P-101 - SULFIDE OXIDATION BY HETEROTROPHIC P. KOREENSIS A9 UNDER AEROBIC CONDITIONS.

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Background

Biological oxidation can be an efficient solution for bioremediation of sulfide contaminated gases and wastewater [1,2]. Microorganisms able to grow chemolithotropically on sulfide compounds are known. Knowledge on heterotrophic sulfur-oxidizing bacteria is scarcer. However, heterotrophs are more metabolically versatile [3]. Heterotrophic bacteria perform sulfide oxidation by the concerted action of three enzymes: sulphide: quinone oxidoreductase (SQR), persulfide dioxygenase (DOP) and rhodanese [1,2,3].

Method

Bacterial strain A9 was isolated from a sulfide enrichment inoculated with the filling of biofilter from a WWTP. After the isolation, the strain was tested for tolerance and degradation of sulfide. Crude extract-cells activity assays were also performed. Sulfide disappearance was monitored by direct potentiometry and sulfate production. The sulfide oxidase activity was measured based on sulfate production, as the major end-product [5].
Total genomic DNA was sequenced by 454-pyrosequencing. The genome was annotated using Rapid Annotation System Technology (RAST) [6], and functional annotation was performed using SEED, SWISS-PROT, COG and KEEG databases.

Results & Conclusions

Maximum sulfide removal (99,8%) and degradation rate (1,6 mmol.h^{-1}) was achieved in GY medium with 16 mM of sulfide. In activity tests using crude cellular extract and 10mM of sulfide, maximum sulfate concentration achieved was 0,858 mM, corresponding to enzyme activity of 6,435 µmol h^{-1}. The specific enzymatic activity ranged 1,828 to 2,927 U. mg^{-1} protein, which are very promising results when compared to bibliography [1, 5]. DNA sequencing of *P. koreensis* A9 and *de novo* assembly, generated the 6376154 bp draft genome with 60,1 % of G+C content. After assembly, 73 contigs with protein encoding genes were produced. RAST annotation disclose that this genome encodes 5738 predicted coding genes, 50% of the detected proteins were annotated in 542 sub-systems from SEED [6]. Functional screening analysis reveals that A9 possesses the genes required for sulfide oxidation to sulfate, with sulfite as the intermediate. In addition, rhodanese-like, glutathione:sulfur transferase, thiol peroxidase, among others, were identified which demonstrate the ability and versatility of A9 for sulfide bioremediation applications.

References & Acknowledgments

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[2] DOI: 10.1155/2016/8137012.
[3] DOI: 10.1038/ismej.2017.125.
[4] DOI: 10.1111/1462-2920.13511.
[5] DOI: 10.1016/j.jbiotec.2006.01.031.
[6] DOI: 10.1093/nar/gkt1226.

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Keywords: Hydrogen sulfide, Heterotrophic sulfur oxidation, Pseudomonas koreensis A9, Genome analysis