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ESTIMATION OF VARIABILITY PARAMETERS FOR YIELD AND ITS CONTRIBUTING TRAITS IN WHEAT (*TRITICUM AESTIVUM* (L.) EM. THELL)

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ABSTRACT

Twenty seven wheat genotypes were evaluated in Randomized block design for the study of variability, heritability and genetic advance among the yield and yield contributing traits. Statistically significant difference was observed among the genotypes tested for important characters indicating the presence of variability. The magnitude of PCV was generally higher than GCV for all fourteen quantitative traits. In addition, the high estimate of PCV along with GCV was observed for grain yield per plant, tiller per plants, biological yield, grains per spike, test weight, flag leaf width, spike length, flag leaf length, harvest index, grain filling period, plant height, days to heading and day to 50% flowering suggesting sufficient variability and thus scope for genetic improvement through selection for these traits. Significant GCV among traits is useful for breeding programme to improvement of yield and its components. High heritability coupled with high expected genetic advance as percent of mean was obtained for grain per spike followed by grain yield per plant, biological yield and spike length, indicating the presence of more additive gene effects for potential crop improvement and so these characters could be improved through selection. This study reveals that greater yield response could be obtained through direct selection.

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INTRODUCTION

Wheat [*Triticum aestivum* (L.) em. Thell] is most important self-pollinated cereal crop particularly in India where it meets the basic food requirements of more than half of the human population. Globally, wheat is being grown in 122 countries and occupies an area of 222.21 million ha producing nearly 645.41 million tonnes of wheat (Anonymous, 2011). The major wheat producing countries are China, India, USA, the Russian Federation, and Australia. These five countries together contribute more than half of the global wheat production. India stands second rank both in area and production next to China in the world. The India's share in world wheat area and production is about 13%. State wise analysis indicated that Uttar Pradesh has registered the highest production (30.24 million tonnes), followed by Punjab (17.04 million tonnes), Madhya Pradesh (13.93 million tonnes), Haryana (11.80 million tonnes), Rajasthan (8.92 million tonnes) and Bihar (5.08 million tonnes). These top six states together contributed around 91 per cent of the total wheat production in the country.

Possibility of achieving improvement in any crop plants depends heavily on the nature and magnitude of variability and heritability in a population. It is one of the prerequisites for successful breeding program in selecting genotypes with desirable characters. The variability for various characters are subjected to selection for changing the genetic architecture of plant characters and consequently of the plant as a whole to develop improved genotypes having higher economic yield. Presence of morphogenetic variations in agronomic characters of a crop would be of considerable importance in determining the best method needed to improve the yield of that crop (Ojo *et al.*, 2006).

Heritability plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value. It is the breeding value which determines how much of the phenotype would be passed onto the next generation (Tazeen *et al.*, 2009). There is a direct relationship between heritability and response to selection, which is referred to as genetic advance. High genetic advance with high heritability estimates offer the most effective condition for selection (Larik *et al.*, 2000). 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.

Keeping the above fact in mind, the objective of the present investigation was to estimate the genetic variability, heritability and genetic advance in wheat lines to identify the genotypes with best potentiality for upgrading yield and its components characters.

MATERIALS AND METHODS

Experimental site and design

The experimental material comprised of twenty five lines of wheat genotypes along with two checks viz., K 9162 and Raj 4037. The test genotypes obtained from

Rajasthan Agriculture Research Institute, Durgapura, exhibited wide spectrum of variation for various agronomic and morphological characters. These were selected on the basis of their diverse geographical origin, wide variation and genotype adaptability for different agro-climatic zones of India (Tables 1). The 27 entries (25 test genotype + 2 checks) were evaluated in Randomized Block Design with 3 replications under normal soil during rabi season of 2012-2013 at Field experimental centre of department of genetics and plant breeding, SHIATS, Allahabad. Each genotype was sown in a two row plots of 2 meter length following inter-row and intra-row spacing of 23 cm and 5 cm, respectively. Thinning was done to maintain a plant to plant spacing. The recommended doses of N: P: K was applied. All the recommended agronomic practices were followed to raise a healthy crop.

Recording of data

Five competitive plants were randomly selected from each genotype in each replication for data collection. However, traits like days to 50% flowering and days to maturity were recorded on whole plot basis. Observations on fourteen quantitative and morphological traits viz., days to heading, days to 50 % flowering, tillers per plant, plant height, flag leaf length, flag leaf width, spike length, grains per spike, grain filling period, days to maturity, biological yield, harvest index, test weight and grain yield were recorded from each replication.

Statistical analysis

The mean value of the recorded data was subjected to analysis of variance (ANOVA) using the statistical analysis procedures of Panse and Sukhatme (1967). The phenotypic and genotypic variances were also estimated according to the method suggested by Burton and De Vane (1952). Heritability (h^2) in broad sense and Genetic advance under selection for each characters was computed using the formula suggested by Burton and Devane (1953) and Johnson *et al.* (1955), respectively.

RESULTS AND DISCUSSION

Analysis of variance for Randomized Block Design for fourteen characters of 27 genotypes have been presented in Table 2. The mean sum of squares due to genotypes found significant at 1% level for all the characters. This indicates that the genotypes selected were genetically variable and considerable amount of variability existed among them. Thus, reveal ample scope for selection for different quantitative characters for wheat improvement. Similar findings in wheat have also reported by Chandra *et al.* (2010) and Priya *et al.* (2013).

Estimation of variance

The estimates of variance for all the fourteen characters studied presented in Table 3. Wide range of phenotypic (VP) and genotypic variance (VG) were observed in the experimental materials for all the traits studied. Phenotypic and Genotypic variance values ranged from (0.09%, 0.07%) for flag leaf width to (129.82%, 127.93%) for grain per spike. The highest phenotypic and genotypic variances were recorded for grains per spike (129.82 and 127.93) followed by plant height (54.54 and 51.92), test weight (33.66 and 31.31), biological yield (41.95 and 29.68) and days to heading (15.07 and 14.79),

while moderate values were observed for grain yield per plant (5.61 and 3.98) and grain filling period (8.65 and 7.16). Whereas flag leaf width (0.09 and 0.05) and spike length (2.21 and 2.09) showed low estimates of variance. Less difference in the estimates of genotypic and phenotypic variance and higher genotypic values compared to environmental variance for all the characters suggested that the variability present among the genotypes were mainly due to genetic reason with minimum influence of environment and hence heritable. These results are in accordance with the finding of Sharman and Garg (2002) and Mohsin *et al.* (2009).

Estimation of coefficient of variation

The estimates of phenotypic and genotypic coefficient of variation for all the fourteen characters studied presented in Table 3. Phenotypic coefficient of variability (PCV) and Genotypic coefficient of variability (GCV) values ranged from (3.27%, 3.04%) for days to maturity to (25.97%, 21.86%) for grain yield per plant. In addition, PCV were found higher than their corresponding GCV, indicating that the little influence of environment on the expression of these characters.

The high magnitude (> 20%) of PCV was observed for grain yield per plant (25.97), tiller per plants (25.33), biological yield per plant (24.66), grains per spike (20.48), test weight (16.73), flag leaf width (15.07), flag leaf length (12.82), spike length(12.31) and harvest index (11.80) while moderate estimate of PCV was depicted by number of grain filling period (9.42), plant height (7.81), days to heading (4.96) and days to 50% flowering (4.61) whereas, days to maturity (3.27) depicted least phenotypic coefficient of variation.

Table 1: List of wheat genotypes

S.N.	Genotype name	Pedigree
1.	AKAW-4731	WAWSN 12,KAUZ//STAR
2.	AKAW-4739	II SSN 98.99/DF ₂ 98.99
3.	DL 1012	SFW/VAISHALI//UP2425
4.	GW 09-211	J96-1/K9533
5.	GW-2010-272	TUSN(NS)NIAW835/CPAN-119 31/WH147
6.	GW-2010-275	SORA/2PLATA12//GW 1102
7.	GW-2010-282	GW 1193/ SULA
8.	GW-2010-287	GW 336/HW 1042//KAZU
9.	GW-2010-288	WR196/CMH 83-2578
10.	GW-2010-289	GW 273/GW 353
11.	GW-2010-290	STAR//KAZU/STAR/3/GW 241
12.	GW-2010-291	W 462//NEE/KOEL/3/PEG
13.	HPW 355	CMH79;1384/4/AGA/3/SN64/C N067//INIA 66/5
14.	J 07- 40	GW 273/MACS 2496
15.	KLY-1090	HUW 468/PBW 343
16.	LBPY 2010-10	BAE 923//SOURAY/ K 8801
17.	LBPY 2010-24	NL 887//NL888//BL 2037
18.	NWL 9-11	NW = 2036/HD 2733
19.	VW 921	VL 830/BUDIFEN//VL829
20.	VW 20107	RAJ3765/CHINA 84-4000022
21.	VW 20143	VL 832/Druchamp/PHR 1010
22.	WSM-30	DWR1331/GREEN 3
23.	WSM-55	EDULT 51.DWR 192
24.	GW-2011-347	CMH 84-3379/PBW 475
25.	JS 6-4	RAJ 4014 X HUW 510
26.	RAJ-4037	CHECK 1
27.	K 9162	CHECK 2

Table 2: Analysis of variance for different quantitative characters in wheat genotypes

S.no	Characters	Mean sum of squares		
		Replications	Treatments	Error
	(df = 2)	(df = 26)	(df = 52)	
1.	Days to heading	0.25	45.34**	0.27
2.	Days to 50% flowering	1.80	1160.76**	14.86
3.	Plant height	3.49	158.37**	2.62
4.	Tillers/ plant	0.27	10.68**	1.39
5.	Flag leaf length	4.77	28.84**	1.95
6.	Flag leaf width	0.02	0.24**	0.01
7.	Spike length	0.02	6.39**	0.11
8.	Days to maturity	1.12	38.98**	1.95
9.	Grain filling period	0.48	22.97**	1.49
10.	Grain /spike	6.90	385.66**	1.89
11.	Biological yield	6.27	101.29**	12.26
12.	Grain yield /plant	0.35	13.56**	1.63
13.	Harvest Index	15.70	42.69**	4.29
14.	Test weight	0.22	95.26**	1.35

*, ** Significant at 5 (%) and 1 (%) level probability, respectively.

Table 3: Estimates of genetic parameters for 14 quantitative characters in wheat

S.N.	Characters	Vg	Vp	GCV	PCV	h ² (bs) (%)	GA	GA as % of Mean
1	Days to heading	15.02	15.30	4.91	4.96	98	7.91	10.03
2	Days to 50% flowering	14.79	15.07	4.57	4.61	98	7.85	9.32
3	Plant height	51.92	54.54	7.62	7.81	95	14.48	15.32
4	Tillers/ plant	3.09	4.49	21.02	25.33	69	3.01	35.93
5	Flag leaf length	8.96	10.92	11.61	12.82	82	5.59	21.68
6	Flag leaf width	0.07	0.09	13.51	15.07	80	0.50	24.95
7	Spike length	2.09	2.21	12.00	12.31	95	2.90	24.08
8	Days to maturity	12.34	14.30	3.04	3.27	86	6.72	5.82
9	Grain filling period	7.16	8.65	8.57	9.42	83	5.01	16.06
10	Grain /spike	127.93	129.82	20.33	20.48	99	23.13	41.57
11	Biological yield	29.68	41.95	20.74	24.66	71	9.44	35.94
12	Grain yield /plant	3.98	5.61	21.86	25.97	71	3.46	37.89
13	Harvest Index	12.80	17.09	10.21	11.80	75	6.38	18.21
14	Test weight	31.31	32.66	16.38	16.73	96	11.29	33.03

Higher magnitude of GCV were recorded for grain yield per plant (21.86), tiller per plants (21.02), biological yield per plant (20.74), grains per spike (20.33), test weight (16.38), flag leaf width (13.51) spike length (12.00), flag leaf length (11.61), and harvest index (10.21) while moderate estimate of PCV was depicted by number of grain filling period (8.57), plant height (7.62), days to heading (4.91), and day to 50% flowering (4.57) whereas, days to maturity (3.04) depicted least phenotypic coefficient of variation. Similar finding by Arya *et al.* (2005) and Verma *et al.* (2013). The high GCV values of these characters suggest that the possibility of improving these trait through selection. Relatively low magnitudinal difference was observed between GCV and PCV for all the traits studied, similar finding by Priya *et al.* (2013). This indicated less environmental influence on the expression of all the attributes.

Estimation of heritability in broad sense and genetic advance

Estimates of heritability in broad sense ranged from 99% for grain per spike to 69% for tillers per plant (Table 3). High estimate of heritability in broad sense was high (>60%) for grains per spike (99%) followed by days to heading (98%), days to 50% flowering (98%), test weight (96%), plant height (95%), spike length (95%), days to maturity (86%), grain filling period (83%), flag leaf length (82%), flag leaf width (80%), harvest index (75%), biological yield per plant (71%), grain

yield per plant (71%) and tillers per plant (69%). This suggested that heritability may be due to higher contribution of genetic component. High heritability estimates were reported by Bergale *et al.* (2001) for 1000 grain weight and Asif *et al.* (2004) for plant height, Rasal *et al.* (2008) has also observed high value of heritability for grain yield and its components in wheat. Heritability alone provides no indication of amount of genetic improvement that would result from selection of individual genotypes hence knowledge about genetic advance coupled with heritability is most useful.

Genetic advance is the improvement in the mean of selected family over the base population (Johnson *et al.*, 1955). Estimates of genetic advance as per cent of mean ranged from 41.57 for grain per spike to 5.82 for days to maturity (Table 3). Maximum genetic advance as percentage of mean was recorded for grain per spike (41.57) followed by grain yield per plant (37.89), biological yield per plant (35.94), tillers per plant (35.93), test weight (33.03), flag leaf width (24.95), spike length (24.08), flag leaf length (21.68), harvest index (18.21), grain filling period (16.06) and plant height (15.32). Low estimates of genetic advance as percent of mean was observed for days to heading (10.03), days to 50% flowering (9.32) and days to maturity (5.82). Similar result were found by Dhanwani *et al.* (2013).

According to Johnson *et al.* (1955), high heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone. The present study reveals high heritability coupled with high expected genetic advance as percent of mean for grain per spike (99, 41.57%) followed by grain yield per plant (71, 37.89%), biological yield (71, 35.94%) and spike length (95, 24.08%). Therefore, these characters could be improved more easily than the other characters. Similar result were found by Shukla *et al.* (2004), Baranwal *et al.* (2012) and Verma *et al.* (2013). Singh *et al.* (2013) also reported similar finding for grain yield per plant and biological yield.

REFERENCES

- Anonymous 2012.** Food and Agricultural Organization, Statistical Databases, www.fao.org.
- Arya, V. D., Pawar, I. S. and Lamba, R. A. S. 2005.** Genetic variability and correlation for yield and quality traits in bread wheat. *Haryana Agric. Uni. J. Res.* **35(1)**: 59-63.
- Asif, M., Mujahid, M. Y., Kisana, S. S., Mustafa, S. Z. and Ahmad, I. 2004.** Heritability, genetic variability and path coefficient of some traits in spring wheat. *Sarhad J. Agriculture.* **20(1)**: 87-91.
- Baranwal, D. K., Mishra, V. K., Vishwakarama, M. K., Yadav, P. S. and Arun, B. 2012.** Studies on genetic variability, correlation and path analysis for yield and yield contributing traits in wheat (Triticum. Aestivum L. em Thell). *Plant Archives.* pp. 99-104.
- Bergali, S., Mridulla, Billore, A. S., Ruwali, K. N. and Prasad, S. V. S. 2002.** Patterns of variability, character association and path analysis in wheat (Triticum aestivum L.) *Agriculture Science Digest.* **22(40)**: 258-260.
- Chandra, D., Sharma, R., Rani S., Singh, D. K. and Sharma, S. K. 2010.** Genetic variability for quantitative traits in wheat [Triticum aestivum (L)]. *Plant Archives.* **10(2)**: 871-874.
- Dhanwani, R. K., Sarawgi, A. K., Solanki, A. and Tiwari, J. K. 2013.** Genetic variability analysis for various yield attributing and quality traits in rice (O. sativa L.). *The Bioscan.* **8(4)**: 1403-1407.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955.** Estimates of genetic and environmental variability in soybean. *Agron. J.* **47**: 314-318.
- Larik, A. S., Malik, S. I., Kakar, A. A. and Naz, M. A. 2000.** Assessment of heritability and genetic advance for yield and yield components in *Gossypium hirsutum* L. *Scientific Khyber.* **13**: 39-44.
- Mohsin, T., Khan, N. and Naqvi, F. N. 2009.** Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. *J. Food, Agriculture and Environment.* **7(3&4)**: 278-282.
- Ojo, D. K., Omikunle, O. A., Oduwaye, O. A., Ajala, M. O. and Ogunbayo, S. A. 2006.** Heritability, character correlation and path coefficient analysis among six inbred lines of maize (*Zea mays* L.). *World J. Agric. Sci.* **2(3)**: 352-358.
- Priya, B., Mukherjee, S., Das, B., Satyanarayana, N. H., Sarkar, K. K., Uikay, B.L., Mukhopadhyay, S. K. 2013.** Studies on characters related to yield and quality of wheat (*Triticum aestivum* L.) grown in gangetic plains of West Bengal, India. *International J. Bio-resource and Stress Management.* **4(3)**: 389-394.
- Rasal, P. N., Bhoite, K. D. and Godekar, D. A. 2008.** Genetic variability and genetic advance in durum wheat. *J. Maharashtra Agriculture University.* **33(1)**: 102-103.
- Sharma, A. K. and Garg D. K. 2002.** Genetic variability in wheat (*Triticum aestivum* L.) crosses under different normal and saline environments. *Annals Agriculture Research.* **23(3)**: 497-499.
- Shukla, R. S., Mishra, Y. and Singh, C. B. 2004.** Variability of some agro-physiological traits in wheat. *J. Applied Biology.* **9(1)**: 25-27.
- Singh, C. M., Suresh Babu, G., Kumar, B. and Mehandi, S. 2013.** Analysis of quantitative variation and selection criteria for yield improvement in exotic germplasm of upland rice (*Oryza sativa* L.). *The Bioscan.* **8(2)**: 485-492.
- Tazeen, M., Nadia, K. and Farzana, N. N. 2009.** Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. *J. Food. Agric. Environ.* **7(3&4)**: 278-282.
- Verma, P. N., Yadav, R. K., Singh, B. N. and Vishwakarma, S. R. 2013.** Genetic studies for yield and component traits in wheat (*T. aestivum* L.) lines under sodic soils. *Trends in Biosciences.* **6(6)**: 747-750.

