

## Genetic parameters in rice (*Oryza sativa* L.)

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### Abstract

The estimates of additional biometrical genetic parameters indicated the importance of dominance in the expression of almost all the traits of interest, among the parents of the present study. Gene symmetric was observed for days to 50 per cent flowering, number of productive tillers per plant, panicle length and seed breadth. Predominance of the presence of dominant alleles was observed for plant height at maturity, number of filled seeds per panicle, seed length, seed L/B ratio, hundred seed weight and seed yield per plant. The ratio of dominance to recessive indicated the prevalence of dominant alleles among the parents except, for number of productive tillers per plant. Similarly, opulence of dominant genetic variation was observed for all the traits of interest, except, seed breadth. The magnitudes of dominance variances were higher than that of additive genetic variance for all the traits of interest except number of filled seeds per panicle. The study amply indicated that the parents utilized for the present inquiry possessed more of dominant alleles. Hence, they may be well utilized in heterosis breeding program.

**Keywords:** rice, genetic parameters

### Introduction

Rice is important food crop. It is cultivated in India 44 million hectares with the production 117.47 million tones. In Tamil Nadu it is cultivated in almost all the districts including Ooty hills and Cumbum valley. It is cultivated in the area of 17.21 lakh hectares with the production 61.32 lakh million tones (Anon, 2020) [2].

The population of Tamil Nadu 8.37 crores. The *percapita* availability of rice per day is 189 g. Hence agricultural scientists have to augment the production and productivity. Heterosis breeding is one of the breeding technology which will improve the productivity and their by production. The choice of parents and their genetic analysis is of paramount importance in getting success with heterosis breeding programme.

### Materials and Methods

Pure, well filled, plumpy and sound seeds of the genotypes *viz.*, (P1) ADT 37, (P2) ADT 43, (P3) ADT 45, (P4) ASD 16, (P5) CO51 and (P6) CO47 were obtained from Tamil Nadu Rice Research Institute (TNAU), Aduthurai and sown on May 30, June 15 and June 30, 2019. Twenty five days old seedlings were planted during June 14, June 29, July 14, 2019. Genotypes were selfed as well as matted in 6 × 6 full diallel fashion. The F1 seeds of 30 cross combinations were evolved. They were sown along with their six parents during July 2019, in raised beds. Twenty five days old seedlings were transplanted in two rows of 3 metre length plots. The spacing adopted was 20 × 15 cm. The seedlings were planted in RBD with three replications. Recommended agronomic practices and need based plant protection measures were followed. Observations were recorded on ten traits *viz.*, X<sub>1</sub>) Days to 50 per cent flowering, X<sub>2</sub>) Plant height at maturity, X<sub>3</sub>) Number of productive tillers per plant, X<sub>4</sub>) Panicle length, X<sub>5</sub>) Number of filled seeds per panicle, X<sub>6</sub>) Seed length, X<sub>7</sub>) Seed breadth,

X<sub>8</sub>) Seed L/B ratio, X<sub>9</sub>) Hundred seed weight and X<sub>10</sub>) Seed yield per plant, on five randomly selected plants per replication. The additional biometrical genetic parameters were computed the as per the procedure outline by Hayman (1954) [4].

### Results and Discussion

The estimates of  $\hat{D}$  components of variation was significant for days to 50 per cent flowering, plant height at maturity, number of filled seeds per panicle, seed length, seed breadth, seed L/B ratio, hundred seed weight and seed yield per plant. It indicated the importance of additive genetic effects of genes, controlling the aforementioned the traits. The result is in conformity with the findings of Thirugnana kumar *et al.* (2008) [10] and Akanksha and Jaiswal (2019) [1].

The estimates of  $\hat{F}$  were positive and significant differing from zero, for plant height at maturity, number of filled seeds per panicle, seed length, seed L/B ratio, hundred seed weight and seed yield per plant. This may indicate the predominance of dominant alleles in the parents for the above said traits. The result is in agreement with the findings of Narasimman (2005) [7] and Senthilkumar and Mudhalvan (2018) [9]. On the other hand gene symmetry existed for the other traits of interest. It is in corroboration with the findings of Narasimman (2005) [7].

The estimates of  $\hat{H}_1$  were significant always, except panicle length, indicating the opulence of dominant genetic variations. A more or less similar trend was observed for the estimate of  $\hat{H}_2$ . The results may indicate there were unequal allelic frequencies. The result is in agreement with the findings of Thirugnanakumar *et al.* (2008) [10] and Bagheri *et al.* (2008).

The estimates of  $\hat{h}^2$  was significant for days to 50 per cent flowering and number of productive tillers per plant only. Probably, it may indicate the overall dominant effects of heterozygous loci. The estimates environmental effect always non-significant (Table 1). The findings are online with that of Narasimman *et al.* (2007) [8].

The ratio of  $(H_1/D)^{1/2}$  were more than one for days to 50 per cent flowering, plant height at maturity, number of productive tillers per plant, panicle length, seed breadth and hundred seed weight, indicating the presence of over dominance for these traits. The other traits had the said ratio with less than one. It may indicate that the traits *viz.*, number of filled seeds panicle, seed length, seed L/B ratio and seed yield per plant may be controlled by incomplete dominance. The ratio of  $H_2/4H_1$  with less than 0.25 indicating the unequal distribution of the dominant and recessive alleles. The ratio of  $(4DH_1)^{1/2+F} / (4DH_1)^{1/2-F}$ , indicated the presence of more proportion of dominant gene for all the traits of interest except plant height at maturity (Table 2). The result with corroboration with the findings of Narasimman (2005) [7] and Iftekharruddaula *et al.* (2008) [5]. The ratio of  $h^2/H_2$  were more than three, indicating that atleast three blocks of genes were controlling days to 50 per cent flowering; and two blocks of genes controlling number of productive tillers per plant. For all the other traits the

ratio is under estimated. That may be due to correlated gene distribution (Jinks, 1954) [6].

The narrow sense heritability estimates were low for almost all the traits except, number of productive tillers per plant and seed yield per plant. These two traits may be controlled by additive genes (Thirugnanakumar *et al.* 2008) [10]. The other traits of interest may be controlled by non-additive genes (Senthilkumar and Mudhalvan, 2018) [9].

The result indicated that gene symmetry existed in the parents for days to 50 per cent flowering, number of productive tillers per plant, panicle length and seed breadth. For all the other traits predominance of dominant alleles was evidenced. The ratio of  $(4DH_1)^{1/2+F} / (4DH_1)^{1/2-F}$  indicated in the presence of more dominant alleles in the expression of all the traits of interest, except, number of productive tillers per plant. The presence of dominance gene effects on the expression of all the traits except seed breadth, were well witnessed. The magnitude of dominance was more prevalent than additivity for all the traits, except, number of filled sees per panicle. It is perceived that, by and large, dominance gene action is important in the expression of almost all the traits of interest among the parents utilized for the present inquiry. These parents could be well utilized in heterosis breeding program.

**Table 1:** Estimate of genetic parameters for ten traits in rice

S. No.	Characters	$\hat{D}$	$\hat{F}$	$\hat{H}_1$	$\hat{H}_2$	$\hat{h}^2$	$\hat{E}$
1	Days to 50 per cent flowering	16.9046±4.29**	20.1622±10.50	64.92±10.91**	55.6663±9.74**	184.5097±6.56**	63.1728±1.62
2	Plant height at maturity	5.1560±1.06**	6.8550±2.59**	9.7036±2.69**	6.1364±2.40**	0.2266±1.62	0.3140±0.40
3	Number of productive tillers per plant	0.5630±0.63	-0.9803±1.55	7.3630±1.61**	6.3886±1.43**	17.8605±0.96**	0.2222±0.24
4	Panicle length	0.5332±0.27	0.9154±0.67	1.7031±0.70**	1.2356±0.62	0.8125±0.42	0.1729±0.10
5	Number of filled seeds per panicle	98.5349±6.55**	62.5867±16.01**	71.3590±16.63**	52.8911±14.86**	7.4109±10.000	0.5494±2.47
6	Seed length	1.7244±0.04**	2.2263±0.11**	1.4807±0.11**	0.7592±0.10**	0.1084±0.07	0.0072±0.01
7	Seed breadth	0.0173±0.001**	0.0235±0.02	0.0392±0.02	0.0324±0.01	0.0195±0.01	0.0065±0.01**
8	Seed L/B ratio	0.2901±0.01**	0.3885±0.04**	0.2808±0.04**	0.1516±0.04**	0.0549±0.02	0.0066±0.01
9	Hundred Seed weight	0.0712±0.01**	0.0814±0.01**	0.0772±0.01**	0.0479±0.01**	0.0289±0.01**	0.0036±0.01
10	Seed yield per plant	29.2682±2.34**	12.7708±5.73**	15.4602±5.96**	12.1708±5.32**	2.9723±3.58	0.1204±0.08

\*\*Significant at 1 per cent level

**Table 2:** Ratio of genetic parameters for ten traits in rice

S. No.	Characters	$(H_1/D)^{1/2}$	$H_2/4H_1$	$\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}$	$h^2/H_2$	Heritability (NS) (%)
1	Days to 50 per cent flowering	1.9597	0.2144	1.8748	3.3146	0.0809
2	Plant height at maturity	1.3719	0.1581	2.8802	0.0369	0.1002
3	Number of productive tillers per plant	3.6164	0.2169	0.6120	2.7957	0.6711
4	Panicle length	1.7871	0.1814	2.8484	0.6575	0.0337
5	Number of filled seeds per panicle	0.8510	0.1853	2.1908	0.1401	0.2641
6	Seed length	0.9267	0.1282	5.5928	0.1427	0.0435
7	Seed breadth	1.5056	0.2070	2.6453	0.6002	0.0084
8	Seed L/B ratio	0.9839	0.1349	5.2614	0.3625	0.0349
9	Hundred Seed weight	1.0408	0.1551	3.4318	0.6035	0.0931
10	Seed yield per plant	0.7268	0.1968	1.8579	0.2442	0.3849

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