

ESTIMATION OF COMPONENTS OF VARIATION OF MORPHOLOGICAL TRAITS AND YIELD IN A-GENOME WHEAT POPULATIONS

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SUMMARY

Recombinant inbred lines (RIL) population (F_7) of two A-genome progenitors i.e. *T. monococcum* and *T. boeoticum* were evaluated for various yield affecting parameters. For all the traits under study enlisting components of variance, genetic advance and heritability were observed to be showing highly significant differences ($P \le 0.01$). Trend of high phenotypic coefficients of variation (PCV) estimates for all the traits under study in all genotypes exhibited the impact of environment. Amongst the yield traits, a minor difference between GCV and PCV was detected for heading time (3.96, 4.36) booting time (3.55, 3.96), flowering time (2.31, 2.56). Huge difference between GCV and PCV was noticed for emergence percentage (16.83, 26.50), flag leaf length (19.26, 28.77) flag leaf sheath length (7.67, 15.08), flag leaf diameter (11.04, 22.51) and grain yield (10.43, 22.94) specifying the environmental impact. Reasonable heritability coupled with high genetic advance was observed for emergence percentage (0.40), booting time (0.81), heading time (0.82), flowering time (0.81), flag leaf length (0.45) and grain yield per plant (0.21) representing that these traits were under the control of additive genetic effects. We have demonstrated the genetic variation in diploid genome blood of wheat through this study which will considerably expand the potential of its genome being used for resistances to various disasters opening the possibility of achieving higher yields.

Key words: Diploid wheat, A-genome, RILs, variability, heritability, genetic advance

Key findings: This study is aimed to set criteria that could be efficiently employed with applicable breeding approaches and curricula to produce value-added varieties and hybrids for farmers use.

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INTRODUCTION

Triticum aestivum, the common wheat consists 3 different genomes; A, B, and D, so an allohexaploid (2n = 6X = 42). *T. monococcum* is the donor of A-genome, *T. speltoides* (*Ae. speltoides*) or close relative of the said species is the donor of B-genome while *T. tauschii* (*Ae.squarrosa*) is of D-genome (Huang *et al.* 2002). Substantial pairing of homeologous chromosomes in the hybrid of diploids indicated that the diploids are still very closely related (Feldman, 1996). Today's wheat is cluster of gene-rich islands having same gene

density as that of small diploid genomes discovered by recent analyses of wheat genome organization (Erayman *et al.* 2004).

Constant exposure of great challenges have been spotted on wheat as with all the crop systems, majorly diseases and pests, among which hot spots are the rust diseases (leaf, stem, and stripe rust). An average loss of approximately 3% is by Leaf rust (causal agent: *Puccinia triticina*) which is the most extensively disseminated malady of wheat. Host resistance is the most effectual and costeffective means of disease control appendaging conventional breeding with direct gene transfer via molecular techniques (Payne, 1984).

One of the effective crop breeding strategies includes heritability estimation that is a necessary catalogue for polygenic attributes transmissibility. Genetic advance together with heritability are necessary for brining improvements via selection (Bhargava *et al.* 2003).

Yield in wheat like other crops, is an intricate character and numerous morphological and physiological traits compose it (Khan et al. 2013; Naeem et al. 2015). Economically valued quantitative traits are highly inclined to ecological condition, advancement of breeding in these traits are principally accustomed by the enormity and variation nature of along with interrelationships among them (Mahmood et al. 2013). Crop breeding triumph is also dependent on the segregation of genetically better-quality genotypes based on the variability at hand. Therefore, information regarding genetic variability residing in assembly of populations of wheat is crucial. Selection in development of novel genotypes along with anticipated attributes has been established by coupling of estimated higher heritability and genetic advance. Considerable quantity of polygenic traits have been found with higher genetic advance and greater heritability viz; plant height, grain yield, grain weight, spikes and grain number (Ajmal et al. 1995, Singh et al. 1999, Ghimirary and Sarkar 2000, Shazly et al. 2000). Estimation of genetic advance vigors the efficacy of heritability designating the character gain due to selection pressure, thereby making genetic advance an important selection parameter aiding breeders in selection program (Shukla et al., 2004). Enormousness in variance of wheat breeding material can be judged by genetic advance, heritability and phenotypic and genotypic variance (Bhutta, 2006).

Therefore, the present study was conducted to assess genetic variability, heritability and genetic advance among 50 genotypes of diploid wheat (2 parents and 48 RILs) with A-genome under winter growing season in order to select the appropriate genotype(s) that are suited to Abbottabad climatic conditions.

MATERIALS AND METHODS

The genetic material used in this study is consisted of fifty genotypes of diploid wheat containing 2 parents and 48 RILs at F_7 stage. The Field experiment was carried out in winter season of the years 2011 and 2012 at COMSATS Institute of Information Technology Abbottabad, Pakistan (Lat: 34.1558 Long: 73.2194)

The experiment was laid out in a randomized complete block design (RCBD) with 3 replications. The experiment site was ploughed and leveled, ridging up was eastwest, 30 cm apart. Sowing date was the 28th of November, 2011. Three to four seeds were casted in each dibble and after emergence thinning was done for maintaining single seedling per dibble. Nitrogen and phosphorus fertilizers were applied in the form of urea and diamonium phosphate (DAP) at 120 and 90 kg ha⁻¹, respectively. Half nitrogen and full dose of phosphorus were applied at sowing and remaining nitrogen was applied with second irrigation. All the recommended cultural and agronomic practices were followed throughout the growing season for optimum growth of wheat. All other weeds were manually removed throughout the crop season. First Irrigation was applied on 40 days after sowing and subsequent irrigations were applied as per requirement. Emergence percentage was counted just after emergence keeping 3 seeds per dibble as slandered. Ten randomly selected plants were used for data collection on all the traits viz., emergence percentage (%), heading time (days after sowing or DAS), booting time (DAS), flowering time (DAS), Flag leaf length (cm), Flag leaf sheath length (cm) and Flag leaf diameter (cm) and the data was collected at the time of maturity. All 10 plants were harvested and threshed individually to get grain yield per plant (g). Analysis of variance was carried out by MSTAT-C, Version 2.11 statistical program (Nissen, 1993) according to the procedures described by Gomez and Gomez (1984). The estimates of Phenotypic $(\sigma^2 ph)$ and Genotypic $(\sigma^2 g)$ variances were worked out according to the method suggested by Johnson et al. (1955) using mean square values from the individual and combined ANOVA tables.

Phenotypic (PCV) and genotypic (GCV) coefficients of variation (individually and combined) were calculated based on the method advocated by Burton (1952).

Heritability percentage in broad sense $h^2_{(bs)}$ and genetic advance (GA) were estimated according to the method suggested by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The outcomes of the analysis of variance are displayed in Table 1. The analysis of variance depicted extensive range of variation as extremely significant differences ($P \le 0.01$) were detected for all the studied traits. No preceding studies have been established for the

studied attributes regarding diploid wheat. Similarly a broad variation for all traits was detected and promising accessions for breeding purposes were identified by Empilli et al., (2000) and Butnaru et al. (2003) while studying diploid wheat genotype for variability for different characters. From a given set of phenotypic observations, reasonably significant variability and superior conclusions can be drawn by following crucial steps of measurement, evaluation and existence of variability. The means diploid wheat genotypes and their RILs regarding yield and agronomic traits are prearranged in Table 1.

Table 1. Mean squares for agronomic and yield of 48 RILS and 2 parents of diploid wheat.

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SOV	Df	Emergence percentage	Booting time	Heading Time	Flowering Time	Flag leaf length	Flag leaf sheath length	Flag leaf diameter	Grain yield
Reps	2	416.66	19.96	46.43	30.34	3.29	0.83	0.02	2064.24
Variety	49	577.63**	77.23**	100.35**	41.57**	30.11**	10.98**	0.04**	581.46**
Error	98	190.81	5.70	6.67	3.01	8.76	5.37	0.02	326.49
Total	149	1185.11	102.88	153.44	74.92	42.16	17.18	0.07	2972.19

*and ** denote significance at 0.05 and .01 % level of probability.

Table 2. Components of variation of morphological traits and yield of 48 rils and 2 parents of diploid wheat.

	G.VAR	P.VAR	GCOV	PCOV	h ² _(bs)	GA (5%)
Emergence percentage	128.94	319.76	16.83	26.50	0.40	14.85
Booting time	23.84	29.54	3.55	3.96	0.80	9.04
Heading time	31.23	37.89	3.96	4.36	0.82	10.45
Flowering time	12.85	15.87	2.31	2.56	0.81	6.65
Flag leaf length	7.11	15.88	19.26	28.77	0.45	3.68
Flag leaf sheath length	1.87	7.24	7.67	15.08	0.26	1.43
Flag leaf diameter	0.01	0.03	11.04	22.51	0.24	0.08
Grain yield per plant	84.99	411.48	10.43	22.94	0.21	8.63

G. Var: genotypic variance, *P.Var*: phenotypic variance, *GCOV*: genotypic covariance, *PCOV*: phenotypic covariance, $h^2_{(B,S)}$: broad sense heritability, GA: genetic advance

Table 2 is depicting the genetic parameters and components of variance for different vield and agronomic traits. Interaction of genotype and environment results in phenotypic expression of the traits. Genotypic coefficient of variation (GCV) estimates the array of variability in crop and also empowers to equate the expanse of variability existing in different traits. Among the diploid wheat genotypes and their RILs with A genome, the estimates of phenotypic coefficients of variation (PCV) were greater than genotypic coefficients of variation (GCV) for all the studied traits which directed the ample impact of environment on the traits

expression. Large GCVs and PCVs were witnessed for emergence percentage and Flag leaf length. Formerly such verdicts for broad variations have been described by Empilli et al. (2000) and Butnaru et al. (2003). Genetic advance guides the formulation of suitable selection procedures while heritability helps in getting information regarding the enormousness of traits inheritance. Information regarding heritability alone may not prove helpful in directing characters for imposing selection. However, the anticipated genetic advance along with heritability estimates will be more consistent. Adequate heritability together with high genetic advance was observed for emergence percentage, booting time, heading time, flowering time, flag leaf length and grain yield per plant specifying that these traits were under the control of additive genetic effects. Higher genetic advance together with higher estimates of broad sense heritability were achieved for booting time, heading time and flowering time exhibited that these traits are having additive genetic effects for inheritance which can be taken as promising traits for diploid wheat enhancement via selection. Analogous verdicts were formerly detected by Fadlalla, 1994.

CONCLUSIONS

Based on outcomes of the current study, it could be determined that an enormous aggregate of variability resides in the genotypes. Higher genetic advance along with higher estimates of broad sense heritability was achieved for emergence percentage, booting time, heading time, flowering time, flag leaf length and grain yield per plant. On the other hand, comparatively low genetic advance with higher estimates of heritability were unveiled for Flag leaf sheath length and flag leaf diameter. This variation in the studied assessed criteria could be efficiently employed with applicable breeding approaches and curricula to produce value-added varieties and hybrids for farmers use.

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