J. Wheat Res. 4 (1) : 49-54

Genetic analysis and traits association in two double haploid populations of bread wheat (*Triticum aestivum L.*)

Gyanendra Singh*, Muneendra Kumar Singh, Mahender Singh Saharan, Charan Singh,
Bhuvdeva Singh Tyagi and Indu Sharma

Directorate of Wheat Research,
Karnal-132 001, India

Abstract

A study was conducted for genetic analysis and estimating association of the traits in double haploid populations of bread wheat (*Triticum aestivum* L.). These populations were planted at Directorate of Wheat Research, Karnal during *rabi* season 2008-09 and 2009-10 in augmented design along with five checks in three blocks, wherein all checks were repeated in each block. The genetic variance and correlation coefficients were carried out for assessment of the performance of double haploid lines derived from the cross (Ducula4/2* Brookton) and (Camm/HD 2329), through six metric traits, *viz.* plant height, days to heading, days to maturity, tillers per plot, 1000-grain weight and grain yield. Analysis of variance on the basis of F- values, revealed wide variability for most of the traits over the year and pooled. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits, while high heritability (<60%) coupled with high genetic advance (<15%) was found for all the traits, excepting the days to maturity and spike length. At phenotypic level, positive and significant correlation coefficients revealed that grain yield is directly influenced by spike length, tillers per plot and thousand grain weight, while significant and negative correlations was found of plant height and days to maturity with grain yield, respectively in both the populations. There is wide genetic diversity available for metric traits, which may be utilized for yield improvement in bread wheat through planned hybridization and selection. The traits plant height, maturity days, tillers per plot, spike length and 1000-grain weight of both populations can be of importance in further yield enhancement.

Key words: Bread wheat, double haploids, genetic variability, correlation coefficient

Introduction

Wheat (*Triticum aestivum* L.) crop is grown over around 29.9 million hectares area with total production of 93.9 million tons (Anonymous, 2012). Wheat occupies the maximum cultivated area on global basis as 22.5 followed by rice with 16.14 and maize with 15.95 billion hectares (Asghar *et al.*, 2011). Though the total production of wheat in the country has increased very significantly, the productivity increase is still comparatively low. Furthermore, the expected demand of 100 million tons of wheat by 2030 and possible adverse impacts of climate change on wheat productivity are the factors to plan and implement strategy for yield enhancement per unit area and the future genotypes need to have high yield with better resistance to biotic factors and increased tolerance to abiotic stresses. This appears to be a difficult task but not impossible to develop high yielding wheat varieties utilizing the available useful variability in germplasm. The production of double haploid lines is a good tool for autogamous species breeding since completely homozygous lines from F_1 crosses are obtained in a single generation (Snape and Simpson, 1984). Another advantage is a substantial reduction in the cost and the time required to produce breeding lines by conventional system (Liu *et al.*, 2002). The success of any breeding programme will depend upon the magnitude of genetic diversity existing in germplasm, heritability index and harnessing genetic advance present in different yield associated parameters. The heritability index alone, that also reflects transmissibility is not enough for selection in advance generations under stress conditions. It must simultaneously be accompanied with substantial amount of genetic advance and interrelationship among yield traits.

Plant breeding using the doubled-haploid system is a key technology used to speed up the breeding process. In traditional plant breeding, it generally takes at least five generations after crossing before a sufficiently homozygous population is obtained, while doubled-haploid produces a homozygous plant in one generation. Therefore, doubled-haploid technology dramatically increases the speed of the inbred developmental processes by reducing several time-intensive generations of inbreeding and by making phenotyping and genotyping more predictive. Doubled-haploid have thus become a key component to the product development process (Tester and Langridge, 2010).

Grain yield is a complex trait and highly influenced by many environmental factors, biotic and abiotic stresses including water-logging, salinity etc. In any crop breeding programme, direct selection for yield under complex environments could be misleading, and therefore, a

* Corresponding author email: *gysingh@gmail.com*

successful selection will depend upon the information on the genetic variability and association of morpho-agronomic traits with grain yield is a pre-requisite. Correlation coefficients provide a better understanding of the association of different trait (s) with grain yield. The study of associations among various traits is useful to breeders in selecting genotypes possessing groups of desired traits. Keeping all this in view, double haploid lines of two crosses and one set of elite lines were included to generate information on genetic variability, relationships of yield and its components and their implication in selection of better genotypes of wheat improvement in India.

Material and methods

The experimental material used here consists of two double haploids cross population of bread wheat, where five checks were included for augmented design planting. The population one is derived from Ducula4/2*Brookton, with 155 lines and population two from Camm/HD 2329, with 79 lines, excluding checks. The checks included were KRL 3-4, PBW 502, HD 2285, HD 2851 and HD 2009. These double haploid lines were obtained from Australia for the characterization. All the materials were planted in an augmented design during *rabi* season of 2008-09 and 2009-10 at Directorate of Wheat Research, Karnal.

All the experimental material were planted in a two-row plot of 1.0 m length with 23 cm row to row spacing and 10 cm spacing between plants and within rows. All the recommended cultural practices were followed to raise normal crop and have proper expression of genotypes. The following observations were recorded on six important metric traits, *viz,* plant height, days to heading, days to maturity, tillers per plot, 1000-grain weight (TGW) and grain yield per plot at appropriate crop growth stage.

The adjusted means of lines have been utilized for estimating genetic variability and other parameters following statistical procedure as given by Johnson *et al.* (1955). Analysis of variance (ANOVA) for estimating phenotypic and genotypic coefficient of variation, heritability and genetic advance as per cent of mean for all six traits was performed by latest statistical software, where adjusted mean values were subjected to statistical analysis for estimation of genetic parameters *viz;* mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2)and genetic advance as percentage of mean (GA%), by commonly used statistical software SAS version 9.2 (SAS Institute, 2008).

Results and discussion

The analysis of variance among double haploids populations over the year and based on pooled data indicated significant differences for all the traits. The F-calculated values along with other estimates are presented in table-1. The results revealed that genotypic variability was high (Table 1) and that prompted for further analysis. The performance of population one and two for six metric traits revealed that grain yield exhibited maximum mean (295 & 225) along with higher range (70-474 & 51-493); followed by tillers per plot with mean of (130 & 141) and range of (97-197 & 103-219); and days to maturity with mean values of (112 & 118) and range varied from (103-126 & 110-129) under population one and two respectively on the basis of pooled data (Table 1).

The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all traits among both populations over the year and pooled. Higher phenotypic coefficient of variation and genotypic coefficient of variation indicate that high variability exists among the genotypes. A close observation of estimates of GCV and PCV suggested that environment had little role in the expression of traits like plant height, thousand grain weight and grain yield, whereas traits like days to maturity, tillers per plot and spike length were having moderate to high influence of the environment among both populations. High GCV was observed for grain yield (19.46); followed by tillers per plot (7.21) in population one, while in population two higher for grain yield (29.99); followed by plant height with 11.96 (Table 1). Higher PCV than GCV indicated that the visible variation in the expression of traits was not only due to genotypes alone but also due to varying influence of environment.

The estimates of high heritability (broad sense) and high genetic advance (GA% of mean) indicate additive gene and hence improvement in these traits could be possible by direct selection (Panse, 1957). High heritability (with more than 80%) was observed for grain yield and 1000-grain weight along with higher genetic advance (more than 20%) in population one and two, whereas moderate heritability with moderate genetic advance was recorded for plant height in population one and for plant height and tillers per plot in population two (Table 1).

In general, grain yield and thousand grain weight revealed high estimates of heritability along with high genetic advance in year one, two and pooled in both the populations. Moderate to high estimates of genetic advance were recorded for all the traits, excepting spike length and days to maturity. Whereas, high values of heritability coupled with moderate to low estimates of genetic advance for traits like plant height, tillers per plot, 1000-grain weight and grain yield indicated role of non additive gene action in the expression of these traits. In case of traits showing moderate values of heritability and genetic advance, slight improvement through direct selection could be possible.

Table 1. Genetic parameters for two double haploids population over years (2008-09 and 2009-10) and pooled.

Trait	Year	F-value	Range	Mean	PCV	GCV	h^2	GA
Population- I (Ducula4/2*Brookton)								
Plant height	Year -I	5.64**	56-100	85	6.90	4.60	61	16.29
	Year -II	6.97**	50-103	90	7.05	4.94	67	17.14
	Pooled	10.43**	53-100	70	6.42	4.72	76	17.25
Days to maturity	Year -I	3.04*	100-126	119	3.23	1.37	30	10.10
	Year -II	3.12*	106-131	122	4.01	1.80	50	10.39
	Pooled	5.04**	103-126	112	2.89	1.01	40	9.09
Tillers per plot	Year -I	4.24**	96-198	139	9.66	6.96	62	14.38
	Year -II	10.66**	91-197	136	8.58	7.49	76	15.46
	Pooled	7.97**	97-197	130	8.63	7.21	70	17.15
Spike length	Year -I	1.19	6-11	8	13.29	9.23	40	7.14
	Year -II	5.28**	7-12	9	7.58	5.81	59	7.85
	Pooled	2.04	6-11	7	9.37	6.75	36	6.44
1000-grain weight	Year -I	35.04**	22-44	31	8.61	7.29	82	24.88
	Year -II	10.94**	20-45	29	9.36	8.24	87	25.60
	Pooled	64.93**	21-45	33	8.78	7.61	86	25.15
Grain yield	Year -I	5.54**	79-462	221	23.53	20.26	80	29.19
	Year -II	33.34**	62-486	272	21.20	20.28	88	29.96
	Pooled	14.71**	70-474	295	21.49	19.46	82	26.32
Population-II (Camm/HD2329)								
Plant height	Year -I	29.05**	40-117	70	14.46	11.85	70	19.00
	Year -II	34.04**	42-114	83	16.64	12.11	62	19.84
	Pooled	56.40**	41-116	92	13.27	11.96	85	19.79
Days to maturity	Year -I	4.09**	112-128	120	3.07	1.57	50	9.26
	Year -II	5.42**	107-132	112	4.13	1.48	63	9.31
	Pooled	3.36*	110-129	118	3.13	1.05	41	8.87
Tillers per plot	Year -I	8.55**	98-220	152	10.55	9.79	72	16.01
	Year -II	19.33**	102-224	170	11.10	9.37	66	17.18
	Pooled	15.37**	103-219	141	12.40	9.47	63	16.98
Spike length	Year -I	1.74	5-12	10	13.37	9.01	40	4.52
	Year -II	8.34**	7-13	9	8.64	5.30	51	5.23
	Pooled	3.24*	6-12	8	10.06	6.61	43	5.85
1000-grain weight	Year -I	54.37**	18-41	29	12.69	10.40	85	26.24
	Year -II	61.22**	19-39	31	13.35	11.25	88	26.83
	Pooled	99.91**	19-40	27	12.90	10.74	87	26.50
Grain yield	Year -I	8.31**	61-491	221	31.77	29.34	82	28.99
	Year -II	51.62**	42-496	229	31.20	30.33	84	30.72
	Pooled	22.51**	51-493	225	31.99	29.99	81	27.92

Where, *,** significant at 5% and 1% level, respectively.

Our results here confirm to the earlier reports of Pawar *et al.* (2002). Gupta *et al.* (2004) who also reported high heritability for days to heading, plant height, tillers per plant, spike length and spikelets per spike, spike weight, seeds per plant and leaf blight. Sardana *et al.* (2007) suggested that high heritability may not necessarily lead to increase genetic gain, unless sufficient genetic variability existed in the germplasm and low heritability has been achieved for the grain number per spike as reported by Ayciceck and Yildirim (2006). Some authors reported moderately high heritability for spikelets per spike (Kashif and Khaliq, 2004). The highest heritability coupled with high genetic advance for plant height and 1000-grain weight whereas, lowest heritability and expected genetic advance for grain yield and test weight was reported by Oguz *et al.* (2011). For plant height and number of tillers per plant, high heritability along with high genetic advance was reported by Gulnaz *et al.* (2011). High heritability along with high genetic advance for some metric traits was reported by Singh *et al.* (2011a, 2011b, 2012). High heritability coupled with high genetic advance and high coefficient of variability for grain yield per plot and 1000-grain weight showed scope for improvement following selections. However, in case of characters like plant height and tillers per plot showing high heritability but moderate to low genetic advance, which may be due to non-additive gene action and presence of G × E interaction, simple selection may not be rewarding (Singh *et al.*, 2003). Different researchers like Ansari *et al.* (2005) and Inamullah *et al.* (2006) in their studies have reported the presence of high heritability and genetic advance in different yield related attributes in wheat. The phenotypic correlation coefficients among six traits were also worked out to see the association between these traits (Table 2). The yield is the end product of contributions made by several component traits that are directly or indirectly associated with grain yield. If the association is positive, improvement in one character will simultaneously bring about an improvement in other. However, the negative association between two economic traits is useful for characteristics, like plant height, maturity duration and days to heading. The significant and positive correlation co-efficient were found between tillers per plot (0.24 & 0.34), spike length (0.16 & 0.22) and 1000-grain weight (0.64 & 0.79) with grain yield, while significant and negative correlation co-efficient of plant height (-0.24 & -0.34) and days to maturity (-0.16 & -0.26) were found with grain yield under populations one and two respectively on the basis of pooled.

Table 2. Phenotypic correlations among six traits in two double haploids populations over years (2008-09 and 2009-10) and pooled.

Trait	Year	Days to maturity	Tillers/ plot	Spike length	1000-grain weight	Grain yield
Population-I (Ducula4/2*Brookton)						
Plant height	Year-I	0.24**	0.05	0.10	-0.23**	-0.16*
	Year-II	0.16*	0.09	0.08	-0.23**	-0.28**
	Pooled	0.24**	0.08	0.11	-0.24**	-0.24**
Days to maturity	Year-I		-0.01	0.34**	-0.15*	-0.17*
	Year-II		-0.01	0.35**	-0.16*	-0.15*
	Pooled		-0.02	0.22**	-0.18*	-0.16*
Tillers per plot	Year-I			-0.04	-0.21**	0.15*
	Year-II			-0.06	-0.22**	0.17*
	Pooled			-0.06	-0.23**	0.24**
Spike length	Year-I				0.20*	0.15*
	Year-II				0.25**	0.16*
	Pooled				0.22**	0.16*
1000-grain weight	Year-I					0.57**
	Year-II					0.66**
	Pooled					0.64**
Population-II (Camm/HD 2329)						
Plant height	Year-I	0.09	0.21*	0.29**	-0.37**	-0.30**
	Year-II	0.10	0.22*	0.26*	-0.39**	-0.37**
	Pooled	0.09	0.21*	0.25*	-0.39**	-0.34**
Days to maturity	Year-I		0.26*	0.42**	0.11	-0.26*
	Year-II		0.22*	0.41**	0.12	-0.23*
	Pooled		0.21*	0.39**	0.12	-0.26*
Tillers per plot	Year-I			0.07	-0.20*	0.26*
	Year-II			0.05	-0.21*	0.29**
	Pooled			0.08	-0.22*	0.34**
Spike length	Year-I				0.21*	0.29**
	Year-II				0.22*	0.25*
	Pooled				0.21*	0.22*
1000-grain weight	Year-I					0.74**
	Year-II					0.81**
	Pooled					0.79**

Where, *,** Significant at 5% and 1% level, respectively at 158 df for population-I and 82 df for population-II.

The plant height (-0.24), days to maturity (-0.18) and tillers per plot (-0.23) significant negatively correlated with 1000-grain weight; while spike length (0.22) significant positively with 1000-grain weight, besides this days to maturity (0.22) significant positive with spike length, plant height (0.24) with days to maturity in case of population one. The performance of populations two is different, here plant height (-0.39) and tillers per plot (-0.22) is significant negative correlated with 1000-grain weight; plant height (0.25 & 0.21) and days to maturity (0.39 & 0.21) significant positively correlated, respectively with spike length and tillers per plot in case of populations two.

At phenotypic level, positive and significant correlation coefficients revealed that under both populations over the year one, two and pooled, grain yield is directly influenced by plant height, days to maturity, tillers per plot and thousand grain weight. While, significant but negative correlation of grain yield with plant height and days to maturity under both populations indicated that height and maturity alone is not the contributor to yield but may be through some other traits which are tillers per plot, spike length and thousand grain weight. It was interesting to note that 1000-grain weight was having negative association with tillers per plot but both these traits were direct contributors of yield under both populations.

Khan *et al.* (2004) also reported significant and positive correlation between grains per spike, effective tillers per plant and spike weight with yield per plant, thus supporting our results. They further reported positive correlation of grain yield with plant height, number of tillers per plant, grains per spike and 1000-grain weight both at genotypic and phenotypic levels. Similar to our findings, the number of effective tillers per plant, number of spikelets per panicle and harvest index gave significant positive correlation with grain yield per plant both at genotypic and phenotypic level as reported by (Kotal *et al.,* 2010). Some authors also reported that grain yield per plant showed highly significant and positive correlation with biological yield per plant, grains per spike, spike weight, tillers per plant and ear length whereas, plant length has significant and positive association with grain yield (Singh *et al.,* 2006 and Singh *et al.,* 2010).

The grain yield was positively and significantly correlated with gain weight, grains per spike, test weight, plant height, spikelets per spike, 1000-grain weight and spike length whereas, negatively correlated with days to 50% flowering as reported by Oguz *et al.* (2011). Significant and positive correlations were also estimated between tillers per meter and 1000-grain weight with grain yield per plot by Singh *et al.* (2012).

In summary, the present study reveals that, wide genetic variability exists in both double haploids populations grown over the two year. Three traits, plant height, thousand grains weight and grain yield showed a high heritability with high genetic advance under both populations over the both year and pooled, indicating a significant scope for improving grain yield through simple hybridization and selection. The high and positive correlations in both populations will help in improving the grain yield through selection and the high heritability and genetic advance will be useful for population improvement through hybridization.

References

1. Anonymous (2012). Progress report of All India Coordinated Wheat & Barley Improvement Project 2011-12, Project Director's Report. Directorate of Wheat Research, Karnal, India, p-01.
2. Ansari KA, Soomro ZA, Ansari BA and Leghari MH (2005). Genetic variability and heritability studied for some quantitative traits in bread wheat (*Triticum aestivum* L.). *Pakistan Journal of Agricultural Sciences and Agricultural Engineering and Veterinary Sciences.* **21**(1): 18-24.
3. Asghar A, Rauf S, Nazir S, Tariq SA and Rehman A (2011). Utilization of wheat species as cultural food. In: Wheat: Genetics, Crops and Food Production. Maria T. Almeida (ed.).Nova Science Publishers, Inc., USA.
4. Ayciceck M and Yildirim T (2006). Heritability of yield and some yield components in bread wheat (*Triticum aestivum* L.). *International Journal of Biological Sciences* **4**: 480-85.
5. Gulnaz S, Sajjad M, Khaliq I, Khan AS and Khan SH (2011). Relationship among coleoptiles length, plant height and tillering capacity for developing improved wheat varieties. *International Journal of Agriculture and Biology* **13**: 130-133.
6. Gupta RS, Singh RP and Tiwari DK (2004). Analysis of heritability and genetic advance in bread wheat (*Triticum aestivum* L.). *Advance in Plant Science* **17**(1): 303-305.
7. Inamullah Ahamad H, Moahammad F, Din SU, Hassan G and Gul R (2006). Evaluation of the heterotic and heterobeltiotic potential of wheat genotypes for improved yield. *Pakistan Journal of Botany* **38**(4): 1159-1167.
8. Johnson HW, Robinson HF and Comstock RE (1955). Estimation of genetic and environmental variability in soyabens. *Agronomy Journal* **47**: 314-318.

9. Kashif M and Khaliq I. (2004). Heritability, correlation and path coefficient analysis for some metric traits in wheat. *International Journal of Agriculture and Biology* **6**:138-142.

10. Khan AS, Ashfaq M and Asad MA (2003). A correlation and path coefficient analysis for some yield components in bread wheat. *Asian Journal of Plant Sciences* **2**: 582-584.

11. Khan MF, Khan MK and Mustaq K (2004). Genetic variability among wheat cultivars for yield and yield components under the agro-ecological condition of districts Rawalkot Azad Kashmir, Pakistan. *Sarhad Journal of Agriculture* **20**(3): 391-394.

12. Kotal BD, Das A and Choudhary BK (2010). Genetic variability and association of characters in wheat (*Triticum aestivum* L.). *Asian Journal of Crop Science* **2**(3): 155-160.

13. Liu W, Zheng MY, Konzak CF (2002). Improving green plant production via isolated microspore culture in bread wheat (*Triticum aestivum* L.). *Plant Cell Reports*. **20**:821-824.

14. Oguz B, Kayihan Z, Korkut, Ismet B, Orhan D, Irfan O, Turhan K and Balkan A (2011). Genetic variation and inter-relationship of some morpho-physiological traits in Durum wheat (*Triticum durum* L.). *Pakistan Journal of Botany* **43**(1): 253-260.

15. Panse VG (1957). Genetics of quantitative character in relation to plant breeding. *Indian Journal of Genetics and Plant Breeding* **17:** 318–328.

16. Pawar SV, Patil SC, Naik RM and Jambhale VM (2002). Genetic variability and heritability in wheat. *Journal of Maharashtra Agriculture University* **27**(3): 324-325.

17. Sardana S, Mahajan R, Gautam N, Ram B (2007). Genetic variability in pea (*Pisum sativum* L.) germplasm for utilization. *SABRAO Journal* **39**(10): 31-41.

18. SAS Institute (2008). What is new in SAS/STAT 9.2, release 3.08, SAS Inst. Inc., Cary, NC.

19. Singh BN, Vishwakarma SR and Singh VK (2010). Character association and path analysis in elite lines of wheat (*Triticum aestivum* L.). *Plant Archives* **10** (2): 845-847.

20. Singh Gyanendra, Chatrath R, Singh GP and Jag Shoran (2003). Shuttle breeding approach for wider adaptability and disease resistance in wheat. In first International Group Meeting on *Wheat Technologies for Warmer Areas. Sept 23-26, 2002. Agharkar Research Institute, Pune, India. Eds.:* Rao V.S., Singh Gyanendra and Misra S.C., Anamaya Publisher, New Delhi . Pp24-35.

21. Singh Gyanendra, Tyagi BS, Singh Charan, Singh Rajender, Sharma P and Singh SS (2011a). Wheat Breeding for increasing productivity in eastern Gangetic plains. In third International Group Meeting on *Wheat Productivity Enhancement under Changing Climate. Feb 9-12, 2011. UAS, Dharwad, Karnataka, India. Eds.:* Singh SS, Hanchinal RR, Singh G, Sharma RK, Tyagi BS, Saharan MS, Sharma I. Pp77-94.

22. Singh KN, Kulshreshtha N, Kumar V and Setter TL (2006). Genetic variability of wheat (*Triticum aestivum*) lines for grain yield and component characters grown under sodic and waterlogged conditions. *Indian Journal of Agricultural Sciences* **76** (7): 414-419.

23. Singh MK, Gyanendra Singh, Saharan MS, Singh SS, Tyagi BS, Verma A and Bind D (2011b). Genetic analysis for yield components traits in bread wheat (*Triticum aestivum* L.). In third International Group Meeting (IGM) on "*Wheat Productivity under Changing Climate*" held at, University of Agricultural Sciences, Dharwad. pp- 43.

24. Singh MK, Gyanendra Singh, Saharan MS, Tyagi BS, Kulshreshtha N, Yaduvanshi NPS, Singh BN, Bind D, Ojha A, Verma A, Sharma I and Setter TL (2012). Characterization of diverse germplasm for waterlogging tolerance in bread wheat (*Triticum aestivum* L.). National Seminar, on "*Plant Genetic Research for Eastern and North Eastern India*", Meghalaya. Pp 193-194.

25. Tester M and Langridge P (2010). Breeding technologies to increase crop production in a changing world. *Science* **327**: 818-821.