International Journal of Bio-resource and Stress Management https://pphouse.org/ijbsm.php

Crossref

IJBSM February 2022, 13(2):122-130 Print ISSN 0976-3988 Online ISSN 0976-4038 **Article** AR2722

Research Article *Natural Resource Management*

DOI: HTTPS://DOI.ORG/10.23910/1.2022.2722

Role of Genetic Variability, Heritability and Genetic Advance for Various Traits of Bread Wheat (*Triticum aestivum* L.) under Variable Sowing Times

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ABSTRACT

The field experiments were conducted with 54 genotypes including 10 lines, 4 testers and 40 F1's. The pure seeds of these 14 selected genotypes were grown in crossing blocks to obtain 40 cross combinations, during November–March of *rabi* 2016–17. These lines and testers along with obtained 40 crosses (F1's) were grown in randomised complete block design with 3 replications in 3 sowing dates during November–March in *rabi* 2017-18 and observations were recorded. Each genotype was sown with spacing of 20 cm between rows and 10 cm between plants. Data recorded for 21 characters including different morphological, physiological and quality traits from 5 randomly selected plants of each replication and mean data used for analysis. In the current investigation, value of PCV is higher than GCV for all the 21 characters. The high values of PCV and GCV were observed for GYPP, BYPP, SV, NEPP, and NTPP in E1, GYPP, BYPP, NEPP, NTPP, HI and SV in E2 and GYPP, BYPP, PL, NTPP, and NEPP in E3. However, we noticed maximum PCV and GCV for GYPP followed by BYPP in E1, E2, and E3. Even though remaining traits showed moderate or low PCV and GCV. High heritability, along with high genetic advance were recorded for the traits GYPP, WG, SV, BYPP, 1000 GW, CC, HI, PL, NEPP, and NTPP. Overall, our findings of various variability parameters may help in the selection of high yielding genotypes under different sowing times in wheat crop.

KEYWORDS: Genetic advance, GCV, heritability, PCV, wheat

Citation* (VANCOUVER)*: Tolwani and Shukla, Role of Genetic Variability, Heritability and Genetic Advance for Various Traits of Bread Wheat (*Triticum aestivum* L.) under Variable Sowing Times. *International Journal of Bio-resource and Stress Management,* 2022; 13(2), 122-130. HTTPS://DOI.ORG/10.23910/1.2022.2722.

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

RECEIVED on 09th November 2021 RECEIVED in revised form on 02nd February 2022 ACCEPTED in final form on 16th February 2022 PUBLISHED on 18th February 2022

1. INTRODUCTION

Common or bread wheat (*Triticum aestivum* L.) is a self-pollinated crop belongs to *poaceae* family, constituted by outstanding group of food plants which can be grown successfully in both tropical and sub-tropical areas (Bharat et al., 2013). Bread wheat accounts for 95% of all the consumed wheat throughout the worldwide and other remaining 5% is made up of durum or hard wheat *T. Turgidum* sp. Durum, used in food production industries. Today bread wheat is occupying 17% of crop acreage, feeding about 40% of the world population with excellent nutritional values (Patricia et al., 2019).

Bread wheat stood as one of the second most important staple crop after rice in India, which shows higher genetic diversity in almost all the countries (Thakur et al., 2018; Soumitra et al., 2016). The production of wheat varies based on the environmental changes; even though the consumption of wheat is increasing day by day because of its higher fibre content than any other diets. The mature wheat grain starchy endosperm consists of 55–75% carbohydrates and 10–20% protein (Gillies et al., 2012). On the other hand, aleurone wheat grain layer has its importance for vitamins, micronutrients, minerals, phytochemicals, and fibres (Liu, 2011; Regvar et al., 2011; Lafiandra et al., 2014).

Grain yield is a complex trait depends on its various component traits (Khairnar et al., 2018). Thus, assessment of variability is essential for the genetic manipulation of grain yield, quality, and other traits in wheat. Genetic variability is an important tool for any successful breeding programme and it is essential to have a critical survey of genetic variability before initiating an improvement programme for development of a high yielding variety (Falconar, 1989). Reduced genetic variability may cause diseases and adverse climatic changes to crop which impacts in yield production (Dargicho et al., 2015). Thus, for selecting a potential genotype, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) is an important variability parameter (Nukasani et al., 2013; Kumar et al., 2014; Negasa and Kumar, 2016; Bharat et al., 2018).

Yield and yield contributing characters are essential to determine crop improvement (Susmita et al., 2021). For selection of a given character in a population, the genetic variability along with heritability and genetic advance (GA) is required (Burton, 1952; Johnson et al., 1955). Heritability is important in a breeding process for determining the extent to which a selected character is transmitted to progenies (Sabesan et al., 2009; Meena et al., 2014). Genetic advance is a measure of genetic gain under selection. Genetic advance depends on magnitude of genetic variability and heritability of a character under consideration. Heritability is the heritable portion of phenotypic variation which is, determining gene expressivity carried by a genotype (Gopal et al., 2020). High heritability along with high genetic advance indicates that heritability is mainly due to additive gene effects and it gives a better idea for selection of desirable characters in developing new genotypes, which reveals the strong relationship between heritability and genetic advance (Mishra and Shukla, 2013; Kumar et al., 2015; Sandeep et al., 2017). In concern with the Indian population, it is a challenging task for breeders to increase the production of wheat crop to cope up with the growing demand to ensure food security. Thus keeping in view, the present investigation was conducted to assess genetic variability, heritability coupled with genetic advance for the genetic improvement of grain yield and its quality traits under varying environments in bread wheat.

2. MATERIALS AND METHODS

This experiment was carried out in seed breeding farm, college of agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.), India. Total 54 genotypes including 10 female lines (GW 273, GW 322, GW 366, JW-1201, JW-1202, JW-1203, LOK 1, HD 2864, HD 2932, and HI 1544) and 4 testers (JW-3336, JW-3288, MP-3269, and JW-3211) was taken under this study. The pure seeds of these 14 selected genotypes was grown in crossing blocks to obtain 40 cross combinations during November-march of *rabi*, 2016–17. These 10 lines and 4 testers along with obtained 40 cross combinations was grown in randomized complete block design with three replications under three different sowing dates (25/11/2017 in E1, 15/12/2017 in E2, 5/01/2018 in E3) during November–March of *rabi* 2017–18. Each genotype was sown in a single row of 5 m length with 20 cm spacing between rows and 10 cm between plants. Data was recorded on 5 randomly selected plants of each genotype in each replication and every environmental condition on 21 morphological, physiological and quality parameters viz. Days to 50% heading, days to maturity, plant height (cm), number of tillers plant^{-1}, number of ears plant^{-1}, number of spikelets ear^{-1}, number of grains ear^{-1}, ear length (cm), ear weight (g), peduncle length (cm), 1000 grain weight (g), biological yield plant^{-1} (g), harvest index (%), canopy temperature, chlorophyll content, sedimentation value (ml), protein content (%), wet gluten content (%), starch content (%), hectoliter weight (g), and grain yield plant^{-1} (g).

2.1. *Statistical analysis*

The analysis of variance was worked out to estimate the differences among the genotypes as per the method suggested by (Panse and Sukhatme, 1967). GCV and PCV were estimated as per the formula given by (Burton, 1952). Heritability in broad sense (%) was calculated by the formula suggested by (Hanson et al., 1956). Genetic advance and Genetic advance as percentage of mean were estimated by the formula suggested by (Lush, 1945; Johnson et al., 1955).

3. RESULTS AND DISCUSSION

In the present investigation, we evaluated the analysis of variance (ANOVA), revealed that the mean sum of squares was found highly significant for all the traits in E1, E2, and E3 along with pooled data (Table 1–4) represents the presence of variability among the genotypes. Similar findings were reported by Thapa et al. (2019) for all the traits under study.

PCV and GCV demonstrate the measure for comparison of variability present in yield and yield attributing traits. PCV is always higher than GCV due to the impact of environmental factors. The higher genetic variability is helpful in the selection of yield attributing traits (Sandeep et al., 2018; Thakur et al., 2020). The high (>15%) GCV and PCV was recorded for grain yield plant^{-1} (26.01%, 26.77%), biological yield plant^{-1} (21.04%, 21.39%) and sedimentation value (18.77%, 19.05%), number of ears plant^{-1} (17.81%, 21.09%) and number of tillers plant^{-1} (16.67%, 20.85%) in E1. In E2, the high GCV and PCV was recorded for grain yield plant^{-1} (23.26%, 24.07%), biological yield plant^{-1} (22.13%, 23.01%),

Table 1: Analysis of variance for different traits (E1)

ANOVA												
SV	DF	DH	DM	PH	NTPP	NEPP	NSPE	NGPE	EL	EW	PL	TGW
Replication	2	0.081	69.593	1.832	0.469	0.334	4.088	20.291	1.75	0.012	5.892	4.981
Treatment	53	34.334*	141.321*	159.30**	31.765**	30.838**	6.261**	49.851**	2.911*	0.500**	20.394**	43.154**
Error	106	20.114	82.827	33.8	5.038	4.491	3.601	22.273	1.792	0.133	4.861	14.936
SV	DF	BYPP	HI	CT	CC	SV	P	WG	S	HW	GYPP	
Replication	2	16.901	5.385	0.023	6.913	7.123	1.104	5.647	0.103	17.841	17.805	
Treatment	53	802.46**	91.193**	3.993**	53.761**	232.248**	2.838**	54.097**	16.541*	27.951**	212.68**	
Error	106	75.196	31.132	1.768	3.147	5.257	0.439	2.889	9.711	16.326	17.582	

*: Significant at (p=0.05); **: Significant at (*p*=0.01); level of significance; SV: Source of variation; DF: Degree of freedom; DH: Days to 50% heading; DM: Days to maturity; PH: Plant height; NTPP: Number of tillers plant^{-1}; NEPP: Number of ears plant^{-1}; NSPE: Number of spikelets ear^{-1}; NGPE: Number of grains ear^{-1}; EL: Ear length; EW: Ear weight; PL: Peduncle length; TGW: 1000 grain weight; BYPP: Biological yield plant^{-1}; HI: Harvest index; CT: Canopy temperature; CC: Chlorophyll content; SV: Sedimentation value; P: Protein content; WG: Wet gluten content; S: Starch content; HW: Hectoliter weight; GYPP: Grain yield plant^{-1}

Table 2: Analysis of variance for different traits (E2)

ANOVA												
SV	DF	DH	DM	PH	NTPP	NEPP	NSPE	NGPE	EL	EW	PL	TGW
Replication	2	14.351	4.13	39.646	2.757	4.395	0.457	3.634	0.627	0.263	15.160*	0.451
Treatment	53	21.538*	72.767*	167.813**	40.24**	39.15**	5.91**	47.94**	3.02**	0.30**	17.65**	43.42**
Error	106	12.631	42.587	27.195	4.398	4.663	2.056	17.241	1.111	0.09	4.604	9.003
SV	DF	BYPP	HI	CT	CC	SV	P	WG	S	HW	GYPP	
Replication	2	61.82	76.946	0.689	10.375	0.793	1.990*	4.532	5.805	3.316	14.081	
Treatment	53	650.38**	182.62**	4.311**	27.26**	209.93**	3.73**	49.25**	21.55**	28.021*	120.07**	
Error	106	73.921	32.34	2.467	6.009	4.96	0.624	2.984	12.581	16.449	11.81	

*: Significant at (p=0.05); **: Significant at (*p*=0.01); level of significance; SV: Source of variation; DF: Degree of freedom; DH: Days to 50% heading; DM: Days to maturity; PH: Plant height; NTPP: Number of tillers plant^{-1}; NEPP: Number of ears plant^{-1}; NSPE: Number of spikelets ear^{-1}; NGPE: Number of grains ear^{-1}; EL: Ear length; EW: Ear weight; PL: Peduncle length; TGW: 1000 grain weight; BYPP: Biological yield plant^{-1}; HI: Harvest index; CT: Canopy temperature; CC: Chlorophyll content; SV: Sedimentation value; P: Protein content; WG: Wet gluten content; S: Starch content; HW: Hectoliter weight; GYPP: Grain yield plant^{-1}

Table 3: Analysis of variance for different traits (E3)

						ANOVA						
SV	DF	DH	DM	PH	NTPP	NEPP	NSPE	NGPE	EL	EW	PL	TGW
Replication	2	1.414	13.758	1.609	2.572	3.159	6.707	4.837	0.907	0.209	5.46	0.121
Treatment	53	17.972**	101.601*	93.376**	43.407**	40.202**	6.420**	61.069**	2.831**	0.294*	16.594**	61.345**
Error	106	8.328	59.651	30.745	3.525	3.374	2.309	17.074	1.14	0.179	2.434	6.934
SV	DF	BYPP	HI	CT	CC	SV	P	WG	S	HW	GYPP	
Replication	2	92.846*	4.526	3.597	6.997	4.024	0.358	0.848	17.319	36.468	7.006	
Treatment	53	374.916**	79.021**	4.538**	58.362**	131.290**	2.883**	40.643**	18.899**	21.390*	58.446**	
Error	106	27.905	29.669	1.718	3.186	5.878	0.483	3.562	11.046	12.521	3.784	

*: Significant at (p=0.05); **: Significant at (*p*=0.01); level of significance; SV: Source of variation; DF: Degree of freedom; DH: Days to 50% heading; DM: Days to maturity; PH: Plant height; NTPP: Number of tillers plant^{-1}; NEPP: Number of ears plant^{-1}; NSPE: Number of spikelets ear^{-1}; NGPE: Number of grains ear^{-1}; EL: Ear length; EW: Ear weight; PL: Peduncle length; TGW: 1000 grain weight; BYPP: Biological yield plant^{-1}; HI: Harvest index; CT: Canopy temperature; CC: Chlorophyll content; SV: Sedimentation value; P: Protein content; WG: Wet gluten content; S: Starch content; HW: Hectoliter weight; GYPP: Grain yield plant^{-1}

number of ears plant^{-1} (19.41%, 22.48%) and number of tillers plant^{-1} (18.63%, 21.79%), harvest index (18.37%, 19.22%), sedimentation value (16.13%, 16.30%). whereas in E3, grain yield plant^{-1} (29.04%, 30.34%), biological yield plant^{-1} (26.21%, 29.81%), number of ears plant^{-1} (26.03%, 29.39%) and number of tillers plant^{-1} (24.47%, 27.52%) and peduncle length (17.50%, 21.63%) had high GCV and PCV respectively. The pooled data shows high GCV and PCV for grain yield plant^{-1} (22.56%, 27.34%), biological yield plant^{-1} (19.46%, 24.58%), number of ears plant^{-1} (18.85%, 24.18%) and number of tillers plant^{-1} (18.06%, 23.14%). Similar results was also reported by Bhushan et al. (2013) for grain yield plant^{-1} and biological yield plant^{-1}; Thakur et al. (2018) for grain yield plant^{-1}; Meena et al. (2014) and Sandeep et al. (2018) for grain yield plant^{-1}; Soumitra et al. (2016) for plant height; Thapa et al. (2019) for grain yield plant^{-1} and number of grain ear^{-1}; Thakur et al. (2020) for grain yield plant^{-1} and number of ears plant^{-1}. The moderate (10–15%) GCV and PCV was recorded for peduncle length (13.96%, 19.45%), wet gluten content (13.45%, 13.83%) in E1. In E2, peduncle length (13.08%, 18.76%), wet gluten content (11.78%, 12.46%) was recorded for moderate GCV and PCV. Whereas, 1000 grain weight (13.70%, 14.38%), harvest index (13.39%, 16.43%) and sedimentation value (11.46%, 11.70%) has moderate GCV and PCV as per E3. The pooled data shows the moderate GCV and PCV for sedimentation value (13.72%, 15.51%), peduncle length (13.5%, 19.85%) and harvest index (12.47%, 16.78%) and wet gluten content (10.91%, 12.23%). All the remaining traits was having low (<10%) values of GCV and PCV in E1, E2, and E3 represented in Table 5. Similar findings was also recorded by Kumar et al. (2014) for 1000 grain weight; Khairnar et al. (2018) for days to 50% heading and number of grains ear^{-1}.

Heritability is an important tool for inheritance of a character and high heritability values indicate least influence of environment. The high heritability (>60%) was found in sedimentation value (98.0%), biological yield plant^{-1} (96.7%), wet gluten content (94.6%), grain yield plant^{-1} (94.4%), chlorophyll content (88.1%), plant height (84.4%), harvest index (82.9%), 1000 grain weight (81.0%), days to 50% heading (72.2%), number of ears plant^{-1} (66.2%), number of tillers plant^{-1} (63.9%), starch content (62.9%), hectoliter weight (62.7%) in E1. In E2, high heritability was recorded for sedimentation value (97.9%), biological yield plant^{-1} (97.0%), grain yield plant^{-1} (93.4%), harvest index (91.3%), wet gluten content (89.4%), plant height (86.5%), 1000 grain weight (81.5%), chlorophyll content (75.9%), number of tillers plant^{-1} (73.1%), days to 50% heading (72.1%), number of ears plant^{-1} (71.1%) and hectoliter weight (63.0%). Whereas in E3, high heritability was recorded in sedimentation value (96.0%), biological yield plant^{-1} (95.6%), grain yield plant^{-1} (91.6%), chlorophyll content (90.9%), 1000 grain weight (90.8%), wet gluten content (86.7%), hectoliter weight (80.4%), number of tillers plant^{-1} (79.0%), days to 50% heading (78.5%), number of ears plant^{-1} (78.4%), plant height (74.1%), harvest index (66.4%) and peduncle length (66.0%). The pooled data of all the three environments had shown high heritability for wet gluten content (79.5%), sedimentation value (78.3%), biological yield plant^{-1} (69.9%), grain yield plant^{-1} (68.1%), 1000 grain weight (63.3%) and number of tillers plant^{-1} (60.9%). Similar findings for high heritability was also demonstrated by Kumar et al. (2015) for grain

Table 4: Analysis of variance for different traits (Pooled)

ANOVA						
SV	DF	DH	DM	PH	NTPP	NEPP
Replication	2	7.062	24.112	12.85	1.519	3.26
Environment	2	2771.367**	13102.25**	8332.104**	617.431**	727.162**
Interactions	4	4.392	31.685	15.119	2.139	2.314
Overall sum	8	696.804**	3297.432**	2093.798**	155.807**	183.762**
Treatment	53	50.757**	165.551**	294.411**	92.207**	86.498**
Error	424	13.154	65.033	38.695	6.141	6.095
SV	DF	BYPP	HI	CT	CC	SV
Replication	2	132.518	28.382	2.439	14.506	10.267
Environment	2	51679.64**	1786.188**	244.901**	718.549**	4550.66**
Interactions	4	19.523	29.238	0.935	4.89	0.836
Overall sum	8	12962.8**	468.261**	62.302**	185.709**	1140.65**
Treatment	53	1371.034**	243.89**	6.584**	69.589**	470.599**
Error	424	101.347	36.904	2.27	11.81	16.883

Table 4: continue...

ANOVA						
SV	NSPE	NGPE	EL	EW	PL	TGW
Replication	0.133	1.996	0.103	0.306	24.554*	1.73
Environment	245.738**	2084.385**	26.748**	76.314**	766.187**	6649.751**
Interactions	5.56	38.383	3.591*	0.089	0.979	1.912
Overall sum	64.248**	540.787**	8.508**	19.199**	198.175**	1663.826**
Treatment	14.696**	125.411**	6.232**	0.829**	40.981**	110.737**
Error	2.479	18.329	1.327	0.134	4.682	12.367
SV	P	WG	S	HW	GYPP	
Replication	0.642	1.192	10.178	41.503	16.342	
Environment	68.367**	1025.651**	63.673**	1893.964**	12377.3**	
Interactions	1.406	4.918	6.524	8.061	11.276	
Overall sum	17.955**	259.17**	21.725*	487.897**	3104.049**	
Treatment	7.366**	125.65**	42.786**	38.778**	292.76**	
Error	0.648	4.652	10.11	16.147	20.599	

*: Significant at (p=0.05); **: Significant at (p=0.01); level of significance

yield plant^{-1} and wet gluten; Thakur et al. (2018) for 1000 grain weight; Soumitra et al. (2016) for grain yield plant^{-1} and number of tillers plant^{-1}; Thakur et al. (2020) for plant height. The moderate heritability (45–60%) in E1 was observed in days to maturity (59.9%), number of grains ear^{-1} (59.2%), protein content (53.7%), peduncle length (51.6%), number of spikelets ear^{-1} (49.8%) and ear weight (48.0%). In E2, protein content (55.5%), starch content (50.6%), peduncle length (48.6%) and days to maturity (48.3%) was recorded for moderate heritability. Where as in E3, protein content (54.9%), and number of grains ear^{-1} (46.2%) had shown moderate heritability. The pooled data of all the three environmental conditions had shown moderate heritability in number of ear plant^{-1} (59.4%), plant height (57.2%), harvest index (55.3%), days to 50% heading (51.8%), hectoliter weight (50.3%), protein content (48.7%), and peduncle length (46.3%). The moderate heritability was also represented Sandeep et al. (2018) for number of grains ear^{-1} and number of spikelets ear^{-1}; Khairnar et al. (2018) for harvest index. Remaining all other traits had

Table 5: Estimates of GCV and PCV for different characters of wheat across varying environments

Character	Co-Variances							
	E1		E2		E3		Pooled	
	GCV	PCV	GCV	PCV	GCV	PCV	GCV	PCV
Days to 50% heading	3.58	4.22	3.57	4.21	3.82	4.31	3.05	4.24
Days to maturity	1.85	2.39	1.37	2.21	1.38	2.35	1.22	2.33
Plant height	7.44	8.10	8.25	8.87	6.54	7.60	6.24	8.25
Number of tillers plant^{-1}	16.67	20.85	18.63	21.79	24.47	27.52	18.06	23.14
Number of ears plant^{-1}	17.81	21.09	19.41	22.48	26.03	29.39	18.85	24.18
Number of spikelets ear^{-1}	4.53	10.19	5.79	9.34	6.39	10.47	5.95	10.01
Number of grains ear^{-1}	5.04	9.34	5.63	9.23	7.24	10.65	6.09	9.71
Ear length	5.42	13.05	7.15	11.82	7.12	12.39	6.70	12.44
Ear weight	9.05	13.06	8.43	12.68	7.83	18.68	8.74	14.46
Peduncle length	13.96	19.45	13.08	18.76	17.56	21.63	13.50	19.85
1000-grain weight	8.08	8.98	9.10	10.08	13.70	14.38	8.64	10.86
Biological yield plant^{-1}	21.04	21.39	22.13	23.01	26.21	29.81	19.46	24.58
Harvest index	12.83	14.09	18.37	19.22	13.39	16.43	12.47	16.78
Canopy temperature	4.72	8.68	4.53	10.77	4.72	7.94	3.70	9.23
Chlorophyll content	9.87	10.52	6.22	7.14	9.70	10.17	5.79	9.32
Sedimentation value	18.77	19.05	16.13	16.30	11.46	11.70	13.72	15.51
Protein	6.59	8.99	7.15	9.60	6.08	8.21	6.24	8.94
Wet gluten	13.45	13.83	11.78	12.46	9.89	10.62	10.91	12.23
Starch	0.98	2.06	1.75	2.46	1.48	2.24	1.41	2.26
Hectoliter weight	2.01	2.54	2.07	2.61	2.85	3.18	1.52	2.77
Grain yield plant^{-1}	26.01	26.77	23.26	24.07	29.04	30.34	22.56	27.34

E1: Normal sown condition; E2: Late sown condition; E3: Very late sown; GCV: Genotypic co-efficient of variation; PCV: Phenotypic co-efficient of variation

low heritability i.e.., (<45%) has been represented in Table 6. Heritability includes the effect of both the additive and non-additive genes. Thus, heritability alone is not sufficient for the selection processes. Genetic advance is the result of additive gene action. Thus, heritability along with the genetic advance as percentage of mean (genetic gain) is essential for the effective selection. The characters having high heritability along with high genetic advance as percentage of mean are effective for selection. The high (>15%) genetic advance as percentage of mean was recorded for grain yield plant^{-1} (52.06%), biological yield plant^{-1} (42.61%), sedimentation value (38.29%), number of ears plant^{-1} (29.84%), number of tillers plant^{-1} (27.44%), wet gluten content (26.97%), harvest index (24.07%), peduncle length (20.66%), and chlorophyll content (19.09%) in E1. In E2, grain yield plant^{-1} (46.29%), biological yield plant^{-1} (44.89%), harvest index (36.15%), number of ears plant^{-1} (33.72%), sedimentation value (32.86%), number of tillers plant^{-1} (32.8%), wet gluten content (22.94%), peduncle length (18.77%), 1000 grain weight (16.93%), and plant height (15.81%) had shown the high values of genetic advance as percentage of mean. Whereas, in E3, the high genetic advance as percentage of mean was recorded for grain yield plant^{-1} (57.27%), biological yield plant^{-1} (52.79%), number of ears plant^{-1} (47.49%), number of tillers plant^{-1} (44.82%), peduncle length (29.39%), 1000 grain weight (26.89%), sedimentation value (23.13%), harvest index (22.47%), chlorophyll content (19.05%) and wet gluten content (18.96%). The pooled data had represented high genetic advance as percentage of mean for grain yield plant^{-1} (38.34%), biological yield plant^{-1} (33.52%), number of ears plant^{-1} (29.93%), number of tillers plant^{-1} (29.03%), sedimentation value (25.00%), wet gluten content (20.03%), harvest index (19.10%) and peduncle length (18.92%) as represented in Table 6. Similar findings was recorded by Yadav et al. (2011) for grain yield plant^{-1} and biological

Table 6: Heritability in broad sense (%), genetic advancement, and genetic advance as % of mean, for all the environmental condition

Character	Heritability in broad sense (%)				Genetic advancement				Genetic advance as % of mean			
	E1	E2	E3	Pooled	E1	E2	E3	Pooled	E1	E2	E3	Pooled
Days to 50% heading	72.2	72.10	78.5	51.8	4.36	4.10	4.27	2.96	6.27	6.25	6.96	4.53
Days to maturity	59.9	48.30	34.2	35.9	3.45	1.83	1.64	1.42	2.95	1.75	1.65	1.32
Plant height	84.4	86.50	74.1	57.2	13.3	13.98	9.36	8.57	14.08	15.81	11.60	9.73
Number of tillers plant^{-1}	63.9	73.10	79	60.9	4.91	6.09	6.67	4.97	27.44	32.80	44.82	29.03
Number of ears plant^{-1}	66.2	71.10	78.4	59.4	4.96	5.89	6.39	4.75	29.84	33.72	47.49	29.93
Number of spikelets ear^{-1}	49.8	38.50	37.2	35.4	0.86	1.45	1.47	1.43	4.14	7.40	8.03	7.29
Number of grains ear^{-1}	59.2	37.30	46.2	39.4	3.37	4.02	5.36	4.46	5.62	7.08	10.13	7.87
Ear length	37.2	36.50	33.1	31.8	0.52	1.00	0.88	0.82	4.63	8.90	8.44	7.44
Ear weight	48.0	44.10	37.6	36.5	0.49	0.37	0.16	0.35	12.91	11.53	6.76	10.88
Peduncle length	51.6	48.60	66	46.3	3.36	3.00	3.63	2.81	20.66	18.77	29.39	18.92
1000-grain weight	81.0	81.50	90.8	63.3	6.76	6.82	8.72	5.57	14.97	16.93	26.89	14.16
Biological yield plant^{-1}	96.7	97.00	95.6	69.9	32.9	29.69	22.31	20.74	42.61	44.89	52.79	33.52
Harvest index	82.9	91.30	66.4	55.3	9.92	14.89	7.96	7.50	24.07	36.15	22.47	19.10
Canopy temperature	39.6	27.70	35.4	26.1	0.96	0.79	1.18	0.60	5.28	3.92	5.78	3.06
Chlorophyll content	88.1	75.90	90.9	38.7	8.00	5.14	8.52	3.28	19.09	11.16	19.05	7.42
Sedimentation value	98.0	97.90	96	78.3	17.8	16.98	13.25	12.98	38.29	32.86	23.13	25.00
Protein	53.7	55.50	54.9	48.7	1.29	1.52	1.32	1.23	9.95	10.98	9.28	8.98
Wet gluten	94.6	89.40	86.7	79.5	8.43	7.74	6.88	6.76	26.97	22.94	18.96	20.03
Starch	62.9	50.60	43.7	39	0.64	1.68	1.30	1.19	0.975	2.57	2.02	1.81
Hectoliter weight	62.7	63.00	80.4	50.3	2.58	2.60	3.81	1.30	3.28	3.39	5.26	1.71
Grain yield plant^{-1}	94.4	93.40	91.6	68.1	16.6	12.43	8.56	9.43	52.06	46.29	57.27	38.34

E1: Normal sown condition; E2: Late sown condition; E3: Very late sown condition

yield plant^{-1}; Mishra and Shukla (2013) for protein content and sedimentation value; Kumar et al. (2014) and Khairnar et al. (2018) for number of tillers plant^{-1}. Soumitra et al. (2016) for grain yield and number of tillers plant^{-1}; Sandeep et al. (2018) for grain yield; Thakur et al. (2020) for grain yield plant^{-1}; Thapa et al. (2019) for grain yield plant^{-1} and number of grains ear^{-1}.

4. CONCLUSION

High GCV and PCV was observed among genotypes with nine important traits having high broad sense heritability and high genetic advance as percentage of mean viz., grain yield plant^{-1}, biological yield plant^{-1}, harvest index, sedimentation value, wet gluten content, number of ears plant^{-1}, number of tillers plant^{-1}, chlorophyll content, and 1000 grain weight in all the three sowing times. Thus, selection based on these traits would be effective for improvement of grain yield and quality attributes in bread wheat.

5. ACKNOWLEDGEMENT

Author is thankful to Department of Science and Technology (DST) for supporting with Inspire fellowship scheme under the Ref.no: DST/INSPIRE/03/2016/000698

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