

GENETIC ANALYSIS OF YIELD AND YIELD CONTRIBUTING TRAITS IN RICE (*Oryza sativa* L.) BC₂F₃ POPULATION DERIVED FROM MR264 × PS2

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ABSTRACT

High yield potential in rice is indirectly determined by yield related traits. These traits are complex and regulated by several genes whose expression is affected by environmental conditions. It is of great importance to disclose the genetic relationships between yield and its yield components for multi-trait improvement in rice. Therefore, present study was aimed to investigate the genetic variability and inheritance patterns of yield and yield attributed traits in BC₂F₃ rice lines to identify the ideal lines from the selection. A total of 36 improved version of blast resistant plant in BC₂F₃ population used in this study were developed from a single cross between a high yielding mutant rice variety but susceptible to blast, MR264 and Malaysian local variety donor for (*Pi-7(t)* and *Pikh* blast resistant genes. Analysis of variance showed that all traits were significantly different for lines except grain length and grain width. High heritability and genetic advance were recorded for plant height, number of tillers, filled grain, 1000-grain weight and seed setting rate. Significant and positive correlation was recorded with most evaluated traits except for grain length and grain width. Thirty-six BC₂F₃ lines were clustered into four major group and the first three principal component (PC3) contributed 71.13% of total variation with 1000 seed weight, yield/hill and filled grain being the main discriminatory characters. Finding in this study showed an adequate genetic variability in the lines and 1000 seed weight, yield/hill and filled grain traits could be consider for indirect selection in breeding programs in next generations.

OBJECTIVES

- To investigate the genetic variability and inheritance patterns of yield and yield attributed traits in BC₂F₃ rice lines to identify the ideal lines from the selection..

METHODOLOGY

BC₂F₃ population was planted from September 2017 to April 2018 in the greenhouse at Agency Nuclear Malaysia Greenhouse, Kajang, Selangor, Malaysia.

Genetic Analysis (Johnson et al. 1955) & Genetic Diversity were analyzed (Oladosu et al. 2020).

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RESULT AND DISCUSSION

Table 1: Variance components and heritability values (*h*²*B*) for yield and yields components

Traits	Mean	MSG	MSE	σ^2G	σ^2P	PCV (%)	GCV (%)	<i>h</i> ² <i>B</i> (%)	GA (%)
DOM	117.04	81.24	23.07	19.39	42.46	5.57	3.76	45.66	5.24
PH	93.27	388.52	19.37	123.05	142.42	12.79	11.89	86.40	22.77
NOT	18.00	71.17	4.50	22.23	26.72	28.72	26.19	83.17	49.20
PL	22.86	10.43	3.09	2.45	5.53	10.29	6.84	44.18	9.37
FG	143.65	4124.92	69.39	1351.84	1421.23	26.24	25.60	95.12	51.42
GL	9.32	3.65	2.57	0.36	2.93	18.37	6.42	12.23	4.63
GW	1.96	0.03	0.03	0.00	0.03	8.24	0.88	1.15	0.20
Y	39.11	32.57	3.26	9.77	13.03	9.23	7.99	75.00	14.26
1000-GW	21.11	28.83	3.89	8.31	12.20	16.55	13.66	68.14	23.23
SS	83.04	331.12	4.29	108.94	113.23	12.81	12.57	96.21	25.40

Note: MSG, mean square of accessions; MSE, mean square of error; 2G, genotypic variance; 2P, phenotypic variance; PCV, phenotypic coefficient of variance; GCV, genotypic coefficient of variance; *h*²*B*, heritability in broad sense; GA, genetic advance

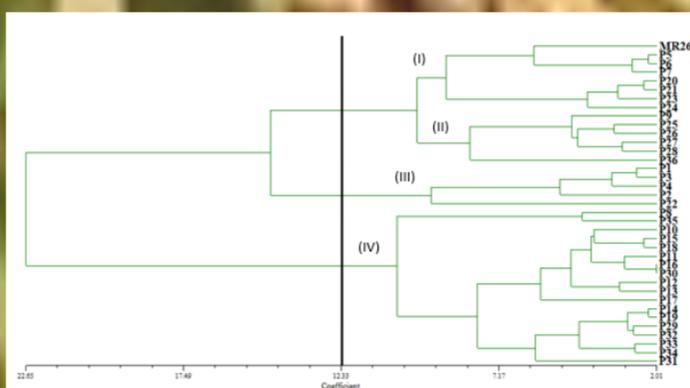


Fig.2: Cluster analysis grouped 36 BC₂F₃ rice lines with MR264 based on 10 quantitative traits

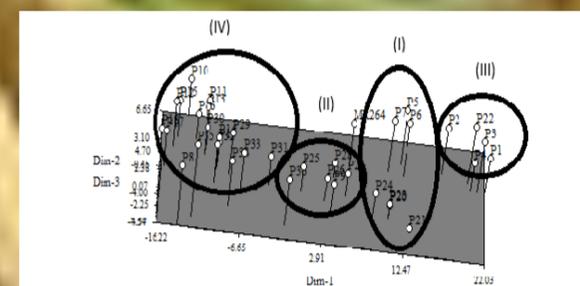


Fig.3: Three-dimensional plots of PCA indicating the 36 BC₂F₃ rice lines with MR264 based on 10 agro-morphological traits

Table 4: Correlation coefficient among 10 quantitative traits for 36 homozygous blast resistant lines with MR264 rice variety

Traits	DOM	PH	NOT	PL	FG	GL	GW	Y	1000-GW	SS
DOM	1	0.3075*	-0.1705*	0.0810	-0.0499	0.0175	-0.3148*	-0.4453*	-0.1320	0.0810
PH	0.3075*	1.0000	-0.4160*	-0.2281*	-0.6525*	-0.0233	-0.2499*	-0.5420*	-0.5661*	-0.4828 *
NOT	-0.2619*	-0.4160*	1.0000	0.2543*	0.2414*	-0.0486	-0.0428	0.2643*	0.5456*	0.3853*
PL	0.0810	-0.2281*	0.2543*	1.0000	0.3198*	-0.0729	-0.1774	0.1964*	0.3009*	-0.0425
FG	-0.0499	-0.6525*	0.2414*	0.3198*	1.0000	0.0551	0.1210	0.4819*	0.6821*	0.4089*
GL	0.0175	-0.0233	-0.0486	-0.0729	0.0551	1.0000	-0.0065	0.0257	-0.0398	-0.1438
GW	-0.3148*	-0.2499*	-0.0428	-0.1774	0.1210	-0.0065	1.0000	0.2902	0.0268	0.0557
Y	-0.4453*	-0.5420*	0.2643*	0.1964*	0.4819*	0.0257	0.2902*	1.0000	0.4393*	0.236*
1000-GW	-0.1320*	-0.5661*	0.5456*	0.3009*	0.6821*	-0.0398	0.0268	0.4393*	1.0000	0.4288*
SS	-0.1705	-0.4828*	0.3853*	-0.0425	0.4089*	-0.1438	0.0557	0.2360*	0.4288*	1.0000

Note: *significant at 0.05 probability level

CONCLUSION

Present study indicated the present of a considerable level of diversity among 36 BC₂F₃ rice lines. The highest heritability and genetic advance found for the plant height, number of tillers, filled grain, 1000-grain weight and seed setting rate remarked crucial for trait selection for hybridization programme. Furthermore, based on the cluster analyses, selected blast resistant lines from 5, 6, 7, 20, 21, 23, 24 which produce high yield, carrying blast resistant genes and ideal morphological traits could be used as parents for future breeding program.