

P.21 Study of the genetic basis of heterosis for cold tolerance in rice as revealed by QTL analysis using molecular markers

Jung-Pil Suh*, Soo-Jin Kwon*, Im-Soo Choi*, Young-Chan Cho*, Sang Nag Ahn**,
Hung-Goo Hwang*, Hak-Soo Suh*** and Hae-Chune Choi*

*National Crop Experiment Station, **Chungnam National University,

***Yeungnam University

벼에서 분자마커를 이용한 내냉성 잡종강세에 관한 유전연구

서정필*, 권수진*, 최임수*, 조영찬*, 안상낙**, 황홍구*, 서학수***, 최해춘*

*작물시험장, **충남대학교, ***영남대학교

Purpose of study

This study was to determine the genetic basis of heterosis to cold tolerance in a cross of cold tolerant variety Stejaree45(*japonica*) and cold susceptible variety Milyang23(Tongil type).

Materials and methods

- Materials : Milyang23, Stejaree45, RILs(Milyang23/Stejaree45 F₉ lines), RILs/Milyang23(BC₁F₈ 143 lines; BC/T), RILs/Stejaree45(BC₁F₈ 143 lines; BC/J)
- Methods :
 - Cold tolerance test : The materials were subjected to cold water stress at 17°C, starting from 20 days after transplanting until maturity.
 - Evaluated traits : heading delay, culm length reduction, leaf discoloration *etc.*
 - SSR analysis : Silver staining method (Panaud *et al.* 1996)
 - Data analysis : Data Desk 4.0 (Data Description Inc. 1992), MAPMAKER/EXP. Version 3.0 (Lander *et al.* 1987)

Results

- For heterobeltiosis (heterosis over the better parent), spikelet fertility reduction showed the strongest significant heterosis (55.20%), followed by PA-tillering (28.57%), number of spikelets reduction (49.82%), panicle exsertion (23.66%).
- Except for culm length reduction in the BC/J, all other traits showed no relationship between the genome heterozygosity and trait performance in both BC₁F₈ populations.
- The genetic basis of heterosis for cold tolerance in the F₁ hybrid examined is largely suggested by dominance.

Table 1. Characteristics of QTLs linked affecting the traits related with cold tolerance in populations backcrossed to Milyang23 and Stejaree45.

Trait	Population	QTL	Markers linked the QTL	P value	iR ² (%)	Phenotypic effect	Phenotype comparison of different genotypes
Heading delay (days)	BC/T	qDTH-10	RM333	0.0024	7.0	1.4	TJ<TT
	BC/J	qDTH-11	RM20B	-0.0090	5.8	-1.7	TJ>JJ
Culm length reduction (%)	BC/T	qICL-4	RM335	0.0103	4.8	2.9	TJ<TT
	BC/T	qICL-4-1	RM255	-0.0106	5.1	-3.3	TJ>TT
	BC/J	qCL-2	RM208	0.0107	5.3	2.7	TJ<JJ
No. of spikelets reduction (%)	BC/T	qISPP-2	OSR11	0.0168	4.4	6.2	TJ<TT
	BC/J	qISPP-7	RM295	0.0182	4.6	5.6	TJ<JJ
Spikelet fertility reduction (%)	BC/T	qIFER-2	RM221	0.0007	9.9	14.9	TJ<TT
	BC/T	qIFER-5	RM163	0.0141	4.3	9.6	TJ<TT
	BC/T	qIFER-7	RM298	-0.0152	4.7	-10.0	TJ>TT
	BC/J	qIFER-1	OSR23	-0.0005	9.6	-14.2	TJ>JJ
	BC/J	qIFER-4	RM335	-0.0090	5.0	-9.8	TJ>JJ
	BC/J	qIFER-11	RM254	0.0015	8.4	12.2	TJ<JJ
	BC/J	qIFER-12	RM20A	0.0000	12.9	-17.4	TJ>JJ
No. of panicle reduction (%)	BC/T	qIPN-1	RM259	0.0264	3.7	9.1	TJ<TT
	BC/T	qIPN-3	RM16	-0.0261	4.4	-9.6	TJ>TT
	BC/J	qIPN-11	RM224	-0.0018	8.5	-12.9	TJ>JJ
	BC/J	qIPN-12	RM20A	-0.0198	4.7	-10.5	TJ>JJ
Panicle length reduction (%)	BC/T	qIPL-3	RM81B	-0.0162	5.5	-4.2	TJ>TT
	BC/T	qIPL-10	RM228	0.0028	7.5	4.9	TJ<TT
	BC/T	qIPL-11	RM167	0.0175	4.7	3.9	TJ<TT
	BC/J	qIPL-1	OSR23	0.0257	4.2	3.6	TJ<JJ
Leaf discoloration (1-9)	BC/T	qDC-1	OSR24	0.0112	4.8	0.35	TJ<TT
	BC/T	qDC-2	OSR8	-0.0145	4.7	-0.35	TJ>TT
	BC/T	qDC-9	OSR12	0.0095	5.3	0.37	TJ<TT
	BC/J	qDC-2	OSR9	0.0054	5.8	0.37	TJ<JJ
	BC/J	qDC-6	OSR21	-0.0095	5.1	-0.35	TJ>JJ
PA-tillering (1-9)	BC/T	qPAT-1	OSR24	0.0032	6.5	0.42	TJ<TT
	BC/T	qPAT-2	OSR8	-0.0165	4.5	-0.35	TJ>TT
	BC/T	qPAT-4	RM335	0.0141	4.4	0.34	TJ<TT
	BC/J	qPAT-2	OSR9	0.0032	6.5	0.33	TJ<JJ
	BC/J	qPAT-6	RM345	-0.0056	5.6	-0.30	TJ>JJ
PA-maturity (1-9)	BC/T	qPAM-3	RM81B	-0.0170	5.4	-0.47	TJ>TT
	BC/J	qPAM-2	OSR26	0.0155	4.3	0.43	TJ<JJ
	BC/J	qPAM-11	RM254	0.0101	5.7	0.47	TJ<JJ
	BC/J	qPAM-12	RM270	-0.0165	4.3	-0.47	TJ>JJ
Panicle exsertion (1-9)	BC/T	qPE-12	RM270	0.0179	4.2	0.41	TJ<TT
	BC/J	qPE-1	RM315	-0.0019	7.6	-0.7	TJ>JJ
	BC/J	qPE-6	RM3	-0.0183	5.0	-0.48	TJ>JJ
	BC/J	qPE-12	RM270	-0.0012	7.7	-0.7	TJ>JJ

P value refers to the probability that the marker listed on the left and having a higher sR² does not have effect on the trait.

The signs, + (omitted) and - preceding phenotypic effects indicate that the heterozygote had a higher phenotypic effect than the respective homozygote, and the heterozygote had higher phenotypic effect than the respective homozygote, respectively. T and J in the genotypes represent the alleles of the locus originating from Milyang23 and Stejaree45, respectively.

BC/T : RILs/Milyang23(BC₁F₈ population), BC/J : RILs/Stejaree45(BC₁F₈ population)