

A1. Introgressions of *Oryza grandiglumis* chromatin into rice affect several traits of agronomic importance

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Objectives

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

Materials and methods

Plant material - Parents (Hwaseongbyeo and HG101), 150 F2:3 lines

Genotyping - SSR markers

Traits evaluated - Twelve traits including days to heading, culm length, 1,000 grain weight

Results and Discussion

150 F2:3 lines from the Hwaseongbyeo/HG101 cross were evaluated for twelve traits. Correlation coefficients between the traits measured in this study on the F2:3 families were calculated and significant ($P < 0.05$) correlations were observed between several traits (data not shown). In agreement with previous studies, yield showed a positive correlation with spikelets per panicle and ripening ratio. The F2 plants were also genotyped with 20 SSR markers which detected *O. grandiglumis* alleles in HG101. To detect association of introgression with morphological traits single point analysis was employed. Significant putative QTL were identified for days to heading, culm length, panicle number and length and grain length (Table 1). At present, we are screening more markers to identify the introgressions undetected previously and mapping those markers in the F2:3 population.

Table 1. OTLs detected for traits based on single-point analysis in an F2:3 population

Trait	SSR marker	Chrom.	P	R ² (%)	Mean			
					H/H [*]	H/G	G/G	Allele effect
Days to heading	RM229	11	0.002	16.0	120	121	123	1.5
Culm length	RM488	1	0.0009	16.7	85.8	81.9	80.8	2.5
	RM229	11	0.01	12.5	82.5	82.1	77.5	2.5
	RM 50	8	0.005	10.1	82.5	82.0	78.2	2.2
Panicle no.	RM224	11	0.046	10.2	11	11	13	1.0
Panicle length	RM144	11	0.03	11.2	19.5	19.7	19.9	0.2
Grain length	RM229	11	0.0001	16.2	5.00	5.11	5.18	0.09

* H/H, H/G, G/G ; Hwaseongbyeo homozygotes, Hwaseongbyeo/HG101 heterozygotes, and HG101homozygotes, respectively

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