indicated by significant *b3* item. This component has been significant for Ys, GMP, YI and STI and non-significant for other traits. Significant *c* and *d* items indicated the presence of maternal and reciprocal effects, respectively. Those two components have been significant for all traits. Mather and Jinks (1982) reported that the advantage of ANOVA components Hayman method are their validity irrespective of whether there are maternal or reciprocal differences among the progeny families and whether the parental lines are a fixed sample or a random sample of a population of inbred lines.

Table 7. Analysis of variance for Yp, Ys and drought tolerance indices according to (Hayman, 1954) method.

SOV	df	Mean Squares				
		Yp	Ys	MP	GMP	YI
a	4	14.752**	5.558**	4.592**	4.437**	0.120**
b	10	32.238**	3.828**	8.920**	5.544**	0.083**
b_1	1	207.335**	1.652^{ns}	61.499**	28.638**	0.036^{ns}
b_2	4	24.544**	5.893**	4.701*	3.359*	0.126**
b_3	5	3.374^{ns}	2.612**	1.779^{ns}	2.674*	0.057**
c	4	29.719**	13.597**	8.262**	9.056**	0.288**
d	6	33.792**	2.443**	8.280**	3.504**	0.051**

SOV	df	Mean Squares				
		Yp	Ys	MP	GMP	YI
Total	24					
Ba	8	0.889	0.182	0.309	0.249	0.004
Bb	20	2.035	0.424	0.607	0.527	0.009
Bb_1	2	2.525	0.493	0.426	0.187	0.011
Bb_2	8	2.247	0.365	0.734	0.598	0.008
Bb_3	10	1.767	0.458	0.543	0.539	0.010
Bc	8	2.165	0.749	0.409	0.237	0.013
Bd	12	2.493	0.301	0.642	0.364	0.006

Yp=Grain yield ander non-stress conditions; Ys=Grain yield under stress conditions; MP=mean prductivity; GMP= Geometric Mean Productivity; YI= Yield Index.

(Continued)

SOV	df	Mean Squares				
		Yr	TOL	STI	YSI	SSI
a	4	0.025**	22.253**	7.084**	0.025**	0.062**
b	10	0.028**	36.453**	8.250**	0.028**	0.072**
b_1	1	0.058^{ns}	171.975**	40.735**	0.058**	0.147**
b_2	4	0.048**	42.070**	5.116*	0.048**	0.122**
b_3	5	0.007^{ns}	4.855^{ns}	4.260*	0.007^{ns}	0.017^{ns}
c	4	0.072**	53.585**	15.041**	0.072**	0.184**
d	6	0.024**	39.350**	5.536**	0.024**	0.062**
Total	24					
Ba	8	0.001	0.907	0.493	0.001	0.001
Bb	20	0.003	2.489	0.742	0.003	0.008
Bb_1	2	0.005	4.331	0.127	0.005	0.012
Bb_2	8	0.004	2.290	0.817	0.004	0.009
Bb_3	10	0.002	2.281	0.804	0.002	0.006
Bc	8	0.007	4.194	0.414	0.007	0.017
Bd	12	0.003	3.020	0.624	0.003	0.008

Yr= Yield Reduction Ratio; TOL=Tolerance Index; STI=Stress Tolerance Index;YSI= Yield Stability Index; SSI=Stress Susceptibility Index

B. Jinks -Hayman analysis: The components of variation and genetic constants: $\hat{D}$, $\hat{F}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{h}^2$, $\hat{E}$, $\sqrt{H_1/D}$, $\bar{p}\bar{q}=H_2/4H_1$, KD/KR, h^2/H_2 *and* $H_{n.s.}$ were computed based on values of statistical constants which are presented in Table (8); these statistical constants consists of variance of parent (i) and its offspring (Vp), mean variance of F_1 arrays ($\bar{V}r$), variance of means of F1 arrays ($V\bar{r}$), mean of covariance between parents and F_1 arrays ($\bar{W}r$) and different square between grand mean and mean of parents ($ML_1 - ML_0$), then by using the equations which are suggested by Ferreria (1988) we computed the components of variation and genetic constants and tests according to Singh and Choudhary (1985) method for further elaboration of the genetic system controlling the drought indices in durum wheat (Table, 9). The results revealed significant role of additive genetic component ($\hat{D}$) for the inheritance of Yr and STI. The positive values of $\hat{F}$ (mean of variance of additive and dominance effects) for all traits indicated that there were more dominant than recessive alleles regardless of positive or negative direction; in other words, this component indicates unequal distribution of dominant and recessive gene frequencies in the parents. The non-additive component ($\hat{H}_1$) was found to be important for the genetic control of all the traits except GMP and STI. Additive and non-additive genetic components were significant for all traits, except GMP, YI and STI. However, the relative magnitude of dominant component ($\hat{H}_2$) was higher as compared to additive component ($\hat{D}$) in all the traits, indicating the preponderance of dominant gene effects in controlling the inheritance of these traits. The genetic component ($\hat{H}_2$) was recorded with low magnitude than ($\hat{H}_1$) for all the traits, indicating that beneficial positive alleles are not proportional to that of deleterious negative alleles at all loci among parents. Non-significant value of ($\hat{h}^2$) for Ys, YI, STI, YSI and SSI indicated the absence of dominance effects due to heterozygous loci. Expected environmental component of variation E was found non-significant for all traits. The average degree of gene dominance ($\sqrt{H_1/D}$) has been >1 for all traits indicates that these traits were controlled by the over-dominance of genes and ample scope for heterosis breeding in durum wheat. The ratio of ($H_2/4H_1$) indicates the symmetry of the frequency of dominant and recessive alleles in all gene location controlling traits. This ratio is less than 0.25 for all traits except Ys. This amount of ratio indicates the unequal frequencies of dominant and recessive allele for this trait. The component (h^2/H_2) measures the number of groups of genes which control the trait and exhibited dominance. In our study, the value of genetic ratio (h^2/H_2) estimated for studied traits indicate that there has been at least one genetic group involved in the control of heredity. The component KD/KR measures the proportion of dominant and recessive genes among the parents. All traits have shown the values for this component above unity, indicating the role of dominant genes in the expression of these traits. The narrow sense heritability $H_{n.s.}$ was moderate for Yp, Ys and MP, while high for remaining traits, indicating that selection for improvement of these traits would be effective.

Table 8. Values of statistical constants values according to Jinks and Hayman (1953b) analysis for Yp, Ys and drought tolerance indices.

Statistics	Yp	Ys	MP	GMP	YI	Yr	TOL	STI	YSI	SSI
Vp	3.047	1.456	0.879	0.928	0.031	0.010	5.489	1.097	0.010	0.026
$\bar{V}r$	12.467	1.297	3.197	1.913	0.035	0.007	15.427	2.931	0.013	0.032
$\bar{W}r$	-0.580	0.331	0.132	0.330	0.006	0.001	-1.131	0.439	0.000	-0.001
$V\bar{r}$	0.834	0.450	0.401	0.574	0.018	0.001	1.754	0.966	0.004	0.009
$(ML_1 - ML_0)^2$	11.327	0.141	3.325	1.547	0.003	0.004	9.634	2.186	0.004	0.009

Yp=Grain yield ander non-stress conditions; Ys=Grain yield under stress conditions; MP=mean prductivity; GMP=Geometric Mean Productivity; YI= Yield Index; Yr= Yield Reduction Ratio; TOL=Tolerance Index; STI=Stress Tolerance Index;YSI= Yield Stability Index; SSI=Stress Susceptibility Index. *Vp* =variance of parent (*i*) and its offspring; $\bar{V}r$ =mean variance of F_1 arrays; $V\bar{r}$ =variance of means of F1 arrays; $\bar{W}r$ = mean of covariance between parents and F_1 arrays; $ML_1 - ML_0$ =different square between grand mean and mean of parents.

Table 9. Genetic constants, ratio of genetic parameters and heritability in narrow sense of (Yp), (Ys) and drought tolerance indices.

	Yp	Ys	MP	GMP	YI
$\hat{D}$	1.909 ± 1.880	1.056 ± 0.612	0.561 ± 0.493	0.638 ± 0.942	0.023 ± 0.024
$\hat{F}$	6.097 ± 4.606	1.140 ± 1.529	0.815 ± 1.231	0.302 ± 2.354	0.027 ± 0.059
$\hat{H}_1$	39.91* ± 5.08	4.64* ± 1.653	8.64* ± 1.331	4.857 ± 2.545	0.13* ± 0.064
H_2	33.27* ± 4.61	3.17* ± 1.499	7.16* ± 1.207	3.396± 2.308	0.065± 0.058
$\hat{h}^2$	22.65* ± 3.11	0.281 ± 1.012	6.65* ± 0.815	3.10* ± 1.558	0.006 ± 0.039
$\hat{E}$	0.660 ± 0.768	0.136 ± 0.250	0.178 ± 0.201	0.131 ± 0.385	0.003± 0.010
$\sqrt{H_1 / D}$	4.572	2.096	3.924	2.759	2.377
$\bar{p}\bar{q}=H_2/4H_1$	0.208	1.703	0.207	0.175	0.130
KD / KR	2.073	1.693	1.454	1.188	1.693
h^2 / H_2	0.739	0.065	1.023	1.048	0.067
$H_{n.s.}$	0.449	0.281	0.421	0.551	0.745

Yp=Grain yield ander non-stress conditions; Ys=Grain yield under stress conditions; MP=mean prductivity; GMP= Geometric Mean Productivity; YI= Yield Index.

(Continued)

	Yr	TOL	STI	YSI	SSI
$\widehat{D}$	0.007* ± 0.001	3.686 ± 2.924	0.71* ± 1.607	0.007 ± 0.004	0.018 ± 0.011
$\widehat{F}$	0.013* ± 0.003	11.554 ± 7.305	0.153 ± 4.015	0.016 ± 0.011	0.041 ± 0.027
$\widehat{H}_1$	0.026* ± 0.004	57.00* ± 7.898	7.538 ± 4.341	0.052* ± 0.011	0.131* ± 0.029
H_2	0.018*± 0.003	43.80* ± 7.163	5.074 ± 3.937	0.031* ± 0.010	0.080* ± 0.026
$\widehat{h}^2$	0.007* ± 0.002	19.27* ± 4.836	4.372 ± 2.658	0.0072 ± 0.007	0.0183 ± 0.018
$\widehat{E}$	0.001*± 0.0006	0.881± 1.194	0.205 ± 0.656	0.001 ± 0.002	0.003 ± 0.004
$\sqrt{H_1/D}$	1.927	3.932	3.258	2.726	2.697
$\overline{pq}=H_2/4H_1$	0.171	0.192	0.168	0.152	0.172
KD/KR	2.833	2.325	1.068	2.435	2.437
h^2/H_2	0.990	0.476	1.025	0.291	0.291
$H_{n.s.}$	0.722	0.546	0.531	0.709	0.709

Yr= Yield Reduction Ratio; TOL=Tolerance Index; STI=Stress Tolerance Index;YSI= Yield Stability Index; SSI=Stress Susceptibility Index. $\widehat{D}$ =variation attributed to additive genetics effects; $\widehat{F}$ =relative frequency of dominant to recessive alleles in the parental populations and the variation level over loci; $\widehat{H}_1$ = variation due to dominance genetics effects; $\widehat{H}_2$ =variation due to dominance genetics effects corrected for gene distribution: $\widehat{h}^2$ =dominance effects due to heterozygous loci; $\sqrt{H_1/D}$ =average degree of dominance; $\overline{pq}=H_2/4H_1$ =frequency product at loci exhibited dominance; *KD/KR* =the ratio of dominant to recessive alleles in all parents; h^2/H_2=number of groups of genes which control the trait and exhibited dominance; $\widehat{E}$ = expected environmental component of variation.

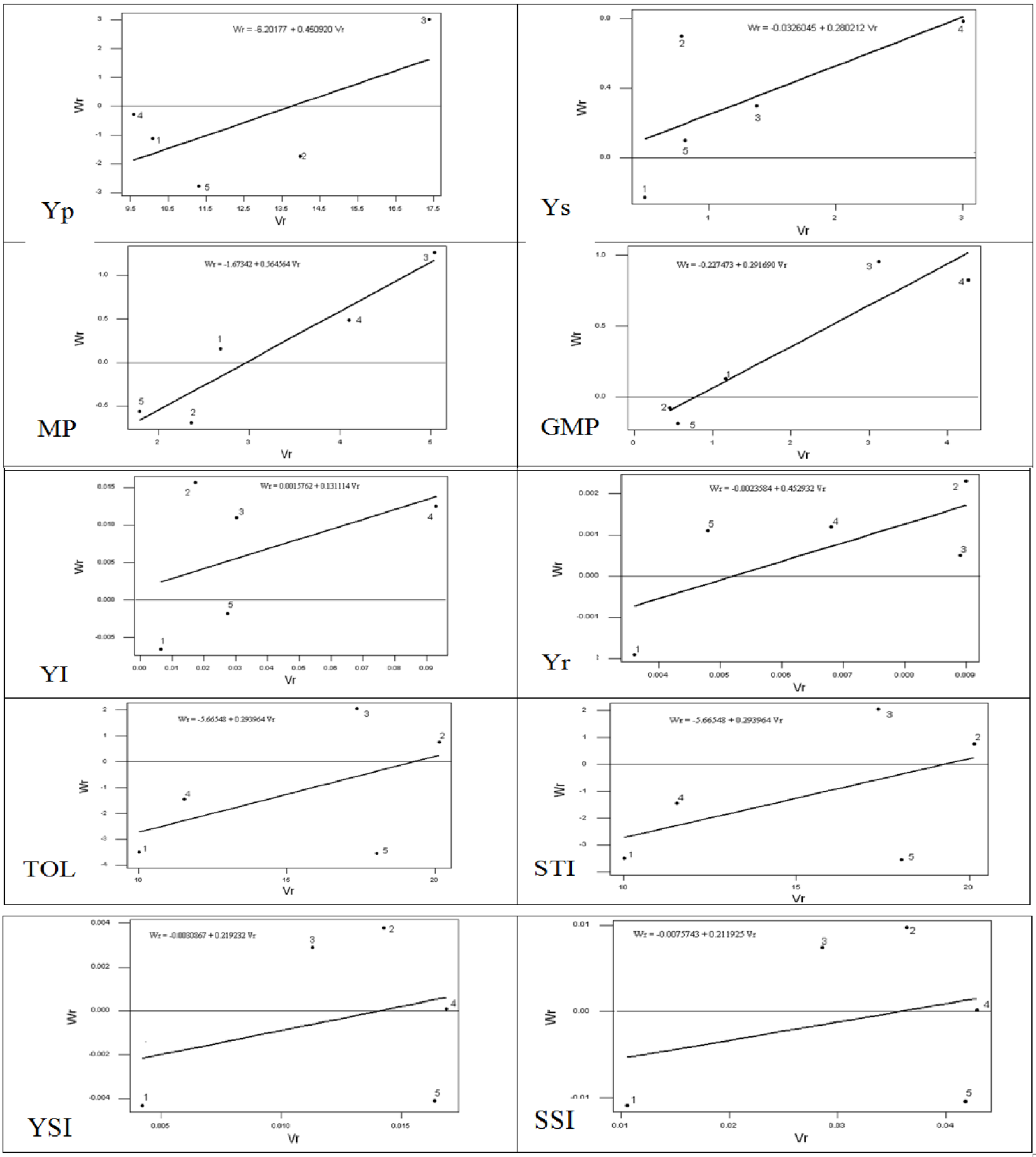
A comparison of degree of dominance for parents with mean values in each trait was shown in the Table (10); it can be noticed that the convergence matching some parents in terms of this comparison, such as parent 5 in Mp and GMP, and it means the possibility to get advantage of this parent to improve these traits, while the other traits and parents differed in the sequence of degree of dominance and means, indicating there are having other effects had an impact in different mean values of the parents. But that does not diminish the importance to refer for some outstanding parents in both sequence degree of dominance or means of traits, for instance: The parent 1 had a first rank in the degree of dominance in the Ys, YI, Yr, TOL, YSI and SSI, while the parent 5 had a first rank in sequence means in Ys, Mp, GMP, YI, STI and YSI, indicates possibility to get advantage of this parent in hybridization breeding programs.

Table 10. Sorting of parents according to degree of dominance and its means for Yp, Ys and drought tolerance indices.

Characters	Sorting parents according to degree of dominance Dominance → → →Recessive					Sorting parents according to means Highest→ → → Lowest				
Yp	3	5	2	1	4	4	1	5	2	3
Ys	1	5	2	3	4	5	2	3	1	4
MP	5	2	1	4	3	5	1	2	4	3
GMP	5	2	1	3	4	5	2	1	3	4
YI	1	5	2	3	4	5	2	3	1	4
Yr	1	5	4	3	2	4	1	2	3	5
TOL	1	4	5	3	2	4	1	2	5	3
STI	2	5	1	3	4	5	2	1	3	4
YSI	1	5	3	4	2	5	3	2	1	4
SSI	1	5	3	4	2	4	1	2	3	5

Yp=Grain yield ander non-stress conditions; Ys=Grain yield under stress conditions; MP=mean prductivity; GMP= Geometric Mean Productivity; YI= Yield Index; Yr= Yield Reduction Ratio; TOL=Tolerance Index; STI=Stress Tolerance Index;YSI= Yield Stability Index; SSI=Stress Susceptibility Index.

C. Graphical Analysis: Regarding to the distribution of parents around the regression line, it's better to know that the cross of regression line from coordinate's center indicates that there is complete dominance, while in case regression line crosses Wr axis in the upper part (positive section) or lower part (negative section) of coordinate center, it shows relative dominance and gene over-dominance are active. From Vr-Wr graph for Yp, Ys and drought tolerance indices (Fig.1) it is evident that the regression line cuts the Wr axis in the positive section above the origin for the traits Ys and YI indicating partial dominance with additive gene action. While the regression line crossed Wr axis in the negative section down the origin for other traits; this indicates that the over-dominance effects of genes are here effective in the control of these traits. The distribution of parents along the regression line shows in turn the ratio of the frequency of dominant and recessive genes [The parent possessed maximum dominant genes being closest to the origin whereas the parent had maximum recessive genes being farthest from the origin]. It means that those parents that are closer to the crossing of regression line and Wr axis have more dominant genes, indicating that the crossing of these parents may lead to the formation of appropriate hybrids. The closest and furthest parents to the origin of coordinates were as follows: 1 and 4 for Ys, YI, YSI and SSI; 1 and 2 for Yr, TOL and STI; 4 and 3 for Yp; 5 and 3 for Mp; 2 and 4 for GMP. Therefore, it can be concluded that the hybridization between 1 and 4 parent leads to get high values of the Ys, YI, YSI and SSI and higher heterosis; and also between 1 and 2 of the Yr, TOL and STI.



Yp=Grain yield ander non-stress conditions; Ys=Grain yield under stress conditions; MP=mean prductivity; GMP= Geometric Mean Productivity; YI= Yield Index; Yr= Yield Reduction Ratio; TOL=Tolerance Index; STI=Stress Tolerance Index;YSI= Yield Stability Index; SSI=Stress Susceptibility Index.

Figure (1): Relationship of covariance (Wr) and variance (Vr) of Yp, Ys and drought tolerance indices of durum wheat.

4. Heterosis: Results of hybrids showing heterosis revealed that maximum number of hybrids showed positive significant heterosis for Mp, Yp, GMP, STI, YS, TOL, YR, SSI, YI and YSI, respectively. The heterosis of F1 hybrids over mid-parents for the drought indices which presented in Table (10) revealed that out of twenty hybrids, fourteen hybrids exhibited significant positive heterosis in Yp; higher significant positive heterosis was estimated in the hybrid [5 × 3] (9.167); no hybrids show significant negative heterosis. The significant positive heterosis in Ys was observed in six hybrids; hybrid [3 × 4] had the highest positive heterosis (4.198). The significant heterosis in desirable direction was observed in most hybrids for MP and GMP. Significant positive heterosis was observed in seven hybrids in YI; the hybrids [3 × 4] showed the highest value for heterosis (0.613). Heterosis values of the hybrids for Yr varied from (-0.180) for hybrid [1 × 4] to (0.243) for hybrid [2 × 3]. Twelve hybrids exhibited significant and positive heterosis for TOL; higher heterosis values estimated from the hybrid [2 × 5] (9.003). As shown in Table (10), a greater significant positive heterosis of TOL was related to [2 × 5], indicating that this hybrid had a larger grain yield/plant reduction under rainfall condition and higher drought sensitivity compared with other hybrids; while a greater negative heterosis of TOL was found in[1×5] (-2.86).Therefore, this hybrid had a lower grain yield/plant reduction under rainfall condition. Significantly and positive heterosis values for STI were found in thirteen out of 20 hybrids; higher heterosis was estimated in the hybrid [3 × 4] (6.064). Heterosis values of the hybrids for YSI varied from (-0.243-0.180); three of twenty showed positive heterosis. [1 × 4] (0.180), [1 × 5] (0.153) and [3 × 4] (0.115) showed high values for heterosis. For SSI, the results indicated that significant positive heterosis was observed in eleven hybrids; higher heterosis values estimated from the hybrid [2 × 3] (0.387). These results indicated that high drought resistance indices involved in the hybrids were predominantly responsible for enhancing this important trait in durum wheat under rainfall conditions.

Table 10. Mid-parent heterosis estimates of studied characters in durum wheat.

Crosses	Yp	Ys	MP	GMP	YI
1 × 2	0.000	0.323	0.162	0.285	0.052
1 × 3	2.467*	0.372	1.419**	1.115*	0.056
1 × 4	1.817	3.747**	2.782**	3.430**	0.548**
1 × 5	-1.083	1.777**	0.347	0.867	0.256**
2 × 3	5.833**	-1.938**	1.948**	0.027	-0.285**
2 × 4	4.683**	0.450	2.567**	1.859**	0.070
2 × 5	7.517**	-1.487**	3.015**	1.044*	-0.218**
3 × 4	5.150**	4.198**	4.674**	4.827**	0.613**
3 × 5	4.083**	1.028*	2.556**	2.139**	0.148*
4 × 5	-0.500	0.803	0.152	0.502	0.118
2 × 1	6.533**	-0.380	3.077**	1.674**	-0.055
3 × 1	4.383**	-1.105*	1.639**	0.561	-0.162
4 × 1	-0.117	-1.680**	-0.898	-1.269**	-0.244**

5 × 1	3.783**	-1.923**	0.930	-0.483	-0.281**
3 × 2	7.483**	-0.055	3.714**	2.137**	-0.010
4 × 2	7.083**	-0.510	3.287**	1.592**	-0.073
5 × 2	1.050	1.727**	1.388*	1.753**	0.254**
4 × 3	6.067**	-0.788	2.639**	1.241**	-0.109
5 × 3	9.167**	1.438**	5.303**	4.011**	0.211**
5 × 4	7.733**	1.423**	4.578**	3.586**	0.211**

Yp=Grain yield ander non-stress conditions; Ys=Grain yield under stress conditions; MP=mean prductivity; GMP= Geometric Mean Productivity; YI= Yield Index.

(Continued)

Crosses	**Yr**	**TOL**	**STI**	**YSI**	**SSI**
1 × 2	-0.017	-0.323	0.292	0.017	-0.027
1 × 3	0.051	2.095	1.218*	-0.051	0.081
1 × 4	-0.180**	-1.930	4.156**	0.180**	-0.287**
1 × 5	-0.153**	-2.86*	1.066	0.153**	-0.244**
2 × 3	0.243**	7.772**	0.009	-0.243**	0.387**
2 × 4	0.077	4.233**	2.086**	-0.077	0.122
2 × 5	0.235**	9.003**	1.267*	-0.235**	0.375**
3 × 4	-0.115**	0.952	6.064**	0.115**	-0.183**
3 × 5	0.057	3.055*	2.585**	-0.057	0.091
4 × 5	-0.069	-1.303	0.482	0.068	-0.109
2 × 1	0.144**	6.913**	1.920**	-0.144**	0.229**
3 × 1	0.183**	5.488**	0.590	-0.183**	0.291**
4 × 1	0.111**	1.563	-1.411*	-0.111**	0.177**
5 × 1	0.191**	5.707**	-0.557	-0.191**	0.304**
3 × 2	0.152**	7.538**	2.395**	-0.152**	0.243**
4 × 2	0.154**	7.593**	1.758**	-0.154**	0.246**
5 × 2	-0.076	-0.677	1.931**	0.076	-0.121
4 × 3	0.195**	6.855**	1.390*	-0.195**	0.311**
5 × 3	0.117**	7.728**	5.022**	-0.117**	0.187**
5 × 4	0.087*	6.310**	4.586**	-0.087*	0.139*

Yr= Yield Reduction Ratio; TOL=Tolerance Index; STI=Stress Tolerance Index;YSI= Yield Stability Index; SSI=Stress Susceptibility Index.

* Significant (P = 0.05), ** Significant (P = 0.01)

5. Genetic correlation: Genetic correlation coefficients, calculated from the data obtained for parental and their F1 hybrids and reciprocals are presented in Table (12). MP, GMP, and STI were highly positive correlated with each other as well as with Ys and Yp. Thus, through these indices it is possible to distinguish high yielding genotypes in either condition. The genetic correlation coefficient of TOL and SSI were highly negative correlated with Ys. While that of TOL with Yp was high and positive. The positive correlation between TOL and Yp and the negative correlation between TOL and Ys suggest that selection can be based on TOL to improve the drought tolerance in durum wheat.

Table 12. Genetic correlation coefficients between (Yp), (Ys) and drought tolerance indices.

	Yp	Ys	Mp	GMP	YI	Yr	TOL	STI	YSI
SSI	0.705**	-0.781**	0.356	-0.128	-0.783**	1.000	0.917**	-0.138	-1.000
YSI	-0.71**	0.781**	-0.356	0.129	0.783**	-1.000	-0.92**	0.138	
STI	0.597**	0.723**	0.871**	0.998**	0.723**	-0.138	0.254		
TOL	0.927**	-0.480*	0.693**	0.266	-0.481*	0.917**			
Yr	0.705**	-0.781**	0.356	-0.129	-0.783**				
YI	-0.117	1.000	0.299	0.716**					
GMP	0.608**	0.717**	0.878**						
MP	0.913**	0.299							
Ys	-0.116								

Yp=Grain yield ander non-stress conditions; Ys=Grain yield under stress conditions; MP=mean prductivity; GMP= Geometric Mean Productivity; YI= Yield Index; Yr= Yield Reduction Ratio; TOL=Tolerance Index; STI=Stress Tolerance Index;YSI= Yield Stability Index; SSI=Stress Susceptibility Index.

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الخصائص الوراثية لمعايير التحمل للجفاف في الحنطة الخشنة

إسماعيل حسين علي[1]

ملخـــص

أجري تهجين تبادلي كامل بين خمسة تراكيب وراثية من الحنطة الخشنة. زرعت حبوب 20 هجيناً فردياً مع الآباء الخمسة في تجربتين منفصلتين واحدة تحت الظروف الديمية والأخرى تحت ظروف الري من أجل دراسة الخصائص الوراثية لمعايير التحمل للجفاف في الحنطة الخشنة. أظهرت بعض الآباء قدرة ائتلاف موجبة عالية، بينما أظهرت بعض الهجن قدرة ائتلاف خاصة في معظم هذه المعايير. هناك تأثير سياديً موجه لجميع الصفات باستثناء حاصل الحبوب تحت الظروف الديمية (Ys) ودليل المحصول (YI) ونسبة انخفاض المحصول (Yr). وعدم الانتظام في توزيع الأليلات السائدة لجميع الصفات ووجود حالة سيادة في بعض الهجن الفردية دون الأخرى في (Ys) و(YI) والمتوسط الهندسي للإنتاج (GMP) ودليل تحمل الشد (STI). أظهرت تقديرات التأثير الوراثي تأثيرا معنويا للمكون الوراثي الاضافي ($\hat{D}$) لــ Yr و STI. كان المكون ($\hat{H}_1$) أعلى عند مقارنته بالمكون الإضافي ($\hat{D}$) وسجل المكون الوراثي السيادي ($\hat{H}_2$) قيمة أقل مقارنة بالمكون ($\hat{H}_1$) لجميع الصفات. كان معدل درجة السيادة ($\sqrt{H_1/D}$)أكبر من واحد لجميع الصفات. كانت نسبة التكرار الجيني للأليلات السائدة الى المتنحية (H2/4H1) أقل من 0.25 لجميع الصفات عدا (Ys). أظهرت جميع الصفات مقداراً أكبر من الواحد في نسبة مجموع عدد الجينات السائدة الى المتنحية في جميع الآباء (KD/KR). كانت قوة التوريث بالمعنى الضيق متوسطة لــحاصل الحبوب تحت ظروف الري Yp (0.449) و Ys (0.281) ومتوسط الانتاجية MP (0.421) بينما كان عالياً لبقية الصفات. تم الحصول على الكثير من الهجن المتفوقة على متوسط الأبوين في جميع الصفات. أظهرت صفات (MP وGMP وSTI) ارتباطاً وراثياً موجباً ومعنوياً مع بعضها ومع ()Ys وحاصل الحبوب تحت الظروف الاروائية (Yp).

الكلمات الدالة: الحنطة الخشنة، معايير التحمل، الخصائص الوراثية.

1) كلية الزراعة/جامعة صلاح الدين/أربيل/ العراق
Dr.ismail@ymail.com
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