

Category: Metagenomics

# Genome sequencing reveals the potential of an indigenous arsenotrophic bacterium; *Achromobacter* sp. KAs 3-5 for sub-surface arsenic mobilization and strategies for bioremediation

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## Abstract

Prevalence of toxic arsenic (As) oxyanion species in oligotrophic groundwater of south-east Asiatic regions (India and Bangladesh) has threatened the health of millions of people. As-transforming bacteria alter the mobility, speciation and bioavailability of As in the aquifer ecosystem, hence play important roles in the biogeochemical cycling of As. Till date, only 19 cultivable As-transforming bacterial strains have been reported but with no description on their detail genomic and physiological perspective of As homeostasis. In this study, the draft genome (5.7 Mbp) of an As-transforming, aromatic hydrocarbon utilizing and iron disproportioning indigenous groundwater bacterium KAs 3-5 has been obtained by Ion-Torrent sequencing revealed 65% genomic GC content, 5100 protein coding genes, and taxonomic affiliation to the members of genus *Achromobacter*, with >85% of genomic completeness. Phylogenomic signatures like MLST of 10 house-keeping genes, cut-off of <95% of average nucleotide/amino acid identity (ANI/OrthoANI/AI), <0.99 of tetra-nucleotide correlations, and <70% value of DNA-DNA homology with nearest phylogenetic neighbors exhibited its species distinctiveness among all the described *Achromobacter* sp. members. Pan-genomic analysis confirmed the strain's potential to adapt wide array of environmental stresses with a higher abundance of unique genes for metabolism of amino acids, polyketide, xenobiotics, nitroso compounds, aromatic hydrocarbons and most necessarily complete operon cluster for As-resistance/transformation/detoxification, as well as genes for transport, and signal transduction mechanisms. The genome analysis also highlighted its genetic determinants for loss of functions for antibiotic resistance, pathogenicity regulations, and gain of new/acquired functions for Fe-transport, fatty acids uptake-metabolism, motility, heavy metal (Cu-Zn-Co) metabolism and several putative/hypothetical proteins owing to its capacity to acquired desired traits through horizontal gene transfer events. The ability of the organism to metabolize mono-poly aromatics like benzene, toluene, naphthalene, anthracene, etc. (by catechol, homogentisate pathways) coupled to As reduction (through *arsHBC*, *arsC*, *ACR3*) found to be well validated by genomic observations. X-ray absorption fine structure (XANES) also enabled us to decipher detailed Fe-based reductive As release process from sediment and its interaction. The obtained genome data provide us with a better understanding of sub-surface mechanisms of hydrocarbon (organic matter) driven As release, which may contribute to the future design of rational strategies for bioremediation of As/other heavy metal contaminated environments.

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