Indian J. Genet., **53** (3): 261–263 (1993)

GENETIC ANALYSIS OF GRAIN NUMBER, GRAIN WEIGHT AND GRAIN YIELD IN RICE (*ORYZA SATIVA* L.)

V. S. CHAUHAN,* J. S. CHAUHAN AND J. P. TANDON

Vivekananda Laboratory for Hill Agriculture, Almora 263601

(Received: April 27, 1988; accepted: December 19, 1992)

ABSTRACT

In a cross of Begunbuchi and IRAT 102 varieties of rice having extreme variations for number of grains and 1000-grain weight, additive and additive x additive interaction effects were found important in the inheritance of grains/panicle and 1000-grain weight. However, grain yield was predominantly governed by dominance effects and additive x dominance and dominance x dominance interaction effects. Complementary type epistasis was observed for grains/panicle and 1000-grain weight, while duplicate type epistasis was prominent for grain yield. The midparent heterosis was maximum (29.3%) for grain yield/plant. Appropriate breeding methodologies for the exploitation of various type of gene effects observed in the present study are discussed.

Key words: Genetics, grain number, grain weight, grain yield, rice.

Information on the nature and magnitude of gene effects for grain yield and its important component characters is quite useful in deciding a sound breeding strategy for the improvement of these traits. Hence an attempt was made in the present study to understand the genetic architecture of rice yield and its two important component characters, viz. grain number and grain weight.

The parents, F_1, F_2, BC_1 and BC_2 generations of a cross between Begunbuchi (a small seeded low-land variety) and IRAT 102 (a bold seeded upland variety) were grown during the wet season of 1982 at the Experimental Farm of Vivekananda Laboratory of Hill Agriculture, Hawalbagh, Almora, Uttar Pradesh. The station is located at 20°N, 79°E and at an altitude of 1300 m. The experiment was conducted in randomized complete block design with three replications. Each replication consisted of two rows each of the parents, F_1, BC_1 and BC_2 and ten rows of F_2. Thirty-day-old seedlings were transplanted at the rate of one seedling/hill. Row length was 1.5 m and the plant spacings were 20 and 15 cm between and

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[*] Present address: Central Rainfed Upland Rice Research Station, Post Box 48, Hazaribag 825301.

within rows, respectively. Standard agronomic practices were followed to raise a normal crop. Ten competitive plants from each parent, F_1, BC_1, BC_2 and 40 plants of F_2 per replication were taken at random for recording observations on number of grains/panicle, 1000-grain weight, and grain yield/plant.

The generation mean analysis was done following Hayman [1]. Heterosis was computed as the percentage increase of F_1 mean over the midparental (MP) value.

The analysis of variance indicated significant differences among different experimental populations for all the three characters. The mean number of grains/panicle (279 ± 3.3) and grain yield/plant (28.9 ± 1.0 g) of Begunbuchi were significantly higher than those of IRAT 102, while 1000-grain weight (35.7 ± 0.5 g) of the latter was significantly higher than that of former (12.9 ± 0.4 g).

Number of grains/panicle in F_1 was closer to the parent with lower number of grains and heterosis for this character was –28.7%. The seeds of cv. Begunbuchi were lighter than those of IRAT 102, with the F_1 value close to the MP value. Heterosis was positive and moderate (7.8%) for 1000-grain weight. Positive heterosis for this trait has been reported earlier [2]. The mean grain yield/plant of F_1 exceeded both the mid-parent and the better parent. The MP heterosis (29.3%) was largest for this trait. Similar results were reported by [3].

The scaling tests revealed the inadequacy of simple additive–dominance model to explain the total genetic variability for all the three traits, indicating the presence of epistasis. Therefore, the six-parameter model of Hayman [1] was used.

Additive effects (d) and three epistatic interactions (additive x additive, additive x dominance, dominance x dominance) were significant for grains/panicle. However, their relative magnitude revealed the predominance of additive x additive (i) type of interactions (Table 1). These results are contrary to those of Singh et al. [4] who reported considerable nonadditive gene action for grains/panicle. Additive effects and additive x additive (i) interaction were also

Table 1. Estimates of gene effects for number of grains/panicle, 1000-grain weight and grain yield/plant in the cross Begunbuchi x IRAT 102 of rice

Parameter	Grains per panicle	1000-grain weight	Grain yield per plant
m	164.7 ± 2.8	24.3 ± 0.4	29.3 ± 0.7
d	$20.5 \pm 4.3^{**}$	$-12.7 \pm 0.7^{**}$	-0.9 ± 1.4
h	0.0 ± 14.5	$4.2 \pm 2.3^{*}$	$9.3 \pm 4.1^{**}$
i	$62.2 \pm 14.3^{**}$	$5.4 \pm 2.2^{*}$	2.4 ± 4.0
j	$-81.8 \pm 9.6^{**}$	2.6 ± 1.6	$-13.0 \pm 3.1^{**}$
l	$-37.2 \pm 18.8^{**}$	-0.8 ± 3.7	$-15.0 \pm 6.6^{**}$

*,**Significant at 5% and 1% levels, respectively.

significant for 1000-grain weight (Table 1). Complementary epistasis was observed for both grain number and grain weight, but the magnitude of dominance effect was very low and nonsignificant (Table 1). The predominance of additive effects and additive x additive gene interaction (fixable component) for these traits suggested the use of simple selection in the segregating generations to improve grain number and grain weight.

The dominance effects (h) along with additive x dominance (j) and dominance x dominance (l) interactions predominantly governed the expression of grain yield (Table 1). Nonadditive gene action for grain yield has also been reported from the earlier studies [2, 5]. However, Ghorai and Pande [6] observed that additive and dominance effects were equally important in the inheritance of grain yield. The presence of significant dominance effects coupled with duplicate type of epistasis restricted the scope of simple selection for the improvement of grain yield. It is, therefore, suggested that for simultaneous improvement of yield and its two important components, viz. grain number/panicle and 1000-grain weight, a single breeding system capable of exploiting additive and nonadditive gene effects should be used. In order to achieve this, the use of recurrent selection is advocated provided the cytogenetic male sterility and restorer systems are available.

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