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Assessing genetic variability, heritability and genetic advance for yield and yield components in common wheat

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Abstract

The present investigation was carried out to study some genetic diversity parameters i.e. the coefficient of variance, heritability and genetic advance for sixteen traits in common wheat. The trial included ten varieties used as phytogenetic material and parents of F1 individuals, whereas F2 individuals are obtained from self – fertilization of F1. The experimentation was conducted in randomized bloc design (RBD) with four replications. Measurements and data notations focused globally on direct and indirect yield components. Analysis of variance revealed significant differences among genotypes for all considered traits. The study showed wide amount of variability for all studied characters. We recorded high magnitude of both PCV and GCV for all the traits except of number of spikelets, spike length and number of grains in linear meter. Moreover, ECV had feeble values except of number of tillers and fertile tillers per plant and number of grains per plant. High values of broad sense heritability associated with high to medium magnitude of genetic advance as per cent of medium were recorded for all traits provided number of grains per plant and per linear meter.

Key words: Common wheat, Morpho –phenologic traits, Genetic diversity, Heritability, Genetic gain.

Introduction

On a worldwide scale, common wheat (Triticum aestivum L), among the cereals, is considered the most cultivated species feeding close to 40 % of the world's population. By their importance in Algerian menus and dishes, cereals in general and common wheat, in particular, occupy a significant part of the Utilized Agricultural Area, especially in the highlands where it has cohabited for a very long time and has become a profitable complement to sheep farming. Various methods and markers can be used to determine the genetic diversity of a species including morphological, biochemical, and molecular markers. Morphophysiological markers are widely used to study genetic diversity in plant species (Singh, G.P 1994; Mwirigi et al., 2009; Dhakar et al., 2012; Fikre et al., 2015; Seyoum and Sisay 2021). Determination of genetic variation in common wheat using morphological traits has been worldwide reported by many researchers (Gill & Brar 1977; Vavilov 1992; Williams et St Clair 1993; MacKey 1993; Zeven 1998; Firouzian et al., 2003; Lang et al., 2004; Garcia-Martinez et al., 2005; Sanchita et al., 2008; Salmi et Haddad 2015; Herison et al., 2018). Up till now, many studies dealt with botanic, morphophysiological and yield potential characterization of native common wheat varieties of Adrar region. However, little had been done in terms of genetic variability parameters studies of which it became a decisive factor for all reproduction program (Sanchita et al., 2008). Therefore, it is important to swipe widely in this direction for identifying the existing genetic capabilities of this local phytogenetic material in order to improve common wheat yield.

Materials and methods

The vegetal material for this trial comprises ten varieties used as parents of series of crossings, of which eight (08) are native to Adrar region, F1 individuals and F2 individuals. The trials were conducted in complete randomized bloc design with three (03) replications at local research station of National Institute of Agricultural Research. Sowing date is in December 29th 2023 distance between grains is 10 cm, while row are distanced every 18 cm. Adopted plot irrigation system is dripping and the frequency of irrigation is two to three times a week, depending on crop requirements and environmental conditions. The crop is conducted under standard technic itinerary and plot harvest was manually done at physiological maturity stage of the crop.

Studied traits:

The studied traits are as follows; tillers ability (Tal. P), Productive tillers (Tal. Ep), Plant height at maturity (H.T), number of grains per spike (Gr.E), number of pikelets per spike (Ept.T), number fertile spikelets per spike (Ept. Ft), spike length (L.E), spike density (D), Thousand grains weight (PMG), earliness to heading and yield (Yld).

Data analysis:

The collected data are subjected to analysis of variance where additive model suggested by Steel and Torrie (1980) is used

Yij = μ + gi + bj+ e(ij), where:
Yij = Observed value of genotype i on bloc j
μ = Trial mean
gi = Effect of genotype i
bj = Effect of bloc j
e(ij) = Residual of model
-The least significant difference (LSD) with p < 5 % was calculated following Steel and Torrie (1980)
LSD 5% = t 5, where:
-Phenotypic variance = $\delta_g^2 + \delta_e^2$ with δ_g^2 as genotypic variance
- Phenotypic, genotypic and environmental coefficient of variation was calculated according to Singh and Chaudhary (1985) formula.
GCV% =(δ_g^2 0.5 /Ȳ)*100 ; PCV% = (δ_P^2 0.5 /Ȳ)*100 ; ECV% =(δ_e^2 0.5 /Ȳ)*100
-Ȳ: is the studied trait mean.
For interpretation of parameters values we utilized Deshmukh et al.. (1986) scale.
-Broad sense heritability (h²bs) was estimated as suggested by Falconer and McKay (1996)
h² (bs) = (δ_g^2 F2 – δ_g^2 F1) / δ_g^2 F2
For values interpretation, we employed the scale of Pramoda and Gangaprasad (2007).
-Genetic advance and genetic advance and GA as % of mean (GAM) were calculated according to Allard (1960):
GA: h² (bs) × $\sqrt{\sigma_p^2}$ × k. with
- $\sqrt{\sigma_p^2}$: Standard deviation of phenotypic variance of 2nd generation (F2)
K = Intensity of selection, the value of which is 2.06 when 5 percent of the individuals are selected from the population, as given by Lush. (1949).
GAM = (GA / Ȳ)*100.

Results and discussion:
Different variance sources, coefficient of variance and the least significant difference for all the sixteen characters are given in table 1. The analysis of variance revealed high significant differences between the genotypes means, resulting in significant effect of genotype for all considered characters (Table 1). Accordingly, the results showed substantial amount of genetic variability among genotypes studied, offering real possibilities of genotypes' improvement through hybridization and selection. Significant differences among genotypes for these traits were earlier mentioned for plant height (Sharma et al., 2020; Dragov et al., 2022), productivity tillering, spike length and number spikelets per spike (Dave et al., 2021; Chauhan et al., 2023; Kumawat et al., 2023), grains number per spike and grains weight per spike (Prasad et al., 2021; Ashebr Baye et al., (2020); Jalal A. Al-Tabbal et al., 2011)), thousand grains weight (Dragov et al., 2022; Sharma et al., 2020; Harshardhan et al., 2016). However, the mean square due to block was significant, only for two traits viz; plant height at maturity period and number of spikelets per spike.

Mean performance:
Regarding range as per cent of mean, it shows an important contrast of diversity among characters ranging from around 12.40 % for number of spikelets per spike to heading up to more than 88 % for mean rate of fertile tillers. High magnitude of diversity (> 20 %) was recorded for number of fertile tillers per plant, yield and number of grains per plant, spike length, tiller capacity, spike density, weight and number of spike grains. thousand grains weight and plant height, respectively. However, relatively low values were recorded for number of spikelets per spike. Indeed, high variability among this material for fourteen traits can constitute the base for a sound breeding program and select genotypes with desired traits for further improvement common wheat yield in such environmental conditions. Comparable findings have been in Harshwardhan et al., (2016); Prasad et al., (2021); Chauhan et al., (2023).
The main reference values (minimum, maximum and maximal) of the studied characters, Phenotypic, genotypic and environmental coefficient of variation, broad sense heritability, genetic gain and genetic advance as per cent of mean for sixteen traits are given in table 2.
A scale was established by Deshmukh et al (1968) regarding phenotypic and genotypic coefficient of variation (PCV, GCV) allow measuring the results extent. Accordingly, values were classified as high (> 20 %) moderate (10 to 20 %) and feeble (< 10 %). High to moderate magnitudes of GCV and PCV means that existing material has a wide range of polymorphisme indispensable for a promising program of selection.
However, low values of these parameters show that available variability rate is feeble within this material and the need to resume works of variability creation (recombination, gene mutation, chromosomal segregation…) followed by selection (Tiwari et al., 2012). Apart from the total number of tillers, fertile tillers and tillers to spike ratio, values of phenotypic coefficient of variation were slightly higher than genotypic coefficient of variation. Furthermore, environmental coefficient of variation values were generally feeble except of these traits, resulting in environment influence on the expression of characters was low for most of these studied characters.

Table 1: Analysis of variance for yield and its contributing traits in common wheat.

Srce/Trait	Tillers-Pte	Spikes/Pte	% Spiks/tillers	Pte-Ht	T Spklts-Spike	Spike-Length	Dens	Wt-Spike Grains	Grains/Spiklt	Grains/Spkls	Grains/Pte	Earliness to heading	TGW	Yield
Total	920.70	604.92	10 839.77	2 748.02	59.24	75.04	327.19	14.69	3 631.65	7.85	608 645.64	1 024,90	993.51	22 752.21
Variety	382.0**	389.67**	7 276.04**	1 564.5**	34.30**	61.7**	256.77	12.16**	1 256.6**	3.69*	264 433.2**	941,77**	453.6**	10 653.56**
Rep	79.35	9.39	116.84	387.03*	11.68**	1.54	10.01	0.35	460.47	0.62	32 984.78	24,33	67.19	1 203.28
Error	459.35	205.87	3 446.89	796.45	13.26	11.76	60.41	2.18	1 914.60	3.54	311 227.63	83,13	472.73	10 895.36
LSD	0.57	1.87	7.66	3.68	0.47	0.45	1.01	0.19	5.71	5.71	72.74	1,84	2.83	13.61
CV %	23.57	25.15	28.28	6.98	3.07	6.54	7.12	12.73	13.10	12.26	26.38	2,10	11.61	25.76

N.B : (*) significant at 0.05 level. (**) significant at 0.01 level.

Table 2: Genetic variability parameters for yield and its contributing traits in wheat.

Trait./Parameter	Tillers-Pte	Spikes/ Pte	% Spiks/tillers	Pte-Ht	Spklts - Spike	**Spike-Length**	**Dens**	Wt-Spike Grains	Grains/ Spike	Grains/ Spkls	Grains/Pte	Earliness to heading	TGW	Yield
Mean	19.18	12.03	75.16	74.45	22.65	10.10	21.39	2.31	64.66	2.94	386.37	76.68	38.15	64.35
Range	16.17 - 23.67	8.00-16.70	28.67-100.00	70.05-86.11	21.17-24.00	8.12-12.42	18.00-25.94	1.98-2.68	56.0-74.0	2.35-3.34	312.46-573.60	72.25-85.16	32.40-43.79	34.10-95.28
% range to Mean	39.11	80.47	84.43	21.58	12.51	42.59	37.12	30.40	27.84	33.51	67.59	16.84	29.86	95.08
Phenotyp variance	43,21	21,14	732.81	305.66	4,16	4.94	50.85	0,73	289,09	0,56	44380,21	68.01	104,91	1496,26
Genotyp variance	27,04	15,94	602.68	289.45	3,80	4.25	47.73	0,67	268,29	0,51	44185,09	63.47	92,80	1301,13
CVP %	41,98	38,24	67.79	23,48	9,28	11,67	31,82	39,11	26,58	25,33	**41,36**	10,76	29,99	48,55
CVG %	33,21	33,21	61.48	20,65	8,87	10,02	31,04	37,46	25,60	24,25	**41,26**	10,65	28,21	45,27
CVE %	55,61	23,77	28.57	11,19	2,73	5,99	7,02	11,24	7,13	7,33	**2,74**	1,47	10,19	17,53
H2 %	0,63	0,61	0.97	0,95	0,91	**0,73**	0,94	0,92	0,93	0,92	**0,99**	0,93	0,88	0,87
GA	8,31	7,78	13.88	9,41	5,71	5,16	10,85	11,76	9,81	9,45	**13,13**	6,27	9,93	12,42
GG %	53,08	64,71	32.39	12,63	25,96	51,49	48,44	539,49	15,33	320,67	**2,58**	8,18	29,08	15,59

Wolde et al., (2016), this is due to the genotype environment interaction. Abinasa et al., (2011), GCV and PCV values convergence shows a minor environmental effect on the expression of these traits and they are controlled by additive gene effects. However, wider difference between the values of GCV and PCV indicate non-additive genetic effects (Governed by dominance genes).

Among fourteen traits, eight possess high values (> 20 %) of phenotypic and genotypic coefficient of variation. It is about yield (48.55 and 45.27 %), number of tillers per plant (41.98 and 33.21 %), number of grains per plant (41.36 and 41.26 %), weight of spike grains (39.11 and 37.46 %), number of plant spikes (38.24 and 33.2 %), thousand grains weight (29.99 and 28.21 %), number of grains per spike (26.58 and 25.60 %), and number of grains per spikelet with 25.33 and 24.25 %, respectively. Additionally, two traits have moderate values (10 to 20 %), namely main spike length (11.67 and 10.02 %) and earliness to heading (10.76 and 10.65 %). Meanwhile, the magnitude of number of spikelets per spike was feeble (< 10 %). In terms of environmental coefficient of variation, its values were mostly feeble and exceptionally moderate to high. In fact, local environmental conditions have apparently significant effect on number of total and fertile plant tillers expression of which it stabilized during early advanced stages which coincides, to a large extent, with progressive resumption of high temperatures. Similar results were reported for the yield elements in early generations in Dragov et al., (2022). Moderate PCV and GCV values for the earliness to heading per main spike are in harmony with those obtained by Bendjama and Ramdani (2022). Feeble values of PCV and GCV for number of spikelets per spike are found (in late sown conditions) by Azimi et al., (2017). Indeed, high magnitude of GCV and PCV indicate existing real chance for selection of promising elite individuals for improvement of the traits.

Heritability is one of the crucial genetic variability parameters applied in breeding and selection for improving genotypes. According to Pramoda and Gangaprasad, (2007) scale, heritability values less than 0.4 (40 %) are considered feeble, average between 0.4 and 0.6 (40 to 60 %), high from 0.6 to 0.8 (60 to 80 %), and very high for

values above 0.8 (80 %). All traits were characterized by a high magnitude of heritability (> 0.80), except for spike length, which has high values of which number plant grains had the highest with 0.99 followed by plante height (0.95) , main spike density (0.94), number spike grains and earliness to heading (0.93), weight of grains per spikelet, weight of spike grains and earliness to heading (0.92), number of spikelets per spike (0.91), thousand weight grains (0.88), mean yield (0.83) and followed by spike length with 0.73. Nevertheless, Weak to moderate heritability values were obtained by Ahmad et al. (2023). According to Khan and Naqvi (2011), the direct selection on one single plant in early generations could be very effective for a character highly heritable. Present findings are comparable with Ali et al., (2008); Wolde et al., (2016), they also suggest that selection by the traits productivity tillers, plant height thousand grain weight can improve yield. Moreover, several researchers (Bhargava et al., 2003; Shukla et al., 2004) highlight the usage only of high heritability is not sufficient for selection and plant improvement programs, in early generation and must be associated with other genetic parameter especially genetic gain. Effectively, when high broad sense heritability values were supported by similar genetic advance magnitudes offer very solid real opportunities and consolidate such wheat improvement program.

According to Johnson et al., (1955) the estimates of genetic advance and genetic advance as percent of mean were classified as low < 10 %, moderate (10-20 %) and high (> 20). High to moderate genetic gain as percent of mean above 20 % associated with high values of heritability were reported for number of spikes per plant (64.71), number of tillers per plant (53.08 %), spike length (51.49 %), main spike density (48.44 %), thousand grains weight (29.08), number of spikelets per spike (25.92), number and weight of grains per spike. Moreover, Three traits possess mean GAM values i.e. yield (15.59 %),number of grains per spike (15.33 %) and plant height (12.63 %). However, two traits had weak values of genetic advance (<10%), namely number of grains per plant and earliness to heading. Moreover, these values have the same tendency as those of the above genetic parameters, except for heritability in the narrow sense. Furthermore, high heritability accompanied with low expected genetic advance signals influence of dominance genetic effects (Salman et al., 2014), which are suitable for heterosis breeding (Ilyas et al., 2019).

Within trial conditions, yield with both direct and indirect yield components traits, were characterized with high magnitude of genotypic parameters (genotypic and phenotypic coefficient of variation. heritability and genetic advance) and associated with relatively low environmental coefficient of variation except of spikes, tillers and tillers to spikes ration per plant. Consequently, direct selection during early generation based on phenotype is effective and would lead to a successful improving of these traits. For Mortez et al., (2018); Dragov et al., (2022), traits productivity, with high or medium genetic advance and high heritability, are controlled by several major genes with additive genetic action and effective selection is possible.

Conclusion

From the above results, it could be concluded that a high amount of genetic variability exists among these genotypes for almost the considered traits. The high magnitude of heritability of broad sense (> 60 %) was recorder for all traits except of density and length spike suggests a strong genetic effect for expression of the studied characters. Furthermore, substantial values of heritability associated with high to medium score of genetic gain as percent of mean (> 10 %) were noticed for nearly all studied traits, especially number of fertile tillers, plant height, number of spikelets per spike, thousand grains weight and yield grain. Consequently, all these mentioned traits expression are most likely governed by several additive genes, resulting in direct selection on individual plant in early generation lead potentially to a genetic improvement in common wheat grain yield.

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