

P017

## Introgression for Agronomic Traits from *Oryza minuta* into Rice, *O. sativa*

F.X.Jin<sup>1</sup>, S.J.Kwon<sup>2</sup>, K.H.Kang<sup>2</sup>, H.G.Hwang<sup>2</sup>, and S.N.Ahn<sup>1\*</sup>

<sup>1</sup>Department of Agronomy, Chungnam National University, Daejeon 305-764;

<sup>2</sup>National Institute of Crop Science, Suwon 441-100, KOREA

### **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**

1. Plant materials
  - o Parent: Hwaseong and OM79006 (Hwaseong/*O. minuta* BC5F6)
  - o Mapping population: 75 F<sub>2:3</sub> lines
2. Genotyping: SSR markers
3. Traits evaluated: Nine traits including heading date and culm length

### **RESULTS AND DISCUSSION**

1. The frequency distribution of 9 traits in 75 F<sub>2:3</sub> lines showed nearly normal distribution, and transgressive segregants exceeding the parental scores were observed.
2. A total of 511 SSR markers were used in the polymorphism survey. Of these, 231 markers (45.2%) showed polymorphism between Hwaseong and *O. minuta*. Among the polymorphic markers, 23 markers detected *O. minuta*-specific fragments in the OM79006 parent, and were used for genotype of the 75 F<sub>2:3</sub> lines.
3. To detect association of introgression with morphological traits, single point analysis was employed. For culm length, the *O. minuta* allele increased culm length at *cl6* which explained 9.6% of the total phenotype variation, and one QTL for 1,000 seed weight, *tsw7*, was identified. These alleles have not been detected in previous QTL studies between *Oryza* cultivars, indicating potentially novel alleles from *O. minuta*. The QTLs detected in this study might provide a rich source of information about the natural genetic variation of rice.

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\*Corresponding author: Tel : 042-821-5728 E-mail : ahnsn@cnu.ac.kr

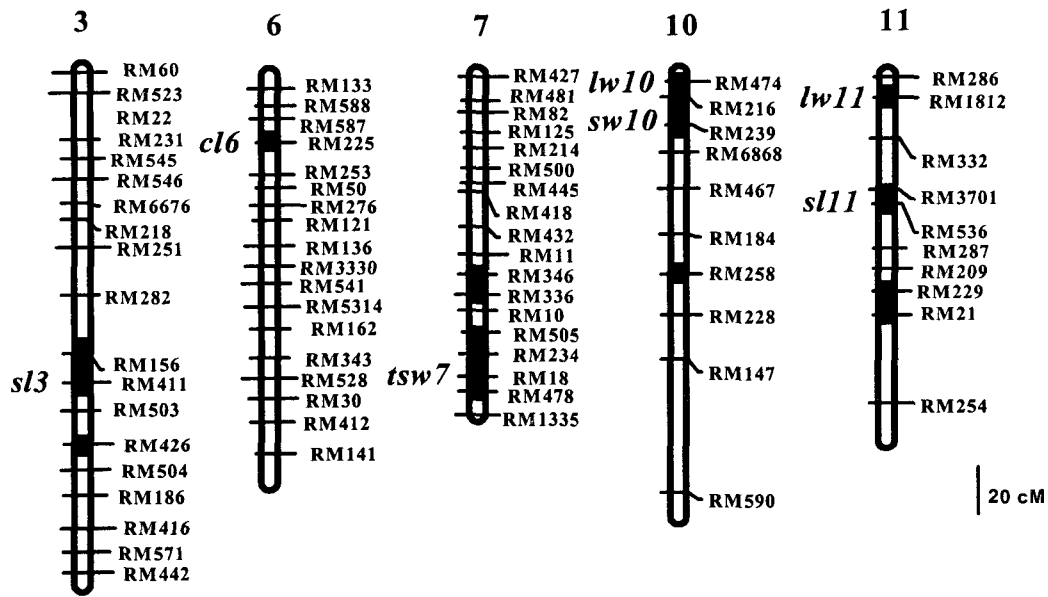


Fig. 1. A map with polymorphic markers between the parents. QTLs are labeled on the left of the chromosome. Dark chromosome regions mark the specific *O. minuta* introgressions.

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

| Trait          | QTL  | SSR    | Chr. | P      | R <sup>2</sup> (%) | Mean             |       |       |               |
|----------------|------|--------|------|--------|--------------------|------------------|-------|-------|---------------|
|                |      |        |      |        |                    | H/H <sup>+</sup> | H/O   | OO    | Allele effect |
| Culm length    | cl6  | RM225  | 6    | 0.0068 | 9.6                | 69.65            | 72.79 | 75.59 | 3.00          |
| Seed length    | sl3  | RM411  | 3    | 0.0288 | 6.4                | 5.23             | 5.31  | 5.30  | 0.04          |
|                | sl11 | RM536  | 11   | 0.0019 | 12.5               | 5.21             | 5.30  | 5.32  | 0.06          |
| Seed width     | sw10 | RM239  | 10   | 0.0466 | 5.3                | 2.93             | 3.01  | 3.00  | 0.04          |
| 1,000 seed wt. | tsw7 | RM18   | 7    | 0.0378 | 5.8                | 24.33            | 24.41 | 26.39 | 1.03          |
| Seed L/W ratio | lw10 | RM474  | 10   | 0.0273 | 6.5                | 1.82             | 1.76  | 1.75  | -0.04         |
|                | lw11 | RM1812 | 11   | 0.0369 | 5.8                | 1.72             | 1.78  | 1.79  | 0.04          |

H/H, H/O, O/O: Hwaseong homozygote, Hwaseong / OM79006 heterozygote, OM79006 homozygote, respectively.

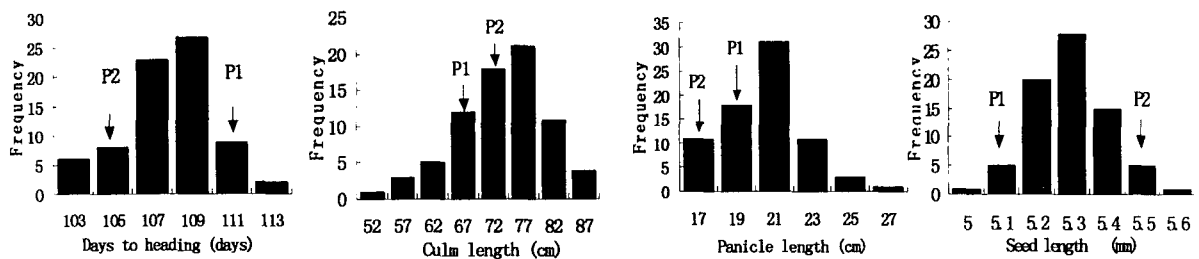


Fig. 2. Frequency distribution of 4 traits in the  $F_{2:3}$  population (P1: Hwaseongbyeo, P2: OM79006).