FULL LENGTH ARTICLE　　　　　　　　　　　　　　　　　　　　　　　　**OPEN ACCESS**

Study of Genetic Variability Parameters For Yield And Yield Attributing Traits in F5 Population of Dicoccum Wheat

H. R. Arpitha*, V. Rudra Naik and G. Anil Kumar.

Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad – 580005, Karnataka, India.
*Corresponding author: arpithasharu@gmail.com

ABSTRACT

A field experiment was conducted to study the genetic variability parameters for ten quantitative characters in F5 population of the two crosses (DDK1025 x DDK-50425 and DDK1025 x DDK-50426) of dicoccum wheat. All the characters showed significant mean sum of squares for varieties in both the crosses, this indicates the presence of significant variability in F5 populations of both the crosses. Mean value in cross II was highest for most of the traits compared to that of cross I. In cross I, the estimates of genotypic and phenotypic coefficient of variability was high for plant height. High PCV and moderate GCV was observed for traits like spike length, number of grains per spike and yield per plot. Moderate levels of PCV and GCV was observed for the traits like number of tillers per meter length, number of spikelets per spike and thousand grain weight. In case of cross II, PCV and GCV was high for plant height and yield per plot. The moderate PCV and GCV was recorded for traits like days to 50 per cent flowering, number of tillers per meter length, number of grains per spike, number of spikelets per spike, thousand grain weight and yield per plot. In cross I population, high heritability coupled with high genetic advance over mean was observed for traits like plant height, spike length, number of grains per spike, number of spikelets per spike, thousand grain weight and yield per plot. But in case of cross II high heritability coupled with high genetic advance over mean was observed for traits like days to 50 per cent flowering, plant height, number of tillers per meter length, spike length, number of grains per spike, number of spikelets per spike, thousand grain weight, grain yield per plant and yield per plot. High heritability coupled with high GAM indicates the involvement of additive gene action for the trait which plays an important role in selection programmes.
Key words: Dicoccum wheat, genetic advance, genetic variability, heritability

INTRODUCTION

Wheat is a crop of global importance and staple food for millions of people around the globe. It provides a large fraction of dietary protein (11-12%) and it supplies more nutrients particularly, essential amino acids than any other single crop. In India mainly three species of wheat *viz*; *Triticum aestivum*, *durum* and *dicoccum* are under cultivation. In India, wheat is grown over an area of 29.30 million ha with production of 95.91 million tones with an average productivity of 3140 kg ha^{-1} (Anon., 2015). The area under wheat in Karnataka is about 1.70 lakh ha with annual production of 1.73 lakh tones and the productivity is 1010 kg ha^{-1} (Anon., 2015). Dicoccum wheat possesses valuable traits like resistance to pests, diseases like leaf and stem rust and tolerance to abiotic stresses compared to durum and bread wheat and thus also represents a valuable genetic resource for the improvement of durum and bread wheat (Dorofeev *et al*., 1987).

Generating information about the genetic variability, genetic diversity relationships and mechanisms of inheritance of the genetic traits involved is the key task in genetic improvement of any crop plant. The genotypic and phenotypic coefficient of variation is helpful in understanding the clear picture of existing variability in the populations whereas, the estimates of heritability and genetic advance provide the indices of transmissibility of characters. Thus, estimates of variability parameters like coefficients of variation, heritability and genetic advance are very useful for devising suitable selection strategy for evolving high yielding genotypes in wheat crop.

Absolute variability values of different characters do not reveal that which of the characters are showing high variability. This could only be accessed through standardized values of the phenotypic and genotypic

variance estimates by obtaining the coefficients of variability. Heritability is a useful quantitative parameter, which considers the role of heredity and environment determining the expression of a trait. Effective selection can be achieved only when additive effects are substantial and environmental effects are small. Expected genetic advance indicates the expected genetic progress for particular trait under selection cycles and measures the extent of its stability under selection pressure.

The heritability estimates along with genetic advance will be more useful than heritability value alone in selecting best individuals. Broad sense heritability gives an idea about portion of observed variability attributable to genetic differences. The difference between PCV and GCV estimates indicates the relative influence of environment on the character, which in turn decides the extent of their heritability. Keeping this in view, a field experiment was conducted to assess the genetic variation present in the segregating population of dicoccum wheat.

MATERIALS AND METHODS

The F_5 populations of the two crosses DDK1025 x DDK-50425 (cross I) and DDK1025 x DDK-50426 (cross II) of dicoccum wheat were evaluated at All India Coordinated Wheat Improvement Project, Main Agricultural Research Station (MARS), University of Agricultural Sciences, Dharwad, following augmented RBD design along with the checks *viz.,* DDK 1001, DDK 1025, DDK 1029 and NP 200 of dicoccum and DWR 1006, HD 4502 and UAS 428 of durum wheat varieties. Each entry was grown at a spacing of 20 x 10 cm, in a plot size of two rows with 2 m length. Two seeds were dibbled per hill and later thinned to retain one seedling per hill. The observations *viz.,* days to 50 percent flowering, days to maturity, plant height (cm), number of tillers per meter length, spike length (cm), number of spikelets per spike, number of grains per spike, thousand grain weight (g), grain yield per plant (g), grain yield per plot (g) were recorded on five randomly selected competitive plants. The mean of five observations were computed for all the characters. The data obtained were subjected to the biometrical analysis that included analysis of variance and genetic variability parameters. Genotypic coefficient of variation (GCV %), phenotypic coefficient of variation (PCV %), broad sense heritability (h^2) and genetic advance as percent mean (GAM) were estimated. Genotypic and phenotypic coefficient of variation were calculated using the method suggested by Burton and Devane (1953). The heritability was categorized as suggested by Robinson *et al.,* 1949 and genetic advance was classified by adopting the method of Johnson *et al.,* 1955.

RESULTS AND DISCUSSION

The analysis of variances for yield and yield attributing traits in F_5 populations of two dicoccum wheat crosses were presented in Table 1. Out of ten quantitative characters studied, all the characters showed significant mean sum of squares for varieties in both the crosses except for thousand grain weight and grain yield per plant in the population of Cross I (DDK-1025 x DDK-50425), this indicates the presence of significant variability in F_5 populations of both wheat crosses. There were significant differences even among the checks for all the characters studied in both the crosses except for thousand grain weight in F_5 population of cross I (DDK-1025 x DDK-50426). Nayeem *et al.* (2003), Dwivedi and Pawar (2004), Bhushan *et al.* (2013), Naik *et al.* (2015) reported high variation for different traits in wheat.

Mean, range, genetic variability and heritability parameters for ten yield attributing traits of the two segregating populations of dicoccum wheat crosses were presented in the Table 2 and the mean of parents and the two crosses of dicoccum wheat were presented in Table 3. The mean value for days to 50 per cent flowering (77.19) and days to maturity (113.72) was highest in cross I (DDK 1025x DDK-50425) compared to cross II (DDK 1025x DDK-50426) with mean value of 73.65 and 109.50, respectively. The parents also had lower mean values for these traits. This indicates, that the population of cross I are of long duration compared to those of cross II and the parents. The mean value for plant height was highest (92.26) in cross I indicating the presence of tall plants compared to the cross II and the parents. These results are in agreement with that of Nuksani *et al.* (2013), Kumar and Shekhar (2014), and Ali *et al.* (2008). Mean value was highest for traits like number of tillers per meter length (71.82), spike length (7.92), number of spikelets per spike (16.48), number of grains per spike (33.01), thousand grain weight (43.24), grain yield per plant (9.77) and grain yield per plot (128.09) compared to that of cross I. The mean values for number of tillers per meter length, spike length, thousand grain weight and grain yield per plot was on par with the parent DDK 1025 and higher than that of parent DDK-50426. The mean value of number of grains per spike in cross II was higher than that of both the parents. The mean values for many traits under study were higher in cross II, so the segregating lines of the population can be further used in breeding programmes. One of the ways in which variability assessed is through a simple approach of examining the range of variation. Wide range of variation for all the traits was observed in both the crosses. Spike length (4.54-10.36), number of spikelets per spike (8.00 - 23.40), number of grains per spike (10.40–48.00), thousand grain weight (29.00 - 59.20), grain yield per plant (5.60 -15.80) and

grain yield per plot (39.23 - 370.00) showed wide gap for maximum and minimum range values in cross II compared to cross I which indicates higher variation in the cross II compared to cross I which can be exploited well for further breeding programmes. Similar results were reported by Tambe *et al.* (2013) and Bhushan *et al.* (2013).

Table 1: ANOVA for two F$_5$ populations of the two crosses ((DDK1025 x DDK-50425 and DDK1025 x DDK-50426) of dicoccum wheat

Source of variation	Crosses	df	DFF	DM	PH	NTPM	SL	NSPS	NGPS	TGW	GYP	GYPP
Block(eliminating Check+Var.)	C$_1$	5	17.08	29.53	187.96	417.74*	0.48	1.80	5.88	7.36	3.53	786.21
	C$_2$	10	8.68	17.07	11.39	241.28	0.19	12.02	11.64	2.62	1.20	337.09
Entries (ignoring blocks)	C$_1$	281	66.91**	56.68**	263.37**	198.26**	3.48**	10.03**	51.05**	28.20	0.83*	676.40**
	C$_2$	156	121.38**	84.38**	228.20**	260.77**	2.88**	9.29**	48.06**	35.06**	3.67**	4257.63**
Checks	C$_1$	6	149.27**	29.74	328.98**	1058.71**	11.43**	33.98**	63.15**	42.70	7.41**	5017.41**
	C$_2$	6	304.78**	98.10**	690.04**	1402.93**	18.67**	46.40**	66.15**	48.08**	10.78**	7856.56**
Varieties	C$_1$	149	61.00**	59.67**	251.86**	152.27**	3.12**	9.10**	48.11**	25.23	0.45	375.44**
	C$_2$	274	108.22**	81.30**	217.57**	224.38**	2.49**	8.44**	46.92**	34.77**	3.26**	4087.51**
Checks vs. Varieties	C$_1$	1	452.91**	83.70	1584.05**	1889.08**	8.79**	4.71*	416.74**	383.21	18.01**	19472.01**
	C$_2$	1	2625.15**	847.88**	371.04**	3377.93**	15.50**	19.73**	258.45**	35.58**	71.97**	29785.90**
Error	C$_1$	30	8.63	22.61	6.16	70.29	0.27	0.73	5.78	1.77	0.34	93.29
	C$_2$	60	5.79	18.09	7.56	42.21	0.21	1.63	4.49	4.71	0.38	112.59

* Significance at 0.05 probability; **Significance at 0.01 probability; C$_1$= DDK1025 x DDK-50425 ; C$_2$= DDK1025 x DDK-50426

DFF: Days to 50 percent flowering **; DM:** Days to maturity; **PH:** Plant height (cm); **NTPM:** Number of tillers per meter length ; **SL:** Spike length (cm); **NSPS:** Number of spikelets per spike, **NGPS:** Number of grains per spike, **TGW:** Thousand grain weight (g)**; GYP:** Grain yield per plant (g); **GYPP:** Grain yield per plot (g)

Table 2: Variability parameters of the two crosses at F$_5$ population for different yield attributing traits of dicoccum wheat

Characters	DDK-1025 x DDK-50425						DDK-1025 x DDK-50426					
	Mean	Range		PCV (%)	GCV (%)	h^2 (bs)	GAM (%)	Mean	Range		PCV (%)	GCV (%)	h^2 (bs)	GAM (%)
		Max	Min						Max	Min				
DFF	77.19	89.00	51.00	9.31	8.48	82.94	15.91	73.65	89.25	45.00	13.00	12.56	93.42	25.02
DM	113.72	125.00	89.00	6.34	4.77	56.77	7.41	109.51	124.00	83.00	7.36	6.55	73.73	11.59
PH	59.38	92.26	35.32	24.62	23.24	95.23	49.20	65.44	73.66	36.44	20.46	20.00	95.71	40.34
NTPM	64.45	98.00	22.00	18.57	12.91	48.30	18.47	71.82	106.00	30.00	19.56	17.23	77.62	31.28
SL	7.76	11.20	4.26	20.88	19.74	89.37	38.45	7.92	10.36	4.54	18.31	17.25	89.63	33.85
NSPS	15.83	23.40	10.20	17.31	16.34	90.12	32.14	16.48	23.40	8.00	16.05	14.09	77.06	25.48
NGPS	31.04	48.20	16.00	20.82	19.24	85.42	36.63	33.01	48.00	10.40	19.07	17.93	88.36	34.72
TGW	40.75	56.00	23.60	11.34	10.83	91.38	21.34	43.24	59.20	29.00	12.47	11.41	83.68	21.50
GYP	8.95	11.40	3.51	7.24	3.33	21.12	3.15	9.77	15.8	5.60	16.42	15.21	85.85	29.03
GYPP	102.35	182.00	41.5	21.83	18.37	70.78	31.84	128.09	370.00	39.30	43.25	42.50	96.59	86.06

DFF: Days to 50 percent flowering; **DM:** Days to maturity ; **PH:** Plant height (cm); **NTPM:** Number of tillers per meter length; **SL:** Spike length (cm); **NSPS:** Number of spikelets per spike, **NGPS:** Number of grains per spike, **TGW:** Thousand grain weight (g); **GYP:** Grain yield per plant (g); **GYPP:** Grain yield per plot (g)

Table 3: The mean performance of the parents and the two crosses in F$_5$ populations for yield and yield attributing traits of dicoccum wheat

	DFF	DM	PH	NTPM	SL	NSPS	NGPS	TGW	GYP	GYPP
DDK 1025	59.00	105	79.24	73.00	8.04	19.60	32.80	44.35	10.02	112.00
DDK-50425	52.00	98.00	62.68	68.00	6.18	13.67	26.33	36.05	9.66	85.30
DDK-50426	50.00	96.00	56.78	43.00	5.54	14.60	33.60	43.30	9.30	150.00
DDK 1025x DDK-50425	77.19	113.72	59.38	64.54	7.76	15.83	31.04	40.75	8.95	102.35
DDK 1025x DDK-50426	73.65	109.51	65.44	71.82	7.92	16.48	33.01	43.24	9.77	128.09

DFF: Days to 50 percent flowering **; DM:** Days to maturity ; **PH:** Plant height (cm); **NTPM:** Number of tillers per meter length ; **SL:** Spike length (cm), **NSPS:** Number of spikelets per spike, **NGPS:** Number of grains per spike**TGW:** Thousand grain weight (g), **GYP:** Grain yield per plant (g), **GYPP:** Grain yield per plot (g)

In Cross I, the estimates of genotypic and phenotypic coefficient of variability was high for plant height. High PCV and moderate GCV was observed for traits like Spike length, number of grains per spike and grain yield per plot. These results are in accordance with Yaqoob (2016) and Naik *et al.* (2015). Moderate levels of PCV and GCV was observed for the traits like number of tillers per meter length, number of spikelets per spike and thousand grain weight. Low levels of PCV and GCV was observed for days to 50 per cent flowering, days to maturity and grain yield per plant. In case of cross II, PCV and GCV was high

for plant height and grain yield per plot. The estimates of genotypic and phenotypic coefficient of variability was recorded to be moderate for traits like days to 50 per cent flowering, number of tillers per meter length, number of grains per spike, number of spikelets per spike, thousand grain weight and grain yield per plot. Similar results are reported by Ali *et al*. (2008). Low GCV and PCV value for the trait indicate the difficulty of improvement for this trait through selection because of the influence of environment on the expression of the trait. In overall the magnitude of GCV was low as compared to PCV for all the characters under study indicating, variability was not only due to genotype but also influenced by environment.

Estimates of heritability and genetic advance are critical for predicting genetic improvement for any quantitative trait. Heritability estimates indicates the effectiveness of selection for phenotypic performance of particular character. The high heritability estimates along with high genetic advance is more useful for the selection (Johnson *et al.,* 1955). In the present study in cross I population, high heritability coupled with high genetic advance over mean was observed for traits like plant height, spike length, number of grains per spike, number of spikelets per spike, thousand grain weight and grain yield per plot. These results are in accordance with Nukasani *et al.* (2013) and Naik *et al.* (2015). High heritability coupled with high GAM indicated, the involvement of additive gene action for the trait which plays an important role in selection programmes. Moderate heritability and GAM was observed for number of tillers per meter length. Days to 50 per cent flowering showed high heritability and moderate GAM. Days to maturity showed moderate heritability with low GAM. But in case of cross II high heritability coupled with high genetic advance over mean was observed for traits like days to 50 per cent flowering, plant height, number of tillers per meter length, spike length, number of grains per spike, number of spikelets per spike, thousand grain weight, grain yield per plant and grain yield per plot which indicate the predominance of additive gene action in controlling the expression of these traits. Therefore, response to selection could be anticipated in improving these traits. Similar results were reported by Ali *et al*. (2008) and Naik *et al.* (2015). The trait days to maturity showed high heritability with moderate GAM.

Considerable amount of genetic variability present in the F_5 populations of the dicoccum wheat, which can utilized well for selection programmes. Most of the traits showed the high heritability with moderate or high GAM in the segregating lines of the crosses of dicoccum wheat. High heritability coupled with high GAM indicates the involvement of additive gene action for the trait which plays an important role in selection programmes. PCV was higher than GCV reflecting the influence of environment. Cross II population performed better than that of cross I and showed high mean values for most of traits studied. So segregating lines of cross II can be well exploited in further breeding programmes.

REFERENCES

1. Anonymous, 2015, Agricrop.statistics.com
2. Ali, Y., Babar, M. A., Javed, A. P. M. and Zahid, L., 2008, Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) germplasm. *Pak. J. Bot.,* 40 (5): 2087-2097.
3. Bhushan, B., Sonu, B., Ashish, O., Manoj, P., Shailendra, S., Gourav, B., Singh, T. and Gyanendra, S., 2013, Genetic variability, correlation coefficient and path analysis of some quantitative traits in bread wheat. *J. Wheat Res.,* 5(1): 21-26.
4. Burton, G. M. and Devane, E. M., 1953, Estimating heritability in tall Festuca from replication clonal material. *Agron. J.,* 45: 478-481.
5. Dorofeev, V. F., Udachin, R. A., Semenova, L. V., Novikova, M. V., Grazhdaninova, O. D., Shitova, I. P., Merezhko, A. F. and Filatenko, A. A., 1987, World wheat. Agropromizdat, Leningrad, 560.
6. Dwivedi, A. N. and Pawar, I. S., 2004, Evaluation of genetic diversity among bread wheat germplasm lines for yield and quality attributing traits. *Haryana Agril. Univ. J. Res.*, 34: 35-39.
7. Johnson, H.W., Robinson, H.F., Comstock, R.E. (1955) Estimates of genetic and environmental variability in soyabean. Agron. J. 47:314-418.
8. Kumar, A. and Shekhar, R., 2014, Genetic variability in relation to qualitative and quantitative traits in wheat (*Triticum aestivum* L.). *Agrica,* 3: 23-28.
9. Naik, R. V., Kumar, Y. L. M., Biradar, S. S., Desai, S. A. and Veeresha, B. A., 2015, Genetic variability parameters for micronutrients, yield and quality traits in wheat. *Int. J. Agric. Sci.*, 7(2):520-522.
10. Nukasani, V. K., Potdukhe, N. R., Bharad, S., Deshmukh, S. and Shind, S. M., 2013, Genetic variability, correlation and path analysis in wheat. *J. Wheat Res.,* 5(2): 48-51.
11. Robinson, H. F., Comstock, R. W. and Harvey, V. H., 1949, Estimation of heritability and degree of dominance in corn. *Agron. J.*, 41: 353-359.
12. Tambe, A., Mehta, D. R., Chovatia, V. P. and Bhatiya, V. J., 2013, Genetic variability, character association and path coefficient analysis in durum wheat (*Triticum durum* Desf.). *Electronic J. Plant Breed.*, 4(4): 1303-1308.

13. Yaqoob, M., 2016, Estimation of genetic variability, heritability and genetic advance for yield and yield related traits in wheat under rainfed conditions. *J. Agric. Res.,* 54(1):1-1