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IDENTIFICATION OF IRON-REDUCING BACTERIA ISOLATED FROM SOIL
FERROSPHERE

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In microbial-induced corrosion processes, conditions for the development of sulfate-reducing bacteria are created by heterotrophs, in particular ammonifying and iron-reducing bacteria.

The aim of the present research was to isolate and identify iron-reducing bacteria from the soil ferrosphere using microbiological, physiological-biochemical and molecular genetic methods, to analyze their ability to produce some corrosive dangerous metabolites.

Iron-reducing bacteria were isolated from the soil ferrosphere and selected on FWA-Fe (III) citrate medium by Koch's method. Analysis of a complex of microbiological, physiological and biochemical characteristics, 16S rRNA gene sequencing and phylogenetic analysis were performed using conventional methods and techniques.

ChNPU ZVB1 strain was isolated and selected as one with iron-reducing and ammonifying properties and the ability to form hydrogen sulfide. According to the Bergey's Manual of Systematic Bacteriology the strain was identified as *Bacillus* sp. on the basis of the complex of microbiological, physiological and biochemical properties. For further identification of the strain 16S rRNA gene amplification followed by sequencing of the PCR product was carried out. The resulting partial sequence was compared with those deposited in the GenBank database. The result of the analysis showed 99% similarity to the different species of *Fictibacillus* and *Bacillus* genera. 16S rRNA gene nucleotide sequence of the ChNPU ZVB1 strain was deposited in the GenBank database as *Fictibacillus* sp. KX349222. To define the phylogenetic position the dendrogram of relationship between various *Bacillus* and *Fictibacillus* species was constructed. There were two large clusters: the first was composed of species belonging to *Bacillus* genus, and the other combined species of *Fictibacillus* genus, including the *Fictibacillus* sp. strain ChNPU ZVB1. The closest neighbors to the *Fictibacillus* sp. strain ChNPU ZVB1 were *F. phosphorivorans* and *F. nanhaiensis* type strains. Thus, based on the obtained results the ChNPU ZVB1 strain belongs to the *Fictibacillus* genus and its species identification require additional molecular-genetic analysis.