World Applied Sciences Journal 27 (8): 944-949, 2013
ISSN 1818-4952

DOI: 10.5829/idosi.wasj.2013.27.08.13710

Estimation of Heritability and Variance Components for Some Quantitative Traits in Bread Wheat (*Triticum aestivum* L.)

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Abstract: The North Carolina Design III has been investigated with respect to the estimation of additive (A) and non additive (D) genetic variation for quantitative traits. Forty crosses with the parental lines were sown using the randomized complete block design with three replications were analyzed by North Carolina Design III. The mean squares of the analysis of variance revealed significant and highly significant differences among families for all the studied characters providing evidence for adequate amount of genetic variability and assured the variability between parents. Additive (A) and dominance (D) genetic variances were significant in all the studied traits. Both additive and dominance components were involved in the inheritance of these characters. The additive genetic variance was more than dominance for days to heading, spikelets/spike and 1000-kernel weight (g).The predominance of additive component indicates that the additive gene effect was more effective than unadditive in the inheritance of these characters. However, the dominance was higher than additive for plant height, number of spikes/plants, spike length, number of kernels/plant and grain yield/plant (g). On the other hand, significant of additive and dominance components indicated that both additive and dominance gene effects were important in the inheritance of these traits. Also, selecting desirable characters may be practiced in the early generations but it would be effective in the late ones. The ratio of $(A/D)^{0.5}$ were higher than units for days to heading, spikelets/spike and 1000-Kernel weight (g) indicating over dominance, However, plant height, number of spikes/plant, spike length, number of grains/plant and grain yield/plant (g) were less than unity, indicating the major of dominance of these characters. Heritability both in broad and narrow senses were found to be high in majority cases indicated higher importance of genetic effects in control of traits. But in some cases these values were moderate or low.

Key words: Bread wheat (*Triticum aestivum* L.) · Salinity · North Carolina Design III · Quantitative genetics

INTRODUCTION

Wheat is the most important cereal crop in Egypt and worldwide. In Egypt, increasing grain yield of cereal crops is considered one of the important national goals in order to face the growing populations needs therefore, it has become necessary to develop genotypes which characterized by showing superior performance [1]. The choice of an efficient breeding program depends to a large extent on knowledge of the type of gene action involved in the expression of the character [2]. The efficiency of breeding program increases by careful choice of parents and populations capable of producing progeny with desirable trait combinations [3]. Before embarking on any improvement program, genetic information regarding the inheritance of quantitative characters, particularly the nature and choice of the most effective breeding procedures depends to a large extent on knowledge of the genetic systems controlling the characters to be selected. Primarily; biological variation presented in the plant population is of three types, viz., phenotypic, genotypic and environmental. The genotypic variance consists of additive, dominance and epistatic components. There is much more evidence that study of epistatic gene action or

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non-allelic interaction in quantitative trait inheritance is important in making a decision for the plant breeders [4, 5]. In the genetic analysis, presence of epistasis is known to cause bias in the genetic components of the variance [6]. Most the genetic studies carried out by wheat breeders [7-9], demonstrated that three epistatic types of gene action were important in the inheritance of quantitative traits in bread wheat. Although, the designs used in the estimation of these genetic components assume the absence of epistasis. Therefore, the presence of epistasis should be studied precisely before deciding any breeding program. Among all the designs available for estimation of gene action, triple test cross is considered the most efficient model as it provides not only a precise test for epistasis, but also biased estimates of additive and dominance components if epistasis is absent. Many investigators studied the type of gene effect in wheat and reported that dominance was relatively more important than additive for grain yield, while additive genetic effect was predominated in the expression of plant height and heading date [10]. Meanwhile, Khalifa *et al.* [11] and El-Sayed *et al.* [12] found that additive-dominance model was adequate for revealing the inheritance of grain yield and its components. On the other hand, Amawate and Behl [13] reported that dominance gene effect was more important than additive one in most traits which indicate the presence of both types of gene effects. The results of Yadav and Nersinghani [14] came to a conclusion that, additive gene effects were predominant for yield and yield components, though non-additive gene effects were also important. Hamada [15], Abd El-Majeed [16] and Tammam [17], revealed that, additive and dominance components of gene actions were detected for most traits studied. In order to detect epistatic effects different methods viz., scaling test in the generation mean analysis. The North Carolina Design III (NCD III) of in which homozygous parents are crossed and F_2 plants are back crossed to each of the parents provides reliable estimates of additive and dominance components and degree of dominance $[(H/D)^{0.5}]$, but it assumes no epistasis.

This type of experiment of North Carolina Design III of [18], that is applicable to any population irrespective of its mating system and its gene and genotype frequencies [19]. The estimate of heritability serves as a useful guide to the breeder. The breeder is able to appreciate the proportion of variation is due to Genotypic (Broad sense heritability) or additive (Narrow sense heritability) effect that is the heritable portion of variation in the first case and the portion of genetic variation that is pure line in the later case. Selection efficiency for a plant trait depends on extent of its heritability and genetic variation [20]. The existing genetic variability shows that the population has high genetic potential for improvement of the characters by selection programmes. The magnitude of heritability was high for most of the plant characters that have been obtained by Awaad [21] and Singh *et al.* [22]. Heritability is a technique used by the plant breeders for effectively isolating the amount of genetic variation from the total phenotypic variation. The objectives of the present investigation were to the estimation of additive (A) and non additive (D) genetic variation for quantitative traits in wheat using the North Carolina Design III analysis. Also, heritability was determined for effectively isolating the amount of genetic variation from the total phenotypic variation. This information could help wheat breeder to plan successful and fruitful breeding program.

MATERIALS AND METHODS

Experimental Site Describition and Field Trials: This work was conducted at the Experimental Farm of the Agronomy Department, Faculty of Agriculture, South Valley University, Qena, Egypt (26°11'N and 32°44'E) during the two growing seasons 2010/11 and 2011/12. In the first season, the F_2 families which were obtained from the crossing between the two introduced lines; SHORAWAKI BW-20313, from Mexico (P_1) and IG 43251 ICBW206015 from Pakistan (P_2) were sown along with their parents. A number of twenty were randomly chosen and grouped to four sets, each of these plants was crossed, as the male parent, (by hand emasculation and pollination techniques) with each of the two introduced lines (taken as f emales) to produce 20 (F_2 x P_1) and 20 (F_2 x P_2) crosses according to North Carolina Design III. During the 2011/2012 growing season, the forty crosses with the parental lines were sown using the randomized complete block design with three replications. Each containing three rows, each row was 3 meters long, spaced 20 cm. apart with 10 cm. between plants within rows. All recommended cultural practices of wheat production in the region were applied. The EC of the experimental site and the used irrigation water were 18.56 ds m^{-1} and 7.90 dS m^{-1}, respectively.

Measurements: Days to heading was measured as number of days from sowing to complete emergence of spike on the main stem for 50% of plants. At harvest, fifteen plants were taken at random from each plot to recording; plant height (cm), number of spikes/plant, spike length (cm), number of spikelets/spike, number of kernels/plant, 1000-kernel weight (g) and grain yield /plant (g).

Statistical Analysis: The procedure followed for detecting epistasis was done according to the method outlined by Kearsey *et al.* [19]. The mean squares of deviations (overall epistasis were tested against pooled error to determine the presence of epistasis. Heritability (h^2), genotypic variance ($\sigma^2 g$) and phenotypic variance ($\sigma^2 ph$) were obtained from the analysis of variance table according to Comstock and Robinson [18].

RESULTS AND DISCUSSION

North Carolina (Design III) Analysis: The mean squares of the analysis of variance as shown in Table 1 revealed significant and highly significant differences among families for all the studied traits except of number of spikes/plant for females and males indicating that families were significantly different from each other, providing evidence for adequate amount of genetic variability and assured the variability between parents. Likewise, the results indicated that families were significantly different from each to other in most studied characters confirming the presence of high amount of genetic variability which could be assessed by means. The females had the largest mean square for plant height (cm), number of spikelets/spike and 1000-kernel weight (g). This indicated that the genetic differences between crosses with different females were major ones and should become a focus in the breeding programmes.

The males had a lower response relative to females for these traits, but the variation caused by the between-males genetic differences still was significant for all traits except for number of spikes/ plant. The various genetic bases among the females, among the males and between the sets also produced a genetically divergent cross progeny. This was indicated by the female-by-male interaction mean square which suggested some divergent dominance could play a role across the specific crosses and across the sets. Further obtain the specific genetic information on the genetic factors that were responsible for the character performance, the related genetic parameters were extracted and used.

Table 1: The analysis of variance for eight studied traits in two wheat crosses

Source of variance	d.f	Days to heading	Plant height (cm)	No. of spikes /plant	Spike length	No. of spikelets /spike	No. of kernels/plant	Grain yield/plant	1000-kernelweight(g)
Sets	3	367.58**	3344.54**	7.38**	27.75**	54.31**	4308.28**	7.750**	8795.79**
Replication in sets	8	6.11**	36.91**	0.85	0.67**	0.76	209.62**	0.35	5084.79**
Females in sets (f)	4	122.67**	1155.74**	0.59	3.14*	26.23**	873.788**	4.62**	17009.08**
Males in sets(m)	16	269.65**	368.120**	1.51	6.86**	21.96**	2013.64**	5.00**	8163.43**
Interaction (m x f) in sets)	16	169.05**	402.55**	3.40**	13.15**	15.27**	2635.722**	8.12**	7082.87**
Error	72	4.06	18.74	0.27	0.61	0.59	107.95	0.37	5295.93

*,** significantly at 5% and 1% probability, respectively

Table 2: Mean values of eight studied character in the wheat crosses

		Days to heading		Plant height(cm)		No. of spikes /plant		Spike length		No. of spikelets/ spike		No. of kernels/plant		Grain yield/plant		1000-kernel weight (g)	
Set	Male	P_1	P_2	P_1	P_2	P_1	P_2	P_1	P_2	P_1	P_2	P_1	P_2	P_1	P_2	P_1	P_2
1	M1	103.00	96.00	83.60	85.10	2.80	4.30	10.50	8.80	18.30	13.60	119.9	99.80	4.46	5.34	37.84	53.47
	M2	97.33	94.33	63.30	70.50	2.25	3.40	7.50	9.23	12.93	13.60	52.05	99.80	2.10	4.23	40.46	48.22
	M3	114.00	96.00	92.80	78.10	1.70	2.90	13.40	8.60	21.00	16.70	63.72	88.50	2.38	4.56	39.30	48.22
	M4	92.66	97.66	87.60	970	4.30	3.00	8.30	7.95	18.30	13.80	163.4	62.10	7.03	2.88	42.95	46.14
	M5	112.00	112.00	87.40	82.90	3.30	3.30	11.20	12.10	17.50	18.30	53.70	68.30	1.71	2.64	31.34	37.98
2	M1	84.33	92.00	51.75	63.80	1.20	2.20	7.06	7.50	12.75	12.60	84.00	27.90	3.38	1.27	39.70	45.13
	M2	110.00	112.00	74.80	52.50	3.20	2.10	9.70	9.10	16.90	17.00	70.00	59.50	1.94	1.74	27.64	29.32
	M3	97.33	93.33	60.00	64.35	2.56	2.30	8.63	10.20	16.90	17.06	70.00	87.10	0.75	4.61	39.70	53.30
	M4	96.00	95.33	73.00	55.35	2.40	4.30	9.00	9.00	12.81	18.70	57.00	59.90	2.91	3.42	51.05	56.83
	M5	97.33	111.00	69.15	74.25	2.66	1.80	10.23	9.15	16.90	15.93	57.00	43.20	2.14	3.43	51.05	49.42
3	M1	107.33	90.33	92.80	77.40	4.40	1.80	11.40	10.23	19.70	13.65	105.7	83.85	3.41	4.17	32.35	50.49
	M2	97.33	109.00	96.60	62.80	2.80	3.60	13.10	6.73	16.50	19.40	86.20	90.60	3.21	2.67	37.52	29.49
	M3	94.33	10800	97.00	80.40	2.30	6.00	7.00	13.10	19.30	17.00	57.90	74.50	3.02	2.12	52.16	28.19
	M4	111.00	110.33	99.00	73.50	4.10	3.00	11.60	10.80	20.20	17.90	67.46	76.30	2.62	2.67	38.91	50.49
	M5	102.33	98.00	85.00	73.43	3.40	3.30	12.40	11.95	20.20	16.50	67.47	139.00	7.98	2.12	38.91	29.49
4	M1	93.33	91.00	73.70	83.60	2.40	3.50	9.10	8.30	10.50	17.20	67.50	112.6	5.07	2.85	56.52	126.67
	M2	92.00	93.00	82.10	49.50	2.26	2.90	9.50	6.40	16.30	12.60	64.20	112.6	3.13	2.85	16.12	99.76
	M3	93.00	84.00	52.80	50.50	2.26	1.50	11.30	7.20	10.50	12.60	67.50	24.00	1.09	2.83	16.12	126.67
	M4	88.33	111.00	58.20	64.70	2.70	2.50	7.20	9.30	16.30	16.40	64.20	38.00	1.49	3.73	23.32	99.76
	M5	94.00	109.00	98.40	49.91	2.40	2.30	8.40	10.20	17.13	18.90	83.20	81.90	3.13	3.73	37.67	42.34
Mean		98.85	100.16	78.95	69.48	2.77	3.00	9.82	9.29	16.54	15.97	75.93	76.47	3.15	3.19	37.53	72.56
L. S.D0.05			3.29		7.06		N S		1.27		1.25		16.96		0.99		118.82
L.S.D.0.01			4.34		9.33		NS		1.68		1.66		22.39		1.30		156.85

Table 3: Estimates of additive (A), dominance (D) components, degree of dominance (A/D) 1/2 for the studied traits in wheat crosses

Type of gene actions	Days to heading	plant height	No. of spikes/plants	Spike length	No. of spekelets/spike	No. of Kernels/plant	Grain yield/plant (g)	1000-kernel weight (g)
Additive variance (σ2 A)	177.05	232.91	0.825	4.16	14.24	1270.46	3.08	1911.66
(σ2D) Dominance variance	109.99	255.87	2.088	8.36	9.78	1685.18	5.16	1191.29
$(A/D)^{0.5}$	1.60	0.91	0.39	0.49	1.45	0.75	0.59	1.60

Table 4: Estimation of genotypic and phenotypic variance and broad and narrow sense heritability for the studied traits in wheat crosses

Type of gene actions	No. of days to 50% flowering	Plant height	No. of spikes/plant	Spike length	No. of spikelets/spike	No. of kernels/plant	Grain yield/plant (g)	1000-kernel weight (g)
σ^2E	1.35	6.25	0.09	0.20	0.20	35.98	0.12	1765.31
σ^2G	287.05-	488.79	2.91	12.53	24.04	2955.64	8.26	3102.9
σ^2Ph	288.40	495.04	3.00	12.73	24.24	2991.62	8.38	4868.27
Hb	99.53	98.74	97.00	98.43	99.17	98.80	98.57	63.74
Hn	61.39	47.05	27.47	32.74	58.79	42.47	36.88	39.27
Dominance ratio	1.24	2.20	5.04	4.01	1.37	2.65	3.35	1.25

Mean Performance: The data presented in Table 2 showed that the mean values of back crosses for P_2 gave inferior values (Lateness) for number of days to heading with the shortest plants and increased number of kernels/plant, grain yield/plant and 1000-kernel weight as compared with back crosses with P_1. Meanwhile, backcrosses to P_1, gave the highest mean for number of spikelets/spike and spike length (cm). The success of any plant breeding programme depends to great extent, on the knowledge of the genetic behaviour of the populations being handled by the breeder. Rreliable information about the nature and magnitude of gene action present efficient. It also has wide applicability as it can be used to investigate both segregating and non segregating plant populations arising from different generations such as F_2, backcross and homozygous lines [19].

Genetic Studies: Estimation of additive (A), dominance (D) components, degree of dominance $(A/D)^{0.5}$ for the studied characters in wheat crosses are presented in Table 3. For the characters with significant mean squares of sums and differences, both additive and dominance components were involved in their genetic control. Therefore, hybridization breeding and selection in segregating generation are recommended for their improvement. Additive (A) and dominance (D) genetic variances were significant in all the studied traits. Estimates of additive (A) were higher than estimates of dominance (D) for days to heading, spikelets/spike and 1000-kernel weight (g.). Generally, it could be concluded that selection procedure in early segregating generations based on accumulation of additive genes would be successful for producing superior inbreeds which could be utilized in hybrid breeding program to exploit non-additive effects [9,23]. However, the dominance were higher than additive for plant height, number of spikes/plants, spike length, number of kernels/plant, number of kernels/plant and grain yield/plant (g). These results indicating the importance role of dominance gene effects in the inheritance of these traits. On the other hand, significant of additive (A) and dominance (D) components indicated that both additive and dominance gene effects were important in the inheritance of these characters. Also, selecting desirable characters may be practiced in the early generations but it would be effective in the late ones. These results are in agreement with those of Koumber [9], Hendawy [23], El-Hosary *et al.* [24] and Hendawy [25].

The values of $(A/D)^{0.5}$ were higher than units for days to heading, spikelets/spike and 1000-kernel weight (g) indicating over dominance, However, plant height, number of spikes/plants, spike length, number of kernels/plant and grain yield/plant (g) was less than unity indicating the existence of incomplete and partial dominance effect (Table 3) similar results were obtained by Abdel-Sabour *et al.* [26] and Hamada *et al.* [27].

Phenotypic (σ^2_{Ph}) and Genotypic (σ^2_g) Variance: Data of phenotypic (σ^2_{Ph}), genotypic $(\sigma_g)^2$ variances and broad and narrow-sense heritability for all the studied traits in wheat crosses are presented in Table 4.The σ^2_{Ph} was greater than σ^2_G for all the studied characters. These results indicated that, the environment had an important role in the expression of these characters and the diverse genotypes can provide materials for a sound breeding programme. These results are in harmony with those obtained by Kotal *et al.* [28] and Zaazaa *et al.* [29], the highest values of σ^2_{Ph} and σ^2_g were recorded for

1000-kernel weight (g) (4868.27) and number of kernels/plant (2991.62) respectively. While, the lowest one was shown by number of spikes/plants (3.00). Genotypic variance indicates the genetic variability present in various quantitative traits without the level of heritability. Genotypic(σ^2_G) variance together with heritability estimates would give the best indication of the amount of gain due to selection.

Heritability: The efficacy of the selections of both yield (a quantitative character) and the yield components depend on the genetic variation and percentage of heritability. Heritability estimates were high It is necessary to identify the components that create the phonotypical difference in order to calculate the genetic variability and heritability based on that variation. In the present investigation broad sense heritability was estimated for various traits. Estimates broad sense heritability (Table 4) showed that it was more than 60 % for all the studied characters. Estimation of broad-sense heritabilities indicated higher importance of genetic effects in control of traits except 1000-kernel weight (g.) (63.74%) was medium which indicated that 1000-Kernel weight (g.) depended highly to environmental factors. Days to heading showed highest heritability (99.53. Comparison between broad and narrow-sense heritabilities revealed equal importance of additive and non-additive effects in genetic control of characters that disagreement with results of degree of dominance estimation High heritable estimates for grain yield per plant were found by Riaz and Chowdhary [30], which support the present findings, intermediate estimates were reported by Mahmood and Chowdhry [31].The narrow sense heritability was high number of days to heading and number of spikelets/spike and moderate for plant height, spike length, number of kernels/plant, grain yield/plant (g) and 1000-kernel weight (g) while, it was low for number of spikes/plants. The high estimates of narrow-sense heritability indicated that the kind additive genetic variance was high while, the low estimates of narrow-sense heritability indicated that the kind additive genetic variance was low compared with dominance genetic variance. These results are in line with those obtained by Adel-Nour [32], Al-Saffar and Al-Sawaf [33] and Foroozanfar and Zeynali [34].

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