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Variovorax beijingensis sp. nov., a novel plant-associated bacterial species with plant growth-promoting potential isolated from different geographic regions of Beijing, China



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ABSTRACT

Two plant-associated bacterial strains were isolated from Beijing, China. The two strains possessed almost identical 16S rRNA gene sequences. However, REP-PCR fingerprint patterns discriminated that they were not from one clonal origin. The average nucleotide identity (ANI) value and the digital DNA-DNA hybridization (dDDH) value between the two strains were 99.4% and 94.7%, respectively, suggesting that they belonged to the same species. The 16S rRNA gene phylogeny analysis indicated that the two strains belonged to the genus Variovorax and were closely related to V. paradoxus NBRC 15149^T and V. boronicumulans BAM-48^T. Their phylogenetic relationship were confirmed in both phylogenetic trees constructed with house-keeping gene sequences and concatenated core genes of the genome. The ANI and dDDH comparisons among 502^T and the most related type strains showed values below the accepted threshold for species discrimination. The genome sizes of strains 502^T and T529 were 6.76 and 6.69 Mbp, respectively. The strain 502^T had 6,227 predicted genes with DNA G + C content of 67.4 %. The respiratory quinone was ubiquinone-8 and the major polar lipids were phosphatidylethanolamine, phosphatidylglycerol and diphospatidylglycerol. The major fatty acids of strain 502^T were C_{10:0}3-OH (26.2%), C_{16:0} (12.9%), C_{17:0} cyclo (14.5%) and summed feature 3 (21.4%). Furthermore, both strains showed the potential of plant growth promotion. Based on these results, the two isolates could be considered to represent a novel species of the genus Variovorax, for which the name Variovorax beijingensis sp. nov., is proposed, with 502^{T} (= DSM 106862^{T} = CGMCC 1.16560^{T}) as the type strain.

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Introduction

The genus *Variovorax* was initially proposed along with the reclassification of *Alcaligenes paradoxus* as *Variovorax paradoxus* [35]. The type species of this genus is *Variovorax paradoxus*. Phylogenetic analyses based on 16S rRNA gene sequences showed that the genus *Variovorax* belongs to the family *Comamonadaceae* of

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https://doi.org/10.1016/j.syapm.2020.126135 0723-2020/© 2020 Elsevier GmbH. All rights reserved. the class *Betaproteobacteria* [35]. At the time of writing, this genus comprised of 12 recognized species (https://www.ezbiocloud.net/taxonomy). Most members of the genus *Variovorax* were isolated from soil [13,17,22,25,26,36], a few species were isolated from other habitats, such as plant [15], sewage [14] and rhizosphere soil [9].

The plant growth-promoting rhizobacteria (PGPR) are considered as important players in plant growth promotion through the production of several growth-related enzymes and hormones. Specifically, the production of 1-aminocyclopropane-1carboxylate (ACC) deaminase and siderophores are the important characteristics of plant growth-promoting bacteria and endophytes. ACC deaminase cleaves ACC, the immediate precursor of the

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