

# Evaluation of Some Genetic Parameters of Grain Yield and Some of its Characters of an Individual Soft Wheat Hybrid (Triticumaestivum L.)

Nizar Harba<sup>1</sup>, Walid Alek<sup>2</sup>, Leila Al-dahhak<sup>3</sup>

<sup>1</sup>Prof, Department of Field Crops, Faculty of Agriculture, Tishreen-University, Lattakia –Syria

<sup>2</sup>Dr. General Commission for Scientific Agricultural Research Center -Damascus- Syria.

<sup>3</sup>PhD Student, Faculty of Agriculture, Tishreen-University, Lattakia –Syria

## Abstract

The research was carried out to study some of genetic parameters for individual hybrid (ACSAD 1115 × Bohouth6) of soft wheat as (days to heading, plant height, peduncle length, spike length, grains per spike, grain yield in individual plant) using an analysis of generations not segregate and second segregate –generation. It was conducted at the Agricultural Research Center in Hamah per to the randomized complete block design (RCBD) in three replications, during two growing seasons. Four genetic populations ( $P_1, P_2, F_1, F_2$ ) of this hybrid were used.

Results showed that act of the over-dominance was controlling on the behavior of the trait (spike length), while behavior of rest of the traits was affected by the partial dominance. The results concluded that significant value of heterosis compared to the average of the parents, for trait grain yield per plant in the first generation  $F_1$  was with non-significant inbreeding depression in the second-generation  $F_2$ .

High heritability in a broad sence associated with a high genetic advance in traits as (plant height, grains per spike), which refers to the possibility of improving these traits through selection in the early generations. While rest of the trait (days to heading, peduncle spike, spike length, grain yield per plant) can be improved through repeated selection in the late segregate generations.

**Keywords:** Soft Wheat, Heterosis, Inbreeding Depression, Heritability and Genetic Advance.

## I. INTRODUCTION

The wheat is the major cereal crop in the world, whether as farming or production. It takes the front besides rice and maize crops because the wheat is among the most importance and usage commodities by human [1]. It exceeds on other kinds of cereal in its foodstuff value, where in addition to contain about 60- 80% starch, also it contains of 8- 15% protein [2].

The wheat is the major food in more than 40 countries, and for more than 35% of people [3].

IFPRI organization was supposed that the international request on wheat will up to 775 million ton during 2020, and will increase of 60% during 2050. These expectances due to the population increasing that cause a threat for international food safety [4].

The promising increasing in the production requires doing on find genetic breeds and types that have ability on acclimatization and production, and that actually one of the most importance purposes for breeding and crossing programs [5].

Re. [6] demonstrated that traits of days to heading, spikes per plant, grains per spike, thousand grain weight, and grain yield in plants were subordinated to over-dominance. Also, re. [7] established that the over-dominance was controlling on traits as days to heading, plant height, spike length, grains per spike, and grain yield in plant.

Re. [8] concluded, after study of five planted breeds of soft wheat and crossing it and analysis using models of [9] and [10] and planting it in two ecological locations, that the dominance act controlling on all traits (days to heading, days to maturity, period of grain plenum, grain yield in plant, and plant height) was from partial dominance form.

Re. [11] bind the genetic depression that causing of immanence breeding with heterosis in opposite relationship, where the hybrid obtained positive values in traits as plant height, grains per spike, thousand grain weight, whereas it obtained negative values in traits as spikes per plant.

Re. [12] totaled low values of genetic advance for traits as days to heading, days to maturity, grains per spike, and grain yield. In his study the partial dominance was controlling on traits as days to heading, plant height, and grain yield in plant. Whereas, the over-dominance was controlling on a trait of grains per spike.

Re. [13] demonstrated of high value to heritability in a broad intention of grain yield trait (0.69). Whereas, it was notable a intermediate to high values for heritability due to low to intermediate genetic advance in traits as days to heading, days to maturity, plant height, spikes per plant, spike length,

grains per spike, thousand grains weight and grain yield [14].

Values of Phenotypic variation were higher compared with values of genetic variation in soft wheat crop, and values of heritability were high to traits as peduncle length and spike length. Whereas values of heritability were intermediate to trait as plant height. And the genetic advance was low to traits as peduncle length, grain yield, plant height and days to heading. It was notable that there are high Phenotypic and genetic variation to traits as plant height, peduncle length and grain yield in plant [15].

Re. [16] studied each of the genetic variation of 50 strains from wheat, besides to heritability in a broad sense, Genotypic and Phenotypic correlation coefficient, in addition to expectant genetic advance for 14 Phenotypic traits. Their results showed high heritability conjugated with high genetic advance to traits as days to heading, days to maturity, plant height, and grain yield (kg/h).

According to reduction of production in area unit, it was necessary to improve efficacy of usage the available genetic resources, and choice the genetic structure that have a high yield energy, in addition to improve traits that detected grain yield and related

with it. That necessary due to that the grain yield considered the final purpose of breeding [17]. Besides that possession of knowledge about quality and size the genetic effects of yield traits consider an important factor in formulation active breeding programs [18].

This research aimed to study some genetic parameters that useful for plant breeders as heterosis, genetic depression, degree of dominance, heritability in a broad sense, genetic advance and its percentage, Phenotypic and genetic variation coefficients of individual hybrid of soft wheat.

## II. MATERIALS AND METHOD

The research was performed at the Agricultural Research Center in Hamah from 2013 to 2016, the center is 316 m above surface of sea in the second steadiness region with rainfall about 250 mm /year.

### A. The Plant Materiality:

The study was performed with individual hybrid of soft wheat (ACSAD 1115 × Bohouth6) That was resulted from crossing between two genetic types which unrelated (table 1).

**Table (1): The Hybrid and Father Strains with Its Relatio**

Relation	Genetic types	Hybrids	N
3918A/JUP//NS732/Her/3/Florkwa-3 ACS-W-9523-6IZ-1IZ-0IZ ( CROW “ S “ ) RSK/5/21931/3/CH53/AN/ /GB56/4/ AN64/6/BOW’S*2/PRL’S’	ACSAD-1115 (P1)	P2×P1	1
	BOHOUTH-6 (P2)		2

### B. The First Season:

The father genetic types were planted at six dates beginning from the first week of November 2013, with distance 10- 15days between the date and the next date. The planting was on lines (3m), 3 lines to each father. The distance between lines was 25 cm, whereas it was 15 cm between plant and another plant. Between each of two types, two lines were let without planting.

The castrate was accomplished from spikes of each mother kind and covered by paper bags. Eunuch spikes inoculated by selected father.

Hybrid spikes were harvested after maturity and grains per spike were removed. Also, fathers spikes were harvested and their grains were removed separately. Then a number of resulted hybrids (H) calculated as following:

$$H = n(n-1) / 2 = 8(8-1) / 2 = 28$$

n: a number of fathers types in crossing program.

### C. The Second Season

Both of the fathers and first generation (F1) were planted in the second section of November 2014. The planting was on 4 lines for each father and 4 for each hybrid. Line length was 3m, with 25cm as distance between lines, and 15cm between plants in

the same line. Three replicates were prepared, and the reading took from ten plants in each replicate.

### D. The Third Season

Grains of populations of father strains and the first generation (F1) and the second generation (F2) were planted in the second section of November 2014. The planting was on 4 lines for each father and four lines for each hybrid from first generation, and 25 lines for hybrid from second generation. Line length was 3m with 25cm as distance between lines, and 15cm between plants in the same line. Hard wheat kind was planted between each of two types. Three replicates were prepared. Reading was taken from ten plants from each father, and ten plants from each first generation hybrid (F1), and fifty plants from second generation hybrid (F2) in each replicate.

### E. The Studied Traits:

The studied traits were days to heading (day), plant height (cm), peduncle length (cm), spike length (cm), grains per spike, and grain yield in individual plant (g).

The randomized complete block design (RCBD) was used.

**F. The Studied Genetic Parameters:**

**1) Heterosis:**

It evaluated as percentage according to [20] as following:

$$H(MP)\% = \{(F1-MP)/MP\} \times 100$$

$$H(BP)\% = \{(F_1-BP)/BP\} \times 100$$

F1: mean of the trait among members of first generation.

MP: mean of the trait in the parent., BP: mean of the trait in the better parent.

T- Test used to evaluate heterosis significance as Wynne *et al.* (1970), where value of (F1-BP) compared with value resulted from followed equation:

$$T = T(\text{TABLET}) * \sqrt{(VBP + VF1)} / 2$$

Where value of (F1-MP) compared with that resulted from followed equation:

$$T = T(\text{TABLET}) * \sqrt{((VP1 + VP2 + VF1))} / 3$$

T: value of calculated T, T (TABLET): value of tabled (P<0.05, P<0.01).

VP1: variation of the first father., VP2: variation of the second father., VF1: variation of the first generation, VBP: variation of the better father.

**2) Potence Ratio (dominance degree)(P):**

It calculated as described by [20] as following:

$$P = (\bar{F1} - \bar{MP}) / 0.5 * (\bar{P2} - \bar{P1})$$

F1: means of trait in the first generation., P1: means of trait in the first father (or the lowest), P2: means of trait in the second father (The better or the highest), MP: means of trait between parent.

**3) Inbreeding Depression:**

It calculated as described by [19] as following:

$$ID = [(\bar{F1} - \bar{F2}) / \bar{F1}] * 100$$

F1, F2: means of the first and second generation, respectively, considering that first generation plants inoculated by itself to produce the second generation [21].

Inbreeding depression significance calculated by compared value of ( $\bar{F1} - \bar{F2}$ ) with value that resulted from following equation:

$$T = T(\text{TABLET}) * \sqrt{((VF2 + VF1))} / 2$$

T: value of calculated T, T (TABLET): value of tabled (P<0.05, P<0.01).

VF1: variation of the first generation., VF2: variation of the second generation.

**4) Broad Sense Heritability:**

$$BSH = S_g^2 / S_{ph}^2$$

S<sup>2</sup>ph: Phenotypic variation = S<sup>2</sup>F<sub>2</sub>(second generation variation).

S<sup>2</sup>g: genetic variation = S<sup>2</sup>F<sub>2</sub>(second generation variation) - S<sup>2</sup>E (ecological variation).

$$S^2E = (S^2P_1 + S^2P_2 + 2 S^2F_1) / 4$$

S<sup>2</sup>P<sub>1</sub>, S<sup>2</sup>P<sub>2</sub>: the two parent variation., S<sup>2</sup>F<sub>1</sub>: the first generation variation.

**5) Phenotypic Coefficient Variation (PCV) and Genotypic Coefficient Variation (GCV):**

PCV AND GCV calculated as [19] as following:

$$PCV = \frac{\sqrt{Sf^2}}{\bar{Xf2}} \times 100 \text{ or } PCV = \frac{Sph \times 100}{\bar{x}}$$

$$GCV = \frac{\sqrt{S^2F_2 - S^2E}}{\bar{Xf2}} \times 100 \text{ or } GCV = \frac{Sg \times 100}{\bar{x}}$$

S<sup>2</sup><sub>p</sub>, S<sup>2</sup><sub>g</sub>: phenotypic and genotypic variation, respectively Sph · Sg: phenotypic and genotypic standard deviation, respectively.  $\bar{Xf2}$ : mean of second generation.  $\bar{x}$ : general mean.

**6) Expected Genetic Advance:**

It calculated as [22]:

GA: genetic advance. σ<sup>2</sup><sub>g</sub>: genetic type variation. σ<sub>p</sub>: stander of deviation phenotypic type of basic society, K: selective difference of certain selective severity level that considering phenotypic value of selective families [23].

Percentage of expected genetic advance (ΔG%) was calculated as following:

$\bar{F}_2$ : mean of trait in the second generation (F2).

**III. RESULTS AND DISCUSSION**

**A. Variation Analysis and Compared Means of Populations to the Studied Hybrid:**

The results showed high significant differences between parent populations and the first and second generations in the studied hybrid (table 2). That means the parent strains which formative the individual hybrid are unrelated. New segregations and good genetic structures could be found in these populations. These new changes can develop breeding programs for improvement yield. It was notable that values of Difference coefficient for studied traits were low to middle (table 2). These values refer to that our evaluation to studied populations was conducted in homogeneous environment as pushing services during the experiment. And the occurred difference among studied replicates was in normal limits.

**Table (2): Variation Among Populations of the First Hybrid (ACSAD 1115 O Bohouth6)**

Sources of variation	The hybrid (ACSAD 1115 × Bohouth6)					
	Days to heading	Plant height (cm)	peduncle length	Spike length (cm)	Grains per spike	Grain yield per plant (g)
Replicates variation	1.2	50.56	0.24	2.18	71.74	16.06
Population variation	4.6**	141.59**	0.89*	34.69**	586.8**	105.54**
Experiential error	0.33	13.3	0.18	0.55	41.2	3.17
Difference coefficient %	0.46	4.22	3.65	2.17	9.13	6.00

\* : significant by level 5%, \*\* significant by level 1%

Results submitted that variation resulted from the second segregate generation (F2) showed higher values compared to that resulted from non segregate generations (F1, P2, P1) (table 3). This result was

notable for all studied traits and these due to that F2 is the population which has the biggest genetic segregations. Results agree with [12].

**Table (3): Variation of Population for the Hybrid (ACSAD 1115 × Bohouth6)**

Genetic structure	No. samples	No. of days to heading			Plant height		
				CV%			CV%
P1	30	127.67	1.33	0.904	94.25	31.69	<b>5.9</b>
P2	30	124.67	0.09	0.79	77.67	4.17	<b>2.6</b>
F1	30	126	1	0.793	88.17	65.58	<b>9.1</b>
F2	150	125.67	9.33	2.43	85.63	147.7	<b>14.1</b>
LSD 5%		1.15			7.29		
Genetic structure	No. of samples	Peduncle length			Spike length		
				CV%			CV%
P1	30	35.96	5.503	6.5	11.81	0.312	<b>4.7</b>
P2	30	29.64	7.32	9.1	11.92	0.37	<b>5.11</b>
F1	30	33.86	8.41	8.5	10.90	0.63	<b>7.2</b>
F2	150	37.47	25.37	13.4	11.90	0.73	<b>7.17</b>
LSD 5%		1.48			0.85		
Genetic structure	No. of samples	No. of grains per spike			Grain yield per plant		
				CV%			CV%
P1	30	35.21	11	9.41	20.40	11.6	<b>16.69</b>
P2	30	67.72	8.92	4.41	35.31	7.55	<b>7.78</b>
F1	30	54.23	11.69	6.31	34.09	16.34	<b>11.85</b>
F2	150	43.96	68.17	18.78	27.82	30.66	<b>19.9</b>
LSD 5%		8.75			3.56		

To trait of days to heading, means of parent ranged from 124.67 day (P2) to 127.6 day (P1). Whereas, means of days to heading in populations of F1 and F2 attained 126 days and 125.6 day, respectively (table 3).

To trait of plant height, P1 was the most height (94.52cm), where P2 was the least height (77.6 cm), whereas means of F1 and F2 were 88.17 and 85.63 cm, respectively (table 3).

To trait of peduncle length, means of parent ranged from 29.64 cm (P2) to 35.96 cm (P1). Whereas, means in populations of F1 and F2 attained 33.86 and 37.47 cm, respectively (table 3).

To trait of spike length, means of parent ranged from 11.81 cm (P1) to 11.92 cm (P2).

Whereas, means in populations of F1 and F2 attained 10.90 and 11.90 cm, respectively (table 3).

And to trait of grains per spike, means of parent ranged from 35.21 grain (P1) to 67.72 grain (P2). Whereas, means in populations of F1 and F2 attained 54.23 and 43.96 grain, respectively (table 3).

To grains yield per plant, P1 attained 20.40g, where P2 attained 35.31g. Whereas, means in populations of F1 and F2 attained 34.09 and 27.82 g, respectively (table 3).

**B. Degree of Dominance and Heterosis Compared with Means of Parents and the Better Parent and Inbreeding Depression:**

Results showed controlling of over-dominance in traits spike length. Where values of dominance degree were > 1 in spike length, it was -18.13 (table 4). In the else traits, (days to heading, plant height, peduncle length, grains per spike, and grain yield per plant), the partial dominance was the controlling because it attained values ranged between (+1, -1). This agree with theory of dominance which explain a phenomenon of heterosis [24], and agree with results of [7].

Both of Heterosis and inbreeding depression consider correlated phenomenon. Moreover values of heterosis and inbreeding depression refer to that the studied traits mostly showed partial dominance effects, except some cases showed over-dominance {[25], [26]}.

Consequently, it was notable that heterosis values in the first generation associated with inbreeding depression in the second generation, where the values were positive in all studied traits except peduncle length and spike length. Grain per spike attained the highest depression (18.94). Inbreeding depression values were insignificant in all traits (table 4).

**Table 4: Dominance Degree (P), Heterosis Compared to Means of Parents (HMP), the Better Parent (HHP), and Inbreeding Depression (DI) of Studied Traits of Individual Hybrid ((ACSAD 1115 × Bohouth6)**

Days to heading (day)					
Number	Genetic type	Degree of dominance	Heterosis		inbreeding depression
			HMP	HHP	
1	ACSAD 1115 × Bohouth6	0.11	-0.13	1.07	<b>0.26</b>
Plant height (cm)					
Number	Genetic type	Degree of dominance	Heterosis		inbreeding depression
			HMP	HHP	
1	ACSAD 1115 × Bohouth6	0.27	2.57	-6.45	<b>2.87</b>
peduncle length (cm)					
Number	Genetic type	Degree of dominance	Heterosis		inbreeding depression
			HMP	HHP	
1	ACSAD 1115 × Bohouth6	0.33	3.21	-5.87	<b>-10.67</b>
Spike length (cm)					
Number	Genetic type	Degree of dominance	Heterosis		inbreeding depression
			HMP	HHP	
1	ACSAD 1115 × Bohouth6	-18.13	-8.15*	-8.56	<b>-9.42</b>
Grain per spike					
number	Genetic type	Degree of dominance	Heterosis		inbreeding depression
			HMP	HHP	
1	ACSAD 1115 × Bohouth6	0.17	5.37	-19.92**	<b>18.94</b>
Grain yield per plant (g)					
Number	Genetic type	Degree of dominance	Heterosis		inbreeding depression
			HMP	HHP	
1	ACSAD 1115 × Bohouth6	0.84	22.38*	3.46	<b>18.39</b>

**C. Phenotypic and Genotypic Coefficients, Heritability, and Genetic Advance:**

Results showed that phenotypic variation coefficient was higher than genotypic variation coefficient for all studied traits in the hybrid (table 5). But the difference between the two coefficients was generally low to all studied traits. This give a guide about that the genotypic variation principally

contributes in the phenotypic variation for the studied hybrid as [15] explained previous.

Evaluation each of genotypic variation coefficient and heritability give the breeders a better idea about selection date. From table (5), heritability values were high to all traits except to spike length (33.49%) and Grain yield per plant (57.74%) were medium. Results agree with [14].



Re. [22] demonstrated that efficacy of selective depended on evaluation of heterosis of trait, in addition to genetic advance value. Where heterosis give information about importance of genetics in quantity traits, whereas genetic advance considers

important parameter to form suitable selective programs. Results showed that genetic advance values were high to all traits except days to heading (4.56%) and spike length which attained 4.96%. The highest value in Grains per spike was 32.59%.

**Table (5): Phenotypic Variation Coefficient (PCV) and Genotypic (GCV), Heritability in a Broad Sense (HBS), Genetic Advance ( $\Delta G$ ), and Percentage Pf Genetic Advance  $\Delta G\%$  to All Studied Traits for the Hybrid (ACSAD 1115  $\times$  Bohouth6)**

Days to heading (day)				
Variation coefficient %		Heritability	Expected genetic advance	
Phenotypic	Genotypic	%	$\Delta G$	$\Delta G\%$
2.43	2.31	90.83	5.72	4.56
Plant height (cm)				
Variation coefficient %		Heritability	Expected genetic advance	
Phenotypic	Genotypic	%	$\Delta G$	$\Delta G\%$
14.06	11.91	71.73	17.98	21.00
peduncle length				
Variation coefficient %		Heritability	Expected genetic advance	
Phenotypic	Genotypic	%	$\Delta G$	$\Delta G\%$
14.71	12.38	70.79	7.35	19.63
Spike length				
Variation coefficient %		Heritability	Expected genetic advance	
Phenotypic	Genotypic	%	$\Delta G$	$\Delta G\%$
7.34	4.25	33.49	0.59	4.96
Grains per spike				
Variation coefficient %		Heritability	Expected genetic advance	
Phenotypic	Genotypic	%	$\Delta G$	$\Delta G\%$
16.42	15.06	84.12	14.33	32.59
Grain yield per plant (g)				
Variation coefficient %		Heritability	Expected genetic advance	
Phenotypic	Genotypic	%	$\Delta G$	$\Delta G\%$
18.83	14.31	57.74	6.59	23.70

**IV. CONCLUSIONS AND RECOMMENDATIONS:**

1. The responsible genes of increase traits (days to heading, plant height, peduncle length, grains per spike, grain yield per plant) dominated partial dominance at genes that lower it. Inbreeding depression attained positive values for some traits, so we prefer selection to it in the lately segregate generations that characterize with very high stability for traits.

2. The environment lightly effected in all studied traits due to the bitty differences between PCV and GCV. This refer to importance of genetic action in traits.

3. Heritability in a broad sense ranged from high to medium in all studied traits of the hybrid. These refer to possibility of improve phenotypic selection for traits.

4. Heritability in a broad sense related with high genetic advance for traits as (plant height, grains

per spike). That refer to possibility of improve these traits by selection across early generations. The other traits could be improvement by repeated selections across lately segregate generations.

5. We advise of continuation the work on this hybrid (ACSAD 1115  $\times$  Bohouth6), with considering a suitable date of selection for each trait until getting homogenous genetic strains that form an important genetic materiality for breeders of soft wheat.

**REFERENCES**

[1] C.P. Wilsie, "Crop adaptation and distribution". Freeman, San Francisco, pp 376–393, 1962.  
 [2] D.Zohary, and M. Hopf, " Domestication of plants in the Old World. The origin and spread of cultivated plants in West Asia", Europe and the Nile Valley. Dec:33(17): 67-78, 1993.  
 [3] P.C. Williams, "The world of wheat. In: Grains and oil-seeds: handling marketing processing."Canadian International Grains Institute, Winnipe. pp 557–602, 1993.

- [4] M.W. Rosegrant, "Biofuels and Grain Prices: Impacts and Policy Responses". International Food Policy Research Institute. 30(12): 12- 22, 2008.
- [5] H.Mohammadi, M. KhodambashiEmami, and A. Rezai, " Estimation of genetic parameters for wheat grain yield and its compenents using diallel crosses" Journal of science and Technology of Agriculture and Natural Resources.,11(40):157- 165. 2007.
- [6] N.K. Sedek, A.G. Eraky, H.A. Rabie, and A.R. ALKadoussi, "Assessment of gene action for grain yield and its attributes in bread wheat using three diallel sizes". Zagazig J. Agric. Res, 36(2): 263-283, 2009.
- [7] S.A. Jadoon, F. Mohammad, H. Ullah, and H. Khalil, "Gene action for pre and post harvest traits in f2 wheat populations", Qscience Connect, 11- 19. 2012.
- [8] M.Zare-kohan, and B.Heidari, "Estimation of Genetic Parameters for Maturity and Grain Yield in Diallel Crosses of Five Wheat Cultivars Using Two Different Models", Journal of Agricultural Science .Vol 4, No 8. ISSN 1916-9752 (Print) ISSN 1916-9760. 2012.
- [9] J.C. Wynne, D. A. Enevy, and P. W. Rice, " Combining ability estimation in Arachis hypogea. II- Field performance of F1 hybrids. Crop Sci. 1: 713- 715. 1970.
- [10] J. L. Jinks, and B I. Hayman, The analysis of diallel crosses. Maize Genetics, Coop Newsletter, 27, 48-54. 1953.
- [11] E. Beche, C.L.da Saliva, E.S. Pagliosa, M.A. Capelin, J. Franke, G. Matei, and G. Benin, " Hybrid performance and heterosis in early segregate populations of Brazilian spring wheat", AJCS, 7(1):51-57, 2013.
- [12] M.E. Abd-El-Rahman, " Estimation of some genetic parameters through generation mean analysis in three bread wheat crosses" Alex. J.Agric .RES. 58 (3): 183- 195, 2013.
- [13] J.Yao, H. Ma, X. Yang, G. Yao, and M. Zhou, "Inheritance of grain yield and its correlation with yield components in bread wheat (*Triticumaestivum* L.)."African Journal of Biotechnology, 13(12), 1379-1385. 2014.
- [14] M.A. Aglan, and W.Z.E. Farhat, "Genetic Studies on some Earliness and Agronomic Characters in Advanced Generation in Bread Wheat (*Triticumaestivum* L.)" IJPSS, 3(6):790-798. 2014.
- [15] S.Ashfaq, H.M. Ahmad, Sh.I. Awan, Sh.A. Kang, M. Sarfraz, and M.A. Ali, " Estimation of Genetic Variability ,Hertability and Correlation for Some Phenotypic Traits in Spring Wheat". J. Biol. Agric and Health, 4(5):10-22. 2014.
- [16] M.F. Amin, M. Hasan, N.C.D. Barma, M.M Rahman, M.M. Hasan, "Variability and heritability analysis in spring wheat (*Triricum aestivum* L .) Genotypes', Bangladesh Journal of Agricultural Research, Vol 40, No 3.ISSN 0258-7122 (Print) 2408-8293. 2015.
- [17] S.PETROVIĆ, M. DIMITRIJEVIĆ, N. LJUBIČIĆ, B. BANJAC, "Diallel analysis of quantitative traits in wheat crosses".47th Croatian and 7th International Symposium on Agriculture. Opatija. Croatia, 13- 17. 02. Proceedings, 313– 317, 2012.
- [18] H.A. Inamullah, "Inheritance of important traits in bread wheat using diallel analysis". Doctoral dissertation. NWFP Agriculturiversity Peshawar, Pakistan. 2004.
- [19] R.K. Singh, and B. D. Chaudhry, " Biometrical methods in quantitative genetic analysis .Kamla Nagar, Delhi. 110007. India. 1977.
- [20] H.H. Smith, " Fixing transgressive vigor in Nicotianarustica. Heterosis, Iowa State College Press. Ames, Iowa, U. S. A, 1952.
- [21] KMather, and J. L. Jinks, "Introduction to biometrical genetics. Chapman and Hall Ltd. London P.231. 1977.
- [22] H.W. Johnson, H. F. Robinson, and R. E. Comstock, "Estimates of genetic and environmental variability in soybean". Agron. J., 47: 314-318. 1955.
- [23] D.S. Falconer, "The inheritance of liability to diseases with variable ageof onset, with particular reference to diabetes mellitus". Ann. Hum.Genet., 31, 1–20. 1967.
- [24] J.F .Crow, "Alternative hypotheses of hybrid vigour. Genetics".33:477-487. 1948.
- [25] A.A. Hamada, E. H. El- Seidy and A. K. Moustafa, "Genetic behavior of some economic characters in two wheat crosses", Egypton Journal of plant breeding, V2(2): 31-50. 2002.
- [26] J.H. Vander Veen, "Test of non-allelic interaction and linkage for quantitative characters in generations derived from two diploid pure lines". Genetic: 30: 201-206, 1959.