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Evaluation of genetic variability in bread wheat (*Triticum aestivum* L. emThell) genotypes

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ABSTRACT
Present investigation was carried out to study genetic variability, heritability and expected genetic advance in bread wheat genotypes for yield and yield contributing traits. The experiment was carried out in randomized block design with three replications and data was recorded on individual plant basis for all the traits except days to 75% heading and days to maturity, which were recorded on per plot basis. The analysis of variance showed significant genotypic differences for all the traits, indicating enough genetic variability in the material studied. Both GCV and PCV estimates were higher for number of grains per spike and grain weight per spike. High heritability was found for 1000-grain weight, grain weight per spike and number of grains per spike. Higher values of genetic advance as percent of mean (GAM) were observed for grain weight per spike and number of grains per spike. High heritability with high GAM were reported for number of grains per spike, grain weight per spike, 1000 grain weight and biological yield indicating additive gene action and improvement through direct selection could be possible for these characters.
Key words Variability, heritability, genetic advance, bread wheat

INTRODUCTION
Wheat is the most important cereal crop of the world and its cultivation has been related to the development of the major civilizations all over the world. Excavation evidences from Mohan-Jo-daroindicate the cultivation of wheat in India more than 5000 years ago [18].Scientists have traced its origin back to the Middle East region, particularly the valley of Tigris and Euphrates Rivers. India is one of the major producers of wheat and occupies second position after china in terms of area and production among wheat growing countries of the world. Wheat is cultivated in almost all parts of India and is contributing about 38 % of the country's total food grain production (MoA&FW, India 2015-16). During 2015-16, India has a production of 93.50 million tonnes from an area of 30.23 million hectares having an average productivity of 3.09 tons/ha[3]. The major wheat producing states in India are Uttar Pradesh (26.9 million tonne), Punjab (16.11 million tonne) and Haryana (11.14 million tonne).Wheat is consumed in the form of a wide range of products from chapatti to processed foods and numerous industrial products for which its flour is specifically suitable. Its baking quality makes it relatively more important as a human food than any other cereal grain. Much of the emphasis in wheat breeding has been placed on increasing productivity of wheat crop in response to the pressure for an adequate food supply caused by continuously increasing population of India and the world as a whole. The choice of parents is of prime importance in breeding programme. Direct selection for yield, may produce misleading results because yield is a complex polygenic trait, influenced greatly by the environmental fluctuations. Knowledge on genetic variability and relationship between various agronomic traits and yield is crucial for the success of a breeding programme.Since, it becomes necessary to divide the present variability into its heritable and non-heritable components with the help of suitable genetic parameters such as phenotypic and genotypic coefficient of variation, heritability estimates, and genetic advance under selection[19].Heritability is the degree to which the variability of a character is transferred to its progeny,

thus denotes the proportion of phenotypic variance that is due to genotype, i.e., heritable. It is a tool to predict the gain from selection in a population **[8]** i.e., genetic advance. Such estimate facilitates evaluation of hereditary and environmental effects in phenotypic variation and thus aid in selection and if these estimates are high the character is least influenced by the environmental factors. Genetic advance is also of considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection **[9].**However, heritability estimates together with genetic advance are more important than heritability alone to predict the resulting effect of selecting the best individuals **[10].**The present investigation was therefore designed to evaluate the degree of genetic variability, heritability and genetic advance indifferent bread wheat genotypes.

MATERIALS AND METHODS
The experimental materials for present investigation comprised of 51 bread wheat genotypes. Out of those genotypes, 12 were female lines, three were testers and 36 were their F1s. All the parents along with their pedigree are presented in **Table 1**. This experiment was carried out in three replications using randomized block design during*rabi* 2014-15 in timely sown conditions at Norman E. Borlaug Crop Research Centre, G. B. Pant University of Agriculture and Technology, Pantnagar. Each genotype was planted in two rows of one metrelength each spaced at 20 cm and theobservations were recorded for 14 metriccharacters. Data was recorded for number of tillers per plant, plant height, flag leaf area, peduncle length, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike, 1000 grain weight, biological yield per plant, grain yield per plant and harvest index on individual plant basis on a sample of five randomly selected competitive plants per plot. However, days to 75% heading and days to maturity were recorded on per plot basis.To test the significance of differencesbetween treatments, the analysis of variancefor randomized block design (RBD) wascarried for all metric characters. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) were calculated according to Singh and Chaudhary,1985.Broad sense heritability values were estimated based on the formula of Falconer *et al.,*1996. The expected genetic advance under selection for the different characters was estimated as suggested by Allard 1960; Singh and Chaudhary1985.Genetic advance as per cent of mean for each character was calculated as suggested by Johnson, Robinson and Comstock 1955.

RESULTS AND DISCUSSION
The analysis of variance showed that the mean squares across the genotypes were highly significant for all the characters studied(**Table 2**). Coefficient of variation (CV) was found to be maximum for flag leaf area (18.41%) followed by number of tillers per plant (12.23%), grain yield per plant (12.09%), harvest index (11.72%) and for rest of the traits less than 10% CV was found.This suggested that genotypes were genetically variable and a considerable amount of variability existed among them, therefore, these wheat genotypes wouldrespond positively to selection.
The genotypic (GCV), phenotypic (PCV) and environmental (ECV) coefficient of variation studied for 14 characters are presented in Table 3.Deshmukh*et al.* (1986) categorized GCV and PCV as low (<10%), moderate (10-20%) and high (>20%).In the present investigation both GCV and PCV estimates were higher for number of grains per spike (19.98 and 21.38) and grain weight per spike (19.39 and 19.66).Moderate estimates of GCV and PCV were observed for the characters *viz.*,1000-grain weight (13.97 and 14.12), biological yield per plant (13.64 and 16.14) and grain yield per plant (12.16 and 17.15). Low GCV and moderate PCV was observed for number of tillers/plant (9.03 and 15.20) and harvest index(8.39 and 14.41) whereas, moderate GCV and higher PCV was found for Flag leaf area (10.49 and 21.19). Low genotypic and phenotypic coefficient of variations were observed for the characters *viz.*, days to 75% heading (1.58 and 2.28), days to maturity (0.71and 1.40), plant height (3.61 and 5.87), peduncle length (7.52 and 9.84), spike length (4.67 and 7.21) and number of spikelets/spike (3.52 and 5.62)[4,11].None of the traits showed higher ECV but moderate ECV was observed for traits *viz.*,flag leaf area (18.41), number of tillers per plant (12.22), grain yield per plant (12.09) and harvest index (11.72). Low ECV was observed for biological yield per plant (8.62), number of grains per spike (7.60), plant height (6.63), spike length (6.52), peduncle length (6.33), number of spikelets/spike (4.38), grain weight per spike (3.15), 1000grain weight (2.01), days to 75% heading (1.64) and days to maturity (1.20).
For effective screening of superior genotypes presence of variability is a pre-requisite and the progress in any breeding programmeis decided by bothnature and magnitude of genotypic variability. In the present investigation PCV were found higher than GCV for all the traits. Traits, number of grains per spike, grain weight per spike, 1000grain weight, biological yield per plant and grain yield per plant showed higher and moderate values of both GCV and PCV but low values of ECV[10, 12, 13, 14, 15].The closeness between GCV and PCV values for these characters and low ECV indicating them to be less influenced by

environment. Therefore, it may be concluded that selection can be employed in the desired direction on the basis of phenotype to improve grain yield.Low GCV, PCV and ECV were observed for days to 75% heading, days to maturity, plant height, peduncle length, spike length and number of spikelets/spike[4,11]. Although these traits are less influenced by environment but variation due to genotype is very low,thus difficult to improve these traits by selection.Number of tillers/plantand harvest index showed low GCV but moderate PCV and ECV indicating that variation was due to environment. Therefore, selection will not be effective for these traits.

The estimates of heritability in broad sense (h²b) showed considerable variation for different characters and presented in **Table 3.** High heritability (≥ 75%) was observed for 1000-grain weight (97.95), grain weight per spike (97.23) and number of grains per spike (87.34).Moderate heritability (50-75%) was reported for biological yield per plant (71.44%), peduncle length (58.52%) and grain yield per plant (50.31%).The remaining characters, days to 75% heading (48.42), days to maturity(26.22),number of tillers/plant (35.28),plant height (37.81),flag leaf area (24.50),spike length (41.95), number of spikelet/spike (39.27)and harvest index(33.91) showed low values of heritability (≤50%).

The high heritability magnitudewas observed for 1000-grain weight, grain weight per spike and number of grains per spike[3, 4, 14], thisindicates the high chance that any genotype can bedistinguished by its phenotype correctly. These results indicated the predominance of additive genetic variation in the expression of these characters and the effectiveness of selection in the early segregating generations in improving these traits [16]. Traits, biological yield per plant, peduncle length and grain yield per plant showed moderate heritability[14],indicating predominance ofnon additive gene effects, so selection for these traits would not be effective.For rest of the traits, since the heritability is low, these traits are difficult to improve [10,11].

Genetic advance as percent of mean (GAM) exhibited considerable variation for different characters. Deshmukh*et al.* (1986) classified genetic advance as percent of mean as low (<10%), moderate (10-20%) and high (>20%).Higher values of genetic advance as percent of mean (GAM) were observed for grain weight per spike (39.39%), number of grains per spike (38.47%), 1000 grain weight (28.47%), and biological yield per plant (23.47%).Moderate GAM was found for grain yield per plant (17.78), peduncle length (11.86), number of tillers/plant (11.05), flag leaf area (10.69) and harvest index (10.07). Low GAM was observed for days to 75% heading (2.27), days to maturity (0.75), plant height (4.57), spike length (6.23) and number of spikelets/spike (4.55).

The heritability estimates are more useful when expressed in terms of genetic advance. High heritability with high genetic advance as percentof mean were reported for number of grains per spike, grain weight per spike, 1000grain weight and biological yield per plant**[1, 12, 13, 15].** These characters show additive gene action and improvement through direct selection could be possible for these characters. Low heritability coupled with low genetic advance was found for days to maturity, plant height, spike length and number of spikelets per spike and this indicate that these traits were highly influenced by environment and selection would be ineffective for these characters.

CONCLUSION

Grain yield is the major character of any crop targeted for crop improvement and selection of desirable genotypes is primarily based on yield contributing traits. Therefore, information regarding the presence of genetic variability, heritability of the various yield contributing traits and genetic advance under selection is much useful. In the present study wide range of variability among genotypes was observed for all the traits studied showing scope of genetic gain through selection. High GCV and PCV were observed for number of grains per spike and grain weight per spike indicating scope for improving these traits by selection. High heritability with high genetic advance as percentof mean were reported for number of grains per spike, grain weight per spike, 1000 grain weight and biological yield per plant indicating additive gene action and improvement through direct selection could be possible for these characters.

Table 1: Genotypes/varieties with their parentage

S. No.	Genotypes/varieties	Pedigree
1	HD 3091	PICUS/3/KAUZ*2/BOW//KAUZ/4/TILHI
2	WH 1139	CHIR/3/SIREN//ALTAR84
3	PBW 681	UP2338/KALYANSONA
4	DBW 88	KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES
5	WH 1126	WBLL1*2/VIVITSI
6	UP 2848	HD2402/4/PVN/CAR422//ANA/3/BOW/CROW//BUC
7	PBW 644	PBW175/HD2643
8	HD 3123	PASTOR//HXL7573/2*BAU/3/CMH82.575/CMH82.801

9	UP 2845	CPAN4022/UP2382//KAUZ//BOW/NKT
10	UP 2696	CDWR9510/NW1027
11	UP 2425	HD2320/UP2263
12	UP 2554	SM4-HSN24E/CPAN2099
13	WH 1105	MILAN/S87230//BABAX
14	UP 2672	UP2382/DLRSN-7
15	HD 3059	KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES

Table2: Analysis of variance (mean squares) for different morphological characters in bread wheat.

S.No.	Characters	Replication (d.f.=2)	Treatment (d.f.=50)	Error (d.f.=100)
1.	Days to 75% heading	2.196	7.796**	2.043
2.	Days to maturity	2.490	4.939**	2.390
3.	Number of tillers/plant	9.773	6.233**	2.365
4.	Plant height (cm)	22.264	50.445**	17.851
5.	Flag leaf area (cm²)	26.736	57.865**	29.320
6.	Peduncle length (cm)	3.969	25.181**	4.812
7.	Spike length (cm)	0.282	1.575**	0.497
8.	Number of spikelets/spike	0.470	2.500**	0.851
9.	Number of grains/spike	12.948	272.302**	12.548
10.	Grain weight/spike (g)	0.007	0.575**	0.005
11.	1000 grain weight	0.712	143.334**	0.992
12.	Biological yield (g)	418.483	486.433**	57.187
13.	Grain yield (g)	24.385	46.495**	11.515
14.	Harvest index (%)	2.988	36.495**	14.370

*, ** significant at 5% and 1% levels, respectively.

Table 3: Evaluation of variability of the genotypes for different characters

S.No.	Traits	GM	Range Min.-Max.	CD5 %	CD1 %	CV %	GCV	PCV	ECV	H²ᵦ %	GA	GAM
1.	DH	87.16	84.00-90.33	2.31	3.06	1.63	1.58	2.28	1.64	48.42	1.98	2.27
2.	DM	128.17	125.67-130.67	2.50	3.31	1.20	0.71	1.40	1.20	26.22	0.97	0.75
3.	T/P	12.61	8.93-16.30	2.49	3.29	12.23	9.03	15.20	12.22	35.28	1.39	11.05
4.	PH	91.15	82.20-100.10	6.84	9.06	4.63	3.61	5.87	6.63	37.81	4.17	4.57
5.	FLA	28.12	17.03-39.20	8.77	11.61	18.41	10.49	21.19	18.41	24.50	3.14	10.69
6.	PL	34.58	28.67-40.50	3.554	4.70	6.33	7.52	9.84	6.33	58.52	4.10	11.86
7.	SL	12.95	11.30-14.60	1.14	1.51	5.49	4.67	7.21	6.52	41.95	0.80	6.23
8.	S/S	20.87	18.87-22.87	1.49	1.97	4.38	3.52	5.62	4.38	39.27	0.95	4.55
9.	G/S	45.33	21.67-69.00	5.73	7.59	7.60	19.98	21.38	7.60	87.34	17.91	38.47
10.	GW/S	2.34	1.36-3.33	0.11	0.15	3.26	19.39	19.66	3.15	97.23	0.88	39.39
11.	TGW	44.67	31.67-57.67	1.61	2.13	2.02	13.97	14.12	2.01	97.95	14.04	28.49
12.	BY/P	87.94	65.09-110.79	12.25	16.21	8.62	13.64	16.14	8.62	71.44	20.82	23.76
13.	GY/P	31.21	22.45-39.97	5.49	7.27	12.09	12.16	17.15	12.09	50.31	4.99	17.78
14.	HI	33.20	25.08-41.33	6.14	8.12	11.72	8.39	14.41	11.72	33.91	3.25	10.07

Where, GM = General mean, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, ECV= Environmental coefficient of variation, h²ᵦ= Heritability in broad sense, GA= Genetic advance under selection, GAM= Genetic advance as % of mean, DH= Days to 75% heading, DM= Days to maturity, T/P= No. of tillers/plant, PH= Plant height (cm), FLA= Flag leaf area (cm²), PL= Peduncle length (cm), SL= Spike length (cm), S/S= Number of spikelet/spike, G/S= Number of grains/spike, GW/S= Grain weight/spike (g), TGW=1000 grain weight, BY/P= Biological yield/ plant (g), GY/P= Grain yield/ plant (g),HI=Harvest index(%).

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