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Research Article

Identification of superior transgressive segregants in F_2 and F_3 populations of wheat (*Triticum aestivum* L.) for yield and its contributing traits

Ayaz Ahamad*, **Sheo Pratap singh, Lal Chandra Prasad, Ravindra Prasad and Padma Thakur**

Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi – 221005, Uttar Pradesh, India
***E-Mail:** ayazahamad2013@gmail.com

Abstract
An experiment was carried out in timely sown condition during *Rabi,* 2018-20 to study the genetic variability, correlation, heritability and expected genetic advance for 13 traits in F_2 and F_3 populations of two wheat crosses and consequently identify superior transgressive segregants. The experimental material consisted of an F_2 population of two crosses K 0307 × LOK 1 (cross 1) and HD 2733 × HUW 234 (cross 2) evaluated in an unreplicated trial and seeds of each identified transgressive segregants in F_2 generation was forwarded to F_3 generation for its evaluation and further sorting the superior segregants to be carry forwarded. The identified transgressive segregants exhibited a wide range of variation for all the traits except for spike length, indicating the presence of enough genetic variability in the material under study. The phenotypic coefficients of variation (PCV) values were higher than genotypic coefficients of variation (GCV) values for most of the traits studied. Estimates of genetic parameters, PCV and GCV in K 0307 × LOK 1 was highest for spikelets per spike and lowest for days to 50% flowering and days to maturity in both F_2 and F_3. While, highest for yield per plant and lowest for days to 50% flowering and days to maturity in HD 2733 × HUW 234. High heritability coupled with high genetic advance was recorded for spikelets per spike, test weight in a cross 1, in both F_2 and F_3. Similarly in cross 2, high heritability coupled with high genetic advance was recorded for grain filling days and yield per plant. Correlation analysis suggested that yield had a positive and significant relationship with test weight, grain per spike, and spikelets per spike for the F_3 families of transgressive segregants of the cross 1. In cross 2, test weight, grain per spike, number of effective tillers, spikelets per spike, peduncle length, days to 50% flowering, and plant height had a positive and significant relationship with yield.

Keywords: PCV, GCV, Heritability, Genetic advance, Transgressive segregants.

INTRODUCTION

Common Bread wheat (*Triticum aestivum* L.) is a major cereal crop grown around the world. Wheat production was 765.4 million tonnes, with an average yield of 3.48 t/ha, and it is accounting for approximately 30% of worldwide cereal production (FAO 2021). Global wheat production is expected to reach a new record of 780 million tonnes in 2021, according to a preliminary forecast issued March 4, 2021 by the Food and Agriculture Organization of the United Nations. In india the production of Wheat during 2020-21 is estimated at record 108.75 million tonnes. It is higher by 8.32 million tonnes than the average wheat production of 100.42 million tonnes (Ministry of Agriculture & Farmers Welfare, Govt. of India). It is grown in a broad range of climates, edaphic and biotic stress conditions across the world, and its extensive adaptability aids in producing sufficient grain yields in a variety of circumstances. Yield is a complex quantitative trait controlled by many genes with minor effects and due to its polygenic nature and genotype × environment interaction it is one of the most difficult traits to study. It is very important to understand the genetic variability and heritability of essential agronomic characteristics to enhance yield (Baker *et al*., 1971).

The collection of progenies resulting from a variety of crosses is expected to have a huge amount of variability, which will aid in the isolation of highly adaptable and superior yielding genotypes in later generations. The present cross is made with the intention to identify the transgressive segregants in terms of yield and yield contributing traits.

MATERIALS AND METHODS

The present investigation was carried for two generations for F2 and F3 in *Rabi* seasons during 2018-19 and 2019-20, respectively in timely sown condition at the Agricultural Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (U.P.), India. The experimental material consisted of an F_2 population of two crosses derived from K 0307 × LOK 1 and HD 2733 × HUW 234 crosses. The parents were selected for their high yield capacity and tolerance to terminal heat stress. In the F_2 generation, a total of eighteen transgressive segregants were identified based on yield performance, nine in each cross 1 and cross 2, respectively. The F_2 population was grown in an unreplicated plot to select the superior transgressive segregants and in F_3 generation, each identified transgressive segregants grown in randomized block design with three replications. Data were recorded on various parameters *viz.,* SPAD chlorophyll meter reading (SCMR), days to 50% flowering, days to maturity, grain filling days, number of effective tillers, awn length , spike length, peduncle length, plant height, spikelets per spike, grain per spike, test weight and yield per plant. Observed data were subjected to the statistical analysis. Analysis of variance (ANOVA) was done to determine the significant differences between the characters as suggested by Panse and Sukhatme (1967). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), Correlation, heritability in broad sense ($h^2_{(b)}$), genetic advance (GA) were estimated according to Burton (1952), Johnson *et al.* (1955) and Lush (1949) respectively.

RESULTS AND DISCUSSION

Analysis of variance for characters studied in two crosses of wheat for F_3 families of transgressive segregants is presented in **Tables 1 and 2.** The result of the analysis of variance showed a significant difference for all the traits except for the spike length as reported by Al-Bakry *et al.* (2011), Naik *et al.* (2015), Khairnar *et al.* (2018) and Rani *et al.* (2018) in both crosses. The findings suggested that the materials selected for the genetic studies are of diverse origin and can be used to improve genotypes through a well-designed breeding programme. The identified superior transgressive segregants can directly be selected for advancement in next generation for further identifying superior types showing high yields in advanced

Table 1. Analysis of variance for yield and yield related parameters in F_3 generation of the cross K 0307 × LOK 1 in wheat

Source	D.F	SCMR	DOF	DOM	GFD	NOT	AL	SPL	PEDL	PH	S/S	G/S	TW	Y/P
Replication	2	0.33	1.00	6.26	6.33	0.26	0.69	2.59	5.38*	4.93	2.81	17.81	31.41	29.76
Genenotypes	8	18.56*	36.33**	97.45**	37.17**	5.98**	0.85*	3.13	4.04**	107.77**	58.18**	51.90**	132.42**	82.88**
Error	16	6.49	2.25	4.13	5.17	1.13	0.30	1.70	0.98	9.57	7.06	13.27	23.12	15.13

Significant at 5 % level; ** Significant at 1% level

Table 2. Analysis of variance for yield and yield related parameters in F_3 generation of the cross HD 2733 × HUW 234 in wheat

Source	D.F	SCMR	DOF	DOM	GFD	NOT	AL	SPL	PEDL	PH	S/S	G/S	TW	Y/P
Replication	2	3.32	7.44*	7.15	0.15	4.59	0.30	0.72	2.36	5.14	1.33	8.04	11.88	3.26
Genenotypes	8	6.17**	41.00**	30.20**	58.70**	4.62*	0.89*	3.38	27.78**	422.20**	9.50**	45.43**	66.54**	84.53**
Error	16	1.19	1.82	2.73	4.06	1.68	0.34	2.19	3.74	5.36	1.46	4.79	11.01	5.79

Significant at 5 % level; ** Significant at 1% level

SCMR: SPAD chlorophyll meter reading; DOF: Days to 50% flowering; DOM: Days to maturity; GFD: Grain filling days; NOT: Number of effective tillers; AL: Awn length; SPL: Spike length; PEDL: Peduncle length; PH: Plant height; S/S: Spikelets per spike; G/S: Grain per spike; TW: Test weight; Y/P: Yield per plant generation thereby, saving resources by reducing the bulkiness of the population size to be carry forwaded for development of new cultivars by biparental cross. This will assist in early generation selection of lines having desirable genes as per the objective of the breeder and the breeding programme. The estimates of mean, range, phenotypic coefficient of variation, genotypic coefficient of variation, heritability and expected genetic advance for 13 traits of two crosses in F_2 and F_3 are presented in **Tables 3 and 4**.

Table 3. Genetic parameters for different traits of both F_2 and F_3 generations of the cross K 0307 × LOK 1 in wheat

Characters	Mean		PCV(%)		GCV(%)		$h^2_{(b)}$ (%)		GA		GAM	
	F_2	F_3	F_2	F_3	F_2	F_3	F_2	F_3	F_2	F_3	F_2	F_3
SCMR	47.99	46.29	7.99	10.33	5.16	8.75	41.78	71.64	3.30	7.06	6.68	15.25
DOF	91.2	88.78	4.94	4.16	3.86	3.79	61.18	83.47	5.68	6.33	6.23	7.13
DOM	117	117.37	4.43	5.05	3.29	4.75	55.26	88.27	5.91	10.78	5.05	9.19
GFD	25.8	28.56	12.13	13.93	9.29	11.43	58.60	67.37	3.77	5.51	14.64	19.29
NOT	8.62	13.59	30.30	12.18	18.85	9.33	38.69	58.67	2.08	1.99	24.15	14.57
AL	3.46	3.65	29.79	18.98	19.12	11.62	41.19	38.33	0.87	0.54	25.258	14.93
SPL	8.82	9.25	23.38	15.96	16.26	7.48	48.37	21.92	2.05	0.66	23.30	7.17
PEDL	14.69	14.85	21.84	9.49	13.34	6.80	37.33	50.98	2.48	1.48	16.79	9.97
PH	88.91	87.27	9.53	7.44	6.84	6.55	51.47	77.37	8.99	10.36	10.11	11.87
S/S	18.92	19.19	23.47	25.53	20.49	21.51	76.20	70.69	6.97	7.14	36.85	37.19
G/S	50.19	49.26	13.53	10.37	10.57	7.28	61.11	49.24	8.54	5.18	17.03	10.52
TW	37.71	36.37	20.83	21.19	18.90	16.59	82.32	61.18	13.32	9.72	35.33	26.72
Y/P	17.35	24.81	27.18	24.74	14.77	19.15	29.54	59.88	2.87	7.57	16.54	30.53

SCMR: SPAD chlorophyll meter reading; DOF: Days to 50% flowering; DOM: Days to maturity; GFD: Grain filling days; NOT: Number of effective tillers; AL: Awn length; SPL: Spike length; PEDL: Peduncle length; PH: Plant height; S/S: Spikelets per spike; G/S: Grain per spike; TW: Test weight; Y/P: Yield per plant

Table 4. Genetic parameters for different traits of both F_2 and F_3 generations of the cross HD 2733 × HUW234 in wheat

Chracters	Mean		PCV(%)		GCV(%)		$h^2_{(b)}$ (%)		GA		GAM	
	F_2	F_3	F_2	F_3	F_2	F_3	F_2	F_3	F_2	F_3	F_2	F_3
SCMR	49.13	47.32	12.35	3.55	8.28	2.72	44.99	58.30	5.62	2.02	11.44	4.26
DOF	88.67	87.67	4.13	4.39	2.57	4.11	38.71	87.77	2.92	6.96	3.29	7.94
DOM	102.92	102.70	3.90	3.35	3.39	2.94	75.79	77.02	6.27	5.46	6.09	5.31
GFD	14.25	15.04	2.26	31.39	39.83	28.37	39.83	81.75	11.30	7.95	79.31	52.86
NOT	8.31	11.04	6.5	14.77	20.40	8.96	30.65	36.93	1.93	1.24	23.26	11.24
AL	2.79	3.81	25.74	18.91	6.59	11.13	6.55	34.96	0.09	0.52	3.47	13.62
SPL	8.82	6.63	20.29	24.13	10.62	9.53	10.62	15.40	0.89	0.51	11.45	7.65
PEDL	13.01	12.44	29.15	27.48	20.20	22.70	48.01	68.16	3.75	4.80	28.84	38.59
PH	89.58	86.96	10.98	13.81	9.32	13.55	72.03	96.28	14.59	23.82	16.29	27.39
S/S	20.87	18.33	17.83	11.07	12.27	8.93	47.41	64.77	3.63	2.71	17.41	14.77
G/S	50.19	45.81	13.24	9.34	10.85	8.03	67.24	73.89	9.59	6.51	18.34	14.22
TW	35.33	38.38	16.68	14.15	9.86	11.2	34.92	62.71	4.86	7.01	12	18.28
Y/P	16.54	19.55	36.67	28.95	28.71	26.20	61.30	81.93	12.18	9.55	46.31	48.87

SCMR: SPAD chlorophyll meter reading; DOF: Days to 50% flowering; DOM: Days to maturity; GFD: Grain filling days; NOT: Number of effective tillers; AL: Awn length; SPL: Spike length; PEDL: Peduncle length; PH: Plant height; S/S: Spikelets per spike; G/S: Grain per spike; TW: Test weight; Y/P: Yield per plant

Estimates of genetic parameters, PCV in cross 1, for both F_2 and F_3 were highest for spikelets per spike, test weight, yield per plant and moderate for grain filling days, grain per spike and lowest for days to 50% flowering, days to maturity, while GCV for both F_2 and F_3 were highest for spikelets per spike and moderate for grain filling days, test weight, yield per plant and lowest for SCMR, days to 50% flowering, days to maturity, plant height.

Similarly, PCV in cross 2, for both F_2 and F_3 were highest for spike length, yield per plant moderate for plant height, spikelets per spike, test weight and lowest for days to 50% flowering, days to maturity while GCV for both F_2 and F_3 were highest for grain filling days, peduncle length, yield per plant and lowest for the SCMR, days to 50% flowering and days to maturity. Similar findings were also reported by Kotal *et al.* (2010) and Ullah *et al.* (2011). For most of the traits, PCV values were greater than GCV values, indicating that the environment had an impact on trait expression as similarly reported by Thakur *et al.* (2020). Both heritability and genetic advance are important selection criteria for crop improvement. Selection based on heritability is not as good as selection based on heritability coupled with genetic advance, because it is not necessary that characters showing high heritability also have high genetic advance. As a result, the breeder must be more cautious when performing selection based on heritability because it can imply both additive and non-additive gene action. Therefore, selection based on heritability coupled with genetic advance would be more reliable and useful in designing suitable selection procedures.

In the present investigation, high heritability coupled with high genetic advance was reported for spikelets per spike, test weight, and moderate heritability coupled with high genetic advance reported for the number of effective tillers, awn length in cross 1, for both F_2 and F_3 generations. Similarly, high heritability coupled with high genetic advance was reported for grain filling days, yield per plant, and moderate heritability coupled with the high genetic advance number of effective tillers in cross 2, for both F_2 and F_3 generations. Similar results were also reported by Abinasa *et al.* (2011), Fellahi *et al.* (2013) and Kumar *et al.* (2013), Because all these characters are important yield contributing traits, direct selection for them would be beneficial for yield improvement.

Correlation coefficients of F_3 families of transgressive segregants for both the crosses are presented in **Tables 5 and 6**. The result showed that F_3 families of transgressive segregants of the cross 1, yield exhibited positive and significant association with test weight, grain per spike, spikelets per spike and spike length with peduncle length, spikelets per spike with grain per spike and test weight (0.490). Similarly, F_3 families of transgressive segregants of the cross 2, yield exhibited positive and significant association with test weight, grain per spike, number of effective tillers, spikelets per spike, peduncle length, days to 50% flowering, plant height and spikelets per spike with grain per spike, test weight, grain per spike with test weight. These conclusions were supported by Ashfaq *et al.* (2014).

Table 5. Correlation coefficients in F_3 generation of K 0307 × LOK 1 among 13 characters of wheat

	SCMR	DF	DM	GFD	NOT	AWNLTH	SPL	PEDLGH	PH	S/S	G/S	TW	Y/P
SCMR	1.000	0.200	0.138	0.021	-0.422*	0.009	0.119	0.144	-0.005	0.409*	-0.053	0.547**	0.257
DF		1.000	0.748**	0.191	-0.483*	0.163	-0.220	-0.449*	0.387*	0.076	0.040	0.375	0.182
DM			1.000	0.794**	-0.401*	0.084	-0.299	-0.251	0.040	0.095	-0.094	0.355	0.154
GFD				1.000	-0.152	-0.024	-0.241	0.040	-0.294	0.071	-0.175	0.182	0.062
NOT					1.000	0.127	0.022	0.039	-0.378	-0.421*	-0.201	-0.656**	-0.247
AWNLTH						1.000	-0.456*	-0.237	0.176	0.037	-0.099	-0.129	-0.126
SPL							1.000	0.410*	-0.084	0.195	.231	0.147	0.259
PEDLGH								1.000	-0.278	0.221	0.290	0.133	0.290
PH									1.000	0.133	0.013	-0.005	-0.189
S/S										1.000	0.549**	0.490**	0.509**
G/S											1.000	0.300	0.692**
TW												1.000	0.791**
Y/P													1.000

Significant at 5 % level, ** Significant at 1% level

SCMR: SPAD chlorophyll meter reading; DF: Days to 50% flowering; DM: Days to maturity; GFD: Grain filling days; NOT: Number of effective tillers; AWNLTH: Awn length; SPL: Spike length; PEDLGH: Peduncle length; PLH: Plant height; S/S: Spikelets per spike; G/S: Grain per spike; TW: Test weight; Y/P: Yield per plant

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Table 6. Correlation coefficients in F_3 generation of HD 2733 × HUW 234 among 13 characters of wheat

	SCMR	DF	DM	GFD	NOT	AWNLTH	SPL	PEDLGH	PH	S/S	G/S	TW	Y/P
SCMR	1.000	0.232	-0.356	-0.460*	-0.045	0.346	0.036	0.041	-0.157	0.257	-0.045	-0.165	-0.096
DF		1.000	0.205	-0.681**	0.439*	-0.108	0.172	0.685**	0.377	0.046	0.319	0.064	0.434*
DM			1.000	0.578**	0.083	-0.154	-0.090	0.379	0.315	-0.265	0.101	-0.076	0.041
GFD				1.000	-0.304	-0.025	-0.211	-0.287	-0.079	-0.237	-0.190	-0.110	-0.331
NOT					1.000	-0.204	-0.299	0.465*	-0.040	0.216	-0.120	-0.035	0.582**
AWNLTH						1.000	0.181	-0.094	-0.575**	0.129	-0.195	-0.219	-0.265
SPL							1.000	0.100	0.211	0.253	0.519**	0.425*	0.189
PEDLGH								1.000	0.401*	0.067	0.382*	0.208	0.540**
PH									1.000	0.125	0.692**	0.413*	0.398*
S/S										1.000	0.397*	0.479*	0.558**
G/S											1.000	0.747**	0.663**
TW												1.000	0.746**
Y/P													1.000

Significant at 5 % level, ** Significant at 1% level

SCMR: SPAD chlorophyll meter reading; DF: Days to 50% flowering; DM: Days to maturity; GFD: Grain filling days; NOT: Number of effective tillers; AWNLTH: Awn length; SPL: Spike length; PEDLGH: Peduncle length; PLH: Plant height; S/S: Spikelets per spike; G/S: Grain per spike; TW: Test weight; Y/P: Yield per plant

The purpose of the study was to identify superior transgressive segregants stacked with desirable genes in early generation so that it can be advanced to further generations and develop a cultivar having the genes as per the objective of the breeder and the programme significantly reducing the bulkiness of the population size which would save resources in all aspect. The identified lines can be additionally screened with molecular markers for trimming the identified population size and it will allow the breeder to focus only on the lines of interest for gene fixation by selfing upto F_7 or F_8 generation.

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