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GENERATION MEAN ANALYSIS FOR YIELD AND QUALITY TRAITS IN F_2 AND BACKCROSS GENERATION OF RICE (*Oryza sativa* L.)

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ABSTRACT

Generation mean analysis in basmati rice was studied for eight traits such as number of effective tillers per plant, panicle length (cm), number of grains per panicle, 1000-grain weight (g), grain yield per plant (g), alkali digestion value (%), gel consistency (%) and amylose content (%) in two crosses UPRI 2003-13×Taraori Basmati (C1) and UPR 2879-98-105× Pusa1121-92-8-1-3-3 (C2) among four basmati/basmati type parental lines. The analysis of variance indicated highly significant differences among genotypes and hybrids for all the traits. Additive, dominance, additive × additive and dominance × dominance interaction effects were present along with either duplicate dominant epistasis or complementary recessive epistasis for grain yield and most of its contributing traits. Hence, selection in the early segregating generations may not give desirable recombinants. Therefore, selection may be delayed to later segregating generations when the dominance and epistasis disappear and resorting to intermating of segregants followed by recurrent selection. Simple selection procedures or pedigree breeding method is sufficient to harness additive gene action. Heterosis breeding procedures are effective in harnessing dominance gene action to the full extent.

Key words : *Rice, Oryza sativa, gene action, generation mean analysis.*

Rice is the most important staple food among the cereals, consumed by more than half of the world's population and contributing to 73 per cent of total calorie intake of the population. Around 11 per cent of the arable land is occupied by rice with a total production of 600 million ton representing 21 per cent of the entire calorie supply (1). The UN/FAO forecasts that global food production will need to increase by over 40 per cent by 2030 and 70 per cent by 2050 (2). India occupies the world's largest area under rice with 42.5 million ha and is the second highest producer with 106.65 million tonnes (2013-14) followed by China, contributing 21 per cent of global rice production. It has a vital role in the food and livelihood security of the country. However, productivity of rice is only 2.54 tonnes/ha as against the global average productivity of 3.28 tonnes/ha (3). Self sufficiency and stability in rice production were made possible by development of high yielding varieties. Sustaining this self sufficiency and to meet out the demand formed by ever increasing population, the production and productivity must be raised again. Development of high yielding genotypes requires a thorough knowledge of genetic variation in yield contributing characters.

MATERIALS AND METHODS

The experimental material consisted of Six populations (P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2) of each cross were grown in compact family block design in three replications in 3m long rows with spacing of 20×10 cm between and within rows, respectively. The numbers of rows were different for different progenies. Each plot consisted of paired rows of parents and back cross each, one row of F_1 and six rows of F_2 generations. The recommended agronomic and plant protection measures for cultivation of basmati rice were followed to raise a healthy crop. Generation mean analysis in basmati rice was studied for eight traits such as number of effective tillers per plant, panicle length (cm), number of grains per panicle, 1000-grain weight (g), grain yield per plant (g), alkali digestion value (%), gel consistency (%) and amylose content (%) in two crosses among four basmati/ basmati type parental lines. The analysis of variance indicated highly significant differences among genotypes and hybrids for all the traits.

RESULTS AND DISCUSSION

Generation mean analysis is a simple but useful technique for characterizing gene effects for a polygenic character (4) and determines the presence & absence of non-allelic interactions. The greatest merit of generation mean analysis is that it helps in the estimation of epistatic gene effects namely additive × additive (i), additive × dominance (j) and dominance × dominance (l). The nature of gene action governing the inheritance of yield and its components was studied using generation mean. The variation among the means of different generation in all the eight characters studied suggesting the usefulness of the estimation of additive, dominance and epistatic interaction. Significant differences among six generation means were found for number of effective tillers per plant, panicle length (cm), number of grains per panicle, 1000-grain weight (g), grain yield per plant (g), alkali

Table-1 : Scaling test of quantitative and qualitative traits of two crosses in basmati rice.

Crosses / Scales		UPRI 2003-13×Taraori Basmati (C1)	UPR 2879-98-105 × Pusa1121-92-8-1-3-3 (C2)	Joint Scaling ^{2} at 3.d.f	Best fit model (parameter)
No. of effective tillers/ Plant	C	-4.02**	-0.97	13.01*	6
	D	-8.24**	-4.52**	53.88*	6
Panicle length	C	-5.09**	0.60	67.66*	6
	D	-25.03**	-8.50**	359.34*	6
No. of grains/panicle	C	-126.13**	-81.40**	1399.90*	6
	D	-13.68**	3.38	13.66*	6
1000–Grain weight	C	-16.97**	3.78**	102.66*	6
	D	-6.80**	0.80*	10.66*	6
Grain yield/plant	C	-13.42**	6.02**	455.74*	6
	D	-6.49	2.75*	134.68*	6
Alkali digestion value	C	-5.81**	-2.65**	86.53*	6
	D	-3.57**	-1.04**	219.85*	6
Gel consistency	C	-27.06**	0.97	296.43*	6
	D	-35.97**	-14.38**	120.31*	6
Amylose content	C	-1.69**	0.09	9.59*	6
	D	-3.11**	-0.91*	3.42 (ns)	6

**Significant at 1% level.

digestion value (%), gel consistency (%) and amylose content (%).

The C, D scaling test for almost all the characters in the two crosses showed that at least one or both were found significant indicating the presence of non-allelic interaction in the inheritance of the characters under study. However the characters under study of cross 2 showed significant values for both C and D scales indicating the interacting mode of inheritance. Any one or both the scaling tests were found to be significant in all the traits indicating the presence of epistasis.

The type of epistasis was determined as complementary when dominance (h) and dominance × dominance (l) gene effects have same sign and duplicate epistasis when the sign was different. Hence, the present study shows that significant additive and epistatic effects exist in this population. Although their presence may vary from cross to cross.

One or both C and D scaling was found significant for all the traits in cross 2 (Table 1). Both the crosses exhibiting non-allelic interaction for inheritance of almost all the traits studied. In general, the interaction effect together i.e., additive × additive (i) and dominance × dominance (l) found in higher magnitude than the combined main effects of additive (d) and dominance (h) effects for all the traits in both the crosses.

For number of effective tillers /plant, the estimates of mean (m) were highly significant for all the crosses. Additive (d) effect was significant only for UPRI 2003-13 × Taraori Basmati while dominance (h) effect was found to be highly significant for cross UPRI 2003-13 ×Taraori Basmati, UPR 2879-98-105 × Pusa 1121-92-8-1-3-3. Additive × additive (i) effect was highly significant for UPR 2879-98-105 × Pusa 1121-92-8-1-3-3. Additive × dominance (j) effect was also found highly significant for UPR 2879-98-105 × Pusa 1121-92-8-1-3-3, whereas for UPRI 2003-13 × Taraori Basmati it was found only significant. The dominance × dominance (l) effect was non -significant for UPRI 2003-13 × Taraori Basmati and significant for UPR 2879-98-105 × Pusa 1121-92-8-1-3-3.

For panicle length (cm), the estimates of means (m) were highly significant for all the crosses. Additive (d) effect was highly significant for this trait for UPRI 2003-13 × Taraori Basmati and it was only significant for UPR 2879-98-105 × Pusa 1121-92-8-1-3-3.The dominance (h) effect was highly significant for UPR 2879-98-105 × Pusa 1121 92-8-1-3-3,while additive × additive (i) interaction was found significant for UPR 2879-98-105 × Pusa 1121-92-8-1-3-3.Additive × dominance (j) effect was also found highly significant for UPRI 2003-13 × Taraori Basmati Dominance × dominance (l) interaction was found significant only for the UPRI 2003-13 × Taraori Basmati.

For number of grains / panicle, the estimates of mean (m) were highly significant for all the crosses. Additive (d) effect was significant for UPRI 2003-13 × Taraori Basmati. Dominance (h) effect and additive ×

Table-2 : Genetic components of generation mean for quantitative and qualitative traits in basmati rice.

Genetic effects	UPRI 2003-13×Taraori Basmati (C1)	UPR 2879-98-105× Pusa1121-92-8-1-3-3 (C2)	Genetic effects	UPRI 2003-13×Taraori Basmati (C1)	UPR 2879-98-105× Pusa1121-92-8-1-3-3 (C2)
Number of effective tillers / Plant			**Panicle length (cm)**		
(m)	9.22±0.21**	11.82±0. 22**	(m)	27.50±0.25**	23.80±0.17**
(d)	-1.96±0.80*	0.23±0.83	(d)	-4.70±0.71**	0.74±0.39
(h)	5.62±1.93**	10.07±2. 00**	(h)	2.94±1.88	22.13±1.22**
(i)	1.95±1.83	9.04±1.89**	(i)	-1.21±1.75	17.00±1.04**
(j)	-2.03±0.86*	-2.66±0.88**	(j)	-2.30±0.73**	-0.96±0.56
(l)	0.11±3.57	-9.84±3.68*	(l)	7.51±3.32*	-8.98±2.12
Type of gene action	Complimentary	Duplicate	Type of gene action	Complimentary	Duplicate
Number of grains / panicle			**1000 – Grain weight (g)**		
(m)	81.50±2.36**	105.79±0.68**	(m)	24.54±0.21**	24.01±0.23**
(d)	23.13±9.14*	0.80±1.51	(d)	3.43±0.58**	-1.70±0.55**
(h)	201.00±21. 4**	7.18±4.46	(h)	10.97±1.57**	2.56±1.54
(i)	162.8±20.59**	-6.77±4.08	(i)	7.57±1.44**	1.60±1.45
(j)	20.06±9.40*	6.03±7.56**	(j)	3.23±0.71**	-1.06±0.64
(l)	-199.46±39.4**	27.24±7.56**	(l)	1.82±2.77	3.60±2.61
Type of gene action	Duplicate	Complimentary	Type of gene action	Complimentary	Complimentary
Grain yield /plant (g)			**Alkali digestion value**		
(m)	9.54±0.22**	15.60±0.97**	(m)	5.25±0.19**	6.04±0.06**
(d)	1.19±1.34*	2.37±1.39*	(d)	0.01±0.09*	0.04±0.10*
(h)	19.56±2.86**	11.40±4.85*	(h)	5.46±0.44**	2.14±0.0.33**
(i)	12.05±2.83**	5.51±4.80	(i)	5.31±0.43**	2.09±0.33**
(j)	1.13±1.37	0.80±1.45	(j)	0.32±0.11**	0.11±0.11
(l)	-10.68±5.50	-4.54±6.94	(l)	-82±0.5**	-4.61±0.49
Type of gene action	**Duplicate**	**Duplicate**	**Type of gene action**	**Duplicate**	**Duplicate**
Gel consistency			**Amylose content (%)**		
(m)	83.75±0.69**	86.42±0.52**	(m)	22.80±0.05**	22.48±0.11**
(d)	10.20±1.36**	-1.50±0.81	(d)	0.09±0.05*	-0.10±0.31**
(h)	8.00±3.99*	28.34±2.84**	(h)	0.58±0.13*	1.960.81**
(i)	-1.93±3.89	28.77±2.64**	(i)	0.82±0.70	1.82±0.77**
(j)	-1.00±1.42	-1.93±1.02	(j)	-0.15±0.31	-0.25±0.35
(l)	30.86±6.38**	-21.57±4.39**	(l)	-0.33±1.1	-0.53±1.41
Type of gene action	**Complimentary**	**Duplicate**	**Type of gene action**	**Duplicate**	**Duplicate**

**Significant at 1% level (m) = mid parental value, (d) = additive effect, (h) = dominance effect,
(i) = additive × additive, (j) = additive × dominance (l) = dominance × dominance

additive (i) interaction were also highly significant for UPRI 2003-13 × Taraori Basmati except for UPR 2879-98-105 × Pusa 1121-92-8-1-3-3.The additive × dominance (j) interaction was found highly significant for UPR 2879-98-105 × Pusa 1121-92-8-1-3-3 and significant for UPRI 2003-13 × Taraori Basmati. The dominance × dominance (l) effect was found to be highly significant for both the crosses.

For 1000-grain weight (g), the estimates of mean (m) were highly significant for both the crosses C1 and C2. Additive (d) effect was significant for both the crosses. Dominance (h) effect was found important for this trait and highly significant for UPRI 2003-13 × Taraori Basmati. Additive × additive (i) interaction was found highly significant only in cross UPRI 2003-13 × Taraori Basmati. Additive × dominance (j) effect was highly significant for UPRI 2003-13 × Taraori Basmati The dominance ×

dominance (l) effect was non- significant for both the crosses.

For grain yield /plant (g), the estimates of mean (m) were highly significant for C1 and C2. The dominance (h) effect was found to be significant in UPR 2879-98-105 × Pusa 1121-92-8-1-3-3 while highly significant for UPRI 2003-13 × Taraori Basmati. Additive × additive (i) interaction was found to be highly significant for UPRI 2003-13 × Taraori Basmati. None of them showed the presence of additive × dominance (j) and dominance × dominance (l) types of interaction.

For alkali digestion value, the estimates of means (m) were highly significant in both the crosses. Both additive × dominance (j) and dominance × dominance (l) interaction was found significant for UPRI 2003-13 × Taraori Basmati

For gel consistency, the estimates of mean (m) were highly significant for both the crosses. Additive (d) effect was the significant in „UPRI 2003-13 × Taraori Basmati, whereas dominance (h) was found significant in C1 and C2. The estimates were high and positive. Additive × additive (i) effect was highly significant in UPR 2879-98-105 × Pusa 1121-92-8-1-3-3.The additive × dominance (j) interaction was found to be non- significant. The dominance × dominance (l) interaction was found highly significant for both the crosses.

For amylose content (%), the chi-square test of goodness of fit for two crosses and estimates of gene effects (Table-1). Additive-dominance model i.e. 3-parameter model was adequate for UPRI 2003-13 × Taraori Basmati and whereas six- parameter model was found to be adequate for remaining cross.

Studies on gene effects in generation mean analysis revealed that additive gene effect (d) was significant in C 1 for all the traits under study except number of effective tillers / Plant, panicle length, Number of grains / panicle and gel consistency in C 2 Table 2). These results indicated that there exist scope for direct selection for grain yield and its contributing traits. Additive effect for number of productive tillers per plant was reported by (5). The dominance gene effect (h) was significant in C 1 for all the traits except panicle whereas in the case of C2 it was observed non-significant effect for Number of grains / panicle 1000 grain weight, and gel consistency. Dominance gene effect for number of productive tillers plant was earlier reported by (6).

The additive × additive (i) interaction effect was significant in C 1 for, 1000-grain weight (g), grain yield per plant (g), alkali digestion value (%), gel consistency (%) and amylose content (%) except number of effective tillers per plant, panicle length (cm) but in the case of C2 the significant effect was noticed for all the traits except Number of grains/panicle 1000-grain weight (g), and grain yield per plant (g) (Table 2). These results were in conformity with (7) for the trait number of productive tillers per plant, (8) for the trait number of grains per panicle, (9).

It could be noted that the presence of additive, dominance, additive × additive and dominance × dominance interaction effects were present along with either duplicate dominant epistasis or complementary recessive epistasis for grain yield and most of its contributing traits. Hence, selection in the early segregating generations may not give desirable recombinants. Therefore selection may be delayed to later segregating generations when the dominance and epistasis disappear and resorting to intermating of segregants followed by recurrent selection. Simple selection procedures or pedigree breeding method is sufficient to harness additive gene action. But the presence of dominance gene action in most of the characters warrants postponement of selection to later generations after effecting crosses. Heterosis breeding procedures are effective in harnessing dominance gene action to the full extent.

Both additive and dominance gene actions play major role in several characters. In such circumstances biparental mating design or reciprocal recurrent selection can be followed for further recombination of alleles to produce desirable segregants. These methods can also be well adopted in order to harness the epistatic interactions by way of breaking the undesirable linkages. Diallele selective mating system proposed by (10) could also be followed to break such undesirable linkages between two or more genes and to produce desirable recombinants.

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