

Identification of QTLs governing hybrid fertility between subspecies in rice

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Objective

The objective of the present study was to identify QTLs associated with inter-subspecific hybrid fertility and to investigate the relationship among the identified hybrid sterility QTLs and QTLs for some agronomic characters.

Materials and Methods

○ Materials:

Dasanbyeo(*indica*)/TR22183(*japonica*)(F₉) RI 166 lines

Indica(Dasanbyeo) backcrossed lines(*i//i/j*) BC₁F₁-I

Japonica(TR22183) backcrossed lines(*j//i/j*) BC₁F₁-J

○ Methods:

Phenotyping for culm length(CL), panicle length(PL), shattering(SH), brown rice length/width ratio(BLWR), grain length/width ratio(GLWR), spikelet fertility(SF), pollen fertility(PF), 1000 grain weight(1000GW), days to heading(DTH), spikelet density(SD), panicle number(PN), cold tolerance at seedling stage(CTS), alkali digestion value(ADV), potassium chlorate resistance(KCL), phenol reaction(PH), spikelet fertility and pollen fertility for BC₁F₁-I and BC₁F₁-J (SFI, SFJ, PFI, PFJ each)

Genotyping marker : 160 microsatellite, STS

○ QTL and epistasis analysis:

Interval mapping using Qgene 3.06 program and Epistacy version 2.0 SAS program.

Results and Discussion

Several QTLs were detected on CL, DTH, PH, KCL, GLWR, SH, PF and SF. QTLs detected in STS509.5~STS5014.1-17.9 on chromosome 5 for spikelet fertility and two adjacent QTLs RM153~STS5030.7 and STS5032.5~RM593 for pollen fertility in the *i//i/j* BC₁F₁ populations. And the neighboring two QTLs, STS509.5~STS5014.1-17.9 and STS5032.5~RM267 for spikelet fertility and wide range QTL RM122~RM593 for pollen fertility found in the *j//i/j* BC₁F₁ populations(Table1, Figure 1). Additional QTL for spikelet fertility in the *j//i/j* BC₁F₁ population was detected in RM126~RM342A on chromosome 8. QTLs for pollen and spikelet fertility in BC₁F₁ populations appeared not to be directly associated with the regions where segregation distortion occurred, implying that different mechanisms might be involved(Figure 2).

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Table 1. List of QTLs for hybrid sterility and agronomic characters in DT RILs

Name	Character	Ch.	Interval	Range(cM)	r^2 (%)	LOD	A	Threshold**
qCL0101	CL	1	RM600-RM312	81-82	7.68	2.88	-3.73	2.88
qCL0102	CL	1	RM237-RM165	178-191	8.11	3.05	-3.4	2.88
qSH01	SH	1	RM237-RM165	166-201	22.01	8.96	11.83	3.00
qDTH03	DTH	3	RM143-RM468	248-249	7.93	2.98	2.61	2.97
qDTH0801	DTH	8	RM25-RM342A	0-26	23.36	9.59	4.1	2.97
qDTH0802	DTH	8	RM342A-RM284	26-45	23.44	9.63	4.45	2.97
qDTH10	DTH	10	RM216	0	7.91	2.97	2.29	2.97
qGW03	1000GW	3	STS302.2-STS3015.2-1	13-15	8.19	3.06	0.84	2.97
qGW0501	1000GW	5	STS5077.4-RM440	83-90	10.64	4.03	1.05	2.97
qGW0502	1000GW	5	RM173-RM538	104-105	7.98	2.98	0.95	2.97
qGW07	1000GW	7	RM248-RM420	142-148	7.95	2.97	0.85	2.97
qGW08	1000GW	8	RM350-RM264	84-91	8.31	3.11	1.39	2.97
qGW12	1000GW	12	RM20A-RM4A	6-16	11.23	4.27	1.23	2.97
qADV01	ADV	1	RM84-RM323	0-16	10.18	3.8	-0.49	2.96
qPH04	PH	4	RM317-RM124	136-210	29.85	12.78	0.64	2.96
qKCL0101	KCIO3R	1	RM600-RM312	79-88	9.03	3.33	0.25	2.94
qKCL0102	KCIO3R	1	RM312-RM128	92-112	9.03	3.33	0.37	2.94
qKCL02	KCIO3R	2	RM475-RM263	210-211	8.02	2.94	0.25	2.94
qBLWR02	BLWR	2	RM53-RM438	61-82	8.77	3.29	0.07	2.85
qSFJ0501	SFJ	5	STS5032.5-RM267	38	8.3	3.05	-8.23	3.05
qSFJ0502	SFJ	5	RM593-RM249	43-46	18.14	7.04	-11.78	3.05
qSFJ0801	SFJ	8	RM72-RM126	19-21	9.34	3.45	8.04	3.05
qSFJ0802	SFJ	8	RM342A-STS8055.4	29-32	9.16	3.38	8.31	3.05
qPFI0501	PFI	5	STS509.5-RM153	4	8.31	3.11	6.84	2.95
qPFI0502	PFI	5	RM593-RM249	43-45	10.61	4.02	6.87	2.95
qPFJ0501	PFJ	5	STS5014.1-17.9	14-20	10.09	3.74	-12.54	3.07
qPFJ0502	PFJ	5	RM593-RM249	22-39	15.73	6.02	-12.52	3.07
qPFJ0503	PFJ	5	RM146-RM430	41-46	16.75	6.45	-13.6	3.07

* Threshold LOD calculated by 'permutation test' 1,000 shuffles by Qgene

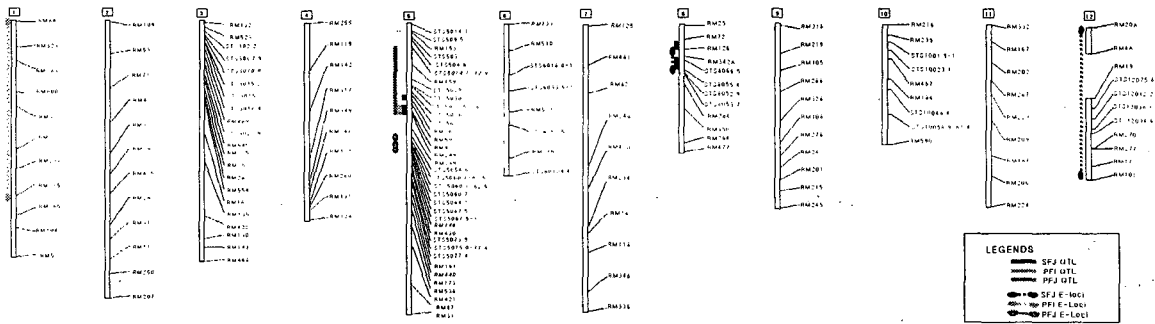


Figure 1. QTLs and digenic epistatic loci for hybrid sterility in DT RILs

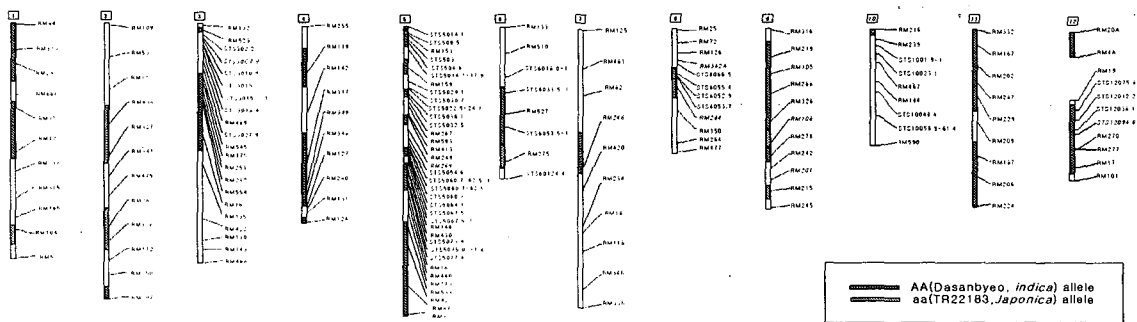


Figure 2. Segregation distortion of 160 loci in DT RILs