



Diversity Trends in Rust Resistant Derived F₄ and F₅ Progenies of Bread Wheat (*Triticum aestivum* L.)

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Abstract: Plant genetic diversity provides opportunity to plant breeders for improving the plant characteristics and helps to tackle the threats of biotic and abiotic stresses. Therefore, present study was envisioned to evaluate the genetic diversity in F₄ and F₅rust- resistant derived progenies of two crosses of bread wheat i.e., WH 1105 × WH 711 and Raj 3765 × WH 711 for grain yield plant⁻¹ and related traits. Moderate to high values of genotypic and phenotypic coefficients of variation were observed for grain weight ear⁻¹, grain yield plant⁻¹, biological yieldplant⁻¹,etc. High heritability with high genetic advance were observed for number of tillers plant⁻¹, grain weight ear⁻¹, 100-grain weight and grain yield plant⁻¹ indicating predominance of additive gene effects and possibilities of simple selection. Based on D² Statistics, the genotypes were distributed into five to six clusters where the highest inter-cluster distances were found between cluster I and V (27.34) in F₄ generation, I and IV (24.38) in F₅ generation of cross-I, I and VI (26.53) in F₄ generation and III and IV (25.16) in F₅ generation of cross-II indicating wider genetic diversity among these clusters. Traits namely, number of grains ear⁻¹, grain weight ear⁻¹, number of tillers plant⁻¹ and number of spikelets ear⁻¹ showed highest contribution (more than 60%) towards genetic divergence. Hence, considering the magnitude of genetic distances, contribution of different traits towards total divergence and magnitude of cluster means for different traits, the genotypes belonging todiverse clusterscould deliver maximum heterosis and good recombinants with desired traits in varietal improvement programs.

Key words: Bread wheat, cluster, diversity, genetic advance, heritability and heterosis.

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aestivum L.) is the most widely grown crop which provides 20% of the total protein and calories in human nutrition (Goel *et al.*, 2018), and supplies ~40% of the dietary intake of essential micronutrients for millions of people, who rely on wheat-based diets (Velu *et al.*, 2017). India is the second largest producer of wheat in the world with area, production and productivity of 30 mha, 104 mt and 34.0 qha⁻¹, respectively during 2021-22 (USDA, 2023).

Further, evolving pathogens and pests pose a major concern for increasing wheat production globally, thus breeding wheat for disease resistance combined with high yield and good quality can undeniably improve wheat productivity to meet the future demands. Rust is the most important disease in wheat causing losses in production and quality of wheat across the world (Keller *et al.*, 2008; Goyal and Prasad, 2010). In order to sustain wheat production, continuous efforts are to be made to develop high yielding and disease resistant wheat genotypes. For achieving this goal, obvious attempts are needed through manipulation of various yield components systematically (Hussain and Qamar, 2007). Due to extensive breeding for a limited number of economic traits, genetic diversity in wheat has been increasingly narrowed which has rendered improved varieties less tolerant to biotic and abiotic stresses (Maqbool *et al.*, 2010).

Grain yield being a complex trait is highly impacted by many genetic factors and environmental fluctuations. For adopting suitable breeding programs, unveiling the proportion of heritable and non-heritable components in the total variability observed is indispensable. The heritable component can be assessed by observing the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability and genetic advance. Genetic diversity studies in wheat have been conducted to estimate the genetic distances between germplasm sources to identify cross combinations that maximize variability (Nielsen *et al.*, 2014). In the present study, Mahalanobis' D² statistics (1936) as described by Rao (1952) was used to quantify the genetic divergence between progenies proficiently. It is true that vast genetic diversity eventually offers greater chances for getting productive recombinants in segregating

generations during genetic improvement (Mohammadi and Prasanna, 2003).

Materials and Methods

About 240 F₄ and F₅ generation progenies derived from two wheat crosses namely, WH 1105 × WH 711 (cross-I) and RAJ 3765 × WH 711 (cross-II) along with parents were sown in the field in paired rows with two replications in a randomized complete block design (RCBD) in research area of Wheat and Barley Section, Department of GPB, CCS HAU, Hisar, during the rabi season of 2015-16 and 2016-17. Infector rows were planted and also artificial inoculation (using spray method) was carried out under field conditions using *Pst* (*Puccinia striiformis*) isolates as a source of inoculum. Resistant and agronomically superior plants were selected from F₄ generation progenies for growing their F₅ progenies in the next year. Five plants selected randomly from the parents, F₄ and F₅ generation progenies were evaluated for recording data on morphological traits like plant height (cm), number of tillers plant⁻¹, ear length (cm), ear weight (g), number of grains ear⁻¹, grain weight ear⁻¹ (g), number of spikelets ear⁻¹, 100-grain weight (g), grain yield plant⁻¹ (g), biological yield plant⁻¹ (g) and harvest index (%). Statistical analysis of recorded phenotypic data was performed using INDOSTAT software. All the traits were measured on individual plants.

Results and Discussion

Analysis of variance

The results revealed that there are highly significant differences among the genotypes for all the characters in progenies of both the crosses (WH 1105 × WH 711 and RAJ 3765 × WH 711) which can be helpful for selecting suitable genotypes (Table 1). Earlier workers including Kaushik *et al.* (2013) and Maurya *et al.* (2014) witnessed high variability for different traits in wheat.

Variability and heritability parameters

Higher values of PCV than GCV for all the characters indicated the influence of environmental conditions on the expression of traits which was also confirmed by findings of Kaushik *et al.* (2013) and Shankarrao *et al.* (2010).

Table 1. Mean sum of squares for 11 morphological characters in F_4 and F_5 generations of cross-I (WH 1105 $\times$ WH 711) and cross-II (RAJ 3765 $\times$ WH 711) in wheat

SV	Cross		d.f.	PH (cm)	NTP ⁻¹	EL (cm)	EW (g)	NGE ⁻¹	GWE ⁻¹ (g)	NSE ⁻¹	100 GW (g)	GYP ⁻¹ (g)	BYP ⁻¹ (g)	HI (%)
Replication	C-I	F ₄	1	42.67	0.54	0.98	0.05	1.68	0.15	0.65	0.19	3.29	18.66	34.35*
		F ₅	1	0.67	0.14	1.27	0.16	12.79	0.09	1.15	0.003	1.92	6.79	6.08
	C-II	F ₄	1	44.91	0.41	0.47	0.04	1.48	0.05	0.16	0.24	1.42	7.97	61.75
		F ₅	1	25.52	0.12	0.67	0.20	1.35	0.004	0.63	0.07	0.99	1.80	0.42
Treatment	C-I	F ₄	115	91.33**	1.99**	0.85**	0.69**	78.60**	0.56**	2.73**	1.20**	16.21**	61.15**	26.93**
		F ₅	115	72.60**	1.33**	0.94**	0.51**	77.09**	0.42**	2.53**	0.67**	13.19**	19.03**	112.59**
	C-II	F ₄	130	59.35**	5.17**	1.03**	0.46**	107.22**	0.52**	3.10**	0.73**	18.56**	29.08**	140.59**
		F ₅	130	67.45**	4.49**	1.02**	0.42**	98.07**	0.52**	3.12**	0.56**	14.84**	19.71**	143.33**
	C-I	F ₄	115	32.89	0.19	0.27	0.05	10.34	0.05	0.54	0.11	1.45	7.52	8.25
		F ₅	115	27.30	0.34	0.39	0.07	16.94	0.03	0.42	0.09	1.88	7.32	31.72
Error	C-II	F ₄	130	22.49	0.26	0.28	0.12	15.48	0.04	1.15	0.10	2.97	7.86	45.36
		F ₅	130	20.60	0.44	0.32	0.18	22.90	0.05	1.06	0.12	1.73	8.32	36.90
CV (%)	C-I	F ₄		6.65	7.43	4.32	7.64	5.23	9.44	3.39	8.82	9.48	10.32	5.94
		F ₅		6.11	10.28	5.24	8.79	6.54	7.16	3.03	8.02	11.99	9.71	13.70
	C-II	F ₄		5.52	7.12	4.44	10.97	6.53	7.98	5.15	7.91	13.26	9.50	15.26
		F ₅		5.38	9.19	4.69	12.72	7.77	8.11	4.83	8.31	9.67	9.33	13.70
CD	C-I	F ₄		11.37	0.86	1.02	0.47	6.38	0.43	1.45	0.65	2.39	5.44	5.70
		F ₅		10.36	1.16	1.24	0.53	8.16	0.34	1.29	0.61	2.72	5.37	11.17
	C-II	F ₄		9.39	1.01	1.04	0.70	7.79	0.39	2.13	0.64	3.41	5.55	13.34
		F ₅		8.99	1.31	1.12	0.83	9.48	0.43	2.04	0.69	2.60	5.71	12.03

PH- Plant height, NTP⁻¹- No. of Tillers plant⁻¹, EL- Ear length, EW- Ear weight, NGE⁻¹- No. of Grains ear⁻¹, GWE⁻¹- Grain weight ear⁻¹, NSE⁻¹- No. of spikelets ear⁻¹, 100 GW- 100 grain weight, GYP⁻¹- Grain yield plant⁻¹, BYP⁻¹- Biological yield plant⁻¹, HI- Harvest index

**Significant at 1%

Cross-I (WH 1105 $\times$ WH 711)

In F_4 generation, PCV ranged from 5.91 for number of spikeletsear⁻¹ to 23.78 for grain weight ear⁻¹ whereas GCV from 4.53 for ear length to 21.83 for grain weight ear⁻¹ (Table 2). In F_5 generation, PCV was observed maximum for grain yieldplant⁻¹ (24.02) and minimum for number of spikelets ear⁻¹ (5.67) whereas GCV was maximum for grain yield plant⁻¹ (20.81) and minimum for ear length (4.38). Bhushan *et al.* (2013) observed moderate values of GCV for harvest index and number of tillers plant⁻¹ while Degewione *et al.* (2013) observed high PCV value for grain yield plant⁻¹.

In F_4 generation, the heritability (broad sense) estimates were significantly high for all the traits, except ear length (52.30%), harvest index (53.10%) and plant height (47.06%). The characters having high heritability estimates are of immense importance for facilitating selection at phenotypic level due to greater correspondence between phenotypic worth

and breeding values. These findings conform well with results of Ali *et al.* (2008) and Ajmal *et al.* (2009). Johnson *et al.* (1955) noticed the importance of combining heritability and genetic advance for deployment of simple selection for desirable individuals due to expression of additive gene action. The traits, number of tillersplant⁻¹, ear weight, grain weight ear⁻¹, 100-grain weight and grain yieldplant⁻¹ were found to have conceivable high heritability with high genetic advance. Furthermore, highest heritability was recorded for grain weightear⁻¹ (87.02%) followed by ear weight (75.74%), 100-grain weight (75.33%), grain yield plant⁻¹ (75.09%) and number of spikeletsear⁻¹ (71.52%), whereas, genetic advance as per cent of mean ranged from 5.80 to 37.15% in F_5 generation. The findings are in close conformity with Khan and Naqvi (2011) and Kumar *et al.* (2012a).

Cross-II (RAJ 3765 $\times$ WH 711)

In F_4 generation, high values of GCV and PCV were observed for number of tillers

Table 2. Genetic variability parameters for 11 quantitative traits in F_4 and F_5 generations of the cross WH 1105 $\times$ WH 711 in wheat

Characters	Cross	Gen.	Mean $\pm$ SE	Range	Coefficient of variation		h^2 (bs) (%)	GA	GA as 5% of mean
					GCV (%)	PCV (%)			
PH (cm)	C-I	F_4	86.27 $\pm$ 5.73	66.27-104.85	6.27	9.13	47.06	7.64	8.86
		F_5	85.58 $\pm$ 5.22	68.3-99.75	5.56	8.26	45.36	6.60	7.72
	C-II	F_4	85.88 $\pm$ 4.74	74.70-98.08	5.00	7.45	45.07	5.94	6.92
		F_5	84.43 $\pm$ 4.54	73.32-98.42	5.73	7.86	53.24	7.28	8.62
NTP ⁻¹	C-I	F_4	5.85 $\pm$ 0.43	3.5-9.1	16.19	17.81	82.61	1.77	30.31
		F_5	5.68 $\pm$ 0.59	4-9.5	12.34	16.06	59.04	1.11	19.53
	C-II	F_4	7.16 $\pm$ 0.51	3.45-10.10	21.87	23.00	90.41	3.07	42.84
		F_5	7.21 $\pm$ 0.66	3.89-9.8	19.73	21.76	82.18	2.66	36.84
EL (cm)	C-I	F_4	11.92 $\pm$ 0.51	9.94-13.86	4.53	6.26	52.30	0.80	6.74
		F_5	11.94 $\pm$ 0.63	10.2-14	4.38	6.83	41.19	0.69	5.80
	C-II	F_4	11.83 $\pm$ 0.52	10.00-13.89	5.22	6.81	58.82	0.98	8.25
		F_5	12.1 $\pm$ 0.57	10.83-14.3	4.89	6.77	52.09	0.88	7.27
EW (g)	C-I	F_4	3.07 $\pm$ 0.23	1.85-4.395	18.30	19.84	85.15	1.07	34.80
		F_5	3.03 $\pm$ 0.27	1.87-4.22	15.53	17.85	75.74	0.84	27.85
	C-II	F_4	3.20 $\pm$ 0.35	2.12-4.62	12.80	16.86	57.64	0.64	20.02
		F_5	3.31 $\pm$ 0.42	2.36-4.81	10.44	16.46	40.25	0.45	13.65
NGE ⁻¹	C-I	F_4	61.50 $\pm$ 3.22	48.25-78.6	9.50	10.84	76.75	10.54	17.14
		F_5	62.95 $\pm$ 4.12	48.65-80.4	8.71	10.89	63.96	9.03	14.35
	C-II	F_4	60.25 $\pm$ 3.93	42.45-79.90	11.24	13.00	74.76	12.06	20.02
		F_5	61.61 $\pm$ 4.78	44.2-80.79	9.95	12.62	62.14	9.95	16.16
GWE ⁻¹ (g)	C-I	F_4	2.32 $\pm$ 0.22	1.295-3.725	21.83	23.78	84.26	0.96	41.28
		F_5	2.39 $\pm$ 0.17	1.34-3.69	18.53	19.87	87.02	0.85	35.61
	C-II	F_4	2.48 $\pm$ 0.20	1.21-3.81	19.75	21.30	85.96	0.94	37.71
		F_5	2.66 $\pm$ 0.22	1.42-3.78	18.30	20.02	83.57	0.92	34.46
NSE ⁻¹	C-I	F_4	21.62 $\pm$ 0.73	17.55-24.55	4.84	5.91	67.08	1.77	8.17
		F_5	21.42 $\pm$ 0.65	18.25-24.03	4.82	5.67	71.52	1.79	8.36
	C-II	F_4	20.86 $\pm$ 1.07	16.50-24.20	4.73	6.99	45.79	1.37	6.59
		F_5	21.35 $\pm$ 1.03	17.05-25.05	4.75	6.78	49.17	1.46	6.86
100 GW (g)	C-I	F_4	3.75 $\pm$ 0.33	1.96-6.01	19.68	21.56	83.29	1.39	37.00
		F_5	3.82 $\pm$ 0.31	2.2-5.73	14.01	16.14	75.33	0.96	25.05
	C-II	F_4	4.10 $\pm$ 0.32	2.20-5.79	13.65	15.78	74.85	0.99	24.34
		F_5	4.21 $\pm$ 0.35	2.62-5.70	11.08	13.85	64.02	0.77	18.26
GYP ⁻¹ (g)	C-I	F_4	12.71 $\pm$ 1.20	6.92-20.96	21.37	23.37	83.56	5.12	40.24
		F_5	11.43 $\pm$ 1.37	7.68-18.81	20.81	24.02	75.09	4.24	37.15
	C-II	F_4	13.00 $\pm$ 1.72	6.14-19.25	21.47	25.23	72.39	4.89	37.63
		F_5	13.59 $\pm$ 1.31	7.13-17.78	18.84	21.17	79.14	4.69	34.52
BYP ⁻¹ (g)	C-I	F_4	26.56 $\pm$ 2.74	15.08-38.9	19.49	22.05	78.09	9.43	35.48
		F_5	27.85 $\pm$ 2.70	22.05-36.10	8.69	13.03	44.45	3.32	11.93
	C-II	F_4	29.54 $\pm$ 2.80	18.73-38.39	11.04	14.56	57.45	5.09	17.24
		F_5	30.92 $\pm$ 2.88	22.25-38	7.72	12.11	40.65	3.13	10.14
HI (%)	C-I	F_4	48.36 $\pm$ 2.87	36.79-53.88	6.32	8.67	53.10	4.59	9.48
		F_5	41.11 $\pm$ 5.63	31.77-52.50	15.47	20.66	56.04	9.81	23.85
	C-II	F_4	44.13 $\pm$ 6.73	29.61-52.49	15.64	21.85	51.22	10.17	23.05
		F_5	44.33 $\pm$ 6.07	30.62-51.93	16.45	21.43	59.05	11.55	26.05

PH- Plant height, NTP⁻¹- No. of Tillers plant⁻¹, EL- Ear length, EW- Ear weight, NGE⁻¹- No. of Grains ear⁻¹, GWE⁻¹- Grain weight ear⁻¹, NSE⁻¹- No. of spikelets ear⁻¹, 100 GW- 100 grain weight, GYP⁻¹- Grain yield plant⁻¹, BYP⁻¹- Biological yield plant⁻¹, HI- Harvest index

plant⁻¹ and grain yield plant⁻¹ (Table 2). In F_5 generation, moderate GCV was observed for traits, viz., number of tillers plant⁻¹ (19.73), grain yield plant⁻¹ (18.84), grain weight ear⁻¹ (18.30) and harvest index (16.45) while, number of tillers plant⁻¹ (21.76), harvest index (21.43)

and grain yield plant⁻¹ (21.17) had high PCV. These results are in agreement with Yadawad *et al.* (2015) and Arya *et al.* (2017) for grain yield plant⁻¹ and Rathwa *et al.* (2018) for number of productive tillers plant⁻¹.

Table 3. Distribution pattern of parents and progenies of F₄ and F₅ generations of cross-I (WH 1105 × WH 711) cross-II (RAJ 3765 × WH 711) in different clusters

Cluster no.	Cross	Generation	Total Number	Details
I	C-I	F ₄	26	WH 711, 5, 8, 11, 12, 14, 17, 19, 25, 26, 27, 28, 29, 31, 34, 36, 38, 41, 43, 64, 69, 75, 86, 91, 93 and 97
		F ₅	15	4, 8, 9, 10, 12, 14, 19, 21, 38, 46, 64, 66, 69, 72 and 93
		F ₄	49	WH 711, 109, 111, 117, 14, 120, 64, 131, 127, 35, 22, 23, 60, 41, 55, 29, 94, 36, 76, 44, 73, 90, 80, 59, 86, 81, 15, 99, 21, 82, 3, 27, 4, 11, 5, 63, 6, 9, 7, 16, 8, 116, 24, 17, 19, 10, 126, 65 and 85
	C-II	F ₅	21	WH 711, 6, 10, 13, 14, 23, 28, 30, 32, 34, 48, 50, 59, 60, 64, 67, 98, 103, 104, 114 and 124
		F ₄	16	10, 18, 23, 24, 42, 47, 48, 51, 58, 61, 74, 88, 98, 99, 106 and 116
	C-I	F ₅	36	6, 11, 16, 17, 18, 23, 24, 26, 27, 28, 29, 32, 33, 36, 39, 41, 42, 43, 44, 45, 47, 59, 60, 67, 75, 82, 91, 97, 98, 99, 103, 107, 111, 114, 115 and 116
II	C-II	F ₄	28	RAJ 3765, 88, 13, 87, 62, 20, 83, 12, 18, 37, 45, 107, 25, 119, 67, 93, 71, 75, 130, 33, 70, 125, 49, 84, 100, 104, 30 and 48
		F ₅	41	3, 4, 5, 7, 9, 11, 15, 16, 20, 21, 22, 27, 29, 41, 42, 44, 57, 58, 63, 69, 72, 73, 75, 80, 81, 82, 83, 86, 89, 90, 94, 99, 102, 105, 107, 108, 109, 112, 113, 115 and 125
	C-I	F ₄	26	WH 1105, 4, 7, 15, 16, 20, 32, 35, 45, 52, 55, 59, 63, 72, 78, 81, 94, 95, 96, 103, 104, 105, 108, 109, 110 and 111
		F ₅	35	WH 711, 3, 7, 15, 30, 31, 34, 35, 48, 52, 55, 57, 61, 63, 65, 68, 73, 77, 78, 79, 81, 84, 85, 88, 89, 92, 94, 95, 96, 104, 105, 108, 109, 110 and 112
III	C-II	F ₄	26	50, 69, 47, 68, 54, 51, 56, 101, 58, 105, 52, 129, 61, 79, 28, 40, 32, 57, 103, 108, 124, 91, 96, 42, 43 and 118
		F ₅	23	RAJ 3765, 36, 40, 46, 47, 51, 52, 54, 55, 56, 61, 68, 76, 79, 95, 101, 106, 111, 120, 121, 123, 128 and 129
	C-I	F ₄	33	3, 6, 9, 21, 30, 33, 40, 46, 56, 57, 60, 62, 65, 66, 68, 71, 73, 76, 77, 79, 80, 82, 83, 84, 85, 89, 90, 92, 100, 101, 102, 107 and 112
		F ₅	25	WH 1105, 5, 13, 20, 22, 37, 40, 49, 50, 51, 53, 54, 56, 62, 70, 74, 76, 80, 83, 86, 87, 100, 101, 102 and 113
IV	C-II	F ₄	14	122, 123, 92, 46, 114, 110, 89, 112, 98, 115, 26, 38, 113 and 72
		F ₅	29	8, 12, 17, 18, 19, 24, 25, 26, 31, 35, 38, 39, 43, 45, 49, 62, 74, 78, 84, 87, 91, 93, 97, 100, 117, 118, 119, 130 and 131
	C-I	F ₄	15	13, 22, 37, 39, 44, 49, 50, 53, 54, 67, 70, 87, 113, 114 and 115
		F ₅	5	25, 58, 71, 90 and 106
V	C-II	F ₄	11	102, 121, 53, 128, 34, 39, 78, 31, 95, 97 and 106
		F ₅	17	33, 37, 53, 65, 66, 70, 71, 77, 85, 88, 92, 96, 110, 116, 122, 123 and 127
	C-II	F ₄	3	74, 66 and 77
VI		F ₅		

In F₄ generation, heritability (broad sense) estimates were witnessed to be high for number of tillers plant⁻¹ (90.41%) followed by grain weight ear⁻¹ (85.96%), 100-grain weight (74.85%) and number of grains ear⁻¹ (74.76%), similar to as found by Choudhary *et al.* (2015) and Rathwa *et al.* (2018). Genetic advance as per cent of mean varied from 6.59 for number of spikelets ear⁻¹ to 42.84 for number of tillers plant⁻¹. High heritability coupled with high genetic advance was exhibited by number of tillers plant⁻¹, number of grains ear⁻¹, 100-grain weight, and grain yield plant⁻¹. Maurya *et al.* (2014) and Dutamo *et al.* (2015) also found the similar trend. In F₅ generation, grain weight ear⁻¹ was found to be with the highest heritability followed by number of tillers plant⁻¹, grain

yield plant⁻¹ and number of grains ear⁻¹. Genetic advance as per cent of mean ranged from 6.86 to 36.84%. Number of tillers plant⁻¹, grain weight ear⁻¹ and grain yield plant⁻¹ had high heritability with high genetic advance. High heritability coupled with high genetic advance was reported by Rajshree and Singh (2018) for number of tillers plant⁻¹ and grain yield by Singh *et al.* (2018).

Genetic divergence analysis

Based on D² analysis, majority of the progenies were clustered into a single cluster in F₄ and F₅ generations of both the crosses, while other clusters have only 1-3 progenies. However, based on an index of similarity and dissimilarity of attributing traits by Euclidean

Table 4. Inter and intra (diagonal) cluster average of D^2 among different clusters in F_4 and F_5 generation progenies of cross-I (WH 1105 $\times$ WH 711) and cross-II (RAJ 3765 $\times$ WH 711)

	Cross	Gen.	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI
Cluster-I	C-I	F_4	12.13	15.84	17.04	16.95	27.34	
		F_5	11.15	15.14	17.59	24.38	20.06	
	C-II	F_4	15.07	19.97	18.42	19.49	21.80	26.53
		F_5	9.60	12.93	14.94	21.34	21.08	
Cluster-II	C-I	F_4		9.82	15.03	14.72	18.46	
		F_5		14.33	16.28	21.99	18.57	
	C-II	F_4		16.07	23.36	22.71	16.46	18.89
		F_5		11.80	18.05	22.54	22.97	
Cluster-III	C-I	F_4			11.38	13.88	19.77	
		F_5			13.52	17.22	15.10	
	C-II	F_4			13.88	16.00	21.03	25.94
		F_5			12.86	25.16	23.31	
Cluster-IV	C-I	F_4				13.64	20.72	
		F_5				14.47	13.54	
	C-II	F_4				12.09	18.50	23.34
		F_5				15.70	14.90	
Cluster-V	C-I	F_4					15.04	
		F_5					7.19	
	C-II	F_4					10.98	14.25
		F_5					13.34	
Cluster-VI	C-II	F_4						11.26
		F_5						-

cluster analysis, there were five clusters in both the generations of cross-I and F_5 generation of cross-II, while six clusters in F_4 generation of cross-II, indicating the presence of ample amount of genetic diversity in the material. The grouping of genotypes based on genetic diversity for different yield contributing components in wheat has also been reported earlier (Vora *et al.*, 2017; Wani *et al.*, 2018 and Krishna *et al.*, 2020).

Cross-I (WH 1105 $\times$ WH 711)- Intra and inter cluster distances

Based on the relative magnitude of D^2 values, cluster IV had maximum (33), whereas cluster V had minimum (15) number of progenies in F_4 generation (Table 3), respectively. The minimum and maximum intra cluster values (9.82 and 15.04) observed for cluster II and V attributed to minimum and maximum differences among progenies grouped in these clusters (Table 4). In F_5 generation, cluster II had a maximum of 36 progenies while cluster V had only 5 progenies. It can be observed that cluster V had the minimum (7.19), while cluster IV had the maximum intra cluster D^2 value

(14.47). When diversity was studied among the clusters, cluster IV and V showed minimum inter cluster distance (13.54), indicating close relationship among the progenies included in these clusters. Inter-cluster distance is the main criterion for selection of genotypes using D^2 analysis (Khare *et al.*, 2015). Clusters showing higher values of inter cluster distances indicate that progenies included in these clusters are genetically diverse and can be used in wheat hybridization program for improving grain yield as promising parents (Birhanu *et al.*, 2017; Rajshree and Singh, 2018).

Cluster means of different clusters for various traits

Table 5 shows that in F_4 generation, the clusters showed considerable differences in mean value for grain yield plant⁻¹ and its component traits, where, cluster V had highest mean values for most of the traits including, number of tillers plant⁻¹ (6.28), ear length (12.41 cm), number of grains ear⁻¹ (70.59), grain yield plant⁻¹ (15.15 g) and biological yield plant⁻¹ (31.14 g) while cluster IV had the highest mean values for 100-grain weight (4.09 g) and harvest

Table 5. Mean values of different clusters for various characters in F_4 and F_5 generation progenies of cross-I (WH 1105 $\times$ WH 711)

Characters	Cluster-I		Cluster-II		Cluster-III		Cluster-IV		Cluster-V	
	F_4	F_5	F_4	F_5	F_4	F_5	F_4	F_5	F_4	F_5
Plant height (cm)	79.76	78.05	85.58	85.83	89.61	86.47	84.70	88.87	95.97	83.71
Number of tillers plant ⁻¹	5.34	5.67	5.35	5.42	6.04	5.66	6.17	6.16	6.28	5.54
Ear length (cm)	11.58	11.89	12.18	11.82	11.90	11.87	11.84	12.23	12.41	12.09
Ear weight (g)	2.61	2.70	2.93	2.78	3.08	3.10	3.28	3.42	3.55	3.51
Number of grains ear ⁻¹	57.63	60.31	66.93	62.51	57.98	60.55	60.57	67.11	70.59	70.09
Grain weight ear ⁻¹ (g)	1.89	2.12	2.15	2.10	2.30	2.47	2.55	2.84	2.79	2.56
Number of spikelets ear ⁻¹	20.68	20.93	22.32	21.18	21.58	21.48	21.55	21.94	22.70	21.71
100-grain weight (g)	3.45	3.82	3.17	3.45	3.93	4.06	4.09	4.08	3.79	3.60
Grain yield plant ⁻¹ (g)	10.00	9.94	11.52	9.50	12.82	11.64	14.24	14.67	15.15	12.14
Biological yield plant ⁻¹ (g)	20.86	29.28	23.85	27.11	27.79	27.16	29.34	29.44	31.14	25.74
Harvest index (%)	48.35	34.08	48.67	35.05	46.89	43.23	49.07	49.82	49.05	47.39

index (49.07%). In F_5 generation, cluster IV had highest mean values for number of tillers plant⁻¹ (6.16), ear length (12.23 cm), number of spikelets ear⁻¹ (21.94), grain yield plant⁻¹ (14.67 g) and harvest index (49.82%), whereas highest mean values for ear weight (3.51 g) and number of grains ear⁻¹ (70.09) were observed in cluster V. Therefore, in both the generation progenies, cluster IV and V having better means for most of the characters, will be better for deploying selection of progenies with desirable characters (Rajshree and Singh, 2018; Santosh *et al.*, 2019).

Per cent contribution towards total divergence

The contribution of characters towards total divergence (Fig.1) shows out of 11 characters studied, number of grains ear⁻¹ (28.98%), grain weight ear⁻¹ (23.90%), number of tillers plant⁻¹ (12.13%) and number of spikelets ear⁻¹ (11.11%) contributed maximum in F_4 generation. In F_5 generation, contribution of number of spikelets ear⁻¹ (36.34%) was maximum, followed by ear weight (14.93%), grain weight ear⁻¹ (14.56%) and number of grains ear⁻¹ (13.25%). Therefore, these traits may be used as selection parameters during hybridization and improvement of grain yield and its component traits (Kolakar *et al.*, 2014; Arya *et al.*, 2017).

Cross-II (RAJ 3765 $\times$ WH 711)

The results revealed that in F_4 generation, cluster I with 48 progenies and WH 711 parent, was the largest, whereas, cluster VI containing 3 progenies was found to be the smallest (Table 3). In F_5 generation, cluster II was largest consisting of 41 progenies, whereas, cluster V being the smallest with 17 progenies.

Earlier also, a random pattern of distribution of bread wheat genotypes in different clusters was observed (Kalimullah *et al.*, 2012; Degewione and Alamerew, 2013; Dutamo *et al.*, 2015).

Intra and inter cluster distances

The intra and inter cluster distance values among F_4 generation progenies (Table 4) showed that cluster V had the minimum intra cluster value (10.98), indicating that presence of closely related progenies in this cluster. The maximum intra cluster D^2 value was observed for cluster II (16.07). Cluster V and VI showed minimum inter cluster distance (14.25), whereas, cluster I and VI showed maximum (26.53). In F_5 generation, the maximum and the minimum average intra cluster D^2 values were shown by cluster IV (15.70) and cluster I (9.60). Cluster I and II showed minimum inter cluster distance indicating close relationship among the progenies included in these clusters. Cluster III and IV showed maximum inter cluster distance of 25.16. This finding was consistent with the past studies in wheat by Singh *et al.*, 2018 and Santosh *et al.*, 2019. Rahim *et al.* (2010) showed that the hybrids developed from the selected genotypes within the limit of compatibility may produce desirable transgressive segregants for varietal improvement.

Cluster means of different clusters for various characters

In F_4 generation (Table 6), cluster IV had a characteristic feature of dwarf plant type (80.50 cm) and highest mean value for number of grains ear⁻¹ (68.92) and number of spikelets ear⁻¹ (21.76). Cluster III had highest mean cluster

Table 6. Cluster mean values of different clusters for various characters in F_4 and F_5 generation progenies of cross-II (RAJ 3765 $\times$ WH 711)

Characters	Cluster-I		Cluster-II		Cluster-III		Cluster-IV		Cluster-V		VI
	F_4	F_5	F_4	F_5	F_4	F_5	F_4	F_5	F_4	F_5	F_4
Plant height (cm)	84.23	86.43	87.98	80.59	88.22	89.52	80.50	83.38	88.28	86.12	89.76
Number of tillers plant ⁻¹	8.10	7.49	6.25	8.16	7.52	7.42	6.49	6.36	6.14	5.76	4.30
Ear length (cm)	11.70	12.10	11.58	12.35	12.36	12.59	12.26	11.48	11.56	11.65	10.93
Ear weight (g)	3.06	3.25	3.05	3.30	3.49	3.57	3.37	3.15	3.28	3.33	3.42
Number of grains ear ⁻¹	55.62	60.92	56.15	59.33	65.94	69.15	68.92	59.12	65.23	61.99	66.00
Grain weight ear ⁻¹ (g)	2.29	2.54	2.21	2.62	2.87	3.14	2.95	2.46	2.47	2.62	2.89
Number of spikelets ear ⁻¹	20.30	21.31	20.70	21.28	21.69	22.27	21.76	20.75	20.85	21.31	20.22
100-grain weight (g)	4.12	4.19	4.20	4.38	4.24	4.13	3.84	4.10	3.82	4.14	4.13
Grain yield plant ⁻¹ (g)	14.08	13.60	10.49	15.68	15.06	15.76	13.76	10.54	10.50	10.82	6.79
Biological yield plant ⁻¹ (g)	29.76	27.54	28.82	31.15	29.88	31.58	29.97	31.37	31.00	32.89	22.49
Harvest index (%)	47.74	49.69	36.27	50.55	50.65	50.01	45.76	33.76	34.27	33.08	30.70

values for ear weight (3.49 g), grain yield plant⁻¹ (15.06 g) and harvest index (50.65%). In F_5 generation, cluster II exhibited lowest mean value for plant height (80.59 cm) with highest number of tillers plant⁻¹ (8.16) and harvest index (50.55%). Cluster III had highest mean value for number of grains ear⁻¹ (69.15), grain weight ear⁻¹ (3.14 g), number of spikelets ear⁻¹ (22.27) and grain yield plant⁻¹ (15.76 g). Therefore, cluster IV and III in F_4 generation while cluster II and III in F_5 generation having better cluster means for most of the characters might be considered better for selecting progenies (Naik *et al.*, 2016; Arya *et al.*, 2017).

Per cent contribution towards total divergence

The analysis of the contribution of each character towards genetic divergence (Fig. 1) indicated that in F_4 generation, number of tillers plant⁻¹ (33.32%) contributed maximum, followed by number of spikelets ear⁻¹ (28.00%) and grain weight ear⁻¹ (13.76%). In F_5 generation, grain yield plant⁻¹ (45.94%) was found to be the most important character, contributing maximum followed by number of spikelets ear⁻¹ (20.45%) and number of tillers plant⁻¹ (12.97%).

These traits contributed more than 60% towards total divergence cumulatively and hence should be given importance during

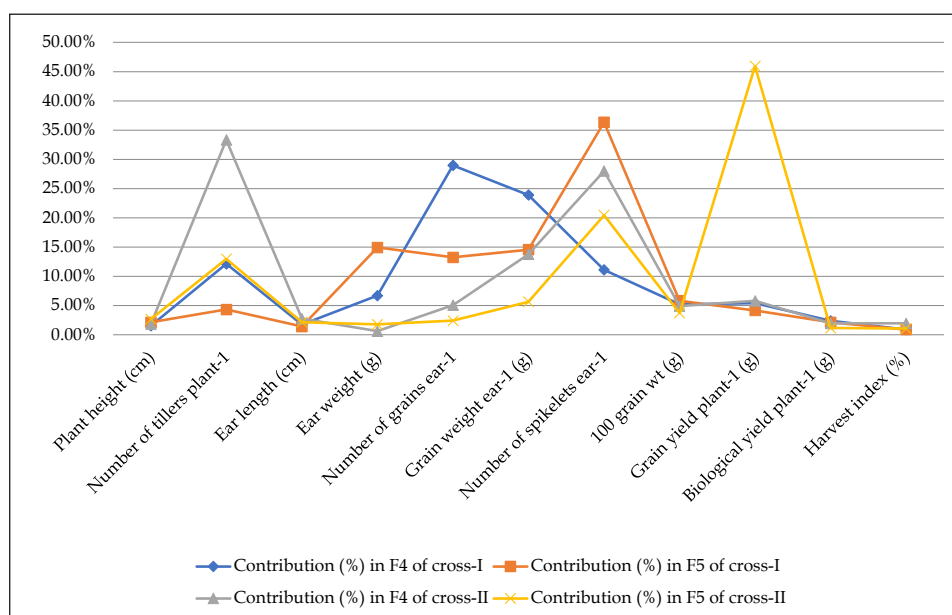


Fig.1. Per cent contribution towards variability of each character in F_4 and F_5 generation progenies of cross-I (WH 1105 $\times$ WH 711) and cross-II (RAJ 3765 $\times$ WH 711).

hybridization and selection in the segregating population for improvement of grain yield plant⁻¹ and its component traits (Singh *et al.*, 2018; Santosh *et al.*, 2019).

A total of 23 diverse and promising progenies derived from cross WH 1105 × WH 711 and 35 progenies derived from cross Raj 3765 × WH 711 were found significantly superior over parents for different traits. These progenies selected on the basis of D² values and superior cluster mean values of characters for which they attributed superior performance, may be used as parents in future breeding programs to further expand genetic variability among populations and to effect selection of elite inbreds for hybridization program. Therefore, in view of the sufficient genetic diversity found in the present endeavor, there is a conceivable scope for genetic improvement through hybridization between the progenies from divergent clusters.

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