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Genetic Studies of Drought Tolerance Indices of F² Generations Population in Bread Wheat (*Triticum aestivum***)**

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المستخلص

The

تمت دراسة ميكانيكية توارث ادلة تحمل الجفاف في عشائر الجيل الثاني من حنطة الخبز باستخدام تطبيقات كرفنك وهايمان وجنكز ـ هايمان بخلال موسم النمو 2012-2013 زرعت خمسة آباء و20 من هجنٍ الجيل الثاني في 15 تشرين الثاني2012 في حقل مركز البحوث الزراعية كويا/أربيل تحت الظروف الديمية باستخدام تصميم القطاعات العشوائية الكاملة بثلاثة مكررات دلت النتائج على اظهار بعض الأباء مقدرة عامة موجبة على الاتحاد بينما أظهرت بعض الهجن مقدرة خاصة موجبة على الاتحاد بالاتجاه المرغوب في معظم هذه الأدلة. كانت قيم متوسطات المربعات لتحليل هايمان معنوية لحاصل الحبوب تحت ظروف الشد المائي (Ys) وعدم الشد (Yp). أشارت تقديرات النأثيرات الجينية الى وجود تأثير معنوي للمكون الوراثي الاضافي في توارث حاصل الحبوب تحت ظروف الشد (Ys) ومتوسط الانتاجية (MP) والمتوسط الهُذسي للانتاج (GMP) ودليل الحاصل (YI) ودليل تحمل
الشعر (Gan) المصل العلم استقلال (Gan) كلمان انتصال على انح محل انحساس انتقلال انتقلال ان ان ان ان ${\widehat{H}}_2$) ودليل الحساسية للشد (SSI). كان التقدير النسبي للمكون السيادي (ر المسين العلمي العلمي العلمي العلمي العلمي العلمي
(أ) أعلى مقارنة بالمكون التجميعي ($\stackrel{\frown}{D}$) في معظم الأدلة_. كان معدل درجة السيادة ($\sqrt{H_1/D}$) اكبر من واحد صحيح في كل الأدلة مما يعني وجود سيادة جينية فائقة تسيطر على هذه الأدلة وهذا يعطي فرصة للاستفادة من قوة الهجين. كانت نسبة تكرار الجينات السئدة الى المتنحية (H2/4H) اقل من 0.25 في جميع الأدلة باستثناء دليل التحمل (TOL). أظهرت خمس صفات مقداراً أكبر من واحد في نسبة مجموع عدد الجينات السائدة الى المتنحية في جميع الآباء (KD/KR). كانت قوة التوريث بالمعنى الضيق (H_{n.s.}) عالية لجميع الأدلة مما يعني فعالية الانتخاب في تحسينها.

Introduction

Wheat is the most important grain crop in Iraq; it is mainly grown on rainfall especially in northern part, therefore, drought can be considered as one of the most important abiotic stresses, causes a reduction in grain yield. So, the improvement of grain yield for drought tolerance is a major purpose in breeding programs under rainfall conditions. It's possible to overcome this problem by developing drought tolerant varieties. Genetic analysis of wheat yield has shown that grain yield is a complex character of varying morphological and physiological traits imposed by their genetic contribute (Farshadfar *et al.,* 2013). More information about physiological traits as the most attractive way to develop new genotypes and the gene effects controlling the highly related traits to drought tolerance makes breeding programs for drought tolerance much more effective (Araus *et al.,* 2008).

Various quantitative criteria have been proposed for selection of genotypes based on their yield performance in stress and non-stress conditions (Taghian and Abo-Elwafa, 2003). These parameters such as, Mean Productivity (MP), Geometric Mean Productivity (GMP), Yield Index (YI), Yield Reduction Ratio (Yr) , Tolerance Index (TOL), Stress Tolerance Index (STI), Yield Stability Index (YSI), Stress Susceptibility Index (SSI), are calculated for a given genotype using grain yield under stress condition relative to its grain yield under non-stressed conditions.

most significant factor restricting plant production on majority of agricultural fields of the world. Wheat is usually grown on arid-agricultural fields and drought often causes serious problems in wheat production on these fields (Tas and Tas, 2007). Therefore, the improvement of drought tolerance in crop is a major objective of most crop breeding programs, particularly in arid and semi-arid areas of the world (Moustafa *et al.,* 1996). Some estimates indicated that 50% of the approximately 230 Million hectares of under wheat cultivation annually in the world is frequently affected by drought (El-Mohsen, *et al.,* 2015). For successful breeding of bread wheat cultivars tolerant to drought through conventional approach, basic information about the breeding material must be available to the breeders. Firstly, there must be significant variability in genotypic responses to water stress and secondly, this variation must be genetically controlled. Thus, an understanding of the knowledge of these two components about the breeding material under consideration is necessary (Mitra, 2001), so wheat improvement for drought tolerance requires reliable assessment of drought tolerance variability among segregating populations (Golabadi *et al,* 2006). Thus, drought indices which provide a measure of drought based on loss of yield under droughtconditions in comparison to normal conditions have been used for screening drought-tolerant genotypes (Mitra, 2001).These indices are either based on

Drought, one of the environment stresses, is the

drought tolerance or susceptibility of genotypes (Fernandez, 1993). On the other hand, understanding of genetic mechanism of drought tolerance is imperative to develop suitable wheat genotypes for the arid and semi-arid areas (Ali, 2015) which can be estimated through Griffing (Griffing 1956), Hayman (Hayman 1954) approaches, furherrmore analysis based on Jinks and Hayman (1953) makes it possible to have access to the genetic information. 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 (Ali, 2015). For that this study aimed to investigate the genetic properties of drought tolerance indices of F2 segregation population in a full diallel between five genotypes of bread wheat.

Materials and Methods

The experiment was conducted at the experimental farm, Agriculture Research Station/Koya, Erbil. Five bread wheat genotypes (Table 1) were crossed in all possible combinations in a 5×5 diallel fashion during the growing season 2009-2010. Grains of 20 F1s and their five parents were cultivated on 15 November 2010. During the growing season, 2012-2013, the 5 parents and their 20 F_2 crosses was cultivated on 15 November 2012 in two experiments, stress (592.6 mm precipitation) and non-stress using Randomized Complete Block

Design with three replications. All the F2 hybrids and their parent cultivars were randomly assigned to experimental units. Each plot comprised one row of 3 m with space of 20 cm between rows and 10 cm between plants within rows. Irrigation was performed in the non-stressed plots at tillering, jointing, flowering and grain filing stage of irrigated water equivalent to 30 mm of fresh water. After harvest the grain yield was recorded for every plot. The drought tolerance indices were calculated for every genotype using the corresponding nonstressed and stressed subplots in each block as follows:

1. Mean Productivity (MP) (Rosielle and Hamblin, 1981): 2 $MP = \frac{Ys + Yp}{f}$

2. Geometric Mean Productivity (GMP) $(Fernander, 1993):$ $GMP = (Yp \times Ys)^{0.5}$

3. Yield Index (YI) (Gavuzzi *et al.,* 1997): *YI* = *Yp* $\sqrt{Y_s}$

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, 1993):

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

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

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

SI $SSI = \frac{1 - Ys/Yp}{s}$, where: $SI =$ stress intensity $= 1 - \overline{Y}_S / \overline{Y}_P$

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

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, method I, random model. The data also analyzed according to Hayman's and Jinks – Hayman approaches (Singh and Chaudhary, 1985).

Parameters used in this experiment were: \hat{D} =variation attributed to additive genetics effects; *F* \widehat{F} =relative frequency of dominant to recessive alleles in the parental populations and the variation level over loci; \hat{H}_1 = variation due to dominance genetics effects; \hat{H}_2 =variation due to dominance genetics effects corrected for gene distribution: h^2 \overline{a} =dominance effects due to heterozygous loci; $\sqrt{H_1/D}$ =average degree of dominance; $\overline{p}q = H_2/4H_1$ =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; $H_{n,s}$ = heritability in narrow sense and *E* \widehat{E} = expected environmental component of variation.

Results and Discussion

The GCA effects of the parents along with their mean performance indicated that there was close relationship between parental mean performance and GCA effects for almost all the (Yp), (Ys) and drought tolerance indices (Table 2). Parent [5] was

found to be desirable combiner for Yp, Ys, MP, GMP, YI and STI. The parent [3] was responsible for Yr, TOL and SSI. Similarly, the parent [1] was responsible for YSI. Thus, the perfect relationship could be established between per se performance and GCA effects of the parents. Similar finding was reported by Kumar *et al.,* (2011).

The desirable SCA effects are presented in Table (3). Out of 10 crosses 4×5 , 1×4 , 1×2 , 1×2 , $1 \times$ 4, 1×2 , 1×2 , 1×2 , 2×5 and 2×3 were observed to be best desirable with positive significant value of SCA effects for Yp, Ys, MP, GMP, YI, Yr, TOL, STI, YSI and SSI, respectively. Some crosses showed desirable SCA effects for more than one characters such as 1×2 which showed significant and desirable SCA effects for five drought indices viz.; MP, GMP, Yr, TOL and STI. Similarly, cross combination 1×4 recorded significant and desirable SCA effects for Ys and YI. On the other hand, the best crosses on the basis of per se performance and SCA effects were 2×4 for Yp, Yr and TOL; 1×4 for Ys, MP, GMP, YI and STI; $2 \times$ 5 for YSI and 2×3 for SSI.

Regarding to reciprocal effects (table, 4) showed that the cross 3×2 had a desirable reciprocal effects for Yp, Yr, TOL and SSI, and a crosses 5×3 for

MP, GMP, STI then a cross 5×4 for Ys, YI and YSI. While the best crosses on the basis of per se performance and performance and SCA effects were 5×4 for Ys and YI. The significant result of GCA and SCA suggests that both additive and nonadditive gene effects were involved in the expression of these indices. Rabbani (2009) concluded that the genotypes possessing dominance and over-dominance are more efficient for producing those traits in hybrid combinations. The results of combining ability revealed that the parents [5 and 3] proved as a best general combiner which can be used in hybridization program for obtaining desirable combinations, while in case of hybrids the results of SCA revealed that the hybrids 1×4 , 1×2 and 3×2] 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 (3). Estimation of SCA effects and corresponding mean performance for (Yp), (Ys) and drought

Table (4). Estimation of reciprocal effects and corresponding mean performance for (Yp), (Ys) and drought tolerance indices in F_2 generation of 5×5 diallel cross.

Mean square values of the Hayman genetic analysis for Yp, Ys and drought tolerance indices are presented in Table (5). Component *a*, which is an estimation of additive variance were significant (p=0.01) for Yp, Ys, MP, GMP and YI while component *b* which is non-additive (dominant) were significant $(p=0.01)$ for all drought indices. This component of variance was divided into *b1*, *b2* and *b3* according to Hayman (1954) component *b1* means the comparison of parents with crosses; it has been significant for Ys, YI, and STI which means that this item displaying the importance of dominance effects (Uni-directional) while nonsignificant 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 for Yp, MP, GMP, TOL and STI which means scattering in dominant allele's distribution for these indices. Important role of specific dominant deviation of genes was indicated by significant *b3* item. This component has been significant for all drought indices. Significant *c* and *d* items indicated the presence of maternal and reciprocal effects, respectively. Component *c* has been significant for all indices while component *d* was significant for all indices except Ys and YI. Similar finding was reported by Ali (2015).

Table (5). Analysis of variance for Yp, Ys and drought tolerance indices according to (Hayman, 1954) method.

E_{b_1}	∠	2.854	0.041	0.894	0.733	0.000
E_{b_2}	O	0.604	0.242	0.215	0.199	0.002
E_{b}	10	1.029	1.172	0.988	1.038	0.010
Ec		0.932	0.585	0.495	0.492	0.005
Ed	$\overline{12}$	0.692	0.834	0.671	0.700	0.007

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

Susceptibility Index.

The components of variation and genetic constants:

D \overline{a} *, F* \overline{a} , \widehat{H}_{1} \mathbf{r} , \hat{H}_2 \hat{H}_2 , \hat{h}^2 \widehat{h}^2 , \widehat{E} տ
թ $\sqrt{H_1/D}$, $\overline{p}\overline{q} = H_2/4H_1$, $\overline{KD}/\overline{KR}$, $\overline{h^2}/H_2$ and $H_{n.s.}$ were computed according to Jinks -Hayman analysis which are described by Singh and Choudhary (1985). The results revealed significant role of additive genetic component (*D* $\frac{1}{2}$) for the inheritance of Ys, MP, GMP, YI, STI and SSI. The positive values of *F* \overline{a} (mean of variance of additive and dominance effects) for all indices indicated unequal distribution of dominant and recessive gene frequencies in the parents. The non-additive

component (\hat{H}_1 (\widehat{H}_1) was found to be important for the genetic control of all the indices except Yp, MP, GMP and STI. However, the relative magnitude of dominant component (\hat{H}_2 (\hat{H}_2) was higher as compared to additive component (*D* \overline{a}) in most indices, indicating the preponderance of dominant gene effects in controlling the inheritance of these indices. The genetic component (\hat{H}_2 (\hat{H}_2) was recorded with low magnitude than (\hat{H}_1) \hat{H}_1) for all the indices, indicating that beneficial positive alleles are not proportional to that of deleterious negative alleles at all loci among parents. Non-significant value of

 (h^2) \overline{a}) for all indices indicated the absence of dominance effects due to heterozygous loci. Similarity, expected environmental component of variation *E* was found non-significant for all indices. The average degree of dominance $(\sqrt{H_1/D})$ has been >1 for all indices indicates that these indices were controlled by the overdominance of genes and ample scope for heterosis breeding. 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 TOL. This amount of ratio indicates the unequal frequencies of dominant and recessive allele for this drought tolerance index. 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 drought tolerance indices have shown the values for this component above unity, indicating the role of dominant genes in the expression of these indices. The narrow sense heritability $H_{n,s}$, was high for all indices, indicating that selection for improvement of these traits would be effective.

In conclusion, based on our studies, it seemed that the information generated as a result of this study on genetic analysis of some important drought tolerance indices of bread wheat will be of great value to the breeders which can be used in future breeding program for the development of cultivars. Furthermore, the drought tolerance indices having high heritability and with additive gene action could be used as indirect selection criteria for the selection of drought resistance genotypes of bread wheat at earlier generation under drought conditions.

drought tolerance indices.									
	Yp	Ys	MP	GMP	YI				
$\hat{\bm{D}}$	4.123 ± 1.980	$1.207 \pm 0.370*$	$2.257 \pm 0.786*$	$2.185 \pm 0.852*$	$0.011 \pm 0.003*$				
$\widehat{\bm{F}}$	6.803 ± 4.946	1.293 ± 0.923	3.181 ± 1.962	3.124 ± 2.127	0.012 ± 0.008				
\widehat{H}_{1}	14.163 ± 5.347	$3.671 \pm 0.998*$	5.091 ± 2.121	5.551 ± 2.300	$0.034 \pm 0.007*$				
H ₂	7.311 ± 4.850	1.091 ± 0.905	0.827 ± 1.924	1.692 ± 2.086	0.011 ± 0.008				
\hat{h}^2	1.012 ± 3.274	0.888 ± 0.611	3.033 ± 1.299	0.846 ± 1.408	0.0078 ± 0.005				
$\widehat{\bm E}$	0.294 ± 0.808	0.294 ± 0.151	0.294 ± 0.321	0.199 ± 0.348	0.002 ± 0.001				
$\sqrt{H_1/D}$	1.893	1.963	1.547	1.689	1.931				
$\overline{p}\overline{q} = H_2/4H_1$	0.129	0.074	0.041	0.076	0.078				
KD/KR	2.605	1.886	2.768	2.627	1.902				
h^2/H_2	0.160	0.138	0.094	0.502	0.094				
$H_{n,s}$	0.807	0.818	0.907	0.881	0.835				
Yp=Grain yield ander non-stress conditions; Ys=Grain yield under stress conditions; MP=mean prductivity; GMP= Geometric									
Mean Productivity; YI= Yield Index.									
	Yr	TOL	STI	YSI	SSI				

Table (6). Genetic constants, ratio of genetic parameters and heritability in narrow sense of (Yp), (Ys), and

Susceptibility Index.

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