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Research Note

Parent Progeny regression analysis in F_2 and F_3 generations of rice

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Abstract:
Parent progeny regression analysis involving F2 and F_3 generation of two crosses in rice was undertaken to estimate the genetic potential transferred from one generation to other by adopting three levels of selection for single plant yield. Significant positive correlation and regression was observed in both crosses at positive level of selection (mean +1SD) between F_3 mean and the corresponding F_2 values, indicating that selection of single plant yield at these levels would be effective in both crosses. It indicates the chances of selecting high yielding genotypes at early generations.

Key words: Rice, parent-progeny correlation, regression analysis, selection.

Rice is life and prince among cereals. This unique grain helps sustain two thirds of world's population. Rice is the backbone of India's economy providing direct employment to about 70 per cent working people in the country. Asia is the biggest rice producer, accounting for 90 per cent of the world's production and consumption of rice. (Anon.,2007). It is considered as the main staple food for more than 50 per cent of the world's population (Child,2004). Globally, India ranks first in area, 43.6 million ha and second in production 91.7 million tonnes with productivity of 2811 Kg ha^{-1} [Amrit Patel,2008].Crop improvement for grain yield has been achieved in rice through effective use of F_2 and F_3 segregating populations and fixing desirable character combinations. However, there are still possibilities to increase the yield output through proper breeding technologies in rice. Grain yield is a complex trait and is the result of interaction of many variables. Parent progeny regression is a method commonly used for estimating the amount of genetic potential transferred from parent to progeny. The present investigation was undertaken to evaluate how far the genetic potential is transferred from F_2 to F_3, based on three levels of selection for single plant yield in F_2.

The F_2 material of the two cross combinations ADT 43 x IRBB 60 and ASD 16 x IRBB 60 were raised along with their parents in non-randomized design with single seedling per hill. Totally 1100 plants were raised as cross derivatives of ADT 43 x IRBB60 and ASD16 x IRBB60 and all the plants were individually tagged before flowering. The F_3 progeny of these two crosses were selected on the basis of mean ± 2SE for single plant yield (Sawant et al. 1994) .One hundred and fifty families (75 families from each cross) of two crosses were raised in F_3 in a Randomized Block Design replicated twice with single seedling per hill adopting a spacing of 20cm between rows and 10 cm between plants at Paddy Breeding Station, Tamil Nadu Agricultural University, Coimbatore. Scheduled cultural operations and need based plant protection measures were carried out. Observations were recorded on days to flowering, plant height(cm), panicle length(cm), effective tillers per plant, grain number per panicle, 100 grain weight(g), single plant yield(g), kernel length(mm), kernel breadth(mm), L: B ratio of kernel ,gelatinization temperature on individual plant basis in F_2 , while in F_3 same observations were recorded in randomly chosen five single plant per family in each replication. The parent progeny regression analysis was carried out by regressing the mean values of a character in the progeny (F_3) upon the value of a character in the parents (F_2) The regression coefficient b was calculated by using the formula suggested by Lush (1940).

In the present study, the selection response of the selected trait, **i e.,** the single plant yield showed a significant correlation and regression for both ADT 43 x IRBB 60 and ASD 16 x IRBB 60 at positive selection level. The chances of identifying the superior genotypes at this level, for both crosses were high. These results indicated that selection would be more effective, when exercised at these levels for respective crosses. (Table 1 and 2). These results are in agreement with the findings of (Ganesan et al. 1998) for three levels of selection in F_2 to F_3 generation of rice.

When unselected traits were taken into consideration at positive level, significant positive association was observed in both the crosses ADT 43 x IRBB 60 and ASD 16 x IRBB 60 for most of the characters, except days to flowering, plant height, grain quality characters. At modal selection level, positive and significant regression and correlation estimates were observed for plant height, grains per panicle (ASD 16 x IRBB 60) (Table 2); and number of productive tillers per plant, number of grains per panicle, 100 grain weight(ADT 43 IRBB 60) (Table 2). These results indicated that selection would be more effective, when exercised at these levels, for respective crosses (Ganesan et al., 1998). The selection importance of these traits had been already suggested by Ganesan et al. (1998) for panicle length; Rao and Saxena (1999) for number of grains per panicle, Smalley et al. (2004) for plant height; Kole (2006) for 100-grain weight and number of tillers per plant.

When all these selection levels are taken in to consideration, positive selection level was found to be suitable for effective selection of desirable segregants for almost all characters in both crosses, especially for ADT 43 x IRBB 60, this was followed by modal level of selection. In the present study, when the two crosses and quantitative characters were taken into account and evaluating them right from the unit analysis, it was found that the cross ADT 43 x IR BB60 performed better than ASD 16 x IRBB60. Among the characters, plant height, panicle length, number of grains per panicle, 100 grain weight were found to be the yield determinants.

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Table 1. Parent –progeny correlation (r) and regression (b) coefficients between F_2 and F_3 generations for single plant yield and its component traits in the cross ADT 43 x IRBB 60, for three level of selection

Characters	Mean+SD (Positive)		Mean±SD (Modal)		Mean-SD (Negative)	
	b	r	b	r	b	r
Single plant yield(g)	0.2106*	0.4371*	0.4229*	0.3897	0.03997	0.0447
Days to flowering	-0.0082	-0.0171	-0.0636	-0.0642	0.0437	0.1496
Plant height(cm)	0.0291	0.1952	-0.1871	-0.1328	0.3826*	0.4456*
Panicle length(cm)	0.5281**	0.5756**	-0.0371	-0.0914	0.5555	0.3125
Number of productive tillers per plant	0.6582**	0.8185**	0.6582**	0.8195**	0.1282	0.2832
Number of grains per panicle	0.3180**	0.4535**	0.5105**	0.5594**	-0.0854	-0.1290
Hundred grain weight(g)	0.1526**	0.4982*	0.2890*	0.3681**	-0.0080	-0.0251
kernel length(mm)	0.2396	0.2256	-0.1906	-0.1327	0.5030	0.2827
kernel breadth(mm)	-0.1311	-0.1798	-0.1311	-0.1798	-0.1311	-0.1798
L/B ratio of kernel	-0.1509	-0.3002	0.0159	0.0407	-0.0549	-0.1350
Gelatinization temperature	-0.0521	-0.0391	-0.0521	-0.0391	-0.0540	-0.0391

*, Significant at 5% level, ** significant at 1 % level.

Table 2. Parent –progeny correlation (r) and regression (b) coefficients between F_2 and F_3 generations for single plant yield and its component traits in the cross ASD 16 x IRBB 60, for three level of selection

Characters	Mean+SD (Positive)		Mean±SD (Modal)		Mean-SD Negative)	
	b	r	b	r	b	r
Single plant yield(g)	0.3790**	0.4646**	0.0804	0.1866	0.3632	0.3040
Days to flowering	0.0341	0.0421	0.1312	0.1082	0.1385	0.1784
Plant height(cm)	0.2295	0.2171	0.5022*	0.6129*	0.0918	0.1343
Panicle length(cm)	0.5891**	0.4647**	-0.0597	-0.0563	0.2857	0.3193
Number of productive tillers per plant	0.7908**	0.7074**	0.1686	0.2176	-0.3932	-0.2828
Number of grains per panicle	0.4827*	0.4480**	0.8026**	0.6070**	0.0409	0.1026
Hundred grain weight(g)	0.3837*	0.4608**	0.1264	0.1900	-0.0240	-0.0506
kernel length(mm)	0.0085	0.1870	0.8077	0.3099	0.1610	0.1848
kernel breadth(mm)	-0.0616	-0.0589	0.2388	0.3244	0.0186	0.0177
L/B ratio of kernel	0.0456	0.0419	0.1380	0.1313	0.3641	0.2139
Gelatinization temperature	-0.0869	-0.0667	-0.0740	-0.1814	-0.0818	-0.1784

*, Significant at 5% level **, significant at 1 % level;