

Genetic Analysis for Spikelet Fertility Related to Cold Tolerance in *Japonica* Rice

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Objectives

This study was conducted to investigate the genetic mode among crosses by using joint scaling test in order to breed cold-tolerant varieties.

Materials and Methods

○ Plant Materials

- P₁, P₂, F₁, F₂, B₁(F₁×P₁), and B₂(F₁×P₂) populations derived from 8 crosses

○ Methods:

- Cold water temperature : 17°C (5cm water depth)

- Treatment Period : 20 days after transplanting to 45 days after heading

- Genetic Analysis : Scaling test by partitioning components of generation means proposed by Mather (1949), Hayman and Mather (1955) and Hayman (1958)

Results and Discussion

In the scaling tests, the values of A, B, and C for spikelet fertility were not significantly at t-values, 0.5 probability level. Therefore, spikelet fertility in eight crosses were fitted to additive-dominance model which is applicable in the case of no interaction among non-allelic genes. The inheritance mode for spikelet fertility was evaluated as additive, dominance, and additive-dominance gene effects. The results of chi-square test of the deviation of the observed mean from the expected mean for each progeny were found as non-significance, proving the employment of the genetic analysis for spikelet fertility in all crosses was adequate. Mean effect of Unbong31/Stejaree45 was higher than that of other crosses. Additive ([d]) effect was higher than dominant ([h]) effect and the average degree of dominance ([h]/[d]) was less than 1, implying partial dominance in all crosses except for Unbong31/Sambaegbyeo.

Table 1. Scaling test and estimates of gene effect of spikelet fertility for six populations using the eight crosses.

Combination	UB/SM	UB/HT	UB/HR	UB/ST
Scaling test				
A	-0.61 ^{ns}	0.49 ^{ns}	-0.07 ^{ns}	-0.04 ^{ns}
B	-0.42 ^{ns}	-0.41 ^{ns}	0.45 ^{ns}	-0.90 ^{ns}
C	-0.87 ^{ns}	-0.37 ^{ns}	-0.96 ^{ns}	-0.27 ^{ns}
Estimates of gene effects				
M	57.7±5.4 ^{**}	67.9±3.1 ^{**}	55.3±3.7 ^{**}	71.3±3.8 ^{**}
[d]	7.6±5.4 ^{ns}	-6.5±3.1 [*]	8.3±3.8 [*]	-10.4±3.8 ^{**}
[h]	17.8±8.7 [*]	5.9±5.8 ^{ns}	0.42±5.8 ^{ns}	4.4±7.8 ^{ns}
[d]/[h]	2.3	0.9	0.05	0.42
Combination	SM/HT	SM/ST	HT/HR	HT/ST
Scaling test				
A	1.39 ^{ns}	-0.09 ^{ns}	-0.43 ^{ns}	-0.16 ^{ns}
B	0.21 ^{ns}	-0.71 ^{ns}	-0.01 ^{ns}	-1.20 ^{ns}
C	0.31 ^{ns}	-0.46 ^{ns}	-0.30 ^{ns}	-0.23 ^{ns}
Estimates of gene effects				
M	60.7±4.3 ^{**}	68.8±5.5 ^{**}	56.5±4.6 ^{**}	57.0±4.1 ^{**}
[d]	-20.4±4.4 ^{**}	-12.2±5.5 [*]	24.6±4.6 ^{**}	-24.1±4.1 ^{**}
[h]	17.8±7.5 [*]	-6.7±9.3 ^{ns}	19.0±7.6 [*]	16.4±12.7 ^{ns}
[d]/[h]	0.87	0.55	0.77	0.68

^{ns}, ^{*}, ^{**} : Non-significant, 0.05 and 0.01 probability levels, respectively

UB : Unbong31, SM : Sambaegbye, HT : Hitomebore, HR : HR19621-AC6, ST : Stejaree 45

Table 2. Generation means and joint scaling test of spikelet fertility for six populations using the eight crosses.

Generation	UB/SM	UB/HT	UB/HR	UB/ST	SM/HT	SM/ST	HT/HR	HT/ST
P ₁	67 [†]	61	64	61	36	57	82	33
	(65.3 [‡])	(61.4)	(63.6)	(60.9)	(40.2)	(56.6)	(81.1)	(32.9)
P ₂	52	75	47	83	81	83	32	82
	(50.1)	(74.4)	(47.0)	(81.7)	(81.1)	(81.0)	(31.9)	(81.1)
F ₁	78	74	56	78	76	64	76	80
	(75.5)	(73.8)	(55.7)	(75.7)	(78.5)	(62.1)	(75.5)	(73.4)
F ₂	56	66	38	71	71	60	60	63
	(66.6)	(70.8)	(55.5)	(73.5)	(69.6)	(65.4)	(66.0)	(65.2)
B ₁	63	70	59	69	73	59	73	53
	(70.4)	(67.6)	(59.6)	(68.3)	(59.3)	(59.4)	(78.3)	(53.2)
B ₂	59	73	60	70	81	61	54	60
	(62.8)	(74.1)	(51.4)	(78.7)	(79.8)	(71.6)	(53.7)	(77.3)
$\chi^2_{(3)}$	0.41 ^{ns}	0.81 ^{ns}	0.07 ^{ns}	0.77 ^{ns}	0.29 ^{ns}	0.55 ^{ns}	0.82 ^{ns}	0.21 ^{ns}

† Observed means, ‡ Expected means.

^{ns}, ^{*}, ^{**} : Non-significant, 0.05 and 0.01 probability levels, respectively

UB : Unbong31, SM : Sambaegbye, HT : Hitomebore, HR : HR19621-AC6, ST : Stejaree 45