

Introgression for agronomic traits from *Oryza minuta* into rice, *O. sativa*

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OBJECTIVES

To identify and characterize alien QTLs underlying traits of agronomic importance in backcross progeny derived from a cross between *Oryza sativa* and *O. minuta* using PCR-based markers

MATERIALS AND METHODS

o Plant materials

- Parent: Hwaseong and WH79006 (Hwaseong/*O. minuta* BC5F6)
- Mapping population: 75 F_{2:3} lines

o Genotyping: SSR markers

o Traits evaluated: heading date, culm length, panicle length and panicle number, seed length, width and thickness, 1,000 seed weight and seed length/width ratio, seeding height

RESULTS AND DISCUSSION

o The frequency distribution of 10 traits in 75 F_{2:3} lines showed nearly normal distribution, and transgressive segregants exceeding the parental scores were observed (Fig.2).

o To detect association of introgression with morphological traits, single point analysis was employed. Total five QTLs were identified and located on chromosome 6, 7, 10, 11, which explained ranging from 5.4-12.5% of the total phenotype variation (Fig.1, Table 1). Among these QTLs identified, four associated with culm length, seed thickness, 1,000 seed weight, L/W ratio of seed, respectively, have not been detected in the previous QTL studies between *Oryza* cultivars, indicating potentially novel alleles from *O. minuta*, while One QTL, *sl11*, was located in the similar region as a grain length QTL from previously QTL studies. The QTLs detected in this study might provide a rich source of information about the natural genetic variation underlying the evolution of rice.

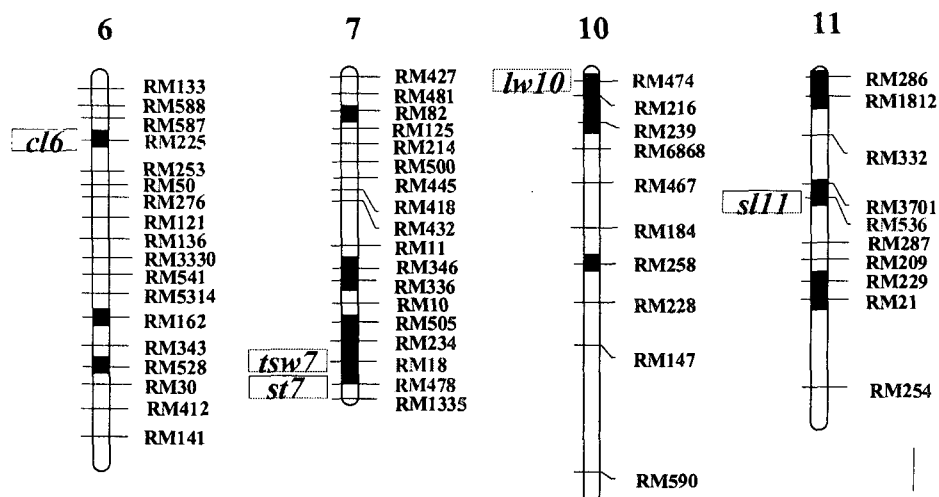


Fig. 1. A map with polymorphic markers between the parents. QTLs are labeled on the left of the chromosome. Dark chromosome regions mark the specific *O. minuta* introgressions.

Table 1. QTLs detected for five traits based on single-point analysis in an $F_{2:3}$ population.

Trait	QTL	SSR	$R^2(\%)$	Mean			
				H/H*	H/W	W/W	Allele effect
Culm length	<i>cl6</i>	RM225	9.6	69.65	72.79	75.59	3.00
Seed length	<i>s111</i>	RM536-RM3701	12.5	5.21	5.30	5.32	0.06
1,000 seed wt.	<i>tsw7</i>	RM18	5.8	24.33	24.41	26.39	1.03
Seed thickness	<i>st7</i>	RM478	5.4	2.11	2.12	2.18	0.04
Seed L/W ratio	<i>lw10</i>	RM474	5.9	1.82	1.76	1.77	-0.03

*: H/H, H/W, W/W: Hwaseong homozygote, Hwaseong / WH79006 heterozygote, WH79006 homozygote, respectively.

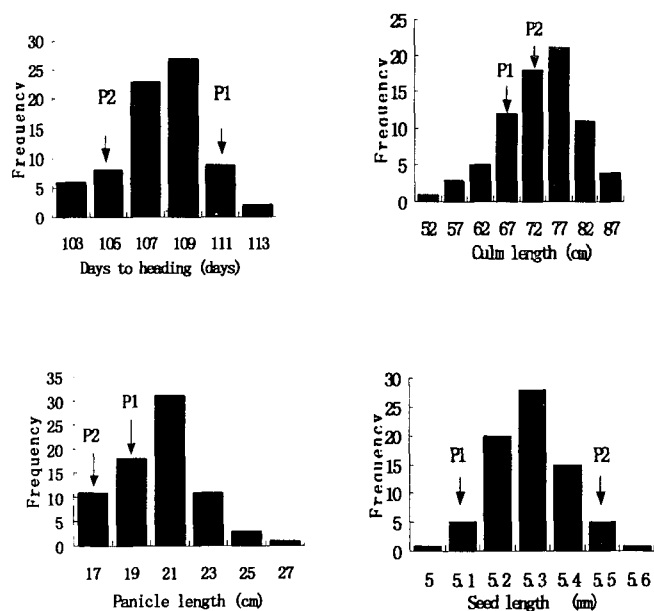


Fig. 2. Frequency distribution of 4 traits in the $F_{2:3}$ population (P1: Hwaseongbyeo, P2: WH79006).