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Genetic studies on F₃ segregating populations in bread wheat (*Triticum aestivum* L.)

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Abstract

The research for this study was conducted out at the farm of the Department of Genetics & Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara, Punjab, to assess the 50 wheat genotypes (Segregating population lines) along with 5 check hybrids. According to the analysis of variance for 50 genotypes (Segregating population-F3 generation) and 5 check varieties the treatments are extremely significant to days to maturity, plant height. The phenotypic coefficient of variation was greater in significance than genotypic coefficient of variation for all the characters under study. High values for both phenotypic and genotypic coefficient of variation was observed in days to heading, number of spikelets per ear, number of grains per ear and thousand grain weight High heritability was recorded for plant height followed number of productive tillers per plant, days to 50% heading, grain yield per plant, number of spikelet's per ear, number of grains per ear.

Keywords: Genotypic, coefficient, spikelets per, breeding

Introduction

Wheat is a segmental allohexaploid ($2n = 6x = 42$) having emanated in the Fertile Crescent area of South-Western Asia (Lupton 1987), its geographical centre of origin and spread globally for cultivation and consumption. Most of the cultivated wheat varieties belongs to main species of genus *Triticum* where common bread wheat (*T. Aestivum*) and durum wheat (*T. durum*, $2n = 4x = 28$) which make up 91% of the global wheat crop. Wheat is grown in 122 countries, covering 224.27 million hectares, and yielding roughly 732.31 million tons per hectare (FAO 2019) [9]. China, India, France, The United States, Russia, Canada, Australia, Turkey and Pakistan are the countries accounting for around 76% of global wheat output. After China India is the largest originator of wheat. The breeding value of a product is based on how much of their phenotype percentage is being passed on to the next generation. In the present study on F₃ segregating population, path analysis was used to assess the direct and indirect effects of various characteristics on grain yield. Heritability, genetic variability and genetic advance for various yield characters were studied.

Studies on genetic variability offer a fundamental understanding of the genetic traits of the population, upon which breeding strategies for crop production are based. More options for variation are created via high heritability and genetic advancement. The second aspect measures a predictor variable's indirect impacts, whereas the path coefficient (or normalised partial regression coefficient) represents a predictive variable's direct impact on its dependent variables. Applying variance and covariance components the connection between characters was evaluated. Heritability analyses are influenced via the environment and the composition of test population. Correlation analysis paired with route analysis is a more effective way for assessing yield-contributing characteristics.

Materials and Methods

Experiment was executed at Lovely Professional University (LPU), Research Farm in Punjab during the Rabi, 2021-2022. The study engaged 50 F₃ (segregating populations) treatments and 5 check varieties of wheat raised in augmented design. Fifty F₃ Treatments were chosen for the experiment from the 6 crosses of the F₂ generation which were grown in Randomised Block Design (Given in Table 1). These 50 treatments (Segregating population) have been sown in 5 blocks and 3 plots (10 Treatments along with 5 check hybrids). Each plot has two rows of 2 m each, spaced 22.5 cm apart and 5 cm within the rows.

Table 1: List of wheat genotypes in F₃ generation

Sr. No	Crosses	Sr. No	Checks
1	DBW - 107 x MP-3382	C1	IC 82187
2	DBW - 93 X MP-3382	C2	IC 57578
3	RUJ - 4037 X MP-3382	C3	IC 532057
4	PBW - 110 X MP-3382	C4	IC 104570
5	DBW - 90 X MP-3382	C5	IC 532502
6	DBW - 110 X MP-3382		

Amongst them 5 plants of each treatment (Segregating population of F₂) along with the check hybrids have been labelled for further studies. The initial objective of making the crosses was the varietal development and 50 F₃ populations were selected based on phenotypic screening for the traits *viz.*, days to 50% heading, days to maturity, plant height, number of productive tillers per plant, spike length, number of grains per ear, economic weight (g), thousand grain weight (g), biological yield per plant (g), harvest index (%), chlorophyll content (%), grain yield per plant (g) from various labelled plants. Statistical analysis was conducted on the mean performance of each treatment. Panse and Sukhatme have given an analysis of variance methodology for testing the significance of various traits. Burton provided methodology for estimating GCV and PCV, Burton and Vane developed heritability in a broad sense (h²), and Johnson provided

genetic advance. The GCV, PCV, and path coefficient analysis are computed using the method proposed via Al-Jibouri and Dewey and Lu.

Result and discussion

To assess the significance of variations between various treatments (checks), analysis of variance for augmented design was performed for thirteen characters and given in the (Table 2). In the analysis it has been found that variation among the blocks was significantly high in days to 50% flowering, plant height, number of grains per spike, spike length, number of grains per ear and grain yield per plant content however the discrepancies among blocks were not substantial for remaining parameters. The differences among treatments have been found significant for days to 50% flowering, plant height, spike length and grain yield per plant the differences among other treatments were not significant for remaining parameters. The differences among check hybrids have been found highly significant for days to 50% flowering, plant height and spike length the differences among the check hybrids were not significant for remaining parameters. Similar conclusions have been noticed via Prasad *et al.*, (2020) [6], Pooja *et al.*, (2018) [15], Avinash *et al.*, (2015) and Sharma *et al.*, (2018) for the various examined.

Table 2: Analysis of variance for grain yield and its component

Source	D.F	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
Block (Ignoring Treatments)	4	108.89 **	28.31 ns	141.91 **	3.08 ns	1.64 ns	1.11 *	59.55 *	0.02 ns	4.15 ns	14.59 ns	7.97 ns	65.31 ns	22.95 *
Treatment (Eliminating Blocks)	54	46.21 **	21.91 ns	250.37 **	0.98 ns	1.13 ns	0.76 *	23.25 ns	0.02 ns	24.29 ns	11.18 ns	4.01 ns	106.83 ns	15.88 *
Treatment: Check	4	134.96 **	27.7 ns	1125.07 **	1.99 ns	0.4 ns	1.48 *	5.84 ns	0.03 ns	18.44 ns	13.43 ns	1.97 ns	120.3 ns	4.63 ns
Treatment: Test and Test vs. Check	50	39.11 **	21.44 ns	180.39 **	0.9 ns	1.18 ns	0.7 ns	24.64 ns	0.02 ns	24.76 ns	11 ns	4.18 ns	105.75 ns	16.77 *
Error	16	9.36	15.28	26.73	1.37	0.65	0.36	12.76	0.01	20.44	14.06	6.11	96.44	7.45
CV%	-	3.2	3.13	6.03	17.82	5.09	7.01	7.95	4.99	10.92	15.26	29.49	28.33	7.24

X1-Days to 50% heading, X2-Days to maturity, X3-Plant height, X4-Number of productive tillers per plant, X5-Number of spikelets per ear, X6-ear length, X7-Number of grains per ear, X8- Economic weight X9- Thousand grain weight, X10- biological yield per plant, X11- Harvest index, X12-chlorophyll content, X13 Grain yield per plant

The calibrated range (Table 3) of days to 50% heading has been (109.68 days to 80.48 days) followed by days to maturity from (139 days to 112.4 days), plant height from (111.4 cm to 48.58 cm), number of productive tillers per plant from (8.32 tillers to 4.4 tillers), number of spikelet's per ear (18.94 spikelets to 13.8 spikelets), ear length (10.13 cm to 5.77 cm), number of grains per ear (53.87 grains to 33.91 grains), economic weight (2.67gm to 2.1gm), thousand grain weight(55.9 gm to 32.42 gm), biological yield per plant (33.47 gm to 17.17 gm), harvest index (74.67% to 19.29%),

chlorophyll content (46.66% to 26.62%), grain yield per plant (14.99 gm to 5.18 gm).

Coefficient of variation (Fig 1) (Table 2) assessed for days to 50% heading has been estimated to be (3.2) followed by days to maturity (3.13), plant height (6.03), number of productive tillers per plant (17.82), number of spikelet's per ear (5.09), ear length (7.01), number of grains per ear (7.95), economic weight (4.99), thousand grain weight (10.92), biological yield per plant (15.26), grain yield per plant (29.49), harvest index (28.33) and chlorophyll content (7.24).

Table 3: Genetic variability parameters for grain yield and its components in Wheat

Character	Range		Mean	GCV%	PCV%	Heritability (BS) %	Genetic advance	GA % mean
	Minimum	Maximum						
Days to 50% heading	80.48	109.68	94.77	5.59	6.45	74.97	9.46	9.98
Days to maturity	112.4	139	124.49	1.95	3.69	27.74	2.63	2.11
Plant height (cm)	48.58	111.14	83.2	13.41	14.78	82.33	20.89	25.11
Number of productive tillers per plant	4.4	8.32	6.44	11.94	15.61	77.87	16.71	19.83
Number of spikelet's per ear	13.8	18.94	15.95	4.86	7.01	47.95	1.11	6.94
Ear length (cm)	5.77	10.13	8.45	7.33	10.19	51.75	0.92	10.88
Number of grains per ear	33.91	53.87	44.17	8.05	11.41	49.76	5.17	11.71
Economic weight (g)	2.1	2.67	2.4	2.65	5.67	21.83	0.06	2.55
Thousand grain weight (g)	32.42	55.9	41.54	4.62	11.82	15.27	1.55	3.72
Biological yield per plant (g)	17.17	33.47	24.53	3.61	13.71	64.45	2.43	6.56
Harvest index (%)	19.29	74.67	34.8	11.41	30.44	14.05	3.07	8.82
Chlorophyll content (%)	26.62	46.66	38.51	6.79	9.82	47.87	3.73	9.7
Grain yield per plant(g)	5.18	14.99	8.4	4.43	26.1	74.91	5.76	11.65

Genetic variability parameters

The phenotypic coefficient of variation was higher in magnitude than genotypic coefficient of variation for all the parameters under study (Table 3). Similar conclusions have been noticed via Rajput (2018) [19], Avinash *et al.*, (2015), Anil *et al.*, (2019), Dagade *et al.*, (2020) [7], Prakash *et al.*, (2021) [17]. High values for both phenotypic and genotypic coefficient of variation was observed in harvest index, plant height, number of grains per spike, spike length and number of productive tillers per plant suggesting that diversity existing among the segregating F3 treatments has scope for the genetic enhancement. Similar findings of PCV and GCV was reported via Anil *et al.*, (2019), Ashish *et al.*, (2020), Jaiswal *et al.*, (2020) [12] and Sharma *et al.*, (2018) reported similar findings for number of grains per spike, ear length.

The estimation of heritability requires an estimate of genotypic variance in a population. The genotypic variance consists of additive, dominance and epistatic variances. The heritability from simple trials (Fig 2), (Table 3) has been assessed higher in plant height (cm) (82.33%) followed by number of productive tillers per plant (77.87%), days to 50% heading (74.97%), grain yield per plant (74.91%), number of spikelet's per ear (51.75%), number of grains per ear (49.76%), chlorophyll content (47.87%) indicating that selection of this traits will be worthwhile in breeding programmes. As the heritability estimates are relatively high in narrow sense that implies the characters are largely administered by additive genes and selection for enhancement of such character would be gratifying. Low heritability has been estimated in days to maturity (27.74%) and economic weight (21.83%), thousand grain weight (15.27%) and harvest index (14.05%). As these estimates of heritability are low in narrow sense it implies that there is preponderance of non-additive gene action. These results confirmatory with previous research done by Bayisa *et al.*, (2020) [5], Anil *et al.*, (2019), Devesh *et al.*, (2018) [8], Gautam (2020) [10]. High genetic advance as a percent of mean was observed for plant height (25.11), number of productive tillers per plant (19.83), number of grains per spike (11.71), grain yield per plant (g) (11.65), spike length (10.88), days to 50% heading (9.98), chlorophyll content (9.7) harvest index (8.82), number of spikelet's per ear (6.94), biological yield per plant (6.56) followed by low values thousand grain weight (3.72), days to maturity (2.11), economic weight (g) (2.55). These results corroborative with the previous experimentation done via Mohapatra *et al.*, (2019), Reddy *et al.*, (2020) and Ashish *et al.*, (2020). High Heritability with high genetic advance was observed for parameters plant height (cm), days to 50%

heading, number productive tillers suggesting that direct selection for these traits will be rewarding as heritability observed is due to additive gene effects. High

Heritability with moderate genetic advance was observed for parameters chlorophyll content (%), spike length, number of spikelet's per ear (g), grain yield per plant indicates preponderance of additive gene action. High heritability with low genetic advance was recorded for days to maturity, number of productive tillers per plant, economic weight, harvest index (%), thousand grain weight advocating high heritability estimates are the repercussion of favourable environmental conditions and low genetic advance is due to non-additive gene. Similar findings were recorded via Ashish *et al.*, (2020), Ibrahim (2019) [11], Devesh *et al.*, (2018) [8].

Genotypic and phenotypic correlation of quantitative traits

Grain yield per plant revealed (Table 4) highly positive significance at phenotypic and genotypic level (0.8645**) (0.8733**) respectively in association with harvest index and (0.5361**) (0.5618**) in association with thousand grain weight, days to 50% flowering revealed highly positive significance at phenotypic and genotypic level (0.6952**, 0.6892**) respectively in association with days to maturity, days to maturity revealed positive significance at phenotypic level (0.2408*) in association with plant height, plant height showed positive significance at phenotypic and genotypic level (0.2752*, 0.2812*) respectively in association with number of spikelets per ear, number of productive tillers revealed negative significance at phenotypic and genotypic level (-0.3536*)(-0.3184*) respectively in association with economic weight, number of spikelets per ear showed positive significance at genotypic level (0.2770*) in association with spike length, number of grains per ear revealed positive significance at phenotypic and genotypic level (0.2721*, 0.2993*) respectively in association with chlorophyll content, thousand grain weight showed highly positive significance at phenotypic and genotypic level (0.5599**, 0.5712**) respectively in association with harvest index, biological yield per plant revealed highly negative significance at phenotypic and genotypic level (-0.4368**) (-0.4355**) respectively in association with harvest index. All results were in close resemblance to the findings reported via Rajput (2018) [19], Kumar *et al.*, (2019), Abbadi *et al.*, (2022), Prabha *et al.*, (2022), Pooja *et al.*, (2018) [15] and Singh *et al.*, (2021) among the segregating F3 treatments has scope for the genetic enhancement

Table 4: Genotypic and phenotypic correlation of quantitative traits in Bread Wheat

		X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
X1	G	1.0000	0.6892**	0.1797	-0.0190	-0.2353	-0.0728	-0.1895	-0.2350	0.1332	-0.1161	0.1150	0.1521	0.0798
	P	1.0000	0.6952**	0.2054	0.0205	-0.1895	-0.0916	-0.2234	-0.2128	0.1680	-0.1559	0.1209	0.1469	0.0504
X2	G		1.0000	0.2264	-0.1209	-0.1667	0.0085	-0.1627	0.0472	0.1167	0.0638	0.0494	-0.0090	0.0964
	P		1.0000	0.2408*	-0.0645	-0.1249	-0.0243	-0.1841	0.0461	0.1538	0.0331	0.0472	-0.0098	0.0669
X3	G			1.0000	0.0834	0.2752*	0.2570	-0.0615	-0.0784	0.1167	0.0140	0.1539	-0.0710	0.1962
	P			1.0000	0.1014	0.2812*	0.2341	-0.0827	-0.0686	0.1298	-0.0165	0.1605	-0.0605	0.1808
X4	G				1.0000	-0.1123	-0.0206	-0.1134	-0.3536*	-0.0710	-0.2054	0.2045	-0.0600	0.0900
	P				1.0000	-0.0814	-0.0321	-0.1249	-0.3184*	-0.0331	-0.1980	0.1950	-0.0524	0.0730
X5	G					1.0000	0.2770*	-0.0529	0.0251	0.0334	0.0409	0.1768	0.0503	0.2182
	P					1.0000	0.2602	-0.0648	0.0333	0.0566	0.0319	0.1749	0.0481	0.2058
X6	G						1.0000	0.1374	-0.1135	-0.0518	0.1905	-0.1809	0.1170	-0.0829
	P						1.0000	0.1472	-0.0953	-0.0585	0.2069	-0.1786	0.1177	-0.0664
X7	G							1.0000	0.0526	-0.0474	-0.1772	-0.1324	0.2993*	-0.2269

	P							1.0000	0.0431	-0.0646	-0.1416	-0.1355	0.2721*	-0.2066
X8	G								1.0000	-0.1166	0.1410	-0.1100	-0.0177	-0.0145
	P								1.0000	-0.0985	0.1480	-0.1099	0.0111	-0.0131
X9	G									1.0000	-0.1351	0.5712**	0.0991	0.5618**
	P									1.0000	-0.1395	0.5599**	0.0991	0.5361**
X10	G										1.0000	-0.4355**	-0.2369	0.0437
	P										1.0000	-0.4368**	-0.2303	0.0586
X11	G											1.0000	0.1048	0.8733**
	P											1.0000	0.0993	0.8645**
X12	G												1.0000	-0.0025
	P												1.0000	-0.0116

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

X1-Days to 50% heading, X2-Days to maturity, X3-Plant height, X4-Number of productive tillers per plant, X5-Number of spikelets per ear, X6-ear length, X7-Number of grains per ear, X8- Economic weight X9-Thousand grain weight, X10- biological yield per plant, X11- Harvest index, X12-chlorophyll content, X13 Grain yield per plant

Genotypic Path Coefficient on Grain Yield per Plant

Analysis of path coefficients divide the correlation coefficient between direct and indirect effects given in (Fig 3) (Table 5). Days to 50% heading imposed positive direct effect (0.0409) on grain yield per plant. Positive indirect effect was imposed via days to maturity (0.0282) plant height (0.0073) and chlorophyll content (0.0062). Days to maturity imposed negative direct effect (-0.0282) on grain yield per plant. Positive indirect effect was imposed via number of spikelet's per ear (0.0047), number of grains per ear (0.0046) and number of productive tillers per plant (0.0034). Plant height imposed positive direct effect (0.0185) on grain yield per plant. Positive indirect effect was imposed via number of spikelet's per ear (0.0051), spike length (0.0048) and days to maturity (0.0042). Number of productive tillers per plant imposed negative direct effect (-0.0191) on grain yield per plant. Positive indirect effect was imposed via test-weight (0.0068), biological yield per plant (0.0039) and days to maturity (0.0023). Number of spikelet's per ear imposed negative direct effect (-0.0082) on grain yield per plant. Positive indirect effect was imposed via days to 50% heading (0.0019), days to maturity (0.0014). Spike length imposed positive direct effect (0.0234) on grain yield per plant. Positive indirect effect was imposed via number of spikelet's per ear (0.0065), plant height (0.0060) and biological yield per plant (0.0045). Number of grains per ear imposed positive direct effect (0.0102) on grain yield per plant. Positive indirect effect was imposed via chlorophyll content (0.0031) and spike length (0.0014). Economic weight imposed positive direct effect (0.0422) on grain yield per plant. Positive indirect effect was imposed via biological yield per plant

(0.0059). Thousand grain weight imposed positive direct effect (0.0002) on grain yield per plant. Biological yield per plant imposed positive direct effect (0.5195) on grain yield per plant. Positive indirect effect was imposed via spike length (0.989), economic weight (0.0733), day to maturity (0.0331) and number of spikes per ear (0.0212). Harvest index imposed positive direct effect (1.1096) on grain yield per plant. Positive indirect effect was imposed via thousand grain weight (0.6337), number of productive tillers per plant (0.2269), number of spikelet's per ear (0.1962), plant height (0.1707), days to 50% heading (0.1276) and chlorophyll content (0.1163). Chlorophyll content imposed negative direct effect (-1.1096) on grain yield per plant. Positive indirect effect was imposed via biological yield per plant (0.0016). Positive and significant correlation along with positive direct effect of days to 50% heading, plant height, spike length, economic weight, biological yield per plant and harvest index with grain yield revealed true relationship between them and direct selection for these traits will be rewarding for yield improvement. On the other hand, days to maturity, number of productive tillers per plant, number of spikelets per ear and chlorophyll content showed negative correlation but imposed positive direct effect, therefore in such situation direct selection for these trait should help in reducing the undesirable indirect effect. Residual effect has been assessed as 0.1112 indicating that the other traits which were excluded in the present investigation should be included as they can also subsidize in the overall yield improvement. These evaluations showed similar findings of Prakash *et al.*, (2021)^[17], Chaudhary *et al.*, (2020)^[6], Devesh *et al.*, (2020) and Ibrahim (2019)^[11].

Table 5: Genotypic path coefficient on grain yield per plant in wheat

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	Genotypic Correlation for grain yield per plant
X1	0.0409	0.0282	0.0073	-0.0008	-0.0096	-0.0030	-0.0077	-0.0096	0.0054	-0.0047	0.0047	0.0062	0.0798
X2	-0.0195	-0.0282	-0.0064	0.0034	0.0047	-0.0002	0.0046	-0.0013	-0.0033	-0.0018	-0.0014	0.0003	0.0964
X3	0.0033	0.0042	0.0185	0.0015	0.0051	0.0048	-0.0011	-0.0015	0.0022	0.0003	0.0028	-0.0013	0.1962
X4	0.0004	0.0023	-0.0016	-0.0191	0.0021	0.0004	0.0022	0.0068	0.0014	0.0039	-0.0039	0.0011	0.0900
X5	0.0019	0.0014	-0.0023	0.0009	-0.0082	-0.0023	0.0004	-0.0002	-0.0003	-0.0003	-0.0015	-0.0004	0.2182
X6	-0.0017	0.0002	0.0060	-0.0005	0.0065	0.0234	0.0032	-0.0027	-0.0012	0.0045	-0.0042	0.0027	-0.0829
X7	-0.0019	-0.0017	-0.0006	-0.0012	-0.0005	0.0014	0.0102	0.0005	-0.0005	-0.0018	-0.0014	0.0031	0.2269
X8	-0.0099	0.0020	-0.0033	-0.0149	0.0011	-0.0048	0.0022	0.0422	-0.0049	0.0059	-0.0046	-0.0007	-0.0145
X9	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0002	0.0000	0.0001	0.0000	0.5618**
X10	-0.0603	0.0331	0.0073	-0.1067	0.0212	0.0989	-0.0920	0.0733	-0.0702	0.5195	-0.2262	-0.1231	0.0437
X11	0.1276	0.0548	0.1707	0.2269	0.1962	-0.2007	-0.1469	-0.1221	0.6337	-0.4832	1.1096	0.1163	0.8733**
X12	-0.0010	0.0001	0.0005	0.0004	-0.0003	-0.0008	-0.0020	0.0001	-0.0007	0.0016	-0.0007	-0.0066	-0.0025

Residual Effect= 0.1112

X1-Days to 50% heading, X2-Days to maturity, X3-Plant height, X4-Number of productive tillers per plant, X5-Number of spikelets per ear, X6-Spike length, X7-Number of grains per ear , X8- Ear weight X9- Thousand grain weight, X10- Biological yield per plant, X11- Harvest index, X12- Chlorophyll content

Conclusion

Therefore, it can be concluded that in wheat the highest positive and significant correlation was recorded in days to heading, thousand grain weight on the dependent character i.e., grain yield per plant. In the path analysis the highest positive direct effect was observed in harvest index, biological yield per plant, economic weight, days to 50% heading, spike length, plant height, number of grains per ear, thousand grain weight. As a result, trait like plant height and thousand grain weight has shown both positive correlation as well as positive direct effect on grain yield per plant. This association among characters must be taken consideration in breeding programmes because changes in one cause changes in another through selection. It is concluded that selection based on association and path analysis for the preceding characters can be effectively used for developing high yielding genotypes. Hence selection of these characters can enhance yield advancement in wheat (F3 segregating population).

References

1. Abbadi AP, Avinash H, Dubey N, Reddy JP, Reddy BT. Genetic studies on F₃ population of bread wheat [*Triticum aestivum* L.] for yield and its components traits. *Electronic Journal of Plant Breeding*. 2022;13(2):369-376.
2. Anil G, SS Dhanda, Renu Munjaland Neelam R Yadav. Assessment of Genetic Variability, Heritability and Genetic Advance for Yield and its Component Traits in Relation to Heat Tolerance in Wheat. *Anal of Biology*. 2019;35(2):214-218.
3. Ashish, Sethi SK, Vikram, Phougat D, Antim. Genetic variability, correlation and path analysis in bread wheat (*Triticum aestivum* L.) genotypes for yield and its contributing traits, *Journal of Pharmacognosy and Phytochemistry*. 2020;9(6):388-391
4. Avinash HA, Dubey N, Shukla RS. Genetic analysis for economic traits in wheat under timely and very late sown conditions. *International Journal Pure and Applied Bioscience*. 2017;5(5):157-162.
5. Bayisa T, Tefera H, Letta T. Genetic variability, heritability and genetic advance among bread wheat genotypes at Southeastern Ethiopia. *Agriculture, Forestry and Fisheries*. 2020;9(4):128.
6. Chaudhary R, Kumar S, Singh S, Prasad J, Jeena AS, Upreti MC. Study of genetic parameters and character association in wheat (*Triticum aestivum* L.). *Int. J. Chem. Stud*. 2020;8(3):2312-2315.
7. Dagade SK, Dodake SS, Magar NM. Genetic variability, character association and path coefficient analysis in bread wheat (*Triticum aestivum* Desf.). *Journal of Pharmacognosy and Phytochemistry*. 2020;9(6):2149-2155.
8. Devesh P, Moitra PK, Shukla RS, Shukla SS, Pandey S, Arya G. Analysis of variability, heritability and genetic advance of yield, its components and quality traits in wheat. *International Journal of Agriculture, Environment and Biotechnology*. 2018;17(4):855-859.
9. FAOSTAT. Crop production. Retrieved 31 January 2019 from; c2019. www.fao.org/faostat/.
10. Gautam S. Studies on germplasm evaluation genetic variability and trait relationship in wheat *Triticum aestivum* Lem Thell; c2020.
11. Ibrahim AU. Genetic variability, Correlation and Path analysis for Yield and yield components in F₆ generation of Wheat (*Triticum aestivum* Em. Thell.). *IOSR Journal of Agriculture and Veterinary Science*. 2019;12(1):17-23.
12. Jaiswal R, Gaur SC, Jaiswal SK, Kumar A. An estimate of variability, heritability and genetic advance for grain yield and yield components in bread wheat (*Triticum aestivum* L.). *Curr J of Appl Sci and Tech*. 2020;39(12):1-6.
13. Kumar M, Avinash H, Dubey N, Kaur S, Kalubarme S, Reddy JP, Ozukum W. Heritability and correlation studies of yield and yield related traits in bread wheat (*Triticum aestivum* L.). *Journal of Pharmacognosy and Phytochemistry*; c2019. p. 97-101.
14. Mohapatra SS, Priya B, Mukherjee S. Studies on Variability, Heritability and Genetic Advance in Some Quantitative and Qualitative Traits in Bread Wheat (*Triticum aestivum* L.) under Rainfed Condition. *International Journal of Current Microbiology and Applied Sciences*. 2019;8(9):1040-1050.
15. Pooja C, Singh V, Yadav S. Path coefficient and correlation studies of yield and yield associated traits in diverse genotypes of bread wheat (*Triticum aestivum* L.). *Int. J. Chem Stud*. 2018;6:73-76.
16. Prabha AA, Avinash H, Dubey N, Reddy JP, Reddy BT. Genetic studies on F₃ population of bread wheat [*Triticum aestivum* L.] for yield and its components traits. *Electronic Journal of Plant Breeding*. 2022;13(2):369-376.
17. Prakash I, Tarkeshwar, Chaudary RP, Singh S, Srivastava A, Gaur SC. Studies on Genetic Variability, Heritability and Genetic Advance in some Bread Wheat (*Triticum aestivum* Lem. Thell) Genotypes. *International Journal of Current Microbiology and Applied Sciences*. 2021;11:503-508.
18. Prasad J, Dasora A, Chauhan D, Rizzarda DA, Bangarwa SK, Nesara K. Genetic Variability, Heritability and Genetic Advance in Bread Wheat (*Triticum aestivum* L.) Genotypes. *Genetics and Molecular Research*. 2020;20:2.
19. Rajput RS. Correlation, path analysis, heritability and genetic advance for morpho-physiological character on bread wheat (*Triticum aestivum* L.). *Journal of Pharmacognosy and Phytochemistry*. 2018;7(2):107-112.
20. Reddy JP, Kumar M, Dubey N, Avinash H, Rohith K, Kalubarme S. Genetic divergence for grain yield and its components in bread wheat (*Triticum aestivum* L.). *Electronic Journal of Plant Breeding*. 2022;13(1):258-261.
21. Reddy JP, Kumar M, Kalubarme S, Avinash H, Dubey N. studies on choice of traits for seed yield improvement through breeding in bread wheat (*Triticum aestivum* L.) Genotypes. *Plant Archives*. 2020;20(2):7813-7819.
22. Sharma P, Kamboj MC, Singh N, Chand M, Yadava RK. Path coefficient and correlation studies of yield and yield associated traits in advanced homozygous lines of bread wheat germplasm. *International Journal of Current Microbiology and Applied Sciences*. 2018;7(2):51-63.
23. Singh T, Singh V, Singh KP, Singh V, Srivastava SP. Analysis of yield components and their association for enhancing grain yield in bread wheat (*Triticum aestivum* L. em Thell.) under sodic soil. *The Pharma Innovation Journal*. 2021;10(7):1265-1269.