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Identification and isolation of transgressive segregants in F_3 generation of blackgram [*Vigna mungo* (L.) Hepper]

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Abstract

An investigation on blackgram (*Vigna mungo* (L.) Hepper) was conducted to elicit the information on superior transgressive segregants generated in respect of seed yield and its components in F_3 generation of blackgram. The F_3 populations were raised in Compact Family Block Design during *Kharif* 2016. High frequency of transgressive segregation (100%) was shown by the different progenies of crosses namely DU-1 x Palampur-93, HPBU-124 x HPBU-111, TU-17-4 x Palampur-93, DU-1 x Him Mash-1, IPU-02-33 x Palampur-93, KU-223 x HPBU-111, KU-553 x Palampur-93, HPBU-126 x HPBU-111, KU-553 x HPBU-111 and HPBU-126 x Palampur-93 for all of the studied traits. The results suggested the existence of large count of transgressive segregants in early segregating generations for almost all the traits which provides a wide scope for the meticulous selection of these genotypes and to bring in the beneficial alleles for blackgram breeding program in later generations for developing the desirable plant type.

Key words: Blackgram, *Vigna mungo*, transgressive segregants and quantitative.

Blackgram is an important short duration and self pollinated *kharif* legume crop belonging to family Fabaceae and originated from *Vigna mungo* var. *silvestris*. India is the primary centre of origin of blackgram with its secondary centre of origin in Central Asia. It is an important pulse crop and cultivated over a wide range of agro-climatic zones of the country. In India, this crop accounts 3.25 million ha area with production of 1.5 million tonnes and 400 kg per ha productivity (Anonymous 2016). It is a vital source of protein (25-28%), micro nutrients (P and Fe), vitamins (niacin, thiamine and riboflavin), amino acids (lysine), carbohydrates (62-65%) and fibre (3.5-4.5%) (Kaul 1982). The yield potential of this crop is low due to narrow genetic base and lack of genetic variability, poor ideotype, lack of high yielding cultivars, planting in marginal lands, susceptibility to biotic and abiotic stresses. Lack of genetic variability, which is the basic requirement for an effective crop improvement programme and suitable cultivars are the major problems and should be resolved by implying selection of superior genotypes for characters of economic importance. Earlier studies on variability has been reported by some other workers *viz.,* Sirisha (2005) on F_3 and F_4 generations of five crosses in groundnut, Kurer (2007) in F_2 and F_3 generations of cowpea, Rana (2013) in F_3 segregating population of urdbean and Gandi *et al.* (2018) in F_2 and F_3 generations of urdbean.

Thus, goal can be achieved by transgressive segregation as it is a useful approach for yield and its contributing characters. Transgressive segregants are observed within the progenies of early segregating generations (Jambormias *et al.*, 2015). The performances of transgressive segregants fall outside the range of their parents, due to the accumulation of favourable genes from both the parents as a consequence of recombination. Complemetary gene action is considered as a primary cause for transgression of quantitative characters, although overdominance and epistasis also contribute in transgression (Rieseberg *et al.* 1999). The objective of present study is to evaluate plants in F_3 generation of blackgram for identification of transgressive segregants.

Materials and Methods

The experimental material for present investigation consisted of F_3 progenies of 12 cross combinations *viz.,* COBG-653 x Palampur-93, DU-1 x Him Mash-1, KU-553 x HPBU-111, COBG-653 x HPBU-111, KU-553 x Palampur-93, DU-1 x Palampur-93, IPU-02-33 x Palampur-93, KU-223 x HPBU-111, HPBU-126 x

HPBU-111, HPBU-124 x HPBU-111, KU-540 x Palampur-93, TU-17-4 x Palampur-93, HPBU-126 x Palampur-93 along with three check varieties i.e. Palampur-93, HPBU-111 and Him Mash-1. The experiment was laid out in Compact Family Block Design with three replications and genetic material was investigated during *kharif* 2016 at Experimental farm of Crop Improvement, CSK HPKV, Palampur. The genotypes were firstly randomized in main plots and then progenies randomized in sub-plots. Three progenies of each genotype were planted in three replications. Each progeny was grown in two rows with 1.5 m length. The row to row distance was 30 cm with plant to plant distance of 10 cm apart. All recommended practices were followed to raise good crop of blackgram. Ten plants were randomly selected from each progeny of 12 cross combinations in each replication and data were recorded for plant height, branches per plant, pods per plant, seeds per pod, biological yield, harvest index, and seed yield per plant. Percentage of transgressive segregation in F_3 generation was obtained progeny wise by defining extreme plants that exceeded corresponding progeny mean and best check mean. Comparisons were made on the foundation value of individual plant and evaluated in positive direction only.

Percentage of transgressive segregation in particular cross = (Number of plants exceeding progeny mean or mean value of check variety Total number of plants in cross) × 100

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Results and Discussion

The mean values of check varieties and progenies of each cross are presented in Table 1 and Table 2 respectively, providing the platform for comparisons between the progenies and identification of transgressive segregants. The percentage of transgressive segregants in F_3 generation is shown in Table 3 and Table 4. The results revealed that progeny-1 of DU-1 x Palampur-93 had high frequency of superior transgressive segregants (60%) over mean value of that particular progeny, while progeny-3 of DU-1 x Palampur-93, progeny-3 of HPBU-124 x HPBU-111, progeny-1 and progeny-2 of TU-17-4 x Palampur-93 and progeny-3 of HPBU-126 x Palampur-93 had high frequency of transgressive segregants (100%) over best check Him Mash-1 (39.47 cm) for plant height. This indicated the accumulation of genes from both the parents lead to increased plant height. In case of branches per plant, progeny-3 of KU-553 x HPBU-111, progeny-1 of KU-553 x Palampur-93 and progeny-2 of KU-223 x HPBU-111 exhibited high frequency of transgressive segregants i.e. 76.67% when scored over the mean value of corresponding progeny and progeny-1 of HPBU-126 x Palampur-93 had highest frequency of segregants (93.33%) over the best check HPBU-111 (2.53). This indicated the involvement of additive and additive x additive epistatic effects along with dominance effects. Similar results were reported by Aditya *et al.* (2013) in soybean crosses.

The highest frequency of transgressive segregants was observed in progeny-1 of HPBU-124 x HPBU-111 (56.67%) when compared to the mean value of corresponding progeny for pods per plant and progeny-6 of HPBU-124 x HPBU-111 had high frequency of transgressive segregants (80%) over best check Palampur-93 (17.73). This indicated the accumulation of favorable genes from the parents resulting in large amount of genetic variability and very high frequency of transgressive segregation (Reddy *et al*., 1989). Similarly, seeds per pod had highest frequency of transgressive segregants (80%) in progeny-3 of DU-1 x Him Mash-1. Progeny-2 of HPBU-126 x Palampur-93 exhibited high frequency of transgressive segregants (73.33%) over the best check Palampur-93 (5.11).

Progeny-3 of KU-223 x HPBU-111 showed high frequency of transgressive segregants (76.67%) for biological yield when compared to mean value of corresponding progeny. Three progenies *viz.,* progeny-1, progeny-2 and progeny-3 of HPBU-126 x Palampur-93 were having maximum transgressive segregants (100%) over the best check HPBU-111 (12.47 g). This may be due to the involvement of additive gene, which is fixed.

The highest frequency of transgressive segregants (90%) was observed in progeny-3 of DU-1 x Palampur-93 over mean value of progeny (14.07%) for harvest index. Likewise, progeny-2 of HPBU-124 x HPBU-111 showed maximum transgressive segregants (100%) over the best check Palampur-93 (17.97%).

Maximum transgressive segregants (100%) were observed in progeny-2 and progeny-3 of DU-1 x

Palampur-93 over the mean value of corresponding progeny for seed yield per plant. The high frequency of transgressive segregants (100%) were exhibited by progeny-1, progeny-2 and progeny-3 of HPBU-126 x HPBU-111, progeny-3 of HPBU-124 x HPBU-111 and progeny-2 and progeny-3 of HPBU-126 x Palampur-93 when compared to the best check Him Mash-1 (2.16 g). This may be due to the recombination of genes from both the parents with positive effects, indicating that the parents involved in developing F_3 families derived were differed for many genes which causes large amount of genetic variability for yield and its contributing traits (Shivakumar *et al.*, 2013).

The promising lines were obtained on the basis of maximum transgressive segregants exceeded over corresponding progeny mean of family and best check mean in F_3 generation of blackgram for yield and yield contributing traits. Out of 36 progenies, 28 progenies were superior for most of the economic traits and these can be used in further breeding program for blackgram improvement.

Table 1. Estimates of mean values of check varieties

Sr. No.	Checks	Plant height (cm)	Branches per plant	Pods per plant	Seeds per pod	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
1.	Palampur-93	39.20	2.33	17.73	5.11	10.77	17.97	1.93
2.	Him Mash-1	39.47	2.53	12.40	4.65	12.47	17.30	2.16
3.	HPBU-111	38.07	2.53	11.53	4.73	10.90	13.21	1.44

Table 2. Estimates of mean values of F_3 progenies

Sr. No.	Crosses	Progenies	Plant height (cm)	Branches per plant	Pods per plant	Seeds per pod	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
			Mean	Mean	Mean	Mean	Mean	Mean	Mean
1	COBG-653 x Palampur-93	Progeny 1	56.90	2.43	18.10	5.04	11.63	21.21	2.45
		Progeny 2	42.40	2.07	15.80	4.74	10.83	17.46	1.90
		Progeny 3	51.28	1.90	17.07	4.89	10.83	22.04	2.37
2	DU-1 x Him Mash-1	Progeny 1	49.67	2.07	17.57	5.01	12.33	18.13	2.24
		Progeny 2	48.95	2.30	18.03	4.40	18.00	21.25	3.76
		Progeny 3	47.18	1.87	16.73	4.62	16.60	14.11	2.35
3	KU-553 x HPBU-111	Progeny 1	53.67	2.53	19.00	4.91	11.53	24.79	3.01
		Progeny 2	58.40	3.07	15.23	5.20	12.37	19.68	2.41
		Progeny 3	52.50	1.80	18.67	4.93	14.40	19.18	2.81
4	KU-553 x Palampur-93	Progeny 1	40.23	2.73	22.40	5.00	9.87	20.59	2.03
		Progeny 2	41.70	3.23	22.40	4.86	14.00	15.81	2.18
		Progeny 3	39.30	3.67	19.77	5.30	11.87	23.42	2.75
5	DU-1 x Palampur-93	Progeny 1	71.27	3.47	21.03	4.95	13.73	15.25	2.10
		Progeny 2	58.30	3.57	16.17	4.97	11.77	14.44	1.68
		Progeny 3	75.10	2.87	14.57	5.06	12.03	14.07	1.64
6	IPU-02-33 x Palampur-93	Progeny 1	41.67	2.13	17.13	4.88	16.37	18.59	3.02
		Progeny 2	43.97	2.73	20.70	4.47	17.97	16.12	2.89
		Progeny 3	50.29	3.37	16.03	4.78	14.25	16.30	2.28
7	KU-223 x HPBU-111	Progeny 1	43.73	2.83	18.53	4.74	14.80	11.27	1.54
		Progeny 2	39.37	2.93	16.67	5.04	14.43	14.31	1.74
		Progeny 3	36.57	2.83	19.30	4.51	9.40	16.04	1.31
8	HPBU-126 x HPBU-111	Progeny 1	51.67	3.20	21.43	5.03	16.33	25.30	3.81
		Progeny 2	43.07	2.47	24.33	5.02	18.60	24.32	4.46
		Progeny 3	53.07	2.87	19.00	4.81	15.17	22.30	3.17

9	HPBU-124 x HPBU-111	Progeny 1	50.93	1.87	22.67	5.02	19.33	32.62	5.21
		Progeny 2	64.93	2.13	19.23	5.29	15.27	40.67	3.71
		Progeny 3	56.83	2.60	22.20	5.06	11.43	46.91	4.80
10	KU-540 x Palampur-93	Progeny 1	47.83	2.47	16.53	4.85	13.03	14.88	1.87
		Progeny 2	51.40	2.73	17.50	5.22	12.77	15.56	1.89
		Progeny 3	53.67	3.00	15.30	4.88	13.33	14.05	1.85
11	TU-17-4 x Palampur-93	Progeny 1	79.83	2.93	17.87	5.14	18.63	11.56	2.15
		Progeny 2	54.07	2.57	16.77	5.27	20.95	12.53	2.63
		Progeny 3	57.71	3.29	21.00	4.81	19.48	13.71	2.67
12	HPBU-126 x Palampur-93	Progeny 1	59.40	4.07	16.57	5.45	34.70	13.84	4.80
		Progeny 2	64.93	3.63	20.77	5.75	40.63	14.47	5.88
		Progeny 3	61.10	3.33	20.63	5.11	36.23	13.17	4.76

Table 3. Percentage of transgressive segregants (TGS) scored over mean value of corresponding progeny and best check in F_3 generation of blackgram

Sr. no.	Families	Progenies	Plant height (cm)		Branches per plant		Pods per plant		Seeds per pod		Biological yield (g)		Harvest index (%)		Seed yield per plant (g)	
			TGS over mean	TGS over best check	TGS over mean	TGS over best check	TGS over mean	TGS over best check	TGS over mean	TGS over best check	TGS over mean	TGS over best check	TGS over mean	TGS over best check	TGS over mean	TGS over best check
1.	COBG-653 x Palampur-93	Progeny 1	30.00	66.67	43.33	43.33	36.67	46.67	53.33	53.33	43.33	36.67	53.33	70.00	26.67	36.67
		Progeny 2	36.67	46.67	33.33	33.33	36.67	26.67	40.00	30.00	40.00	30.00	63.33	63.33	26.67	40.00
		Progeny 3	43.33	80.00	56.67	36.67	50.00	46.67	53.33	40.00	56.67	46.67	46.67	53.33	36.67	43.33
2.	DU-1 x Him Mash-1	Progeny 1	43.33	93.33	33.33	33.33	36.67	36.67	43.33	40.00	20.00	20.00	60.00	60.00	43.33	43.33
		Progeny 2	40.00	76.67	50.00	50.00	36.67	40.00	26.67	33.33	40.00	53.33	53.33	56.67	30.00	70.00
		Progeny 3	46.67	80.00	53.33	43.33	50.00	46.67	80.00	43.33	36.67	53.33	46.67	30.00	36.67	40.00
3.	KU-553 x HPBU-111	Progeny 1	33.33	63.33	60.00	60.00	20.00	26.67	66.67	50.00	40.00	46.67	36.67	63.33	23.33	46.67
		Progeny 2	40.00	76.67	30.00	66.67	36.67	30.00	73.33	33.33	36.67	40.00	53.33	63.33	46.67	46.67
		Progeny 3	40.00	86.67	76.67	50.00	43.33	43.33	36.67	26.67	43.33	53.33	63.33	70.00	50.00	60.00
4.	KU-553 x Palampur-93	Progeny 1	53.33	56.67	76.67	76.67	50.00	60.00	46.67	43.33	46.67	36.67	83.33	80.00	56.67	53.33
		Progeny 2	40.00	46.67	53.33	83.33	43.33	53.33	53.33	36.67	40.00	53.33	63.33	40.00	43.33	43.33
		Progeny 3	50.00	73.33	60.00	60.00	40.00	56.67	60.00	60.00	43.33	36.67	43.33	43.33	43.33	43.33
5.	DU-1 x Palampur-93	Progeny 1	60.00	90.00	53.33	86.67	43.33	60.00	56.67	40.00	36.67	43.33	83.33	66.67	93.33	93.33
		Progeny 2	53.33	90.00	46.67	60.00	40.00	33.33	50.00	43.33	36.67	36.67	83.33	60.00	100.0	90.00
		Progeny 3	43.33	100.0	56.67	56.67	33.33	23.33	46.67	33.33	40.00	43.33	90.00	50.00	100.0	96.67
6.	IPU-02-33 x Palampur-93	Progeny 1	40.00	56.67	63.33	63.33	40.00	46.67	56.67	36.67	46.67	63.33	53.33	60.00	60.00	83.33
		Progeny 2	46.67	66.67	53.33	53.33	40.00	46.67	46.67	26.67	73.33	66.67	60.00	53.33	63.33	86.67
		Progeny 3	36.67	66.67	33.33	56.67	26.67	20.00	40.00	33.33	43.33	50.00	43.33	40.00	50.00	50.00
7.	KU-223 x HPBU-111	Progeny 1	40.00	63.33	66.67	66.67	40.00	46.67	46.67	56.67	50.00	36.67	43.33	40.00	26.67	6.67
		Progeny 2	50.00	50.00	76.67	76.67	40.00	33.33	40.00	40.00	53.33	43.33	50.00	50.00	40.00	20.00
		Progeny 3	36.67	33.33	70.00	70.00	43.33	26.67	36.67	23.33	76.67	40.00	53.33	40.00	33.33	0.00

8.	HPBU-126 x HPBU-111	Progeny 1	36.67	80.00	40.00	63.33	36.67	46.67	26.67	43.33	30.00	43.33	43.33	76.67	96.67	100.0
		Progeny 2	43.33	80.00	50.00	50.00	40.00	50.00	50.00	36.67	40.00	40.00	46.67	80.00	86.67	100.0
		Progeny 3	46.67	76.67	56.67	66.67	43.33	50.00	23.33	43.33	10.00	20.00	53.33	66.67	80.00	100.0
9.	HPBU-124 x HPBU-111	Progeny 1	56.67	70.00	56.67	20.00	56.67	66.67	50.00	23.33	40.00	66.67	40.00	90.00	70.00	93.33
		Progeny 2	36.67	96.67	30.00	30.00	50.00	56.67	40.00	30.00	30.00	56.67	33.33	100.00	46.67	100.0
		Progeny 3	36.67	100.0	50.00	33.33	50.00	80.00	46.67	20.00	43.33	46.67	36.67	86.67	56.67	93.33
10.	KU-540 x Palampur-93	Progeny 1	40.00	73.33	60.00	46.67	40.00	33.33	40.00	50.00	50.00	36.67	46.67	56.67	46.67	36.67
		Progeny 2	46.67	73.33	50.00	50.00	40.00	40.00	26.67	36.67	43.33	43.33	60.00	40.00	43.33	30.00
		Progeny 3	33.33	76.67	53.33	53.33	30.00	20.00	43.33	50.00	53.33	40.00	40.00	26.67	46.67	36.67
11.	TU-17-4 x Palampur-93	Progeny 1	53.33	100.0	63.33	63.33	46.67	46.67	53.33	40.00	40.00	60.00	46.67	30.00	50.00	50.00
		Progeny 2	30.00	100.0	36.67	56.67	23.33	33.33	20.00	26.67	36.67	50.00	50.00	36.67	33.33	63.33
		Progeny 3	43.33	83.33	46.67	46.67	43.33	53.33	53.33	46.67	46.67	56.67	33.33	20.00	50.00	56.67
12.	HPBU-126 x Palampur-93	Progeny 1	50.00	66.67	43.33	93.33	36.67	33.33	46.67	56.67	50.00	100.00	50.00	16.67	56.67	93.33
		Progeny 2	33.33	70.00	60.00	73.33	30.00	46.67	46.67	73.33	46.67	100.00	50.00	43.33	46.67	100.0
		Progeny 3	50.00	100.0	50.00	70.00	43.33	53.33	36.67	43.33	50.00	100.00	53.33	20.00	43.33	100.0

Table 4. Progenies showing maximum number of transgressive segregants for all traits

Characters		Best progeny	Maximum percentage of transgressive segregants
Plant height (cm)	Progeny mean	Progeny-1 of DU-1 x Palampur-93	60.00
	Best check mean	Progeny-3 of DU-1 x Palampur-93, progeny-1 and progeny-5 of TU-17-4 x Palampur-93 , progeny-3 of HPBU-126 x Palampur-93 and progeny-6 of HPBU-124 x HPBU-111	100.00
Branches per plant	Progeny mean	Progeny-3 of KU-553 x HPBU-111, progeny-1 of KU-553 x Palampur-93 and progeny-2 of KU-223 x HPBU-111	76.67
	Best check mean	Progeny-1 of HPBU-126 x Palampur-93	93.33
Pods per plant	Progeny mean	Progeny-1 of HPBU-124 x HPBU-111	56.67
	Best check mean	Progeny-6 of HPBU-124 x HPBU-111	80.00
Seeds per pod	Progeny mean	Progeny-3 of DU-1 x Him Mash-1	80.00
	Best check mean	Progeny-2 of HPBU-126 x Palampur-93	73.33
Biological yield (g)	Progeny mean	Progeny-3 of KU-223 x HPBU-111	76.67
	Best check mean	Progeny-1, progeny-2 and progeny-3 of HPBU-126 x Palampur-93	100.00
Harvest index (%)	Progeny mean	Progeny-3 of DU-1 x Palampur-93	90.00
	Best check mean	Progeny-2 of HPBU-124 x HPBU-111	100.00
Seed yield per plant (g)	Progeny mean	Progeny-2 and progeny-3 of DU-1 x Palampur-93	100.00
	Best check mean	Progeny-1, progeny-2, progeny-3 of HPBU-126 x HPBU-111, progeny-3 of HPBU-124 x HPBU-111, progeny-2 and progeny-3 of HPBU-126 x Palampur-93	100.00

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