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DETERMINATION OF CHARACTERS FOR PANICLE YIELD IN EARLY MATURING, SEMIDWARF VARIETIES OF RICE UNDER TWO FERTILITY ENVIRONMENTS

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ABSTRACT

Beyond a certain panicle number per unit area, further increase in rice yield would depend on increase in mean panicle yield. To identify panicle yield characters 18 elite, early maturing, semidwarf rice varieties were grown under high fertility (N_{100}:P_{50}:K_{50}) and low fertility (N_{50}:P_{25}:K_{25}) levels. Results from stepwise regression analysis showed that the number of spikelets per panicle was the most important determinant of panicle yield which accounted 65% and 45% of the total variation in panicle yield under high and low fertility levels, respectively. The number of sterile spikelets/primary branch and 1000-grain weight were next in order of importance. Together, these three characters accounted 82% and 86% of the total variation in panicle yield at high and low fertility levels, respectively. Thus, if selection for panicle yield is to be based on spikelet number/panicle alone, high fertility should be preferred. However, for maximum gains, selection should be based on increased number of spikelets/panicle, reduced number of sterile spikelets/primary branch, and higher 1000-grain weight. If selection for panicle yield is based on all these three determinants of panicle yield, the fertility levels would make little difference in the effectiveness of selection.

Key words: Correlation, fertility, panicle yield, rice, stepwise regression.

Yield of rice per unit area is primarily determined by the mean panicle yield and the number of effective tillers or the number of panicles. Beyond a certain limit, accommodating more tillers per unit area through choice of cultivar and/or agronomic management can not be expected to enhance yield; further increase in yield per unit area would necessarily come from increase in mean panicle yield. Information on panicle yield determination should be of considerable value in the development of heavy-panicle type rice varieties having very high yield potential and productivity. Since semidwarf rice cultivars have characteristically short panicles, there is a possibility of increasing their yield potential through genetic

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improvement of panicle yield. In order to learn whether the rice panicle is amenable to favorable genetic modification, panicle morphology of 18 elite semidwarf rice genotypes was examined to identify characters determining panicle yield and assessed effects of fertility levels on character relationships.

MATERIALS AND METHODS

Eighteen early, semidwarf rice cultivars were grown at J. N. Agricultural University, Jabalpur, during the 1972 wet season in a three-replicate split-plot experiment with two fertility levels: $N_{50}P_{25}K_{25}$ and $N_{100}P_{50}K_{50}$. Observations were recorded on 2 plant characters, 40 panicle characters, 5 grain characters, and 3 kernel characters [1].

The analysis of variance (ANOVA) was carried out for all characters. Estimate of intercharacter correlation coefficients were obtained using standard procedures. Stepwise multiple regression analysis [2] was carried out on character means to identify characters that accounted for relatively large proportion of variance for panicle yield.

RESULTS AND DISCUSSION

In the present study, the presence of high magnitude of genetic variation for panicle traits in the experimental materials having similar tiller number per plant in high as well as low fertility levels indicate that it was possible to modify panicle structure and grain characters to improve panicle yield to a certain extent without affecting tiller number. Stepwise regression analysis indicated that the most important determinants of panicle yield spikelets/panicle, sterile spikelets/primary branch, and 1000-grain weight (Table 1). The No. of sterile spikelets/primary branch appeared in the final regression equation for panicle yield in high fertility environment but was replaced by number of sterile spikelets/ secondary branch in the final regression equation for low fertility environment. Appearance of the number of sterile spikelets/primary branch in the regression equation using pooled data indicated its greater importance relative to sterile spikelets/secondary branch. Besides, these two sterility parameters were closely correlated in both high ($r = 0.92$) as well as low fertility ($r = 0.98$) levels. In the final equation from stepwise regression analysis using pooled data, primary branches/panicle and effective tillers/plant also showed up, but their effects were very small and may be ignored.

Using all the three determinants of panicle yield, there was little difference in the efficiency of the final regression equation at the two fertility levels. Therefore, if all the three determinants were to be considered simultaneously, selection may be practiced at any fertility level. These three determinants of panicle yield, together accounted for 82.4 and 85.9% of the variance for panicle yield in high and low fertility environments, respectively. Similarly, simultaneous selection for spikelets/panicle and sterile spikelets/primary branch would be almost equally effective at the two fertility levels because these two determinants

Table 1. Stepwise regression of main panicle yield on component characters for 18 cultivars analyzed under high fertility, low fertility, and pooled data in rice

Cfmponent character added to the equation	Total reduction SS (%)	Const-ant	Regression coefficients				
			b_1	b_2	b_3	b_4	b_5
High fertility:							
Number of spikelets/panicle	64.9	0.98	0.009				
Number of sterile spikelets/primary branch	75.2	0.84	0.013	–0.127			
1000-grain weight	82.4	–0.81	0.015	–0.146	0.060		
F value for coefficients in final equation:			96.10**	77.34**	78.07**		
Low Fertility:							
Number of spikelets/panicle	44.8	1.11	0.010				
Number of sterile spikelets per secondary branch	72.3	0.77	0.018	–0.97			
1000-grain weight	85.9	–1.95	0.020	–0.977	0.102		
F value for coefficients in final equation:			42.18**	66.68**	101.84**		
Pooled data:							
Number of spikelets/panicle	52.6	1.07	0.009				
Number of sterile spikelets per secondary branch	68.2	0.79	0.015	–0.184			
1000-grain weight	79.3	–1.45	0.018	–0.200	0.083		
Mean length of primary branches	80.7	–1.9	0.016	–0.199	0.079	0.070	
Number of effective tillers/plant	81.7	–1.59	0.016	–.206	0.076	0.083	–0.039
F value for coefficients in final equation:			117.40**	112.75**	132.76**	107.92**	91.02*

**Significant at 1% level.

put together accounted for 75.2 and 72.3% variance for panicle yield in the high and low fertility conditions, respectively. It is significant, however, that selection based on spikelets/panicle alone could be more effective in high than in low fertility conditions. The reduction in panicle yield variance due to spikelets/panicle was 64.9% in high as against 44.8% in the low fertility environment.

Among the three components of panicle yield, only spikelets/panicle had significant correlation with panicle yield at both fertility levels (Table 2). The No. of sterile spikelets per primary branch was significantly correlated with panicle yield only at high fertility, whereas

1000-grain weight had low and nonsignificant correlation with panicle yield at both fertility levels. It is interesting that of all the characters having significant correlation with panicle yield at both fertility levels, only spikelets/panicle considerably contributed to panicle yield as shown by stepwise regression analysis. These findings illustrate the limitations of simple correlation coefficients.

Table 2. Estimates of correlation coefficients (r) of different characters with panicle yield in low and high fertility environments (characters having nonsignificant value of r with panicle yield omitted)

Character	Correlation coefficients with panicle yield	
	low fertility	high fertility
Panicle length	0.67**	0.56**
Ineffective length of panicle (%)	–0.27*	–0.33*
Nodes/panicle	0.66**	0.62**
Spikelets/panicle	0.67**	0.80**
Sterile spikelets/panicle	0.30*	0.43**
Primary branches/panicle	0.57**	0.72**
Mean length of primary branches	0.62**	0.48**
Mean ineffective length of primary branches	0.35**	0.15
Spikelets/primary branch	0.63**	0.78**
Sterile spikelets/primary branch	0.23	0.31
Density of primary branches	0.35**	0.70**
Mean length of primary branch bearing spikelets directly on its main rachis	–0.07	–0.43**
Secondary branches/primary branch	0.61**	0.73**
Mean length of seconday branches	0.46**	0.35**
Spikelets/secondary branch	0.65**	0.54**
Total length of all primary plus secondary branches	0.65*	0.74**
Panicle density	0.34**	0.16
Mean length of two terminal branches of the panicle	–0.18	–0.38**
Density of two terminal branches of the panicle	0.30*	0.23
Mean length of the grain	–0.01	–0.26*

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

Simple correlations between component characters, nevertheless, provide useful information to the plant breeder. For instance, significant positive correlation between spikelets/panicle and sterile spikelets/ primary branch under high fertility (r = 0.68) and low fertility (r = 0.80) would make it difficult to select for higher number of spikelets/panicle and reduced number of sterile spikelets/primary branch at the same time. Breeders would do well to compromise by attempting to select for an optimum balance between the two components rather than going for the extremes. Also, it should be more advantageous to practise selection under high fertility where correlation between these two determinants of panicle yield was low. Similarly, significant negative correlation, though moderate in magnitude, between spikelets/panicle and 1000-grain weight (high fertility, r = –0.46; low fertility r = –0.43) would mean that instead of going for extremes, a compromise between the levels of these two characters may prove more rewarding.

Genetic advance estimated as percentage of mean was high for spikelets/panicle as well as sterile spikelets/primary branch, and was accompanied by high estimates of heritability at both fertility levels. However, high heritability estimates (84% at high fertility, 82% at low fertility) for 1000-grain weight were accompanied by low genetic advance (19.5% at high and 16.0% at low fertility). Panse [3] indicated that if the heritability of a character in a given environment was due to predominantly nonadditive gene action, the genetic advance would be low, whereas if the heritability was due to predominantly additive gene action, the genetic advance would be high. Thus, while nonadditive gene action was predominant for 1000-grain weight, predominantly additive gene action was indicated to control the other two determinants of panicle yield. This also suggests that while striking a balance between 1000-grain weight and spikelets/panicle, greater weight may be given to spikelet number/panicle which would be relatively more amenable to genetic fixation because of its predominantly additive genic control.

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