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NATURE OF GENETIC CONTROL OF SUBMERGENCE TOLERANCE IN RICE

N. MANDAL*, K ROY AND S. GUPTA**

Department of Genetics and Plant Breeding,
Bidhan Chandra Krishi Viswavidyalaya, Mohanpur 741 252

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ABSTRACT

Inheritance of submergence tolerance in rice was investigated in a 10 × 10 diallel cross. A strong prepotency of parents was found in transmitting the character to their offsprings. Tolerance was dominant over susceptibility and the average dominace was within the range of incomplete dominance. Wr-vr graphic analysis suggested the involvement of both major and minor genes. Additive and non additive gene effects were highly significant. A high narrow sense heritability (71%) indicated that additive gene effects were more prominent. Parents highly tolerant to submergence also had high gca effects. The hybrids CNL31 × FR-13A, Pankaj × FR-13A, Mahsuri × FR-13A, CNL 31 × ***rufipogon*****, Pankaj ×** ***rufipogon*****, Mashsuri ×** ***rufipogon*****, IR 42 ×** ***rufipogon*** **and CNL 31 × FR-43B appeared to be promising for incorporating an adequate level of tolerance to submergence into susceptible cultivars as indicated by their significant sca estimates.**

Key words: *Oryza sativa* L., *O. rufipogon* Griff, submergence tolerance, inheritance.

The genetics of submergence tolerance is not entirely known [1]. A few genetic studies have been made on tolerance to complete submergence in rice [2-4] and breeding for submergence tolerance has already been started [5, 6]. Thorough knoweldge of the genetics of submergence tolerance in rice will increase efficiency for breeding submergence tolerant varieties. Therefore, the present expriment was designed to study the nature and magnitude of genetic variation of submergence tolerance in 10 rice genotypes crossed in a half diallel fashion.

MATERIALS AND METHODS

Three submergenc etolerant genotypes viz FR-13A (P1) [IRRI, Acc. No 6144], FR-43B (P2) [IRRI, Acc. No. 6143] and *O. rufipogon* (P3) obtained from Chinsurah

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*Present address: Biotechnology, Instrumentation and Environmental Science Unit, BCKV, Mohanpur, Nadia
**Bose Institute, 93/1, A.P.C. Road, Calcutta 700009

Rice Research Station, Chinsurah, West Bengal] and seven susceptible cultivars viz CNL 31 (P4), Pankaj (P5), Mahsuri (P6), C-64-31 (P7), IR 5744 (P8), Meghna (P9) and IR 42 (P10) were crossed in half diallel fashion. The 45 F1's and 10 parents were grown in pots and studied for submergence tolerance in the greenhouse submergence tank. The test of submergence tolerance was conducted under artifical conditions using the method descirbed by Vergara and Mazaredo [7]. The experiment was laid out in a randomized block design with four replications. The method involved submerging 10 days old seedlings (100/ genotype/replication) in 30 cm water for seven days. At the end of the experimental period, the pots were taken out and placed outside the submergence tank for recovery of the plants. On the 10th day of the recovery period a survival count was taken and sunmergence tolerance (based on survival percentage) was scored on a 1 to 9 scale [4]. Lower score indicated higher tolerance. Combining ability analysis as per Griffing [8], Graphical and variances components analyses as per Hayman [9] were done.

RESULTS AND DISCUSSION

Mean scores for the parents and their arrays showed FR-43B, FR- 13A and *O. rufipogon* to be top tolerant parents in that order (Table 1). Performances of F1's differed greatly from one cross to another depending on the level of tolerance of

Table 1. Mean phenotypic score, array, parent-offspring covariance (W_r) and variance (V_r) for submergence tolerance in a 10 × 10 diallel cross in rice

S. No.	Parents	1	2	3	4	5	6	7	8	9	10	Array means	V_r	W_r
1.	FR-13A	2.24	2.25	2.48	1.98	1.77	2.62	2.38	2.12	2.61	3.15	2.36	0.149	0.110
2.	FR-43B		1.93	2.73	2.64	3.15	3.60	2.47	3.00	2.73	3.51	2.80	0.278	1.038
3.	*O. rufipogon*			3.10	2.26	2.01	2.52	2.50	3.47	3.33	2.16	2.66	0.245	–0.234
4.	CNL 31				5.25	5.70	7.45	8.24	4.81	7.76	6.75	5.28	5.462	4.014
5.	Pankaj					7.51	6.22	5.39	4.60	5.61	3.89	4.59	3.474	3.352
6.	Mahsuri						8.48	7.52	6.23	7.70	7.40	5.96	4.978	4.150
7.	C-64-31							5.03	5.21	6.29	4.80	4.98	4.251	3.197
8.	IR 58 44								6.11	4.76	5.52	4.58	1.801	2.573
9.	Meghna									5.97	6.15	5.29	3.563	3.379
10.	IR 42										6.78	5.01	3.173	2.878

the parents used in the cross. The close correspondence between the parental means and their array means (r = 0.9) suggests a high prepotency of the parents in transmitting submergence tolerance to their offspring.

A regression graph of parent offspring covariance (W_r) and variance (V_r) showed a regression coefficient, b = 0.7609 ± 0.2294 (Fig. 1) which was significantly different

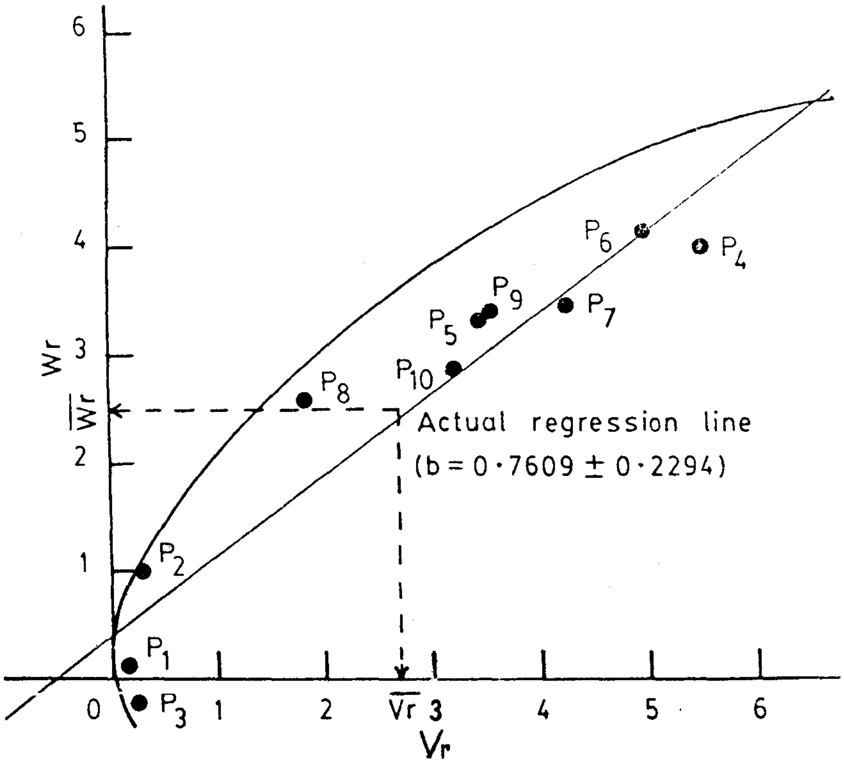

Fig. 1. (W_r, V_r) Regression graph for submergence tolerance in a 10 × 10 diallel cross in rice

from zero but not from unity, thus indicating the absence of epistasis. The regression line cutting the Wr axis above the orign suggested that the tolerance was dominant over susceptibility and the average dominance was within the range of incomplete dominance. The position of the array points on the graph showed that the dominant alleles were concentrated in the three tolerant parents. viz. FR-13A, *O. rufipogon* and FR-43B in that order. Mahsuri the most non-tolerant parent had the highest concentration of recessive alleles. This striking discontinuity between the array points of the tolerance versus non tolerant group suggested the possible involvement of one or more major genes in the inheritance of the trait. In a preliminary study Mohanty and Khush [4] also reported the involvement of both major and minor genes.

Genetic parameters like additive genetic variance (D) and three components of dominance variance (H_1, H_2 and h^2) were highly significant (Table 2), indicating the importance of both additive and non additive type of gene action in the inheritance of the trait. The low estimate and non significance of F value and the ratio $H_2/4H_1 = 0.19$. which was less than the maximum expected value of 0.25, suggested low order of gene asymmetry. The average dominance $(H_1/D)^{1/2}$ was within the range of incomplete dominance and was in agreement with the conlusion drawn from the graphical analysis. However, the near zero value (–0.06) for the ratio $1/2\ F/[D\ (H_1-H_2)]^{1/2}$ indicated an inconsistency of dominance over loci.

Table 2. Estimates of genetic parameters for submergence tolerance in rice

Genetic parameters	Estimates
D	4.5009 ± 0.5094
H_1	4.8705 ± 1.0843
H_2	3.7232 ± 0.9215
h^2	31.2605 ± 0.6168
F	–0.7526 ± 0.6617
E	0.3760 ± 0.1536
$(H_1/D)^{1/2}$	1.0402
$(H_2/4H_1)$	0.1911
h^2/H_2	8.3961
Heritability (narrow sense)	0.71
$1/2\ F/[D(H_1 - H_2)]^{1/2}$	–0.16

The ratio of $h^2/H_2 = 8.3$ suggested the involvement of at least eight groups of genes having dominance. The estimate of narrow sense heritability value (0.71) showed the greater importance of additive gene action in the control of submergence tolerance.

The significant mean squares due to general combining ability (gca) and specific combining ability (sca) (Table 3) suggested that both additive and non-additive gene actions were important for the character under investigation. The higher magnitude of the former component indicated the predominance of additive gene action.

Table 3. ANOVA for combining ability for submergence tolerance in 10 × 10 diallel cross in rice

Sources	D.F.	Mean Squares
gca	9	11.028**
sca	45	1.317**
error	162	0.307

Estimates of gca effects revealed that the tolerant parents FR-13A and *O. rufipogon* were good general combiners (Table 4). Among the hybrids invoving tolerant × non tolerant crosses $P_1 \times P_4$, $P_1 \times P_5$, $P_1 \times P_6$, $P_2 \times P_3 \times P_4$, $P_3 \times P_5$, $P_3 \times P_5$, $P_3 \times P_6$ and $P_3 \times P_{10}$ were highly heterotic, with significant sca effects for higher tolerance. The high sca estimates in these crosses again indicated the prepotency of FR-13A and *O. rufipogon* parents in transmission the submeragence tolerance trait.

Table 4. General combining ability (g_1) and specific combining ability (s_{ij}) effects for submergence tolerance in rice

Parent	S_{ij}									+
	1	2	3	4	5	6	7	8	9	10
1.	-1.911**	1.296*	1.549**	-1.320**	-1.135*	-1/524**	-0.651	-0.667	-0.756	-0.050
2.		-1.569*	1.458**	-1.001*	-0.097	-0.886	-0.902	-0.129	-0.977	-0.031
3.			-1.592**	-1.358**	-1.214*	-1.942**	-0.849	0.365	-0.354	-1.358**
4.				0.777*	0.107	0.619	2.522**	-0.665	1.707**	0.863
5.					0.398*	-0.217	0.066	-0.481	-0.049	-1.603**
6.						1.621**	0.958	-0.089	0.083	0.669
7.							0.508*	0.005	0.506	-0.818
8.								0.264	-0.781	0.145
9.									0.843**	0.917
10.										0.676**

Diagonal values are gca effects (gi) of the parents; *,** Significant at 5% and 1% levels, respectively

Hence, improved lines of high yielding submergence tolerance could possibly be developed from the crosses of CNL 31 × FR-13A, Pankaj × FR-13A, Mahsuri × FR-13A, CNL 31 × FR-43B, CNL31 × *rufipogon*, Pankaj × *rufipogon*, Mahsuri × *rufipogon* and IR 42 × *rufipogon* as indicated by the high sca estimates of the relevant crosses.

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