Detection of Desulfovibrio oryzae polysaccharide deacetylase gene

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The geochemical activity of sulfate-reducing bacteria is manifested, in particular, in the form of participation in the biodamage of materials. Preventing the growth of their biofilms is one of the areas materials protection. It is known that biofilm exopolysaccharides

modifications after polymerization change the physicochemical properties of the biopolymer, which, in turn, can affect bacterial pathogenicity, virulence and environmental adaptability. Deacetylation is the important reaction for the exopolysaccharide processing and production in biofilms of many bacteria, it is associated with the cell aggregation, surface attachment, exopolysaccharide secretion, and biofilm maturation. Previously, we isolated and identified the strains of sulfate-reducing bacteria Desulfovibrio oryzae NUChC SRB1 and NUChC SRB2 from the surface of the corroded metal structure. The purpose of the present study was to search and detect genes encoding exopolysaccharide deacetylase in D. oryzae strains by performing bioinformatic and molecular-genetic analysis. Genomes of phylogenetically close related species were analyzed and compared. The primer sequences were designed on the basis of gene encoding polysaccharide deacetylase family protein in D. termitidis genome in 714723-715856 positions. As a result of amplification with selected primers 337-bp PCR-fragment was obtained for D. oryzae NUChC SRB1 and NUChC SRB2 strains. The defined primers could be used as the DNA-markers of D. oryzae polysaccharide deacetylase gene. Since the development of exopolysaccharide deacetylase inhibitors is a promising anti-biofilms approach, the prospect of further research is to find eco-friendly approaches to prevent deacetylation in D. oryzae and formation of biofilms by them.