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VALIDATION OF GENES INVOLVED IN STRIGOLACTONES BIOSYNTHETIC PATHWAY IN *LOTUS JAPONICUS*

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As sessile organisms, plants elaborate their development of branches in response to environmental and developmental signals to maximize reproductive success. Hormones play a critical role in determining the diversity of plant branching. One of the signaling pathways regulating branching involves MAX/RMS/D (more axillary branching) genes, which are apparently highly conserved in higher plants. Strigolactones, a group of terpenoid lactones, have been recently identified as products of the MAX/RMS/D pathway that travel acropetally from root through xylem to inhibit bud outgrowth. Here we report the cloning of the first catalytic enzyme for strigolactones (*CCD7*) from *Lotus japonicus* (*LjCCD7*) by RACE-PCR. *LjCCD7* contains a 1866bp ORF encoding 621 amino acids, and is most closely related phylogentically to *RMS5* of pea, *CCD7* of soybean, Arabidopsis and tomato. *LjCCD7* was then prokaryotically expressed as GST fusion protein, and detected by both SDS-PAGE and western blot analysis. As in other species, enzymatic activity of the purified GST-LjCCD7 indicated that it encodes an enzyme capable of cleaving carotenoids such as beta-carotene. Plants silenced for *LjCCD7* were generated, and are being molecularly characterized. Their phenotype is currently being analyzed under different stress conditions.