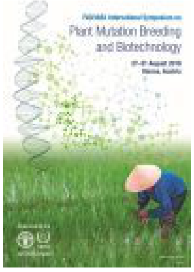

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CHARACTERIZATION OF A NEW GENE CONTROLLING LEAF SENESCENCE USING PROGENY FROM AN INTERSPECIFIC CROSS IN RICE

An analysis of quantitative trait loci (QTL) controlling chlorophyll content was conducted using introgression lines (CR7501 and CR2002) derived from a cross between the Oryza sativa japonica cultivar 'Hwaseong' as a recurrent parent and wild species O. grandiglumis as a donor parent. These two lines showed higher chlorophyll content than Hwaseong. For QTL analysis, we constructed 58 F3 and 17 F4 lines from the cross CR7501/Hwaseong. SSR markers were used for genotyping the lines. One-way ANOVA indicated the presence of a QTL for chlorophyll content (qCC2) on chromosome 2 and qCC2 explained 24.6% of the phenotypic variance. To examine whether qCC2 is also involved in senescence, a series of dark-induced senescence (DIS) experiments were conducted. Detached leaves from Hwaseong and CR2002 were incubated in 3mM MES buffer (pH 5.8) at 27 ℃ under complete dark condition. CR2002 showed higher chlorophyll content with delayed senescence than Hwaseong. To know whether qCC2 maintains leaf functionality during DIS, ion leakage test and Fv/Fm measurement were performed. The Fv/Fm value displayed significant difference between CR2002 and Hwseong at 6 days after incubation, while ion leakage rate was not significantly different. These results might imply that qCC2 is associated with chlorophyll content and stay-green phenotype. The qCC2 QTL region harbours GW2 locus encoding the RING-type E3 ubiquitin ligase controlling grain size. To know the possible relationship between the GW2 activity and senescence, gw2-knockout mutant (gw2-ko) and the wild type plants were incubated under dark condition. gw2-ko showed delayed senescence in DIS, suggesting that GW2 is possibly related to stay-green phenotype.

Country or International Organization

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Track Classification: New challenges and technologies in plant genomics and breeding