I -40

Stenotrophomonas ginsengisoli sp. nov., isolated from soil of a ginseng field

Sathiyaraj Srinivasan, Myung Kyum Kim, Yeon Ju Kim and Deok-Chun Yang*

Korean Ginseng Center for Most Valuable Products & Ginseng Genetic Resource Bank, Kyung Hee University

Seocheon-dong, Giheung-gu Yongin-si, Gyeonggi-do 449-701, South Korea

Objectives

In a series of studies, we attempted to isolate microorganisms from ginseng field soil in order to investigate the community structure based on a culture dependent method. In this study, one strain was isolated and characterized by polyphasic taxonomy approach which included phylogenetic analysis based on 16S rRNA gene sequences, genomic relatedness, and chemotaxonomic and phenotypic properties in order to determine the precise taxonomic position of the strain.^{T}.The strain DCY33^{T}was isolated from soil in a ginseng field via direct plating onto ten-time diluted R2A agar (Difco). The results obtained in this study indicated that DCY33^{T} can be assigned as a new member of the genus *Stenotrophomonas*.

Materials and Methods

Oxidase activity was evaluated using 1% (w/v) tetramethyl-p-phenylene diamine. Catalase activity was determined by the measurements of bubble production after the application of 3% (v/v) hydrogen peroxide solution. Isoprenoid quinones were extracted with chloroform/methanol (2:1,v/v), purified via TLC (thin-layer chromatography). The crude n-hexane quinine solution was purified and subsequently analyzed by HPLC, as previously described (Collins and Jones, 1981; Shin *et al*.,1996). Fatty acid methyl esters were prepared, separated, and identified with the Sherlock Microbial Identification System (MIS), produced by MIDI, Inc., Newark, DE., USA (Sasser, 1990). For determination of G+C content, the genomic DNA was extracted and purified with the QIAGEN Genomic-tip system analyzed using reverse-phase HPLC as previously described (Tamaoka and Komagata, 1984; Mesbah *et al*.,1989).

Result

The cells were found to be Gram-negative, motile, rod-shaped, oxidase and catalase positive. The strain DCY33^{T}was able to grow at a temperature range of 25-37°C but not at 4°C and 42°C. The optimum growth temperature was 30°C. The strain DCY33^{T} contained ubiquinone Q-8 as the predominant respiratory lipoquinone which was commonly found in the *Stenotrophomonas* species. The major cellular fatty acids in the strain DCY33^{T} included: 15:0iso (38.45%), 15:0anteiso (16.58%), 11:0iso (6.63%), 16:010methyl (5.98%), 17:0iso (5.38%) and 13:0iso3OH (4.71%). The fatty acid profile of the strain DCY33^{T} is actually different from those of other *Stenotrophomonas* species. The G+C content of the genomic DNA of the strain DCY33^{T} was 69.9 mol% that was similar too their *Stenotrophomonas* species (65 - 69mol%). Based on these data, DCY33^{T} (= KCTC 13155^{T}) should be classified as the type strain for a novel species, for which the name *Stenotrophomonas ginsengisoli* sp. nov. has been proposed.

Corresponding author : 양덕춘, e-mail : dcyang@khu.ac.kr, Tel : 031-201-2688

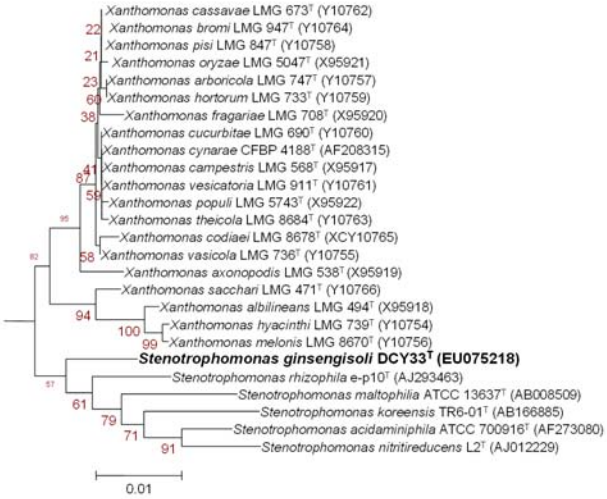

Fig. 1. Phylogenetic tree based on 16S rRNA gene sequences, showing the phylogenetic relationships between strain DCY33^T and related species (all *Stenotrophomonas* species and other related genera). Neighbor-joining method was used and a bar represents 0.01 substitutions per nucleotide position.