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Genomic insights into a plant growth-promoting *Pseudomonas koreensis* strain with cyclic lipopeptide-mediated antifungal activity

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Abstract

Strain S150 was isolated from the tobacco rhizosphere as a plant growth-promoting rhizobacterium. It increased plant fresh weight significantly and lateral root development, and it antagonized plant pathogenic fungi but not phytobacteria. Further tests showed that strain S150 solubilized organic phosphate and produced ammonia, siderophore, protease, amylase, and cellulase, but it did not produce indole-3-acetic acid. Using morphology, physiological characteristics, and multi-locus sequence analysis, strain S150 was identified as *Pseudomonas koreensis*. The complete genome of strain S150 was sequenced, and it showed a single circular chromosome of 6,304,843 bp with a 61.09% G + C content. The bacterial genome contained 5,454 predicted genes that occupied 87.7% of the genome. Venn diagrams of the identified orthologous clusters of *P. koreensis* S150 with the other three sequenced *P. koreensis* strains revealed up to 4,167 homologous gene clusters that were shared among them, and 21 orthologous clusters were only present in the genome of strain S150. Genome mining of the bacterium *P. koreensis* S150 showed that the strain possessed 10 biosynthetic gene clusters for secondary metabolites, which included four clusters of non-ribosomal peptide synthetases (NRPSs) involved in the biosynthesis of cyclic lipopeptides (CLPs). One of the NRPSs possibly encoded lokisin, a cyclic lipopeptide produced by fluorescent *Pseudomonas*. Genomic mutation of the *lokA* gene, which is one of the three structural NRPS genes for lokisin in strain S150, led to a deficiency in fungal antagonism that could be restored fully by gene complementation. The results suggested that *P. koreensis* S150 is a novel plant growth-promoting agent with specific cyclic lipopeptides and contains a lokisin-encoding gene cluster that is dominant against plant fungal pathogens.

KEYWORDS

biological control, Cyclic lipopeptides, non-ribosomal peptide synthetase, *Pseudomonas koreensis*, secondary metabolite

Yilin Gu and Yi-Nan Ma are contributed equally to this work.

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