

Serratia oryzae sp. nov., isolated from rice stems

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Abstract

A novel endophytic bacterium, strain J11-6^T, was isolated from rice stems. Its taxonomic position was investigated using a polyphasic approach. The novel strain was Gram-staining-negative, facultatively anaerobic, motile and rod-shaped. Although the results of phylogenetic analysis based on 16S rRNA gene sequences indicated that J11-6^T represented a member of the genus *Rahnella*, multilocus sequence analysis (MLSA) on the basis of concatenated partial *atpD*, *gyrB*, *rpoB* and *infB* gene sequences showed a clear distinction of J11-6^T from the type strains of species of the genus *Rahnella* but indicated that it lay within the clade of the genus *Serratia*. The phylogenetically closest species were *Serratia fonticola* and *Serratia aquatilis* on the basis of the results of the MLSA phylogenetic analysis. The predominant cellular fatty acids were C_{16:1ω7c} (38.7%) and C_{16:0} (25.0%). The DNA G+C content was 53.2 mol%. The DNA–DNA relatedness was 17.4% between J11-6^T and *Rahnella aquatilis* CIP 78.65^T, and 29.2% between J11-6^T and *S. fonticola* LMG 7882^T which indicates that this strain represents a novel species of the genus *Serratia*. Characterization by genotypic and phenotypic analysis indicated that J11-6^T (=ACCC 19934^T=KCTC 52529^T) represents a novel species of the genus *Serratia*, for which the name *Serratia oryzae* sp. nov. is proposed.

In a prior experiment that used high-throughput sequencing techniques to reveal the correlation between rice genotypes and their endophytic bacterial flora, we found that the family *Enterobacteriaceae* was the most dominant group in rice seeds and stems. Subsequent culture-dependent experiments were used to isolate the endophytic bacteria in stems. One of these isolates, designated as J11-6^T, was a monophyletic cluster associated with the family *Enterobacteriaceae* of the class *Betaproteobacteria*. The results of polyphasic analysis indicated that J11-6^T represented a member of the genus *Serratia*. At the time of writing, 18 species of the genus *Serratia* have been reported with *Serratia glossinae* as a later synonym of *Serratia fonticola* (<http://www.bacterio.net/~allnamesz.html>) [1]. Strains of members of the genus *Serratia* are frequently isolated from some hospitalized patients [2]. In addition, they have been found in bats [3,4], water [5] and plant surfaces [6]. Species of the genus *Serratia* have frequently been found associated with plants: *Serratia rubidaea* has been repeatedly isolated from coconuts bought in France and California [7]; *Serratia ficaria* is especially associated with the fig–wasp ecosystem [6]; and vegetables used in salads might bring strains of members of the

genus *Serratia* to hospitals and contaminate the patient's digestive tract [8]. Some plant-associated species of the genus *Serratia* have been isolated from diseased roots or leaves, however, those strains only caused a hypersensitivity reaction on plants [2]. In this study, we examined the taxonomy of a novel strain, J11-6^T, which was isolated from sterilized rice stems, and identified it as representing a potentially novel species of the genus *Serratia*.

Rice stems were collected from Qiyang County of Hunan Province, PR China. Surface sterilization of stems was implemented by using sodium hypochlorite solution: Samples were washed twice with sterile water, and then immersed in 2.5% NaClO for 4 min, and finally washed six times with sterile water. To check for surface contamination, samples were imprinted on triplicate plates of trypticase soy agar (TSA; Difco) and cultured for 3 days at 30 °C. Meanwhile surface sterilized stems were cut into pieces and ground evenly in a mortar. Finally, endophytes from rice stems were isolated using the standard dilution plating technique. Trypticase soy agar (TSA; Difco) medium was used to culture the bacteria at 30 °C for 3 days. J11-6^T was stored

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Abbreviations: ANI, average nucleotide identity; MLSA, multilocus sequence analysis.

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The GenBank/EMBL/DDJB accession number for the 16S rRNA gene, *gyrB*, *rpoB*, *infB* and *atpD* gene sequences of strain J11-6^T are KX421209, KY808397, KY808395, KY808396 and KY808398. The genome accession number of J11-6^T is PRJNA352343.

Two supplementary tables and one supplementary figure are available with the online Supplementary Material.