

Research Note

Genetic variability, heritability and association studies in bread wheat (*Triticum aestivum* L.) genotypes

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Abstract

A field study was carried out under rainfed conditions during the growing seasons 2010/11 and 2011/12 in Setif (Eastern part of Algeria) to study the genetic variability, heritability and expected genetic advance for ten traits in 29 bread wheat genotypes. The genotypes showed wide range of variation for all the traits. Genetic coefficient of variation ranged from 1.55 for days to 50% heading to 15.86 for number of spikes per plant. Highest values of heritability were observed for chlorophyll content (60.44%), spike length (63.05%), number of spikes per plant (61.19%), number of grain per spike (67.65%), grain yield (63.96%) and thousand kernel weight (65.35%). The genetic gain ranged from 1.73% for days to 50% heading to 68.55% for number of spikes per plant. The traits plant height, number of spikes per plant and thousand kernel weight showed high heritability and genetic coefficient of variation along with high genetic advance. Results also revealed a positive genotypic association for grain yield with chlorophyll content (0.601), plant height, (0.331), spike length (0.301) number of spikes per plant (0.883), thousand kernel weight (0.468) and harvest index (0.561). Path analysis identified that plant height (1.135) and number of spikes per plant (1.122), exhibited the highest direct effect on grain yield. Therefore, these traits could be considered as suitable selection criteria develop high yielding genotypes.

Keywords: PCV, GCV, Genetic advance, Genotypic and Phenotypic correlation, Yield components.

Wheat is an important cereal and main food crop for people over the entire world. Materialization of wheat yield fluctuates widely as a result of its interaction with environment because grain yield in wheat is a polygenic inherited trait and is the product of several contributing factors affecting yield directly or indirectly (Akram et al., 2008). The need and importance of wheat is increasing day by day due to increase in human population. Different methods could be used to increase cereal production, such as increasing area of production, effective cultural practices, and using improved cultivars (Benbelkacem, 1996; Hannachi et al., 2013). Use of varieties with better yield potential and wide range of adaptability is of prime importance for increasing wheat production. Thus development of high yielding wheat cultivars has always been a major objective of wheat breeding programs throughout the world (Bhutta, 2006). Generating information about the genetic variability, relationships and mechanisms of inheritance of the genetic traits involved is the key task in genetic improvement of any crop plant. The knowledge of heritability helps the plant breeder in predicting the behavior of the succeeding generation and making desirable selections. Thus, genetic advance is yet another important selection parameter that aids breeder in a selection program. According to Evans and Fischer (1999), knowledge of genetic association between grain yield and its components under water limited environments play significant role in identifying appropriate indices for selecting wheat varieties. Genotypic and phenotypic correlations are important statistical methods in determining the degree to which various yield contributing traits are associated and which can help wheat breeders in selection for higher yields. Throughout the years, many physiological, morphological and developmental traits have been suggested to be useful in improving drought tolerance (Ludlow and Muchow, 1990). Genetic advance is also of

considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection (Hamdi et al., 1992). The present research with nine wheat genotypes and their 20 F₁ crosses was conducted to estimate the level of genetic coefficient of variation, heritability and genetic advance, and to get information on the correlation of yield components with grain yield for the purpose to ascertain and develop appropriate selection indices for the increased grain production under rainfed conditions.

This investigation was undertaken to estimate statistical genetic parameters for yield and its component characteristics in Line x Tester analysis in bread wheat. The experimental work was conducted at the Field Crop Institute, Agricultural Experimental Station of Setif (ITGC-AES, 36°12'N and 05°24'E and 1.081msl), Algeria. In 2010/11 crop season for achieving crosses and in 2011/12 season for evaluating F₁ hybrids plants. Nine bread wheat genotypes involving five female parents, *viz.*, Acsad₉₀₁, Acsad₈₉₉, Acsad₁₁₃₅, Acsad₁₀₆₉ and Ain Abid and four male parents *viz.*, Mahon-Demias, Rmada, Hidhab (HD₁₂₂₀) and Wifak were the source material of this investigation (Table 1). The parents were chosen on the basis of wide variability existing between them for the yield contributing traits for this study. Resulting 20 hybrids along with their parents were planted in a randomized block design with three replications. Each genotype was planted in one row of 2.50 m length by 0.30 m between rows and 0.15 m between plants. The recommended package of practices and cultural operations were followed during its growth. At maturity, five guarded plants

were randomly selected from each plot and data were collected for chlorophyll content (CCI), estimated with a CCM-200 (Opti-Sciences, Tyngsboro, Massachusetts, USA); proline content ($\mu\text{g/g}$ fresh weight) measured by method of Monneveux and Nemmar (1986); plant height; spike length; number of spikes per plant; 1000 grain weight; kernel per spike; harvest index and grain yield.

Data recorded for various parameters were analyzed following Steel and Torrie (1984) to establish the significant differences among genotypes including crosses. Genotypic variance (σ^2_g), phenotypic variance (σ^2_p), genotypic coefficient of variation (GCV %), phenotypic coefficient of variation (PCV %), broad sense heritability ($h^2_{(bs)}$ %) and genetic advance in per cent mean (GAPM) were estimated by the formula suggested by Singh and Chaudhary (1985). The estimate of GCV and PCV were classified as low, medium and high (Sivasubramanian and Madhavamenon, 1973). The heritability was categorized as suggested by Robinson *et al.* (1949). Again, genetic advance was classified by adopting the method of Johnson *et al.* (1955). Genotypic and phenotypic correlations between traits were calculated using variances and covariances according to Singh and Chaudhary (1985). Path coefficient analysis was performed according to the method of Dewey and Lu (1959) by solving simultaneous equations using genotypic correlations.

The result of variance analysis of ten yield related traits for the twenty-nine genotypes (nine parents and twenty F_1 's) showed significant differences between genotypes for all studied traits, indicating that there is variability between studied genotypes to measured traits (Table 2). Parents and crosses showed significant effects for all traits. This result implied that this population of wheat cultivars would respond positively to selection.

The genotypic coefficient of variation (GCV) ranged from 1.55% to 15.86% and phenotypic coefficient of variation (PCV) from 1.95% to 25.36% (Table 2). The result of genotypic coefficient of variation revealed that number of spikes per plant exhibited highest genotypic coefficient of variation (15.86%) similar with the studies of Kashif and Khaliq (2004) followed by chlorophyll content (13.73%), number of grains per spike (13.16%), grain yield (11.97%) and plant height (10.37%). The highest phenotypic coefficient of variation was found for proline content (35.26%) followed by number of spikes per plant (29.21%), grain yield (28.45%) and chlorophyll content (23.33%). The high PCV and GCV observed are evident from their high variability that in turn offers good scope for selection (Table 2). In their study, Ali *et al.* (2008)

reported high GCV and PCV estimates for grain yield per plant, number of productive tillers per plant and number of grains per spike. The lowest GCV and PCV were recorded for days to heading (1.55% and 1.95%), indicating difficulty of improvement for this traits through selection (Table 2). The PCV values were higher than GCV values for all the traits which reflect the influence of environment on the expression of traits.

Heritability is a useful quantitative parameter, which considers the role of heredity and environment determining the expression of a trait (Allard, 1960). Effective selection can be achieved only when additive effects are substantial and environmental effects are small. Heritability estimates ranged from 3.66% for proline content to 65.34% for plant height (Table 2). Days to 50% heading (63.91%), thousand kernel weight (60.42%), number of grains per spike (56.30%) and spike length (52.70%) also, gave relatively higher broad sense heritability values emphasizing that the additive genetic variation was the major component of genetic variation in the inheritance of these traits and the effectiveness of selection in the early segregating generations of the studied hybrids for improving these traits (Panse, 1957). High heritability estimates for plant height (Tripathi *et al.*, 2011), days to 50% heading (Baranwal *et al.*, 2012), thousand kernel weight (Ashraf *et al.*, 2002), number of grains per spike (Abinasa *et al.*, 2011) and spike length (Ali *et al.*, 2008), were also, reported.

Expected genetic advance indicates the expected genetic progress for particular trait under selection cycles and measures the extent of its stability under selection pressure. Altogether a different trend was noticed for the values of expected genetic advance (Table 2). The highest value was recorded in total number of grains per spike (20.34%) and lowest for days to 50% heading (2.57%). Chlorophyll content (16.71%), plant height (17.26), number of spikes per plant (17.73%) and thousand kernel weight (15.76%) also gave high values. Johnson *et al.*, (1955) have reported that heritability estimates along with genetic advance will be more useful than heritability value alone in selecting best individuals. High heritability along with moderate genetic advance was noticed for spike length suggesting predominance of additive and non-additive gene action in the expression of this trait. Therefore, this trait can be improved by mass selection. High heritability accompanied by low genetic advance for days to 50% heading is indicative of predominance of non-additive gene actions which could be exploited through heterosis breeding. Similar findings have been reported by Eid (2009) and Rangare *et al.* (2010). Besides, Akanda *et al.* (1997) reported that high genotypic coefficient of variation along with high heritability

and genetic advance provide better information than other parameters alone. In the present study, plant height, number of grains per spike and thousand kernel weight showed high genetic advance in conjunction with high heritability and genotypic coefficient of variation (Table 2). These traits are the most important quantitative traits to be taken into consideration for effective selection in wheat. Similar results have been reported by Ali *et al.* (2008) and Sharma and Garg (2002). On the other hand, low genotypic coefficients of variation, heritability and genetic advance manifested by proline content and harvest index suggest that these traits cannot be relied upon for the purpose of selection.

The knowledge of association and relationship between grain yield and its components is of paramount importance to the breeder for making improvement in complex quantitative trait like grain yield for which direct selection is not much effective. Hence, association analysis was undertaken to determine the direction of selection and number of traits to be considered in improving grain yield. The results of phenotypic and genotypic correlations among different attributes are presented in Table 3. The genotypic and phenotypic associations of grain yield with chlorophyll content (0.601 and 0.223), plant height, (0.331 and 0.464), spike length (0.301 and 0.491) number of spikes per plant (0.883 and 0.850), thousand kernel weight (0.468 and 0.305) and harvest index (0.561 and 0.292) were positive and significant both at genotypic and phenotypic levels. A strong correlation of these traits with grain yield indicated that, simultaneous improvement of all the traits is possible. Other researchers also reported significant positive association of grain yield per plant with different attributes like number of spikes per plant (Rangare *et al.*, 2010), thousand kernel weight (Baranwal *et al.*, 2012), chlorophyll content (Wani *et al.*, 2011), plant height, (Kashif and Khaliq, 2004), spike length (Shahid *et al.*, 2002) and harvest index (Singh and Diwivedi, 2002). Relationship between grain yield and days to 50% heading (- 0.264 and - 0.376) and number of grain per spike (- 0.640 and - 0.009) was negative at both levels. These results suggested that selection of early heading genotypes would give high grain yield under rainfed conditions.

Path-coefficient analysis using grain yield as dependent variable and other traits as independent variables is presented in Table 4. The highest positive direct effects on yield were exhibited by plant height (1.135) followed by number of spikes per plant (1.122), harvest index (0.800), number of grains per spike (0.577), proline content (0.902), days to 50% heading (0.247) and chlorophyll content (0.224) (Table 4). Kumar *et al.* (1986) also reported highest direct positive effect of plant

height on grain yield in wheat under normal conditions. Positive direct effects of these traits on grain yield indicated their importance in determining this complex trait and therefore, should be kept in mind while practicing selection aimed at the improvement of grain yield. On the other hand, the maximum negative direct effect was exhibited by thousand kernel weight (-0.589), followed by spike length (-0.452) and had a negative direct effect on yield. Similar results were reported by Shahid *et al.* (2002). The highest positive indirect effects on yield were observed for thousand kernel weight via plant height (1.032) and number of spikes per plant (0.850), followed by plant height, number of grain per spike and chlorophyll content through number of spikes per plant (0.721), thousand kernel weight (0.595) and harvest index (0.606), respectively.

From the present study, it is evident that genotypes studied may provide good source of material for further breeding program. Therefore, information on the genetic parameters such as genetic correlation coefficient, coefficient of variation, heritability and genetic advance can help the breeder to evolve suitable cultivars within a short time. On the basis of results as summarized above, it is concluded that traits like number of spikes per plant, plant height and thousand kernel weights can be considered as suitable selection criteria for the development of high yielding bread wheat varieties.

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Table 1. Name, pedigree and origin of the bread wheat parental genotypes

Name	Pedigree	Origin
Lines		
Acsad ₉₀₁	ACSAD529/4/C182.24/C168.3/3/CNO*2/7C//CC/TOB-	ACSAD (Syria)
Acsad ₈₉₉	0S	ACSAD (Syria)
Acsad ₁₁₃₅	ACSAD529/4/C182.24/C168.3/3/CNO*2/7C//CC/TOB-	ACSAD (Syria)
Acsad ₁₀₆₉	1S	ACSAD (Syria)
Ain Abid	PRL/VEE#6//MYNA/VUL/3/PREW ZAHRAI-14//HD2169/BOW'S' AS8189'A'	Spain
Testers		
Mahon-	PLC/RUFF/GTA'S'/RoletteCm17904	Balearic Islands (Spain)
Demias	K134/4/Tob/Bman/Bb/3/Cal/5/Bucc	CIMMYT (Mexico)
Wifak	HD1220/3*Kal/NalCM40454	CIMMYT (Mexico)
HD ₁₂₂₀	Vee's/Bow's//Alondra's/Pavon's	ACSAD (Syria)
Rmada		

Table 2. Estimates of mean values, phenotypic and genotypic coefficients of variation, broad sense heritability and genetic advance for grain yield and its components in bread wheat genotypes.

	MS	Mean	σ_p^2	σ_g^2	PCV (%)	GCV (%)	$h^2_{(bs)}\%$	GAPM
Chlorophyll content (CCI)	114.6**	35.2	67.59	23.50	23.33	13.76	34.78	16.71
Proline content ($\mu\text{g g}^{-1}$)	109.1**	28.6	101.65	3.73	35.26	6.74	3.66	2.66
Days to 50% heading	15,62*	134.4	6.85	4.38	1.95	1.55	63.91	2.57
Plant height (cm)	226.85*	77.4	98.33	64.26	12.82	10.37	65.34	17.26
Spike length (cm)	2.91*	13.2	1.42	0.75	9.05	6.57	52.70	9.82
Number of spikes per plant	23.48*	13.2	14.78	4.35	29.21	15.86	29.45	17.73
Number of grains per spike	152.87*	48.4	71.91	40.48	17.53	13.16	56.30	20.34
Grain yield (g)	39.78*	19.1	29.39	5.20	28.45	11.97	17.69	10.37
Thousand kernel weight (g)	33.22*	30.7	15.04	9.09	12.66	9.84	60.42	15.76
Harvest index (%)	26,90*	38.3	19.05	3.93	11.40	5.17	20.60	4.84

MS: Mean square, σ_p^2 : Phenotypic variance, σ_g^2 : Genotypic variance, PCV: Phenotypic coefficient of variation, GCV: genotypic coefficient of variation, h^2_{bs} : Broad sense heritability and GAPM: Genetic advance in per cent mean. *, **: Significant at 5% and 1% level, respectively.



Table 3. Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients between grain yield and its components in bread wheat genotypes

	<i>ChI</i>	<i>PC</i>	<i>DH</i>	<i>PH</i>	<i>SL</i>	<i>SN</i>	<i>GN</i>	<i>GY</i>	<i>TKW</i>	<i>HI</i>
<i>CCI</i>		0.059	-0.453**	-0.120	0.240*	0.161	0.170	0.223*	-0.149	0.068
<i>PC</i>	-0.095		-0.153	0.174	0.265*	0.172	-0.050	0.117	-0.157	-0.235*
<i>DH</i>	-0.735**	0.565**		-0.013	-0.558**	-0.159	-0.398**	-0.376**	0.210*	-0.315**
<i>PH</i>	-0.438**	-0.224*	0.353**		0.254*	0.568**	-0.491**	0.464**	0.616**	-0.153
<i>SL</i>	0.244*	0.090	-0.485**	0.046		0.331**	0.285**	0.491**	-0.076	0.122
<i>SN</i>	0.295**	0.443**	0.161	0.643**	-0.012		-0.414**	0.850**	0.257*	-0.080
<i>GN</i>	0.160	0.205	-0.403**	-0.973**	0.262*	-0.917**		-0.009	-0.522**	0.387**
<i>GY</i>	0.601**	-0.086	-0.264*	0.331**	0.301**	0.883**	-0.640**		0.305**	0.292**
<i>TKW</i>	-0.280**	-0.083	0.325**	0.909**	-0.149	0.758**	-1.010**	0.468**		0.204
<i>HI</i>	0.757**	0.165	-1.109**	-0.414**	0.644**	0.031	0.557**	0.561**	-0.380**	

CCI: Chlorophyll content, PC: Proline content ($\mu\text{g g}^{-1}$), DH: Days to 50% heading, PH: plant height (cm), SL: Spike length (cm), SN: Spikes number per plant, GN: Grains number per spike, GY: grain yield (g), TKW: Thousand kernel weight (g) and HI: Harvest index. *, **: Significant at 5% and 1% level, respectively.

Table 4. Direct (diagonal) and indirect effect (off-diagonal) of yield contributing characters on bread wheat yield at genotypic level.

	<i>CCI</i>	<i>PC</i>	<i>DH</i>	<i>PH</i>	<i>SL</i>	<i>SN</i>	<i>GN</i>	<i>TKW</i>	<i>HI</i>	<i>Genotypic correlation with grain yield</i>
<i>CCI</i>	0.224	-0.028	-0.182	-0.497	-0.110	0.331	0.092	0.165	0.606	0.601**
<i>PC</i>	-0.021	0.290	0.140	-0.254	-0.041	-0.497	0.118	0.049	0.132	-0.086
<i>DH</i>	-0.165	0.164	0.247	0.401	0.219	0.181	-0.233	-0.191	-0.887	-0.264*
<i>PH</i>	-0.098	-0.065	0.087	1.135	-0.021	0.721	-0.561	-0.535	-0.331	0.331**
<i>SL</i>	0.055	0.026	-0.120	0.052	-0.452	-0.013	0.151	0.088	0.515	0.301**
<i>SN</i>	0.066	-0.128	0.040	0.730	0.005	1.122	-0.529	-0.446	0.025	0.883**
<i>GN</i>	0.036	0.059	-0.100	-1.104	-0.118	-1.029	0.577	0.595	0.446	-0.640**
<i>TKW</i>	-0.063	-0.024	0.080	1.032	0.067	0.850	-0.583	-0.589	-0.304	0.468**
<i>HI</i>	0.170	0.048	-0.274	-0.470	-0.291	0.035	0.321	0.224	0.800	0.561**

CCI: Chlorophyll content, PC: Proline content ($\mu\text{g g}^{-1}$), DH: Days to 50% heading, PH: plant height (cm), SL: Spike length (cm), SN: Spikes number per plant, GN: Grains number per spike, GY: grain yield (g), TKW: Thousand kernel weight (g) and HI: Harvest index. *, **: Significant at 5% and 1% level, respectively.