Research Paper

Simple Correlation and Some Genetic Parameters of Yieldbread Wheatgenotypes and Itscomponents.

Mohammed Ali Hussain
University of Duhok

Mohammed Othman Mohammed
University of Zakho

College of Agricultural Engineering   College of Sciences
SciencesBiology Depart.
Field CropsDepart.

ABSTRACT:
The experiment was carried out to estimate correlation and some genetic parameters of twelve bread wheat genotypes,the experimental units was laid out in Randomize Complete Block Design with three replications.The results revealedthat, highly significant between genotypes for plant height,flag leaf area,No.of spike^{-1}, weight of grain spike,1000 grain weight and grain yield plant^{-1}.Also, the results showed the Tamoz-2 was superior in No.of seed spike^{-1} and grain weight spike, while the BABAGA-3 genotypes had the maximum 1000 grain weight. The research-4 gave the maximum grain yield 302.60 gmand followed by Abu-graib-1gave 299.33gm the results showed the genotypic coefficientvariation was medium for the most characters and low for leaf area and the heritability in broad sense was high for most characters and low for flag leaf area and grain yield.The genetic advance as mean was high for weight grain spike and number of grain spik^{-1}and medium for plant height,1000 grain weight and grain yield and low for flag leaf area .The simple correlation between six characters, the results indicated that significant positive correlated between weight grain spike and number of grain spike^{-1} with value 0.612, while the week positive or negative relationship with many characters.From this result can be useful of using the weightgrain spike, number of grain spike^{-1} to improve the yield in bread wheat after putting in program wheat breading.
Keywords: *Correlation, bread wheat, components, parameters of yield.*

I.   INTRODUCTION

Wheat is one of the most important and strategic cereal crops over the entire world, providing on average 20% of the total calories and 22% the total protein inhuman diet (FAOSTAT, 2018). The evaluation of genotypes by continued genetic recombination is the need of the day. Several researches have reported that genotypic correlation is important in determining the degree to which various yield contributing characters are associated and also the high phenotypic and genotypic coefficient of variability detected for most of the yield and yield components traits studied in wheat genotypes are indicatorsfor their wide range of variation. The phenotypic coefficient PCV values are close to the Genotypic coefficient variationGCV value indicated least influence of the environment on the traits and selection more successful for thistraits (Singh and Choudury 1985; Saleem *et al.,*2006; Abinasa*et al.,* 2011; Bhushan *et al.,*2013; Tahmasebi *et al.,*2013; Zeehan*et al.,*2014; Desheva and Cholakov2015; Khan *et al.,* 2015; and Abde Aziz *et al.,*2017.

In wheat, many breeders try to explain the relations ships between grain yield and agronomic and morphological traits by using simple correlation coefficients. Although correlation coefficient is very important to determine the traits that directly affectedgrain yield. Therefore, one needs to know more about these traits and how they affectedgrain yield so one can breed new genotypes that have high yields (Saif*et al*., 2009 and Khaliq *et al*., 2009)

Heritability with value genetic advance helps the plant breeder to predict the grainunder selection, and also heritability estimates provide the information about index of transmissibility of the quantitative traits of economic importance and are essential for effective crop breeding strategy, the genetic advance gives clear picture and higher estimates of heritability coupled with better genetic advance confirm the scope of selection in

---

developing new genotypes with desirable traits. (Topal*etal*.,2004: Bhushan *et al*., 2013; Haman, 2014 and Abdel Aziz *et al*., 2015). The study was carried out to estimate simple correlation coefficient and inheritance of yield and some related plant traits to develop desirable wheat genotypes.

II. MATERIALS AND METHODS:

Twenty-genotypes of bread wheat were used in this study, Table-1

The experiment site is studied in semi-arid zone characterised by semi rainfall during the season. The soil in the experimental field was a clay loam in texture with a pH of around 8 to 8.5. The experimental unit was laid out in Randomised Complete Block Design (RCBD) with three replications. The experiment units consisted three rows for each genotype with three-meter length and 0.25 between rows. For studied different genotypic parameters and relationships between six traits were taken into consideration, plant height, leaf area no. of grain spike, grain spike weight, 1000grain wheat and grain yield (g). The data analysed for different components, phenotypic and genotypic and variance were estimated by the formula used from Johnson *et al*.,1955.

The genetic parameter was estimated as follow,

Genotypic and phenotypic variance was estimated according to the formula of Johnson *et al*., 1955.

Genotypic variance $^2\sigma g = \frac{MSG - MSE}{r}$

Where MSG = Mean sum of square for genotypes

MSe = Mean sum of square for environments

r = number of replications

$^2\sigma p$ = phenotypic variance = $^2\sigma G + {}^2\sigma E$

Where; = $^2\sigma G$ = Genotypic variance

$^2\sigma E$ = Environment variance

Estimation Genotypic and phenotypic coefficient of variation:

Genotypic and phenotypiccoefficient of variation was calculated by following formula Burton, 1952

$Gcv = \frac{\sigma g \times 100}{\bar{x}}$

$Pcv = \frac{\sigma p \times 100}{\bar{x}}$

Where, Gcv = Genotypic co-efficient of variation

Pcv = Phenotypic co-efficient of variation

σg = Genotypic standard deviation

σp = Phenotypic standard deviation

x̄ = Population mean

Estimation of heritability: Bread sense heritability was estimated by the formula suggested by Singh and Chaudhary, 1985

$h_{b.s}\% = \frac{^2\sigma g}{^2\sigma p} \times 100$

Where, $h_{b.s}$ = heritability in bread-sense

$^2\sigma g$ = Genotypic variance

$^2\sigma p$ = Phenotypic variance

Genetic advance was estimated by the formula

$GA = \frac{k \times \sqrt{^2\sigma p} \times \sigma g}{^2\sigma p}$

K constant value = 2.063

$GAM = \frac{GA}{\bar{x}} \times 100$

Table 1: Number and sources of bread wheatgenotypes using in this study

No	Name	Source
1	Resarch-4	Central of Agriculture Research Duhok
2	Abu-graib-1	Abu-graib Central of Agriculture Research
3	IPA-99	IPA
4	TAWAHI-3	International Center for Agricultural Research in the Dry Area.
5	Sham-6	International Center for Agricultural Research in the Dry Area.
6	Maxipak	International Center for Agricultural Research in the Dry Area.
7	BABAGA-3	International Center for Agricultural Research in the Dry Area.
8	D-7	Abu-graibCentral of Agricultural Research.
9	Azadi	Central of Agriculture Research Duhok
10	IPA-95	IPA
11	SETTAR-85	International Center for Agricultural Research in the Dry Area
12	Tamoz-2	Central of Agriculture Research Duhok

III. RESULTS AND DISCUSSION

Table 2 exhibited the analysis of variance of six characters of bread wheat genotypes according to Randomize Complete Block Design method, the results in the same table showed that genotypes mean square was highly significance for plant height, No. of grain spike^{-1}, weight of grain spike^{-1}, 1000-grain weight and grain yield and non-significance for flag Leaf area.

Table 2. Analysis of variance for twelve bread wheat genotypes

s.o.v	df	M.S					
		characters					
		Plant height. cm	Flag Leaf area cm^2	No.of seed spike^{-1}	Weight of grain spike(g)	1000-grain weight(g)	Grain yield plant $^{-1}$(g)
replication	2	9.41	21.63	49.95	0.03	13.19	3498.18
genotypes	11	** 202.56	* 25.72	** 173.00	** 0.33	** 83.36	** 6633.61
error	22	19.91	9.45	14.70	0.04	8.70	1874.56
Total	35						

*.** Significant difference at 0.05 and 0.01 respectively.

The means performance of twelve genotypes for all characters was presented in Table 3. For plant height, the results exhibited that the highest value was recorded by Azadi which was (87.43 cm) and the lowest value was (57.81 cm) which obtained byResearch-4.Regarding to Leaf area, the Research-4 had the largest flag leaf area (53.28 cm^2), while, the smallest value (44.17 cm^2) recorded by Shame-6.Also the results revealed, the maximum number of grains spike^{-1}(66.88) was noticed in Tamoze-2, whereasthe Shame-6 gave the minimum number of grains spike^{-1}which was(47.46).Concerning the weight of grain spike, the Tamoze-2 showed maximum value 2.78, while the Azadi variety recorded the minimum value 1.63 .For 1000-grain weight, the BABAGA-3 gave the maximum value (52.339) and the IPA-99 had the minimum value (34.079),in trait grain yield the Research-4 and Ab-graib-1 were superior over all genotypes and giving 302.60 and 299.33g respectively, whilstthe Tamoze-2 had the lowest value 168.13g. From the result in the Table 3, the Research-4 had the maximum flag leaf area and this traitplays avery important role in the grain filling in bread wheat crop small grain crops such as wheat because of its position on the culm and It is the top most leaf and as such it intercepts quite a lot of radiation. Assimilation translocation from the flag leaf (Source) to panicle (reproductive Sink)is enhanced by the proximity of the flag leaf to the sink when the flag leaf of a small grain cereal crop is lost or destroyed grain yield is lost as a result.Many researches pointed to the same results such as Saleem *et al.,* 2006 and Abinasa*et al*., 2011.Abdul- Aziz. *et al.,*2017.

Table 3. Means of twelve bread wheat genotypes for studied characters.

genotypes	Plant height cm	Flag leaf area cm^2	No.of seed spike^{-1}	grain weight spike (g)	1000-grain weight(g)	Grain yield(g)
1	70.10 cd	53.28 a	55.70 bcd	2.31 bcd	41.55 c	302.60 a
2	75.60 bc	48.97 abc	62.57 ab	2.18 cde	34.89 de	299.33 a
3	57.81 e	50.12 ab	57.32 bc	1.94 def	34.07 e	250.23 abcd
4	69.00 cd	47.40 abc	47.58 e	1.80 ef	37.76 cde	253.23 abc
5	68.83 cd	44.17 c	47.46 e	2.24 bcd	47.26 b	223.00 abcd
6	81.36 ab	52.25 a	54.86 cd	2.62 ab	43.39 bc	170.00 d
7	72.05 cd	47.88 abc	50.12 de	2.83 abc	52.33 a	223.53 abcd
8	63.58 de	49.21 abc	61.03 abc	2.44 abc	40.04 cd	268.53 ab
9	87.43 a	49.12 abc	40.33 e	1.63 f	40.68 c	172.23 cd
10	76.55 bc	45.92 bc	60.30 abc	2.12 cde	35.18 de	258.17 ab
11	63.50 de	45.14 bc	58.53 bc	2.45 abc	42.03 bc	212.50 bcd
12	66.80 d	44.45 bc	66…88 a	2.78 a	41.69 c	168.13 d

Mean bearing different letters within each column differ significantly at 0.05 level probability.

The data in Table 4 described the estimation of variance (genetic, environment, and phenotypic),GCV, PCV, heritability genetic advance and genetic advance as mean. The GCV was medium for all characters, and low for flag leaf area. While the PCV was medium for plant height, weight of grain spike[-1],Numberof grain spike[-1] and 1000-grain weight,while was high for grain yield and low for flag leaf area.Regarding to heritability was high for most characters and medium for flag leaf area and grain yield. The results in the same table showed genetic advance as means was high for weight grain spikeand number of grain spike[-1] medium for plant height, 1000-grain weight and grain yield and low for flag leaf area. The weight grain spike[-1] and number of grain spike[-1] exhibited high broad sense heritability, and associated with high genetic advance as mean. From this result can be useful of these characters to improve the yield in bread wheat after putting in program of wheat breeding. These results were in agreement with obtained by Johnson *etal*., 1955 and Abinasa*etal.,* 2011 and Abdel-Aziz *etal*.,2017

Table4. Heritability and some genetic parameters of traits bread wheat genotypes.

character	VG	VE	V P	G CV	P CV	h.$_{b.s}$	GA	GAM%		GAM%
Plant height cm	60.8	19.91	80.71	10.97	12.64	75	11.85	16.67%		16.67%
Leaf area cm^2	5.42	9.45	14.87	4.83	8.00	36	2.44	5.07%		5.07%
Weight of grain (g)	0.095	0.048	0.143	13.75	16.88	66	0.43	30.91%		30.91%
Number of grains	53.1	14.70	67.80	13.19	14.19	78	11.30	20.47%		20.47%
1000 grain weight (g)	27.88	9.70	37.58	12.90	14.98	74	7.98	19.52%		19.52%
Grain yield (g)	1586.35	1874.56	3460.91	17.06	25.20	45	46.59	19.95%		19.95%

The results in Table 5 revelaed the simple correlation between six studied characters, the results in the same table indicated that significant positive correlation between weight of grain spike[-1] and No. grain, spike[-1] and the value was 0.612, while, the week positive or negative relationships with a many character. The results in Table 5emphasizes the role of these traits in selection of wheat genotypes when putting a good program to improving wheat genotypes.

Table .5 simple correlations Coefficient between studied traits

	Grain yield (g)	Plant height cm	Leaf area cm^2	No. grain spike[-1]	Weight of grain spike
Plant height cm					
Leaf area cm^2	0.291	0.22			
No. grain spike[-1]	0.247	-0.446	-0.096		
Weight of grain spike (g)	-0.138	-0.321	-0.21	0.612	
1000 grain weight(g)	-.0408	0.108	-0.154	-.365	** 0.51

*Significant at level 0.05 probability

REFERENCES

[1]. Abdel Aziz. N.S., Kamal. H.G, and A.S. Mohamad. 2017. Estimation of Genetic parameters for yield and its components in bread wheat (*Triticum aestivum* L.) genotypes under pedigree selection interanion. J. of Agronomy and Agric. Res. 10.2: 22-30.

[2]. Abinasa. M, Ayana. A, G. Bultosa. 2011. Genetic variability, heritability and trait association in durum wheat (*Triticum turgidum L. var durum*) genotypes. African Journal Agric. Res. 6(17): 3972-3979.

[3]. Allard. R.W. 1960. Princinple of plan breeding. John Willey and Sons Inc. New York, pp. 36.

[4]. Bhushan. B, Gaurav. SS, Kumar. R, Pal. R, Panday. M, Kumar. A, and vp. Rahul. 2013. Genetic variability, heritability and genetic advance in bread wheat (*Triticum aestivum* L.) Environmental and Ecology. 31(2): 405-407.

[5]. Burton, G.W. 1952. Quantitative inheritance in grass pea. Proc. 6th Grassel Cong. 1: 277-283.

[6]. Desheva. G and T. Cholakov. 2015. Variability, heritability and genetic progress for some yield cmponents in common winter wheat genotypes (*T. estivum* L.) Genetics and plant physiology-Conference-Bulgarian Academy Science 4(3-4): 191-200.

[7]. FAO. 2013. (Food and Agriculture organization of the United Nations). FAOSTAT, world crop production data. Accessed on 23 March, 2014. Available at www.faostat.fao.org/site.

[8]. Haman. K. A. 2014. Late and early pedigree selection for grain yield with three selection criteria in two populations in bread wheat. Journal Plant Production. Mansoura University. 5(11): 1831-1847.

[9]. Johnson, Herbert; W, H.F. Robinson and R.E. Comstock-1955. Estimates of genetic and environmental variability in soybean. Agrom. J. 47: 314-318.

[10]. Khaliq. I, I.R. Noorka and R. Khaliq. 2009. Estimation of heritability and genetic advances for quantitative characters in spring wheat. Int. J. Agric. Appl. Sci. (1): 76-78.

[11]. Khan. I, Mohammad. F, Fu. Khan. 2015. Estimation of genetic parameters of yield and tield traits in wheat genotypes under rainfed conditions. International. J. Envir. 4(2) 193-205

[12]. Saif.U.A,Nahid.I,and Y.M.Muhammed.2009.Estimationof Genetic Parameters and characters Association in wheat. J. Agric. Biol. Sci. (1)1:15-18.
[13]. Saleem. U, Khaliq. I, Mahmood. T and M. Rafique. 2006. Phenotypic and genotypic correlation coefficient between yield and yield components in wheat. J. Agric. Res. 44(1): 1-8.
[14]. Singh, R.K. and B.D. Chaudhary. 1985. Biometrical methods in quantitative genetic analysis. Kalyani: Publisher, New Delhi, India, pp. 56.
[15]. Tahmasebi. Gh, Heydarnezhadian. J and Ap. Aboughadareh. 2013. Evaluation of yield and yield components in some of promising wheat lines. Inte. J. Agric. and Crop science. 5(20) 2379-2384.
[16]. Topal. A, Aydin. C, Akgun. N and M. Babaog Lu. 2004. Diallel cross analysis in durum wheat. Field Crops Research. 87. 1-12.
[17]. Zeehan. M, Arshad. W, Khan. M, Ali. S and M. Tariq. 2014. Trait association and casual effect of polygenic traits in spring wheat (*Triticum aestivum*L.) genotypes. Inter. J. Agric. Forestry and Fisheries. 2(1):16-21.