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E-mail address of corresponding author is added from order viewer, kindly check.



Authors: Bhagya Iyer, Shalini Rajkumar

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Genome sequence and comparative genomics of *Rhizobium* sp. Td3, a novel plant growth promoting phosphate solubilizing *Cajanus cajan* symbiont

Bhagya Iyer and Shalini Rajkumar*

Institute of Science, Nirma University, Ahmedabad –382 481, Gujarat, India

*shalini.rjk@nirmauni.ac.in Phone:+91-79-30642757; Fax: +91-2717-241916

Abstract:

Rhizobium sp. Td3 is a *Sesbania* plant growth promoting, *Cajanus cajan* nodulating rhizobia. Studying its whole genome was important as it is a potent phosphate solubilizer with constitutive gluconic acid production ability through operation of the periplasmic glucose oxidation pathway even under conditions of catabolite repression. This is in contrast to the other explored phosphate solubilizers. Rhizobial isolates sequenced so far are known to lack components of the direct glucose oxidation pathway and cannot produce gluconic acid on its own. Here, we present the genome sequence of *Rhizobium* sp. Td3. Genome comprises of a single chromosome of size 5,606,547 bp (5.6 Mb) with no symbiotic plasmid. *Rhizobium leguminosarum* bv. *viciae* USDA2370 was the closest whole genome known. 109 genes responsible for diverse plant growth promoting activities like P solubilization, synthesis of acetoin, nitric oxide, indole-3 acetic acid, exopolysaccharide, siderophore and trehalose have been identified. Flagellar proteins, genes encoding antibiotic and metal resistance, enzymes required for combating oxidative stress as well as attachment and colonization in the plant rhizosphere are also present. Availability of genome sequence of such a versatile plant growth promoting agent will help in exploiting all the phyto-beneficial traits of Td3 for its use as a biofertilizer.

Keywords: rhizobia; P solubilization; gluconic acid; plant growth promotion

1. Introduction

Advances in DNA sequencing technology have drastically changed the strategies for studying genetic systems of various organisms. Complete genomic sequences not only provide the information obligatory to perform functional analysis of the genes but also furnishes new insights into gene function, gene evolution and genome evolution. Development of ultra-high throughput sequencing (UHTS) has been exceedingly influential in advancing research in all scientific areas, particularly in microbiology, where genomes are small (Bertelli and Greub,

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