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Different expression levels of *OsPLS1* control leaf senescence period between indica and japonica-type rice

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Abstract

Leaf senescence is the process of aging in plants. Chlorophyll degradation during leaf senescence has the important role translocating nutrients from leaves to storage organs. The functional stay-green with slow leaf yellowing and photosynthesis activity maintenance has been considered one of strategy for increasing crop productivity. Here, we have identified two QTLs on chromosome 9 and 10 for leaf senescence with chlorophyll content of RIL population derived from a cross between Hanareum 2, early leaf senescence *Indica*-type variety, and Unkwang, delayed leaf senescence *Japonica* variety. Among these QTLs, we chose *qPLS1* QTL on chromosome 9 for further study. *qPLS1* was found to explain 14.4% of the total phenotypic variation with 11.2 of LOD score. Through fine-mapping approach, *qPLS1* QTL locus was narrowed down to about 25kb in the marker interval between In/del-4-7-9 and In/del-5-9-4. There are 3 genes existed within 25kb of *qPLS1* locus: LOC_Os09g36200, LOC_Os09g36210, and LOC_Os09g36220. Among these genes, transcript level of LOC_Os09g36200 was increased during the leaf senescence stage and the expression level of LOC_Os09g36200 in *Indica* was higher than in *Japonica*. Finally, we chose LOC_Os09g36200 as candidate gene and renamed it as *OsPLS1-In* and *OsPLS1-Jp* from *Indica*- and *Japonica*-type rice, respectively. *OsPLS1-In* and *OsPLS1-Jp* overexpressing transgenic plants showed both early leaf senescence phenotype. These results indicate that *OsPLS1* functions in chlorophyll degradation and the difference of expression level of *OsPLS1* cause the difference of leaf senescence between *Indica* and *Japonica* in rice.

Keywords: Rice, leaf senescence, chlorophyll degradation, Plant Leaf Senescence (PLS)

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