

## **CORRELATED RESPONSE TO SELECTION FOR YIELD COMPONENTS IN SEGREGATING POPULATIONS OF RICE (*ORYZA SATIVA* L.)**

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### **ABSTRACT**

Correlated response to selection was worked out for number of tillers/plant, panicle length, number of grains/panicle and 1000 grain weight in 280 F<sub>3</sub> progenies of the cross UPR 83-34/Sita during *Kharif*, 1993 in random and biased (on the basis of grain yield/plant) populations selected from four different plant spacings viz., 15 × 10 cm, 20 × 10 cm, 20 × 15 cm and 20 × 20 cm during *Kharif*, 1992. Though no definite trend could be established, random selection by and large, resulted in positive correlated response for different yield components. The correlated response varied from character to character in the plant progenies selected on the basis of grain yield alone (biased selection)

**Key Words :** Rice, correlated response, random selection, biased selection

### **INTRODUCTION**

Indirect selection becomes imperative if the attribute in question has low heritability and/or is not easily and precisely measurable. In such a condition some criteria of early diagnosis have to be developed to rationalize the selection programme. The aim of correlation studies is primarily to know about the suitability of various characters for indirect selection because selection for one character results in correlated response for several other characters [1] resulting into changed patterns of variability [2]. Such changes would be quite substantial with the dwarfing genes and intense selection pressure for a plant type which involves several component traits related to productivity. The studies on indirect selection response are, therefore, necessary for simultaneous and sequential improvement of component traits. In the present investigation an attempt was made to find out correlated response for yield components in random and biased populations.

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## MATERIALS AND METHODS

The experimental material comprised  $F_2$  population of cross UPR 83-34 / Sita. The  $F_2$  progenies of this cross were transplanted at four different plant spacings viz.  $15 \times 10$  cm,  $20 \times 10$  cm,  $20 \times 15$  cm and  $20 \times 20$  cm from row-to-row and plant-to-plant, respectively in a well puddled field at the Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar during *Kharif* (wet) season, 1992. At each spacing a minimum population of 2000 plants was maintained. These were further divided into two equal parts, each having 1000 plants. From each plant spacing 200 plants (20%) were selected randomly (before flowering) as well as on the basis of their grain yield (at maturity).

During *Kharif*, 1993 the  $F_3$  progenies ( $F_3$  plants) of 35 random and 35 top yielding (biased) plants from each spacing (a total of 280 plant progenies) were evaluated alongwith the parents,  $F_1$  hybrid and local check (Pant Dhan 10) in a Randomised Complete Block Design in two replications. Each  $F_3$  progeny was grown in a single row of 5 metre length. A row to row spacing of 20 cm and plant to plant spacing of 15 cm was maintained. At the time of maturity, five plants from each progeny were selected on the basis of their phenotypic performance for detailed study. Data were recorded on number of tillers/plant, panicle length (cm), number of grains/panicle, 1000 grain weight (g) and grain yield/plant (g), during both the years. Correlated response to selection was estimated as per Falconer [3].

## RESULTS AND DISCUSSION

The correlated response for various characters (Table 1) indicated that for number of tillers/plant, the response was maximum in the population selected from a close spacing of  $15 \times 10$  cm in the biased group of genotypes (1.128). On the other hand, the progenies selected from a wide spacing of  $20 \times 20$  cm gave maximum correlated response to selection in the random group (1.265). Though both the methods by and large, resulted into positive correlated response for this trait, the gains were affected by plant spacing, while a closer spacing was found to be better for biased selection, comparatively wider spacing was needed for random selection.

The above trend was reversed for panicle length. The correlated response to selection was positive only at a wider spacing of  $20 \times 20$  cm in the biased population. Other spacings gave negative estimates of correlated response. This indicated that wider spacings encouraged the formation of longer panicles. Randomly selected populations, by and large, gave positive estimates for this trait and the value was maximum at a closer spacing of  $15 \times 10$  cm (0.921).

A moderate spacing of  $20 \times 10$  cm was found to be better for number of grains/panicle in both the groups of genotypes. Among the biased groups, the genotypes selected from  $15 \times 10$  cm and  $20 \times 10$  cm spacings gave negative correlated response to selection. Among the random groups of genotypes, the correlated response was maximum at  $20 \times 10$  cm spacing (1.263). It seems that at this spacing plants were able to utilize the resources in an optimum way.

**Table 1. Correlated response to selection for yield components in biased and random groups of genotypes under different plant spacings**

Sl. No.	Characters	Method of selection	Plant spacings (cm)			
			$15 \times 10$	$20 \times 10$	$20 \times 15$	$20 \times 20$
1.	Number of tillers/plant	Biased	1.128	0.306	-0.085	0.160
		Random	0.507	0.225	0.896	1.265
2.	Panicle length (cm)	Biased	-0.181	-0.028	0.019	1.139
		Random	0.921	0.562	0.516	-0.211
3.	Number of grains/panicle	Biased	-0.033	0.380	-0.326	0.139
		Random	1.195	1.263	0.585	-0.380
4.	1000-grain weight (g)	Biased	0.358	-0.012	-0.060	0.828
		Random	0.693	0.502	0.603	0.279

For 1000 grain weight, random selection gave positive correlated response at all the spacings and it was maximum at  $15 \times 10$  cm spacing (0.683). On the other hand, this response was maximum at  $20 \times 20$  cm spacing in the biased selection. However, 1000 grain weight is highly heritable [4] and least affected by spacing [5]. It is the method of selection which made the difference.

Normally, in the study of correlated response the selection is directed towards better expression of the component character and its indirect effect is observed on the grain yield. Studies in wheat have indicated indirect response for grain yield/plant through direct selection of kernel weight, number of tillers/plant and number of grains/spike [6]. Similar observations have also been made in urdbean [7]. In the present study there were two groups of populations. In one group (biased), the selection was directed towards higher grain yield/plant and indirect response of main components viz. number of tillers/plant, panicle length, number of grains/panicle and 1000 grain weight. In the other group selection was random. Though no definite trend could be established due to the confounding effect of selection methods and

plant spacings, it emerged that random selection by and large gave positive indirect response to grain yield through major yield components. In the biased selection this response varied for different characters depending upon the spacing and many of these were negative. This would be possible if a higher proportion of plants still heterozygous at a number of loci in the  $F_2$  generation for favoured during biased selection due to superior morphological expression. The selection differential will be high under these circumstances, but the selection response will be low. On the other hand, in random selection both the homozygous and heterozygous genotypes are equally likely to be retained in the selected groups. In this case the selection differential will be low, but the selection response may be high. This probably was the main cause of the deviation in the correlated response to selection between the two groups of populations.

The results are also likely to change because of the environmental variations and intensity of selection. The other major factor which influences the correlated response is the genetic constitution of the population i.e., whether the material under study are fixed genotypes or segregating populations [3].

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