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Analysis of the genetic components of F₁ and F₂ generations for bread wheat (*Triticum aestivum* L.) seed yield and its component attributes

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Abstract

The present study involved 100 treatments (10 parents, 45 F₁s, and 45 F₂s) and 10 advanced lines, arranged in a Randomized Block Design during the 2024 *Rabi* season at three locations: Crop Research Farm (Aligarh), Crop Research Farm (Kaushambi) and Student Instructional Farm (CSAUAT, Kanpur). The experimental material consisted of 10 parental lines (DBW-173, DBW-187, DBW-222, DBW-398, HD-3059, K-1006, PBW-386, PBW-644, HI-1563 and HI-1612). On the partitioning of treatment variances, the mean squares of parents, F₁s, and F₂s were highly significant for all the 14 traits. Parents vs. F₁s were highly significant for all the traits except the number of spikelets per spike, protein content, and seed hardness while parents vs. F₂s were also found highly significant for almost all the traits except days to 50% flowering, plant height, spike length, number of grains per spike, grain yield per plant indicating much variability in different populations. These lines were crossed using a diallel design to develop 45 F₁s, which were evaluated for 9 traits: number of productive tillers per plant, spike length, number of spikelets per spike, 1000-seed weight, harvest index, plant height, grain yield per plant, biological yield per plant and protein content. Pooled analysis of variance revealed highly significant differences among the varieties and environments for all the characters. The results, therefore, satisfied the basic requirement for the present study.

Keywords: Wheat, genetic variability, genetic components

Introduction

Wheat (*Triticum aestivum* L.) is one of the leading food crops of the world farming and occupies significant position among the cultivated cereals. Cultivation of wheat has been the symbolic of green revolution that played pivotal role in making the nation a food surplus nation. Wheat is a member of the Poaceae family and a self-pollinated crop. India's wheat production is projected to reach 111.32 million tonnes in 2023-2024, up from 109.52 million tonnes in 2022-2023, reflecting a compound annual growth rate (CAGR) of 1.64%. Wheat is used for both human and animal nutrition and plays an important role in the nutrition of rapidly growing populations both in our country and the world (Patil *et al.*, 2024) [12]. The common wheat (*Triticum aestivum* L.) which is good for chapatti making, bread making and bakery products is grown in whole of North India and also in Central and South India. The durum wheat which is good for 'suji', 'semya', 'sphagti' and 'macaroni' is grown only in central and south India and that too under rainfed conditions. The dicoccum wheat is good for the south India dish 'Uppumav' (Singh *et al.*, 2018) [15]. Durum wheat (*Triticum turgidum* L.) is the main tetraploid type, its large, very hard grains yield low gluten flour that is the main source of semolina suitable for pasta, couscous, burghul and other local end-products. (Nachit 1995) [11]. It is grown under a wide range of climatic conditions from Kashmir and other mountainous regions to semi-arid regions with mild to severe winter. (Yadav *et al.*, 2021) [17]. since ages, wheat has been playing an important role in the economy of several countries (Singh *et al.*, 2010) [16]. A number of biometrical techniques are extensively used for genetic evaluation of plants. Out of them, diallel, partial diallel and line X tester analyses have been frequently used by breeders for genetic study because they provide more genetic information about the material studied. Diallel mating design is used to evaluate several material in terms of combining ability variances and effects.

Its provides information about general combining ability (gca) and specific combining ability (sca) variances and effects and additive (D) and dominance (H) components of genetic variance. Diallel analyses helps in the selection of suitable parents for use in the hybridization programme as well as in the choice of appropriate breeding for the genetic improvement of various quantitative traits in a crop species.

Materials and Methods

The current study was conducted during *Rabi* 2024 at three locations: Crop Research Farm at Kalai, Aligarh, and Crop Research Farm at Saini, Kaushambi and Student Instruction Farm at CSAUAT, Kanpur. It involved 100 treatments (10 parents, 45 F₁'s and 45 F₂'s) in a Randomized Block Design. The experimental material comprised 10 parental lines: DBW-173, DBW-187, DBW-222, DBW-398, HD-3059, K-1006, PBW-386, PBW-644, HI-1563 and HI-1612. The 100 treatments (10 parents, 45 F₁'s, and 45 F₂'s) were evaluated for genetic analysis of nine quantitative traits in wheat. Half diallel analysis was analyzed as suggested by Griffing (1956) [5] Fisher divided the component of variance into additive, dominance and epistatic.

Results and Discussion

The analysis of variance revealed considerable variability among the treatments for all the traits namely, days to 50% flowering, days to maturity, plant height, number of productive tillers per plants, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike, biological yield, grain yield per plant, 1000-grain weight, harvest index, seed hardness and protein content. It reflected significant variability in Table 1 the base material and the material generated subsequently involving all possible combinations in both generations. Similar result reported by Ahmad *et al.*, (2011) [3], Hassan *et al.*, (2013) [6] and Kumar *et al.*, (2015) [10]. The mean performance of F₁s was greater than parents for plant height (cm), number of productive tillers per plant, spike length (cm), number of spikelets per spike, number of grains per spike, weight of grains per spike (gm), biological yield per plant (gm), grain yield per plant (gm), 1000-grain weight (gm), harvest index (%), seed hardness (kg) and protein content while the mean performance of F₁s were lower than parents for days to 50% flowering, days to maturity. The variance component analysis for F₁ and F₂ generations in respect of genetic components of variation was performed according to the model proposed by Hayman (1954) [7].

The estimated of all the six components *viz.*, \hat{D} , \hat{H}_1 , \hat{H}_2 , \hat{F} , \hat{h}^2 , and \hat{E} along with their standard error and related parameters are given in Table 2 for all the 14 traits in F₁ and F₂ generations, separately. The estimates of additive (\hat{D}) component were recorded highly significant for days to 50% flowering, days to maturity, plant height, number of productive tillers per plant and number of grains per spike in both the generations and protein content in F₁ generations, while it was not significant for number of productive tillers per plant, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike, biological yield per plant, 1000-seed weight, seed hardness and grain yield per plant in both the generations

and protein content in F₂ generation. The estimated values of dominant components (\hat{H}_1 and \hat{H}_2) were found highly significant for all the 14 traits. The values of \hat{H}_1 were recorded higher than the values of \hat{H}_2 for all the characters.

The positive and highly significant values of \hat{F} component were found for plant height and protein content in both the generations; protein content in F₁ generations and number of seeds per plant in F₂ generation. Positive and non-significant values of \hat{F} component were found for days to 50% flowering, days to maturity, number productive tillers per plant, spike length, number of spikelets per spike, grain weight per spike, biological yield per plant, 1000-seed weight, harvest index, seed hardness and grain yield per plant in both the generations; number of grains per spike in F₁ generation; protein content in F₂ generation. The estimated values of \hat{h}^2 genetic component were found positive and highly significant for spike length and number of grains per spike in F₁ generations and days to 50% flowering, days to maturity and protein content in F₂ generation. Non-significant values of \hat{h}^2 were found for plant height, number of productive tillers per plant, number of spikelets per spike, grain weight per spike, biological yield per plant, 1000-seed weight harvest index, seed hardness and grain weight per plant in both the generations; for days to 50% flowering, days to maturity and protein content in F₁ generation and for spike length and number of grains per spike in F₂ generation. The estimated of components were found significant for protein content in F₁ generation only. The estimated value of average degree of dominance (\hat{H}_1/\hat{D})^{0.5} was observed more than unity for all the 14 characters in both the F₁ and F₂ generations except plant height in F₂ generation. The ratio of positive and negative genes effect ($\hat{H}_1/4\hat{H}_2$) was estimated less than the theoretical value (0.25) for all attributes in the both generations. The proportion of dominant and recessive genes [(\hat{D}/\hat{H}_1) ^{0.5} + $\hat{F}/(4\hat{D}\hat{H}_1)$ ^{0.5} \hat{F}] was observed more than unity for all the attributes namely days to 50% flowering, days to maturity, number of productive tillers per plant, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike, grain yield per plant, harvest index, seed hardness, protein content in F₁ and F₂ generations excepts biological yield per plant and 1000-seed weight in F₁ generation and plant height in F₂ generation. The value of \hat{h}^2/\hat{H}_2 were found less than unity for all the attributes namely, days to 50% flowering, days to maturity, plant height, number of productive tillers, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike, biological yield, grain yield per plant, 1000-seed weight, harvest index, seed hardness, protein content. Similar result reported by Rabbani *et al.*, (2009) [13], Jadoon *et al.*, (2012) [9], Din *et al.*, (2020) [4] and Sharma *et al.*, (1991) [14].

Table 1: Analysis of variance for 14 characters in wheat

Source of variation	d. f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of productive tillers per plant	Spike length (cm)	Number of spikelets per spike	Number of grains per spike	Grain weight/spike (g)	Seed hardness (kg/seed)	Protein content (%)	Biological yield/plant (g)	1000-grain weight (g)	Harvest index (%)	Grain yield/plant (g)
Replication	2	0.28	24.57	2.44	0.08	0.68	0.41	9.08	0.03	2.71	0.19	4.41	0.76	2.31	0.31
Treatment	99	26.58**	60.58**	19.95**	3.16**	1.40**	2.87**	41.94**	0.80**	2.35**	2.16**	125.83**	6.92**	15.12**	23.83**
Parents	9	5.91**	6.96**	7.48**	0.61**	0.68**	0.76**	16.59**	0.12**	0.91**	1.03**	6.76**	1.31**	9.86**	1.57**
F1	44	7.31**	2.95*	5.72**	1.36**	0.93**	2.93**	46.47**	0.19**	2.10**	1.25**	130.34**	4.09**	19.72**	21.78**
Parents vs F1	1	1632.59**	250.19**	1358.23**	100.55**	53.76**	16.33**	735.33**	42.23**	31.20**	106.53**	2177.32**	210.44**	133.32**	474.94**
F2	44	9.34**	0.87	1.35	0.66**	0.77**	2.99**	26.61**	0.07**	2.08**	0.70**	95.15**	4.57**	8.82**	20.14**
Parents vs F2	1	608.19**	885.83**	448.19**	3.84**	23.18**	9.39**	694.32**	6.31**	8.28**	110.55**	798.47**	44.93**	143.43**	223.58**
Error	198	2.41	2.09	1.05	0.33	0.20	0.56	4.00	0.06	0.28	0.11	3.91	0.80	2.26	0.51
Total	299	10.40	21.61	7.32	1.26	0.60	1.33	16.60	0.30	0.98	0.79	44.28	2.83	6.52	8.23

* significant at 5%, ** significant at 1%

Table 2: Estimates of D, H₁, H₂, F, h² and E component and related statistics for 14th attributes in 10 parent-diallel cross in F₁ generation of wheat

Parameters		Days to 50% flowering	Days to maturity	Plant height (cm)	Tillers/plant	Spike length (cm)	Spikelets/spike	Grains/spike	Grain weight/spike (g)	Seed hardness (kg/seed)	Protein content (%)	Biological yield/plant (g)	1000-grain weight (g)	Harvest index (%)	Grain yield/plant (g)
D	F1	1.47	1.48**	2.22*	0.140	0.151	0.080	4.08	0.022	0.221	0.307**	0.42	0.09	2.40	0.35
	SE±	0.82	0.47	0.98	0.254	0.107	0.220	3.94	0.029	0.323	0.117	13.15	0.89	4.63	3.86
	F2	0.85	1.47**	1.94**	0.057	0.168	0.071	4.35	0.016	0.186	0.305**	1.50	0.25	2.58	0.37
F	SE±	0.91	0.56	0.51	0.070	0.107	0.328	3.91	0.012	0.255	0.157	10.70	0.53	0.86	2.62
	F1	2.47	1.98*	2.33	0.271	0.233	0.131	17.91*	0.035	0.173	0.328	-0.29	0.98	8.47	1.48
	SE±	1.90	1.09	2.25	0.585	0.247	0.508	9.08	0.066	0.746	0.270	30.35	2.06	10.68	8.90
H1	F2	0.65	2.50*	3.60*	0.131	0.410	0.072	9.29	0.030	0.169	0.632*	2.51	0.53	3.50	1.12
	SE±	2.11	1.29	1.19	0.162	0.247	0.756	9.02	0.028	0.589	0.362	24.68	1.21	2.00	6.05
	F1	36.04**	6.84**	28.59**	3.251**	1.937**	3.000**	68.31**	0.907**	3.038**	3.202**	152.69**	8.13**	31.58**	29.10**
H2	SE±	1.75	1.01	2.08	0.540	0.228	0.469	8.38	0.061	0.688	0.250	28.00	1.90	9.85	8.21
	F2	18.67**	15.53**	10.32**	0.632**	1.469**	3.131**	46.07**	0.166**	2.457**	2.995**	46.07**	5.59**	12.34**	22.96**
	SE±	1.95	1.19	1.09	0.150	0.228	0.697	8.32	0.026	0.543	0.334	22.77	1.12	1.84	5.58
h ²	F1	34.35**	5.90**	27.03**	2.903**	1.711**	2.127**	37.66**	0.875**	2.996**	2.953**	104.88**	6.38**	23.95**	20.01**
	SE±	1.49	0.85	1.77	0.459	0.194	0.399	7.12	0.052	0.585	0.212	23.80	1.62	8.37	6.98
	F2	17.54**	14.55**	8.60**	0.467**	1.124**	2.543**	36.87**	0.143**	2.253**	2.584**	64.28**	4.22**	9.39**	14.66**
E	SE±	1.65	1.01	0.93	0.127	0.194	0.593	7.08	0.022	0.462	0.284	19.35	0.95	1.56	4.75
	F1	215.32**	32.72**	179.17**	13.249**	7.070**	2.092**	96.54**	5.568**	4.089**	14.049**	286.75**	27.66**	17.28**	62.63**
	SE±	1.00	0.57	1.18	0.307	0.130	0.267	4.77	0.035	0.391	0.142	15.93	1.08	5.61	4.67
((H1D)0.5)	F2	79.88**	116.62**	58.96**	0.455**	3.040**	1.174**	91.22**	0.826**	1.052**	14.578**	105.13**	5.86**	18.68**	29.46**
	SE±	1.11	0.68	0.62	0.085	0.130	0.397	4.74	0.015	0.309	0.190	12.95	0.64	1.05	3.18
	F1	0.50	0.84	0.28	0.064	0.074	0.174	1.45	0.017	0.082	0.037	1.83	0.34	0.89	0.18
H2/4H1	SE±	0.25	0.14	0.29	0.076	0.032	0.066	1.19	0.009	0.098	0.035	3.97	0.27	1.40	1.16
	F2	1.12	0.85	0.55	0.147	0.057	0.183	1.18	0.023	0.116	0.039	0.75	0.19	0.71	0.15
	SE±	0.28	0.17	0.16	0.021	0.032	0.099	1.18	0.004	0.077	0.047	3.22	0.16	0.26	0.79
((4DH1)0.5+F)/((4DH1)0.5-F)	F1	4.96	2.15	3.59	4.81	3.58	6.12	4.09	6.45	3.71	3.23	19.02	9.33	3.63	9.14
	SE±	4.68	3.25	2.31	3.32	2.95	6.64	3.26	3.21	3.63	3.14	8.21	4.71	2.19	7.85
	F2	0.238	0.215	0.236	0.223	0.221	0.177	0.138	0.241	0.247	0.231	0.172	0.196	0.190	0.172
h2/H2	SE±	0.235	0.234	0.208	0.185	0.191	0.203	0.200	0.216	0.229	0.216	0.159	0.189	0.190	0.160
	F1	1.410	1.902	1.342	1.503	1.548	1.309	3.317	1.280	1.236	1.396	0.965	3.579	2.898	1.606
	SE±	1.179	1.709	2.344	2.046	2.404	1.165	1.977	1.810	1.286	1.989	1.227	1.575	1.899	1.476
r	F2	6.268	5.547	6.629	4.565	4.131	0.984	2.564	6.366	1.365	4.757	2.734	4.337	0.722	3.130
	SE±	4.554	8.014	6.853	0.973	2.705	0.461	2.474	5.765	0.467	5.643	1.636	1.388	1.989	2.009
	F1	10.80	-0.62	1.15	14.78	13.26	26.37	16.98	7.24	13.99	5.77	51.66	30.57	24.95	49.70
Parameters	SE±	0.864	0.926	-0.968	-0.791	-0.867	-0.592	-0.629	-0.985	-0.625	-0.930	-0.163	-0.761	-0.153	-0.746
	F1	Days to 50% flowering	Days to maturity	Plant height (cm)	Tillers/plant	Spike length (cm)	Spikelets/spike	Grains/spike	Grain weight/spike (g)	Seed hardness (kg/seed)	Protein content (%)	Biological yield/plant (g)	1000-grain weight (g)	Harvest index (%)	Grain yield/plant (g)

Conclusion

Significant genetic variability in the base and created materials was indicated by the analysis of variance, which revealed highly significant variations across all nine characters. In both the F₁ and F₂ generations, dominance variance was found to be greater than additive genetic variance, indicating over-dominance gene activity for all traits. The fact that the ratio of genotypic variance to phenotypic variance is less than unity emphasizes how important environmental influences are in determining how traits manifest. These findings are in line with earlier research and highlight the significance of both additive and non-additive genetic elements in breeding programs, especially when it comes to enhancing economically significant features.

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