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## Genetic variability and association studies for yield and its attributes in wheat (*Triticum aestivum* L.)

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### Abstract

The present investigation entitled "Genetic variability and association studies for yield and its attributes in wheat" was carried out to assess genetic variability, correlation and path analysis for grain yield and its attributes having 26 genotypes of bread wheat at Agricultural research field, School of Agriculture, Lovely Professional University during *rabi* 2020-21 in randomized block design (RBD) with three replications. Analysis of variance revealed the presence of significant variation among genotypes. On the basis of mean performance, thirteen genotypes *viz.*, K 68, HP 1761, FASILABAD 2008, PBW 502, VL 829, WH 1105, JWS 17, SUJATA, SKW 196, WH 147, HD 3086, HD 2967, HW 2004, MP 3020 H1 8627, HD 3059, K 1006, PBW 343 and RUJ 4037 were found significantly superior than the best check DBW 222. Phenotypic coefficient of variation was higher than the genotypic coefficient variation which indicated the influence of environmental factors. Moderate genotypic coefficient was observed for seed yield per plant, harvest index, 1000 seed weight, biological yield per plant, ear weight, number of grains per spike. High heritability coupled with high genetic advance as percent mean were observed for seed yield per plant, 1000 seed weight, harvest index and biological yield per plant. Correlation coefficient analysis revealed that the traits *viz.*, plant height, peduncle length, number of tillers per plant, number of spikelets per spike, number of grains per spike, 1000 seed weight, biological yield per plant had positive significant correlation with seed yield per plant. Path analysis revealed that plant height, days to 50% flowering, number of grains per spike, ear weight, 1000 seed weight, biological yield per plant and harvest index had direct effect on seed yield per plant.

**Keywords:** Bread wheat, genetic variability, Heritability, correlation coefficient, Path coefficient analysis

### Introduction

Wheat (*Triticum aestivum* L.) ( $2n=6x=42$ ) is a self-pollinated Poaceae family member and one of the world's top cereals in many nations, including India. Because of its vast area, good production, and significant role in the worldwide food grain trade, it has been called as "King of Cereals." Wheat is India's second-largest food crop, after rice, in terms of both acreage and production. Wheat is used to make bread, chapatti, porridge, flour, and suji, among other things. In 2012-13, India produced 255.36 million tonnes of food grains, with wheat accounting for 92.46 million tonnes of the total production (Anonymous, 2013). India is the world's second-largest wheat producer, accounting for around 34% production of global food grain. Wheat is cultivated on 35.05 lakh hectares in Punjab, with 176.20 million tonnes production (Anonymous 2021). Despite the fact that India's per capita grain production has decreased over the last five decades, wheat consumption has risen and is predicted to continue to rise as the population grows. The pace of rise in production in India is anticipated to be slower than the rate of increase in population. As a result, meeting the massive target of increasing wheat production is a huge challenge that will not be met solely by increasing the area under production and improving production technology unless and until the genetic potential of wheat varieties for various areas and environments is significantly increased. Germplasm is the backbone of a successful breeding programme for increasing yield and yield contributing characteristics in wheat cultivars. Plant populations with a lot of variation in terms of adaptability across years and location are always favoured by nature. True, higher plant variety means more diversified plants and a better possibility of producing high heterotic crossings and a wide range of variability in segregating generations during genetic improvement. Techniques such as selection and hybridization are mostly used to improve a genotype's genetic makeup.

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Selection is commonly used to pool beneficial genes, whereas hybridization is mostly used to aggregate beneficial genes in a genotype for improved performance. Because germplasm serves as the most useful natural reservoir for giving superior attributes, donors can be found from accessible germplasm for this reason. To design a successful breeding programme, it is necessary to identify donor parents for relevant traits by assessing genetic variance in available germplasm.

**Materials and Methods**

The present research has been carried out at research farms of lovely professional university, Jalndhar, Punjab. For the present study, 26 genotypes were used, out of which DBW - 222 is used as check variety. These genotypes were sown

using RBD design with 3 replications during rabi 2021. Each variety is sown in 4 lines of 1 meter length with the spacing between the rows is 15cm and plants is 5cms. Parameters like Days to 50% flowering, days to 75% flowering, plant height, number of tillers per plant, number of spikelets per spike, peduncle length, spike length, ear weight, biological yield per plant, number of grains per spike, seed yield per plant, harvest index and 1000 seed weight were recorded. Statistical analysis viz. ANOVA as per panse and sukhatme (1985), genotypic, phenotypic and environmental coefficient variation as prescribed by Burton and De Vane (1953) [2], Heritability as per Johanson *et al.* (1955), Correlation coefficient and Path analysis by Dewey and Lu (1959) [4] were analysed.

**Table 1:** Showing list of genotypes

S. No	Genotypes	S. No	Genotypes	S. No	Genotypes
1	HD 2643	10	WH 147	19	HW-2004
2	GW 273	11	VL 829	20	HD-3086
3	K 1006	12	SUJATA	21	HD-3059
4	K 68	13	H1-8713	22	PBW-343
5	MP-3336	14	H1-8627	23	DBW-222
6	UP 2565	15	HP 1761	24	UNNAT PWB-550
7	RUI-4037	16	SKW 196	25	WH-1105
8	JWS-17	17	MP-3020	26	HD-2967
9	FASILABAD 2008	18	PBW 502		

**Table 2:** Showing analysis of variance for different traits in wheat

Source of variation		Sum of mean squares			Source of variation		Sum of mean squares		
		Replication	Treatment	Error			Replication	Treatment	Error
Traits	dff	2	25	50	Trait	dff	2	25	50
1 Days to 50% flowering		7.090	11.758*	1.796	8 Ear weight (g)		0.199	0.394*	0.119
2 Days to 75% maturity		0.500	14.185*	2.940	9 Number of grains per spike		2.109	102.151*	10.668
3 Plant height (cm)		269.713	194.335*	39.213	10 Biological yield per plant per plant (g)		0.127	40.766*	2.772
4 Peduncle length (cm)		266.615	143.926*	32.676	11 Harvest index		13.413	131.190*	6.912
5 Spike length (cm)		0.979	10.499*	3.986	12 1000-seed weight (g)		4.420	107.358*	0.473
6 Tiller per plant		1.173	3.078*	1.205	13 Seed yield per plant (g)		1.049	21.762*	0.838
7 Spikelets per spike		0.254	11.449*	1.168					

**Table 3:** Showing genotypic and phenotypic correlation among traits in wheat

Traits		Days to 50% flowering	Days to 75% maturity	Plant height	Peduncle length	Spike length	Tiller per plant	Spikelets per spike	Number of grains per spike	Ear weight	1000-seed weight	Biological yield per plant per plant	Harvest index
Days to 75% maturity	P	0.737**											
	G	0.838**											
Plant height	p	0.284*	0.262*										
	G	0.458**	0.441**										
Peduncle length	P	0.228*	0.201NS	0.970**									
	G	0.395**	0.390**	0.990**									
Spike length	P	0.332**	0.342**	0.571**	0.358**								
	G	0.644**	0.588**	0.449**	0.304**	1.014**							
Tiller per plant	P	0.222NS	0.288*	0.298**	0.271*	0.261*							
	G	0.421**	0.579**	0.449**	0.304**	1.014							
Spikelets per spike	P	-0.126NS	-0.071NS	-0.006NS	-0.054NS	0.134NS	0.115NS						
	G	-0.187NS	-0.088NS	0.093NS	0.047NS	0.238*	0.146NS						
Number of grains per spike	P	-0.125NS	-0.069NS	-0.004NS	-0.051NS	0.134NS	0.116NS	0.999**					
	G	-0.189NS	-0.088NS	0.090NS	0.043NS	0.238*	0.149NS	1.000**					
Ear weight	P	-0.203NS	-0.081NS	-0.191NS	-0.185NS	-0.110NS	-0.135NS	0.157NS	0.154NS				
	G	-0.369**	0.126NS	-0.253*	-0.234*	-0.301**	-0.352**	-0.038NS	0.037NS				
1000-seed weight	P	-0.290*	-0.241*	0.100NS	0.140NS	-0.096NS	0.108NS	0.157NS	0.157NS	-0.285*			
	G	-0.349**	-0.318**	0.120NS	0.182NS	0.180NS	0.158NS	0.169NS	0.171NS	-0.456**			
Biological yield	P	-0.116NS	-0.069NS	0.217NS	0.231*	0.047NS	0.160NS	0.233*	0.233*	0.045NS	0.584**		

per plant per plant														
	G	-0.177NS	-0.120NS	0.273*	0.316*	0.011NS	0.159NS	0.216NS	0.215NS	-0.057NS	0.660**			
Harvest index	P	-0.140NS	-0.240*	0.015NS	-0.023NS	0.121NS	-0.001NS	0.179NS	0.177NS	0.024NS	0.272*	0.012NS		
	G	-0.202NS	-0.303**	0.104NS	0.065NS	0.214NS	0.186NS	0.195NS	0.194NS	-0.002NS	0.292**	0.068NS		
Seed yield per plant	P	-0.197NS	-0.240*	0.152NS	0.133NS	0.118NS	0.095NS	0.302**	0.301**	0.047NS	0.583**	0.638**	0.774**	
	G	-0.274*	-0.311**	0.241*	0.237*	0.165NS	0.225*	0.298**	0.297**	-0.035NS	0.625**	0.654**	0.797**	

**Table 4:** Showing direct indirect effects of traits on seed yield in wheat

Traits	Days to 50% flowering	Days to 75% maturity	Plant height	Peduncle length	Spike length	Tiller per plant	Spikelets per spike	Number of grains per spike	Ear weight	1000-seed weight	Biological yield per plant per plant	Harvest index	Correlation with yield
Days to 50% flowering	0.00968	-0.01461	1.92295	-1.40430	-0.49054	0.01425	0.93598	-0.94041	0.01203	-0.02623	-0.09802	-0.14221	-0.274*
Days to 75% maturity	0.00811	-0.01744	1.85058	-1.38569	-0.44810	0.01959	0.43984	-0.43848	0.00410	-0.02395	-0.06680	-0.21310	-0.311**
Plant height	0.00444	-0.00769	4.17543	-3.51955	-0.62486	0.01520	-0.46570	0.44768	0.00826	0.0899	0.15175	0.07354	0.241*
Peduncle length	0.00382	-0.00680	4.15550	-3.55338	-0.55891	0.01028	-0.23348	0.21295	0.00762	0.01372	0.17567	0.04555	0.237*
Spike length	0.00623	-0.01026	3.44108	-2.60682	-0.76185	0.03433	-1.18723	1.18432	0.00982	-0.01352	0.00612	0.15074	0.165 <sup>NS</sup>
Tiller per plant	0.00407	-0.01009	1.88380	-1.07886	-0.77244	0.03386	-0.73050	0.74975	0.01146	0.01188	0.08809	0.13060	0.225*
Spikelets per spike	-0.00181	0.00154	0.39117	-0.16610	-0.18109	0.00495	-4.99480	4.98306	0.00122	0.01273	0.11997	0.1379	0.298**
Number of grains per spike	-0.00183	0.00153	0.37693	-0.15186	-0.18107	0.00505	-4.99488	4.98298	0.00120	0.01284	0.11960	0.13629	0.297**
Ear weight	-0.00357	-0.00219	-1.06256	0.83057	0.22936	0.01190	-0.18742	0.18304	0.03261	-0.03433	-0.03167	-0.00123	-0.035 <sup>NS</sup>
1000-seed weight	-0.00337	0.00555	0.50147	-0.64796	0.13694	0.00535	-0.84504	0.85029	0.01488	0.07523	0.36632	0.20558	0.625**
Biological yield per plant per plant	-0.00171	0.00210	1.14683	-1.12437	-0.00840	0.00537	-1.07941	1.07346	0.00186	0.04964	0.55516	0.04802	0.654**
Harvest index	-0.00196	0.00528	0.43826	-0.22994	-0.16313	0.00628	-0.97338	0.96468	-0.0006	0.02197	0.03787	0.70398	0.797**

Residual effect: 0.00282

## Results and Discussion

Analysis of variance indicated sufficient amount of variation for all the traits among all genotypes. Mean performance revealed that 13 genotypes viz., K 68, HP 1761, FASILABAD 2008, PBW 502, VL 829, WH 1105, JWS 17, SUJATA, SKW 196, WH 147, HD 3086, HD 2967, HW 2004, MP 3020 H1 8627, HD 3059, K 1006, PBW 343 and RUJ 4037 were superior to check variety. Phenotypic coefficient of variation is found to be higher compared to genotypic coefficient of variation. Similar results reported by Ali *et al.* (2008) [5] and Kumar *et al.* (2014) [6]. PCV and GCV are found moderately high for the traits seed yield / plant, 1000 seed weight, harvest index, Biological yield/ plant, grains/spike and ear weight. Similar results reported by Reena *et al.* (2018) [7], Mele *et al.* (2017) [8], Bayisa *et al.* (2020) [9], Kumar *et al.* (2013) [10], Bahudar *et al.* (1994) and Jagshoran *et al.* (1995) [12]. High to moderate PCV and GCV values indicated the presence of partial additive gene action which might be useful for selection. Lower values GCV & PCV were observed for rest of the characters.

Traits viz., 1000 seed weight, seed yield / plant, harvest index, biological yield / plant and grains / spike has high heritability whereas the traits like days to 50% flowering and 75% maturity, plant height, tiller / plant, spike length, ear weight were having moderated heritability. Similar findings reported

by Kumar *et al.* (2014) [6], Bilgin *et al.* (2011) [13], Ali (2008) [5], Sial (2007) [14], Khan *et al.* (2003) [15] and Ketata *et al.* (1976) [16].

High heritability coupled with high genetic advance is observed for seed yield / plant, 1000 seed weight, biological yield / plant, harvest index whereas moderate heritability coupled with moderate genetic advance is observed for grains/spike, days to 50% flowering, plant height, peduncle length, tillers per plant and ear weight indicating the dominance of additive gene action. Priority should be given in selection of these traits for crop improvement will be beneficial. Similar type of results were noted by Kumar *et al.* (2014) [6].

Correlation helps in finding the degree of relationship in between the characters. At phenotypic level, seed yield/plant exhibits positive correlation with spikelets/spike, grains/spike, 1000 seed weight, biological yield/plant, and harvest index and negative correlation with rest of characters. Akram *et al.* (2008) [18], Ali *et al.* (2008) [5] reported similar results. At genotypic level traits like plant height, peduncle length, tiller/plant, spikelets/spike, grains/spike, 1000 seed weight, biological yield / plant, harvest index exhibited positive correlation with the trait seed yield / plant and rest of the traits shown negative correlation with seed yield. Similar results observed by Chandar and Singh (2008), kumar *et al.* (2010) [20]

and sahu (2011)<sup>[17]</sup>. Traits which exhibits positive correlation with seed yield can be used as best selection indices for increasing seed yield/plant.

Path analysis helps in portioning correlation coefficient values into the direct and indirect effect values. At genotypic level, days to 50% maturity, plant height, grains/spike, ear weight, 1000 seed weight, Biological yield / plant and harvest index shown positive direct effect on seed yield / plant indicating selection for these traits is useful in improving seed yield / plant whereas spikelets/spike, tiller/plant, spike length, peduncle length, days to 75% maturity had negative direct effect on seed yield/ plant which indicated selection of these character is negligible.

### Conclusion

Analysis of variance revealed significant differences among the mean square due to genotype for all the characters indicating presence of variation for all the traits among all genotypes studied. Genotypic coefficient of variation was found to be lower than the phenotypic coefficient variation. Further moderate magnitude of genotypic coefficient of variation (GCV) was observed for the traits viz., seed yield per plant, harvest index, 1000 seed weight, biological yield per plant, ear weight and number of grains per spike which indicated presence of partial additive gene action which might be useful for selection. High heritability coupled with high genetic advance were observed for seed yield per plant, 1000 seed weight, harvest index, biological yield per plant indicating dominance of additive gene action. Seed yield per plant had positive significant correlation with the traits viz., plant height, peduncle length, number of tiller per plant, number of spikelet per spike, number of grains per spike, 1000 seed weight, biological yield per plant and harvest index which can be used as best selection indices for increasing seed yield per plant. Path coefficient analysis reveals that the traits like days to 50% flowering, plant height, number of grains per spike, ear weight, 1000 seed weight, biological yield per plant, harvest index had direct positive effect on seed yield per plant which means selection for these characters will be helpful in improving seed yield per plant

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