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Mutation in the GRAS family gene, OsGRAS32, affectedvegetative development in rice

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The GRAS gene family encodes plant-specific transcription factors that have diverse functions in plant development and growth. They are involved in gibberellin signal transduction (GAI, RGA), root radial patterning (SCR, SHR), phytochrome A signaling (PAT1), and axillary meristem formation (LAS). Among 57 OsGRAS family genes in the rice genome, only a few genes have been characterized. OsGAI/SLR1 and MOC1are involved in GA signal transduction and controlling the tiller number, respectively. Other rice GRAS genes, CIGR1 and CIGR2, were induced by N-acetylchitooligosaccharide elicitor, while OsSCR and OsSHR were expressed in root tips. To elucidate functional roles of the GRAS family genes in rice, we have examined the 21 T-DNA knockout mutant lines in the OsGRAS family genes. In this report, we describe characterization of one of them, OsGRAS32. The homozygotic mutants showed phenotypes of semi-dwarf, rolled leaves, and dark-green leaves. This gene was constitutively expressed in both vegetative organs and reproductive organs. We will report detailed analysis of the mutantphenotypes.

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