

ABSTRACT:

Pseudomonas sp. strain S3 was isolated from Paddy (rice) field agricultural area. This organism, which can utilize a halogenated compound of D,L-2-Chloropropionic acid as sole carbon and energy source, catalyses the hydrolytic dehalogenation of both D- and L- isomers of 2-Chloropropionic acid. Identification of *Pseudomonas* sp. S3 is still ambiguous due to the lack of basic studies, especially their molecular genetic information. In this study, the amplified 16S rRNA gene sequence of *Pseudomonas* sp. S3 (Accession No. FJ968758) was compared to other nine selected gene sequences from the same group of *Pseudomonas* sp. and/or dehalogenase producing bacteria using in silico method. Their phylogenetic relationships were then determined. The results were analysed using MEGA4 software to ascertain its evolutionary distance by reconstructing a phylogenetic tree of these organisms. The evolutionary history and bootstrap consensus tree were inferred using the Neighbour-Joining method from 500 replicates. The tree is drawn to scale, with branch lengths (next to the branches) in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the p-distance method and were in the units of the number of base substitutions per site. Based on this analysis, *Pseudomonas* sp. S3 16S rRNA gene was closely related to the *Pseudomonas chlororaphis* with genetic distance 0.170 base substitutions per site. S3 gene was also compared among known dehalogenase producing bacteria 16S rRNA genes. Results suggested that S3 was closely related to the *Pseudomonas* sp. R1 with a genetic distance 0.040 base substitutions per site. From present study, evolutionary relationships of 16S rRNA gene of *Pseudomonas* sp. S3 were elegantly illustrated by phylograms, comparable to a pedigree showing which microorganisms are most closely related.