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과제 일련번호: 11

Characterization of Pathogen inducible OsLEUZIP Gene from rice (*Oryza sativa* L. cv. Dongjin)

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We cloned the full length cDNA, OsLEUZIP, encoding leucine zipper containing protein from rice (*Oryza sativa* L. cv. Dongjin) treated with *Xanthomonas oryzae* pv. oryzae 10331. The OsLEUZIP contained 1,227 bp nucleotides and encoded a protein of 408 amino acid residues with predicted molecular weight of 47,229 Da. The deduced amino acid sequence of OsLEUZIP had consensus sequence of leucine zipper from PROSITE (PDOC00029), L-X(6)-L-X(6)-L-X(6)-L. The OsLEUZIP gene were preferentially induced in rice during incompatible interaction with *Xanthomonas oryzae* pv. oryzae 10331 and *Pyricularia grisea* KJ-301. Expression of OsLEUZIP gene was also induced by treatment of ethephon and ABA. To analyze the biological function of OsLEUZIP in planta, overexpression vector was prepared by Gateway system. Thirteen tobacco transformants were generated and analyzed their defense activity by infiltration with Pseudomonas syringae pv.tabaci. Disease resistance to *Pseudomonas syringae* pv. tabaci was increased in OsLEUZIP overexpressed lines. Our data represented in this study was suggesting that OsLEUZIP gene may play an important role in rice defense-related. Further studies of this gene, over expression and knock-out in rice and northern blot analyses of transgenic plant, would be useful to elucidate the role of the OsLEUZIP gene in defense responses of rice.

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