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Genetic analysis of agromorphologic traits under normal and delayed planting in rainfed lowland rice (*Oryza sativa*)

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Rainfed lowlands are the major rice (*Oryza sativa* L.) ecosystem in eastern India spread over 13 million ha, and its productivity in this region is around 1.5 tonnes/ha. Early drought and flood cause delayed planting, resulting in further yield decline. More than 50% of rainfed lowland rice, transplanting is frequently delayed (Mackill *et al.* 1996).Yield stability is another major problem of rainfed lowland ecosystem. Traditional rice cultivars grown in rainfed lowlands provide stable protection against flood, drought and delayed planting-related problems, but they are less responsive to favourable environments or higher inputs. Drought or flooding often makes it impossible to transplant at optimum age of seedlings. Rice farmers need improved genotypes with better yields and stability under delayed planting conditions across environments.

The choice of suitable breeding procedure depends upon the relative magnitude of different kinds of genes and an understanding of the mode of inheritance of complex quantitative characters. Generation means analysis used to estimate the components of genetic variance which provides information about the predominant type of gene action for the different traits under improvement. This analysis is one of the several tools used in estimating additive, dominance and epistatic variations. Literature survey revealed that voluminous work has been done for gene action of various traits in rice (Singh *et al.* 2004).But reports on lowland rice is very scanty. Furthermore, work on gene action under delayed planting condition is not available. Therefore, the present investigation was undertaken to know the additive, dominance and epistatic gene action involved in the expression of different traits in lowland rice under normal and delayed planting conditions.

The experiment was conducted at Central Rice Research Institute, Cuttack, Orissa during rainy season of 2004–06. The experimental materials comprising the parents (P_1 and P_2), F_1, F_2 and its back cross generations (BC_1P_1 and BC_1P_2) of the cross 'SBIR 66876-11-M-1-1-1-1'×'Rajshree' were used. The test materials were transplanted under normal as well as delayed transplanting conditions in randomized complete block design in three replications. The spacing was 20 cm between rows and 15 cm within rows. Twenty-five plants/replication were transplanted for parents, F_1 and back cross generations while 300 plants were tested in F_2 generation in each replication. Observations on days to 50% flowering, plant height (cm), tillers/plant (number), panicle length (cm), grains/panicle (numbers), 1000–grain weight (g.), biological yield (g.), harvest-index (%) and grain yield/plant (gm) were recorded for 20 plants each on P_1, P_2, and F_1; 150 plants for F_2 and 25 plants each in BC_1P_1 and BC_1P_2 generations. The means and variance of means of 9 metric traits were computed for each generation of the cross. Mather's scaling test (1949) was applied to detect the presence of epistasis. Cavalli's joint scaling tests (1952) were also applied to confirm the presence of epistasis. The significance of scales and gene effects were tested by t-test (Singh and Chaudhary 2004). The genetic effects were estimated using the models suggested by Mather and Jinks (1971) and Jinks and Jones (1958).

Simple scaling tests, A, B, C and D were applied to find

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Table 1 Simple scaling test for different characters under normal and delayed transplanting conditions

Character	Normal transplanting				Delayed transplanting			
	A	B	C	D	A	B	C	D
Day to 50% flowering	–13.2** ±0.67	–18.40** ±1.98	17.40** ±0.93	24.50** ±1.67	–25.70** ±4.43	–22.33** ±1.26	42.93** ±2.83	45.93** 2.67
Plant height (cm)	–21.24** ±0.87	–26.89** ±1.21	2.50 ±0.99	25.31** ±2.56	33.76** ±0.60	–52.30** ±0.82	–71.4** ±4.91	–26.44** 2.47
Tillers/plant	–1.73** ±0.60	–0.96** ±0.29	–10.5** ±2.56	–3.93** ±1.33	–6.10** ±0.95	–1.50* ±0.74	–8.53** ±1.05	–0.46 0.72
Panicle length (cm)	0.48 ±1.89	–3.52** ±1.00	3.14* ±1.49	2.98* ±1.28	–6.23** ±1.87	–4.93 ±0.93	0.56 ±1.33	5.86** 1.21
Grains/panicle	–31.80** ±4.07	–42.20** ±1.54	5.13** ±2.65	39.56** ±1.99	–25.36** ±6.62	–18.73** ±7.00	–94.7** ±13.7	–25.20** 2.25
1 000-grain weight (g)	–0.66** ±0.17	–0.43** ±0.16	–0.16 ±0.84	0.46 ±0.41	–0.66* ±0.30	–0.30 ±0.20	–0.56 ±0.72	0.20 0.35
Biological yield/ plant (g)	–1.04 ±1.15	–7.72** ±1.97	–14.5** ±2.06	–2.89** ±1.12	–18.27** ±0.92	–18.14** ±0.64	0.32 ±3.77	18.76** 1.90
Harvest index (%)	1.09 ±4.17	–2.01 ±5.90	17.40** ±3.01	–9.16* ±3.74	–7.79** ±1.32	8.90** ±1.27	–5.05** ±1.76	–3.18** 1.11
Grain yield/plant (g)	–0.18 ±0.98	–3.74** ±0.88	–2.06 ±1.33	0.93 ±0.66	–7.53** ±0.29	–1.48** ±0.73	–2.20 ±1.36	3.40 0.75

* P=0.05, ** P=0.01

out presence or absence of non-allelic gene interactions or epistasis in the expression of nine traits under normal and delayed transplanting conditions (Table 1). Significant values of all the four scales (A, B, C and D) for days to 50% flowering, tillers/plant and grains/panicle indicated the presence of (i), (j) and (l) type of non-allelic gene interactions for expression of these traits under normal transplanting condition. Significance of scales A, B and D for plant height; B, C and D for panicle length and biological yield/plant; A and B for 1 000-seed weight; C and D for harvest index and A for grain yield/plant also indicated the presence of various non-additive gene action for expression of these traits under normal planting condition. All the four scales A, B, C and D were significant for days to 50% flowering, plant height, grains per panicle and harvest index under delayed planting condition. Significance of Scales A, B and C for tillers/plant; A, B, and D for biological yield; A and B for grain yield/ plant; A and D for panicle length and A for 1 000-seed weight also revealed the importance of non-additive gene action for expression of these traits under delayed planting conditions. Joint scaling test was also applied to detect the presence of epistasis in the expression of nine traits under normal and delayed transplanting conditions. The chi-square values of joint scaling tests presented in Table 2 were significant under both the conditions of planting except 1 000-seed weight under normal planting. This confirmed the presence of epistasis and inadequacy of additive-dominance model.

After the presence of non-allelic gene interactions was confirmed, the data were further analyzed employing six

Table 2 Chi-square estimates for joint scaling test for nine characters under normal and delayed planting

Character	Normal planting	Delayed transplanting
Day to 50% flowering	938.8**	1 144.2**
Plant height (cm)	9 043.0**	1 095.4**
Tillers/plant	1 195.0**	337.6**
Panicle length (cm)	41.8**	26.3**
Grains/panicle	744.8**	981.1**
1000–grain weight (g)	8.06	15.5**
Biological yield/plant (g)	1 115.5**	165.9**
Harvest index (%)	107.0**	79.9**
Grain yield/plant (g)	663.7**	28.1**

* P=0.01, ** P=0.05

parameters (m, d, h, i, j, l) model of generation mean analysis. The estimates of gene effects under both the conditions of transplanting are given in Table 3. In case of days to 50% flowering, dominance (h), additive×additive (i) and dominance×dominance (l) type of non-allelic gene interactions were significant under both the conditions of planting. All type of gene interactions were significant under both planting situations for plant height except additive (d) under delayed planting. For tillers/plant showed additive, additive×dominance (j) and dominance×dominance under normal planting while dominance, additive×additive and dominance×dominance type of interactions under delayed planting condition. Significance of all the five types of gene effects were observed under normal condition for the

Table 3 Gene effects for different characters under normal and delayed transplanting conditions in rice

Character	Normal transplanting						Delayed transplanting condition					
	m	(d)	(h)	(i)	(j)	(l)	m	(d)	(h)	(i)	(j)	(l)
Days to 50% flowering	107.61 ±0.69	–0.72 ±2.28	–77.27** ±5.36	–90.97** ±5.35	–1.68 ±2.30	139.1** ±9.57	118.21 ±0.18	4.59 ±1.02	–36.60** ±0.21	–49.00** ±2.17	2.59* ±1.03	80.60** ±4.20
Plant height	107.60 ±1.21	19.30** ±0.43	79.62** ±4.96	58.88** ±4.94	43.03** ±0.46	–34.34** ±5.22	96.60 ±1.23	–0.19 ±0.69	33.46** ±5.14	50.63** ±5.13	2.82** ±0.73	98.76** ±5.70
Tillers/plant	8.56 ±0.24	–3.86** ±0.53	2.53 ±1.45	0.93 ±1.44	–2.29** ±0.55	6.66** ±2.39	6.08 ±0.64	–0.56 ±0.31	8.41** ±2.67	7.86** ±2.67	–0.38 ±0.32	–5.16* ±2.89
Panicle length	26.66 ±0.31	–2.27* ±1.03	–8.97 ±2.44	11.73** ±0.24	–0.65** ±0.10	22.90** ±4.35	24.50 ±0.36	–3.22 ±1.06	–4.68 ±2.57	–5.97* ±2.56	1.90 ±1.07	8.80 ±4.49
Grains/panicle	117.88 ±0.94	–2.40 ±1.30	51.08** ±7.97	50.60** ±4.50	–3.31** ±1.25	–6.50 ±1.55	112.25 ±0.33	9.20** ±1.87	**±4.14 –81.06	–79.13** ±3.98	5.20* ±2.16	153.1** ±7.95
1 000-grain weight	2.66 ±0.16	0.39** ±0.12	–0.28 ±0.72	–0.40 ±0.71	–0.18 ±0.71	1.36 ±0.87	2.43 ±0.20	0.20* ±0.08	–0.75 ±0.83	–0.95 ±0.82	–0.11 ±0.08	2.03* ±0.90
Biological yield/plant	43.12 ±0.92	–3.59** ±0.46	–25.10** ±3.83	–37.53** ±3.81	–0.33 ±0.52	74.74** ±4.20	23.64 ±0.29	4.78** ±0.95	5.77* ±2.40	5.78** ±2.24	3.34** ±0.98	2.97 ±4.35
Harvest index	26.37 ±0.37	–8.69** ±0.82	7.10** ±2.27	6.53** ±2.22	–8.24** ±0.87	–7.67** ±3.75	45.48 ±0.61	7.68* ±3.53	–11.46** ±7.53	–18.32** ±7.48	1.55 ±3.58	19.24** ±14.46
Grain yield/ plant	11.37 ±0.33	–4.26** ±0.36	–3.07* ±1.52	–6.81** ±1.51	–3.02** ±0.38	18.82** ±2.00	10.75 ±0.20	3.99 ±0.53	–0.07 ±1.43	–1.86** ±1.33	1.77** ±0.55	5.79** ±2.50

*P=0.05, **P=0.01

character panicle length but additive (d) gene effect along with (i) gene interactions were observed under delayed planting condition. Grains/panicle exhibited significant (h), (i) and (j) under normal planting and expressed all five type of interactions under delayed planting condition. Significant estimates of (d),(h) and (i) was observed under both the planting situations but dominance×dominance under normal and additive×dominance for delayed planting noted for the trait biological yield/plant. Harvest index manifested with significant values of all gene effects under normal planting. But the action under delayed planting was additive, dominance and additive×additive only. In case of grain yield/plant, all the three types of epistatic gene action was observed under both the conditions of planting.

The simple scaling tests, A, B, C and D were significant for majority characters under both normal and delayed transplanting situations. This indicated inadequacy of additive-dominance model. Hence, estimation of epistatic components of gene interaction was essential for better understanding of the expression of these traits. The 6-parameter model of Jinks and Jones (1958) was utilized for generation mean analysis. The results of joint scaling test also supported the results of simple scaling tests. In joint scaling test, the chi-square estimates were highly significant for all the nine characters under both the conditions of planting. In case of days to 50% flowering, dominance (h), additive×additive (i) and dominance×dominance (l) effects played a role under both the situations of transplanting. Duplicate type epistasis observed for the trait would slow the progress under selection. Saleem *et al.* (2005) observed significant role of additive gene effects for days to 50% flowering, while Sharma *et al.* (1987) and Singh *et al.* (2004) reported importance of both the additive as well as non-additive gene action for days to 50% flowering. Significant estimates of dominance and epistatic gene effect were observed for plant height under both the situations of transplanting. Importance of additive genes was also noticed under normal planting while dominance as well as epistatic gene effects were important under both the situations. Importance of additive and non-additive gene effects for plant height has also been reported by Saleem *et al.* (2005), while preponderance of non-additive gene action was observed by Saleem *et al.* (2005) and Singh *et al.* (2004). Perraju and Sarma (1999) and Ram *et al.* (2007) reported significant role of additive gene action for plant height. Results indicated that expression of trait, tillers/plant was governed by both additive and non-additive gene action. Therefore, the cross material may be subjected for exploitation of tillers/plant through non-additive gene effects. However, Ram *et al.* (2007) reported importance of additive and non-additive gene action with preponderance of additive gene action in expression of tillers/plant.

In case of panicle length, predominant role of additive×additive (i) interaction under delayed planting was noticed, while all the gene effects were important under normal transplanting. This indicated the importance of both the gene effects under normal transplanting while most of the genes got suppressed under delayed transplanting. Saleem *et al.* (2005) recorded importance of additive as well as non-additive gene effects with predominance of additive gene

effects for panicle lengh. Perraju and Sarma (1999) reported that panicle length was under the control of non-additive gene effects, while Singh *et al.* (2004) and Sharma *et al.* (1996) found the role of additive genetic variance only. Grains per panicle exhibited dominance, additive× additive and additive×dominance type of gene action for expression of the trait. The epistatic gene effect was duplicate epistasis under both the conditions of planting. This indicated the predominance of epistatic gene effects along with additive gene effect for expression of the trait. Perraju and Sarma (1999) observed predominance of non-additive gene action.

The expression of character, 1 000-seed weight exhibited significant estimates for additive gene effect under both normal and delayed planting conditions. This indicated the predominance of additive gene effect in inheritance of the character. Thus, selection may be advocated for taking care of presence of fixable additive gene effects. Importance of additive gene effects for this trait was also recorded by Ram *et al.* (2007), Saleem *et al.* (2005) and Singh *et al.* 2007 Biological yield/plant was governed by additive and non-additive gene effects. The trait was found to be controlled by duplicate epistasis under normal transplanting and it may slower the selection process. This result is in agreement with Sharma *et al.* (1996) where significant role of additive and non-additive gene action with predominance of non-additive component was reported for expression of biological yield/plant. For harvest index, both additive and non-additive gene expression governed the trait. Predominant role of non-additive gene action with presence of duplicate epistasis exhibited for inheritance of the trait. Therefore, use of breeding methods like recurrent selection for exploitation of non-additive gene effects may be recommended for further generations of the cross. Similar results have been reported earlier by Sharma *et al.* (1996) for expression of the trait. Grain yield/plant manifested dominance, additive×additive, additive×dominance and dominance×dominance gene action under normal planting. The results indicated that there was a predominant role of epistatic gene effect under normal planting. In case of delayed planting, (d), (i) and (l) parameters were significant. This indicated the predominance role of non-additive gene effects comprising dominance and epistatic gene effects in inheritance of grain yield/plant under delayed planting condition. Importance of additive and non-additive gene effects with predominance of non-additive gene effect for expression of traits was reported earlier by Singh *et al.* (2007) and Saleem *et al.* (2005).

The estimate of gene effects obtained for nine traits under normal and delayed transplanting conditions exhibited both additive and non-additive gene effects with preponderance of non-additive gene effects. The substantial additive gene effects can be utilized for development of pure line through conventional breeding procedure. But the non-fixable components may be exploited through heterosis breeding. Besides the methods, like biparental mating and diallel selective mating may also be suggested for exploitation of dominance and epistatic effects for the purpose of isolating transgressive segregants to develop pure line varieties.

SUMMARY

Six generation means (P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2) of cross 'SBIR 66876-11-M-1-1-1-1'/'Rajshree' were utilized to study the additive, dominance and epistatic components of variations in lowland rice under normal and delayed planting conditions. Simple and joint scaling tests indicated the presence of epistastic gene interaction and fitness of digenic interaction model under normal and delayed transplanting conditions. Six parameter model of generation mean analysis revealed importance of additive (d), dominance (h) and epistastic gene interactions (i, j, l) for nine characters with pre-dominance of non-additive gene action for majority of traits under normal and delayed transplanting conditions. Grain yield/plant exhibited dominance, additive×additive, additive×dominance and dominance×dominance types of genetic effects under normal planting while additive, additive×additive and dominance ×dominance components were expressed under delayed planting situations. The role of duplicate epistasics was found to important in majority of the traits studied. The dominance and epistastic components of variation could be exploited for the development of hybrids while bi-parental mating and diallel selective mating could be adopted for isolation of transgressive segregants for development of pureline(s).

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