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Heritability, Trait Association and Path Coefficient Studies for Some Agronomic Characters in Synthetic Elite Lines of Wheat (*Triticum aestivum* L.) Under Rainfed Conditions.

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Research Article

ABSTRACT

50 synthetic elite lines of wheat were evaluated to their genetic variability, heritability for quantitative traits and the direct and indirect contributions of important yield components towards grain yield to identify the characters of utmost importance that may be used as selection criteria in a wheat breeding program. The experimental material consisted of. Agronomic characters were recorded including days to heading, days to flowering, days to anthesis, days to physiological maturity, grain filling period, plant height, plant biomass, number of spikes / plant, number of spikelets /spike, spike length, harvest index, 1000-grain weight and grain yield / plant. Harvest index exhibited highest heritability value of 83.31% while 1000-grain weight showed minimum value of 42.32%. Grain yield correlated positively with flag leaf area, plant height, biomass, number of spikes, spike length, number of spikelets / spike, number of grains / spike, 1000-grain weight and harvest index. Path coefficient analysis indicated that grain yield had a positive direct effect with spike length and number of grains per spike. The traits having a positive direct effect on grain yield can be considered as a selection criteria for evolving high yielding wheat elite genotypes.

INTRODUCTION

Synthetic hexaploid wheat (*Triticum aestivum* L.) has proven to be very useful as a source of resistance to diseases and pests, as well as for tolerance to environmental stresses. Introgression of alleles from synthetic hexaploids into wheat has modified the expression of quantitative traits such as grain yield and its components. This suggests that introgression of germplasm from *A. tauschii,* durum, or a combination of both into wheat may result in positive transgressive segregation for yield. Hence, synthetic hexaploids are a promising source to improve quantitative traits in wheat [1, 2].

Towards a clear perceptive of the type of plant traits, their association and causal effect on dependent variable is a reliable statistical technique which provides means not only to quantify the interrelationships of different yield components but also indicates whether the influence is directly reflected in the yield or takes some other pathway for ultimate effects [3]. Path analysis can be used to calculate the quantitative impact on yield of direct or indirect effects caused by one or the other components [4]. Scientists in wheat [5], barley [6], bean [7] and cowpea [8] commonly use path coefficient analysis to explain clearly the relations among yield components. Several studies involving genetic correlation and path coefficient analysis have been conducted in wheat. Number of grains had an

important indirect effect via grain weight [9]. Similarly, yield was strongly and positively correlated with spike length, grains per spike, plant height and flag leaf area [10].

Heritability plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value. It is understood that only the phenotypic value can be measured directly while breeding values of individuals are derived from appropriate analyses. It is the breeding value, which determines how much of the phenotype would be passed onto the next generation [11]. There is a direct relationship between heritability and response to selection, which is referred to as genetic progress. The expected response to selection is also called as genetic advance (GA). High genetic advance coupled with high heritability estimates offers the most effective condition for selection [12]. The utility of heritability therefore increases when it is used to calculate genetic advance, which indicates the degree of gain in a character obtained under a particular selection pressure. Thus, genetic advance is yet another important selection parameter that aids breeder in a selection program [13]. Phenotypic and genotypic variance, heritability and genetic advance have been used to assess the magnitude of variance in wheat breeding material [14].

Therefore, present research was conducted to identify the characters of utmost importance which may be used as selection criteria in a wheat breeding program by studying heritability and genetic advance and further to evaluate there casual effects on grain yield, the ultimate objective of every breeding program.

MATERIALS AND METHODS

Plant material

The experimental material consisted of 50 synthetic elite lines of wheat for which seeds were obtained from CIMMYT, Mexico. Experimental material was sown at premises of Barani Agricultural Research Station, Fatehjang, Attock, Pakistan. The experiment was sown according to Randomized Complete Block Design with three replications during the wheat sowing season of 2012-13 under rainfed conditions, where source of irrigation is natural rainfall. The experimental unit comprises of $7.2m^2$, having six rows of each entry of 4 meter in length and 30cm apart. Ten guarded plants from each experimental unit were selected for recording data of days to heading, days to flowering, days to anthesis, days to physiological maturity, grain filling period, flag leaf area, plant height, biomass, number of spikes, spike length, spikelet per spike, number of grains, grain yield, 1000-grain weight and harvest index.

Statistical analysis

Correlation coefficient studies were done according to Kown and Torrie [38]. Path analysis was carried out according to Dewey and Lu [15]. Grain yield was the dependent variable and number of spikes, spike length, spikelet per spike and number of grains were taken as the causal variables.

Broad sense heritability (h^2_B) [16] and genetic advance under selection (GA) [17] were estimated in 50 wheat genotypes by partitioning the variance in plant traits into between accessions and within accessions components and applying these in the following function: $h^2_B = Vg/Vp$, where Vg genetic variance = (variance between-accessions - variance within-accessions)$/n$, Vp phenotypic variance = [(variance between-accessions – variance within-accessions)/n] + variance within-accessions, n = number of replications. [39]

$$Genetic\ advance\ (GA) = K \times (Vp)^{0.5} \times h^2_B ,$$

where K = selection intensity at 5% (2.06), Vp = phenotypic variance, h^2_B = heritability (broad sense).

Phenotypic coefficient of variability (PCV) =

$$Phenotypic\ variance\ (Vp) / Mean\ value\ of\ the\ trait \times 100$$

Genotypic coefficient of variability (GCV) =

$$Genotypic\ variance\ (Vg) / Mean\ value\ of\ the\ trait \times 100$$

RESULTS AND DISCUSSION

Correlation and path coefficients

Simple correlation coefficients between all possible combinations of the four yield components are shown in Table 1. Results indicate that grain yield is positively and significantly correlated with spike length, number of spikes per plant, number of spikelets per spike and number of grains per spike. The four components also showed positive correlations with each other. The high positive correlation coefficient indicates that selection based on number of spikes, spike length, number of spikelets per spike and number of grains per spike have an equal contribution towards increasing the grain yield.

The pathway through which the four yield components operate to produce their phenotypic association with grain yield reveal direct and indirect contribution (Table 2) The correlation coefficient of grain yield with spike length (r = 0.521) consists of four components, direct effect points out that with other variables held constant, increasing average spike length will increase seed yield (P_{15} = 0.219**). The indirect effect through spikes per plant and spikelets per spike seems to be negligible.

However, the influence via number of grains per spike is positive and more; the net effect in increasing the yield seems to be contributed by number of grains per spike which may be greater because of large size of spikes, but a longer spike does not seem to have more spikelets. Although the coefficient of correlation between grain yield and spikelets per spike is positive (r = 0.519) when the correlation is partitioned into its components, the spikelets per spike had a non-significant direct effect on grain yield, while indirect effect of spike length, number of spikes per plant and increase in spike length is contributing little (0.041 and 0.029). The main contribution is from number of grains per spike (r = 0.569). Comparing grain yield and number of spikes the correlation coefficient was r = 0.488. Number of spikes have a non-significant indirect effect on grain yield. At this stage again the main contribution in yield is through indirect effect of number of grains (r = 0.361). Number of grains had direct significant effect on grain yield (P_{45} = 0.711**).

Correlation and path coefficient analysis can be used as an important tool to bring information about appropriate cause and effects relationship between yield and some yield components [18]. In the present study, grain yield was positively and significantly correlated with spike length, number of spikelets per spike and number of grains per spike. This is in good agreement with the findings of Gupta and Khan [18, 19]. High positive correlation coefficient reveals that selection based on number of spikes, spike length, number of spikelets per spike and number of grains per spike has an equal contribution towards increasing the grain yield. Path coefficient analysis provides an effective means of partitioning correlation coefficients into unidirectional pathway and alternate pathways and thus permits a critical examination of specific factors that produce a given correlation and can be successfully employed in formulating an effective selection strategy [20].

Results show that the direct effects of grain yield with spike length were positive indicating that increase in spike length is directly associated with increase in number of spikelets per spike, grain numbers per spike, grain weight and ultimately the grain yield per plant [3]. Direct effects of spikelets per spike on grain yield were non-significant. The total effects of spikelets on grain yield have a value of 0.519, which was mainly due to its indirect effect through grains per spike. Hence, spikelets cannot be regarded as a reliable source of getting high yield in wheat [21]. The direct effects of number of spikes on grain yield per plant were non-significant (0.060). Total correlation coefficient (0.488) between grain yield and number of spikes was mainly because of indirect effect through number of grains per spike. Therefore, selection for spikes cannot guarantee for high yield. Number of grains has a direct effect on grain yield as reflected by high correlation (0.711) value. Number of grains per spike did increase substantially over the selection period, showing that more grains per spike could aid in conferring high yields of newer germplasm [22]. Additive effects as well as genetic interactions have been reported to condition grains per spike [23].

The highest and positive direct effect on yield comes from kernel number per spike [6, 24]. This led us to suggest that kernel weight and kernel numbers are two easily measured characters that would be valuable in selecting for yield improvement. Other comparisons revealed negligible indirect effect that include spike length, number of spikes and number of spikelets per spike.

Table 1: Phenotypic correlation (r) between yield and yield components.

Character	Correlation coefficient (r)
Number of spikes	0.765**
Spike length	0.446**
Number of spikelets spike	0.474**
Number of grains per plant	0.935**

Table 2: Direct and indirect influences of spike length, No. of spikes plant^{-1}, No. of spikelets spike^{-1} and No. of grains plant^{-1} on grain yield.

Grain yield vs. spike length	0.521
Direct effect, P_{15}	0.219**
Indirect effect via No. of spikes plant^{-1}, $r_{12}P_{25}$	-0.022
Indirect effect via No. of spikelets spike^{-1}, $r_{13}P_{35}$	0.034
Indirect effect via No. of grains spike^{-1}, $r_{14}P_{45}$	0.290
Total	0.521
Grain yield vs. No. of spikes	0.488
Direct effect, P_{35}	0.060 ^{ns}
Indirect effect via spike length, $r_{13}P_{15}$	0.126
Indirect effect via No. of spikelets spike^{-1}, $r_{23}P_{25}$	-0.059
Indirect effect via No. of grains spike^{-1}, $r_{34}P_{45}$	0.361
Total	0.488
Grain yield vs. No. of spikelets spike^{-1}	0.519
Direct effect, P_{25}	-0.120 ^{ns}
Indirect effect via spike length, $r_{12}P_{15}$	0.041
Indirect effect via No. of spikes plant^{-1}, $r23P35$	0.029
Indirect effect via No. of grains spike^{-1}, $r_{24}P_{45}$	0.569
Total	0.519
Grain yield vs. No. of grains	0.734
Direct effect, P_{45}	0.711**
Indirect effect via spike length, $r_{14}P_{15}$	0.089
Indirect effect via No. of spikes, $r_{24}P_{25}$	-0.096
Indirect effect via No. of spikelets spike^{-1}, $r_{34}P_{35}$	0.030
Total	0.734
Residual effect P_{xy}	0.620

Heritability

Broad sense heritability (h^2_B %), genetic advance under selection (GA) and genetic advance under selection as percentage of the mean (GA %) are shown in Table 3. High heritability was estimated for days to heading (79.22) and the expected genetic gain upon selecting the best 5% for days to heading was 23.85. High heritability (broad sense) estimates 76.47 with genetic advance of 21.40 were obtained for days to flowering. Number of spikes showed a high value of heritability (70.76) along with 2.60 of genetic advance. The value of the heritability obtained for grain yield was 77.45; this value can be considered as high with 7.25 of genetic advance. Estimation of heritability for number of spikelets per spike in the wheat population gave a high value (82.02) with high genetic advance of 71.46. For harvest index per plant the heritability estimate was 83.31, which can be considered as a high value. Upon selecting the best 5% of the wheat lines, the expected genetic gain for harvest index of 2.93 was noted.

Heritability estimate was moderate for days to anthesis (69.82) and the expected genetic gain for days to anthesis would be 16.18. Physiological maturity showed moderate value for heritability (63.49) with 14.16 of genetic advance. Heritability estimate obtained for flag leaf area was moderate (67.22) with a low genetic advance (7.16).

The broad sense heritability (h^2_B %) for plant height in the wheat population gave a value of 49.31%. Expected genetic gain upon selecting the tallest 5% of the wheat lines would be 15.86. Spike length gave an estimate of43.72, which is considered a low value while expected genetic gain for spike length was 2.71. Heritability for biomass gave an estimate of 45.43, which was considered as low. The expected genetic gain upon selecting the best 5% of the wheat lines for biomass was 2.53. The broad sense heritability for number of grains gave an estimate of 42.54 which was considered to be a low value. The genetic advance of 14.96 was observed. The value of heritability for 1000-grain weight was obtained

as 42.32, which was a low value. The expected genetic gain upon selection for 1000-grain weight would be 20.38.

Table 3: Mean squares, means, genotypic and phenotypic coefficients of variability, heritability and genetic advance.

Agronomic traits	Mean squares	Mean	GCV	PCV	h^2_B	GA
Days to heading	214.906**	101.49	167.76	211.75	79.22	23.85
Days to flowering	184.549**	103.01	137.01	179.15	76.47	21.40
Days to anthesis	126.698**	103.96	85.09	121.87	69.82	16.18
Physiological maturity	117.320**	121.43	61.34	96.61	63.49	14.16
Grain filling period	29.133n.s	22.04	-	-	-	-
Flag leaf area	26.753**	7.98	191.28	387.87	67.22	7.16
Plant height	244.085*	62.92	109.74	334.86	49.31	15.86
Number of spikes	3.195**	2.06	109.75	155.09	70.76	2.60
Biomass	7.333**	15.108	161.74	355.97	45.43	2.53
Spike length	9.057*	11.59	34.16	78.14	43.72	2.71
Number of spikelets	1789.248**	25.43	5771.29	7035.97	82.02	71.46
Number of grains	291.701**	31.55	393.30	924.33	42.54	14.96
Grain yield	20.696**	3.53	454.00	586.15	77.45	7.25
1000-grain weight	546.783**	25.40	1304.58	2152.07	42.32	20.38
Harvest index	2.930**	0.989	246.76	296.19	83.31	2.93

Heritability is a significant parameter for the selection of an efficient population improvement method. Single plant selection and that in the earlier generations may be much effective for a character that is highly heritable as compared to that a character which is less heritable. Further more, environment may also interact with the genotypic constitution to influence heritability [25]. High values for the heritability related to time to heading were obtained in the studies that were conducted previously [26]. These findings suggest that selection can be practiced for this character in subsequent generations. Broad sense heritability for number of spikes gave a relatively high estimate with low genetic advance under current study. The present results are similar with the earlier finding of Ehdaie and Waines [27]. Low heritability has been achieved for the grain number per spike [28]. During current studies, number of grains showed relatively low value of heritability. Moderate to high heritability estimates with high genetic advance have been reported for number of grains per spike [29]. High heritability for grain yield indicated that this trait was affected by genetic factors [30]. High estimates of variability, heritability and genetic advance for grain yield would be helpful for the breeders to select for the best combinations and to reach to the desirable level of yield potential [31].

Present research gave results that are in agreement with the above. During current work moderate values of heritability have been observed for days to anthesis, physiological maturity and flag leaf area whereas plant height, spike length, number of grains, 1000-grain weight and biomass have low values. Low values of heritability for these traits have been observed [28], while moderate [30] and mostly high values have also been obtained for the plant height in the studies conducted previously [32, 33]. Nabi and Jedynski [34, 35] reported very low heritability estimates for spike length. Their results are similar with findings of Mandal [36] and Kashif and Khaliq [3] who reported moderately high heritability for spikelets per spike. Our values for heritability obtained for 1000- grain weight were low and match with the values obtained by Al- Marakby [37].

CONCLUSIONS

The above analysis led us to suggest that the number of grains per spike mainly contribute to a better grain yield with some contribution by spike length as well. It may therefore be concluded that number of grains per spike is a trustworthy measure of higher yield and can be used as a selection criteria in an effective and successful breeding program. High heritability and positive, moderately high genetic advance were shown by the different characters, especially heading, flowering, number of spikes, grain yield and harvest index. These traits therefore, deserve greater attention in future breeding programs for evolving better wheat.

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