A07

Mapping of QTLs for Agronomic traits using an introgression line from a cross between an *Oryza sativa* and *O.minuta*

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Objectives

To identify quantitative trait loci (QTLs) for yield components and morphological traits using a backcross population between the *Oryza minuta* and the Korean cultivar Hwaseongbyeo

Materials and methods

1. Plant materials

- Parents: Hwaseongbyeo and HW29001 (*Hwaseongbyeo/O.minuta* BC5F4)
- Mapping population: 197 F2:3 lines

2. Genotyping: SSR markers,
3. QTL mapping: standard analysis of variance (ANOVA)

Results and discussion

1. The frequency distributions of phenotypes for each trait in F2population showed approximately normal distribution except for 1000 grain weight and secondary branch number. Five traits (DTH, PB, SP, GD, and SPP) showed transgressive variation, giving a large apparent variation in the F2 population (Fig. 1).

2. One-way ANOVA was carried out to detect associations of introgression with agronomic traits. A total of fourteen QTLs were identified for ten traits, and at six loci of the fourteen QTLs for traits including panicle number (*pn9*), and spikelets per panicle (*spp7*), the *O. minuta*alleles were beneficial in the Hwaseongbyeo background (Table 1 and Fig. 2). One QTL for heading date was located near the marker RM587 on chromosome 6. This allele from *O. minuta* increased the days to heading and this QTL explained 43.2% of the phenotypic variation. The four QTLs on chromosome 7 for primary branch number (*pb7*), seed per panicle (*sp7*), spikeles per panicle (*spp7*) and grain yield (*gd7*) were colocalized in the same interval. Among these QTLs identified, QTL for secondary branch number and awn have not been detected in previous QTL studies between *Oryza* cultivars, indicating potentially novel alleles from *O. minuta.*

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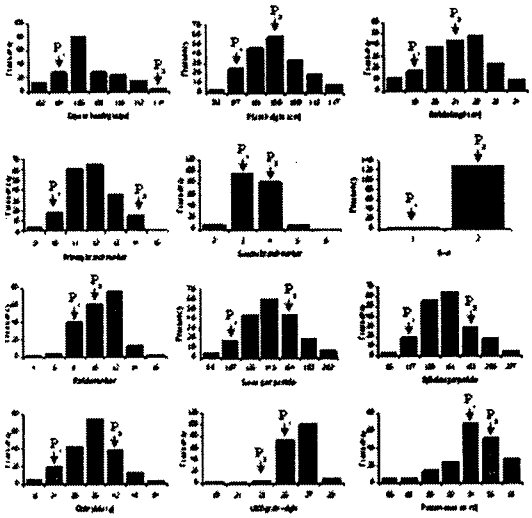

Fig. 3. Frequency distribution of 12 traits in the F2 population. (P1: Hwaseongbyeo, P2: HW29001)

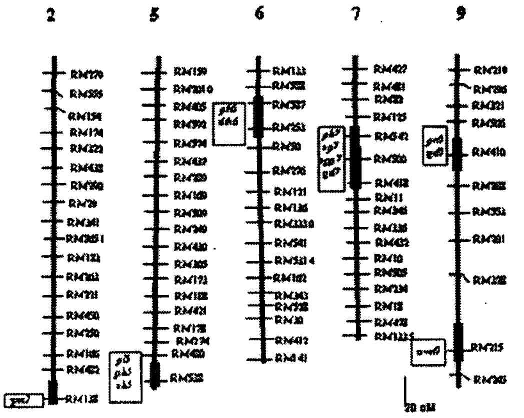

Fig. 4. A map with polymorphic markers between the parents. Chromosome number is on the top, and loci names are listed to the right. QTLs detected are labeled on the left of the chromosome. Dark chromosome regions mark the *O. minuta*-specific introgressions.

Table 1. QTLs detected for ten traits based on single-point analysis in an F_2 population

Trait	QTL locus	SSR marker	Chr.	*P*	R^2(%)	Mean			
						H/H*	H/W	W/W	Allele effect
Days to heading	*dth6*	RM587	6	0.0001	43.2	104.4	105.8	109.5	2.55
Plant height	*ph6*	RM587	6	0.0001	11.9	100.9	103.4	106.0	2.55
Panicle length	*pl5*	RM538	5	0.0018	6.2	21.6	21.2	20.5	-0.55
	pl7	RM542	7	0.0009	4.3	21.1	21.5	20.0	-0.55
Panicle number	*pn2*	RM138	2	0.0124	2.5	10.0	10.4	9.3	-0.40
	pn9	RM410	9	0.0004	2.9	9.7	9.7	10.9	0.60
Primary branch	*pb5*	RM538	5	0.0464	3.0	12.1	11.9	11.5	-0.30
	pb7	RM418	7	0.0017	6.1	11.3	11.9	12.2	0.45
Secondary branch	*sb5*	RM538	5	0.0238	3.2	3.6	3.5	3.2	-0.20
Seeds per panicle	*sp7*	RM445	7	0.0090	4.8	129.2	137.9	145.6	8.20
Spikelets per panicle	*spp7*	RM445	7	0.0125	4.4	138.6	147.3	155.9	8.70
Grain yield	*gd7*	RM418	7	0.0300	3.8	30.2	33.4	34.2	2.00
	gd9	RM410	9	0.0051	3.0	31.0	32,3	35.5	2.25
Awn	*awn9*	RM215	9	0.0001	12.1	1.9	2.4	2.7	0.40

H/H, H/W, W/W: Hwaseongbyeo homozygotes, Hwaseongbyeo / HW29001 heterozygotes, and *O. minuta* homozygotes, respectively.