

SHORT COMMUNICATION

QUANTITATIVE GENETIC ANALYSIS ON AMYLOSE CONTENT IN RICE (*Oryza sativa* L.)

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High grain amylose content is the main feature of leading rice cultivars in the Mekong Delta. Attempt to improve this trait (intermediate amylose) is one of the CLRRRI's breeding objectives. High amylose content is incompletely dominant to low and it is controlled by a major gene and several modifiers (Ghosh and Govidaswami 1972).

Genetic components of combining ability estimates of amylose content in rice were analyzed using eight-parent complete diallel set. They are Khao Dawk Mali 105, Jasmine 85, IR64, IR48, OM987, CNA 6820, Tung sa, Ba Nguon. Seeds of 56 F_1 's and eight parents were grown in randomized complete block design with three replications. Amylose content was analyzed according to Sadavisam and Manikam (1992). The genetic components of variation were calculated following Hayman's procedure, general combining ability (gca), specific combining ability (sca) analyses were implemented following Griffing's procedures, method I, model I (Singh and Chaudhary 1985)

Mean degree of dominance $(H_1/D)^{1/2} = 1.54$ showed that genes controlling amylose are overdominance. Proportion of genes with positive and negative effects in the parents $H_2/4H_1 < 0.25$ indicated unequal allelic frequency. Proportion of dominant and recessive

genes in the parents $K_d / K_r = 2.23 > 1$, and $F > 0$ means that dominant gene action is more predominant than recessive gene action in term of amylose trait.

The variance ratio $(2\sigma^2_{gca} / [2\sigma^2_{gca} + \sigma^2_{sca}])$ was computed from the expected components of the mean square of gca and sca, assuming a fixed model to assess the relative importance of additive and non-additive gene effects in predicting progeny performance (Ram et al. 1989). This value indicated that non-additive gene action was more important than additive gene action in the inheritance of amylose content. High significant mean squares for the trait for both gca and sca indicated the importance of both additive and non-additive gene action (table 1). However, the σ^2_{gca} was higher than σ^2_{sca} suggesting the prevalence of non-additive gene effect for amylose.

The merits of the parents were evaluated on the basis of gca effects (table 2). Khao Dawk Mali was the top general combiner for lower amylose trait. The gca value of Jasmine 85 was not significant. Specific combining ability effects were studied in top hybrids for lower amylose content (negative value), however, no hybrid was selected due to no significance

Table 1. ANOVA for combining ability

Source	df	Mean square	F
Gca	7	5.72	62.86**
sca	28	567.81	6239.67**
rec	28	0.25	2.74**
Error	126	0.091	

Table 2. General combining ability effects (diagonal values), specific combining ability effects (above diagonal), and reciprocal effects (below diagonal)

	P1	P2	P3	P4	P5	P6	P7	P8
P1	-1.08*	0.43	0.43	0.22	0.64	-0.49	0.73	1.78
P2	-0.73	-0.49	-0.20	0.35	0.21	-0.42	0.20	-0.51
P3	-0.37	-0.42	0.08	-0.29	-0.21	-0.44	-0.34	0.64
P4	0.73	-0.01	0.25	0.42	-0.36	-0.11	-0.43	-0.72
P5	-0.12	0.37	0.22	0.08	0.32	0.11	-0.28	-0.053
P6	0.17	0.43	0.78	-0.25	0.23	-0.39	0.63	-0.42
P7	0.42	-0.03	0.00	0.25	0.30	0.33	0.56	-0.89
P8	-0.33	-0.37	0.35	0.00	-0.08	0.35	-0.13	0.59

P1: *Khao Dawk Mali 105*, P2: *Jasmine 85*, P3: *IR64*, P4: *IR48*, P5: *OM987*, P6: *CNA6820*, P7: *TUNG SA*, P8: *BA NGUON*.

References

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TÓM TẮT

Phân tích di truyền số lượng tính trạng amylose

Hàm lượng amylose cao là một đặc tính của các giống lúa phổ biến đang trồng ở Việt Nam. Mục tiêu cải tiến giống hiện nay nhằm giảm hàm lượng amylose xuống ở mức trung bình (#20%). Trước tiên, bố mẹ trong chương trình lai tạo cần được đánh giá thông qua phân tích diallel, với thông số di truyền Hayman và Griffing. Mặc dù chúng ta biết amylose do một gen điều khiển, nhưng cùng tham gia còn có những gen phụ (modifiers) được ghi nhận trong nhiều phân tích trước đây. Tám vật liệu bố mẹ là Khao Dawk Mali 105, Jasmine 85, IR64, IR48, OM987, CNA6820, Tung sa, Ba Nguơn. Thông số Hayman cho thấy hoạt động gen mang tính siêu trội kiểm soát hàm lượng amylose cao, với tần suất gen trội và gen lặn không bằng nhau, alen trội chiếm ưu thế. Thông số Griffing cho thấy hoạt động của gen không cộng có ưu thế hơn hẳn hoạt động nhóm gen cộng. Giống Khao Dawk Mali 105 có giá trị khả năng phối hợp chung tốt cho mục tiêu giảm hàm lượng amylose trong chương trình lai tạo giống hiện nay.