



## Microbacterium Paraoxydans: A Strain with Potential for Arsenic Bioremediation and Plant Growth Promotion, Its Genome Has Been Sequenced, Annotated and Applied

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### Abstract

Bhagobangola I block's garden soil, which contained arsenic, produced a heavy metal hypertolerant bacterium that encouraged plant growth (Murshidabad district). The bacterial isolate was classified as a member of the genus *Microbacterium* by metagenomic analysis. The isolated strain's maximum average nucleotide identity (89.99%) with the *Microbacterium paraoxydans* strain DSM 15019 was discovered through taxonomic analysis. Prokka, DFAST, and RAST were used to annotate bacterial genomes. The genome's total base count was 3365911, with 69.90% GC. In the bacterial genome, Prokka found 3216 coding sequences (including 1461 hypothetical sequences), 3283 genes, 10 miscellaneous RNAs, 3 rRNAs, 53 tRNAs, and 1 tmRNA. In the bacterial genome, DFAST found 3257 coding sequences (1217 hypothetical sequences), 3 rRNA sequences, and 53 tRNA sequences.

**Keywords:** Arsenic; Bioremediation plants; Genome sequencing

### Introduction

An international environmental hazard is soil and groundwater contaminated by arsenic. Groundwater and soil contamination by arsenic is more common in deltaic alluvial regions surrounding the Ganga Brahmaputra Meghna river basin in Bangladesh and India. The majority of the arsenic found in groundwater and soil comes from geological sources. The WHO and USEPA's maximum allowable limit for arsenic in groundwater is exceeded in some areas of West Bengal, India [1-3].

### Methodology

Some areas of Murshidabad, Nadia, Bardhaman, Malda, South and North 24 Pargana district in West Bengal have extremely high levels of arsenic contamination in their groundwater. There have been reports of groundwater contamination containing arsenic from 24 blocks in the Murshidabad district. The maximum amount of arsenic detected in the Murshidabad district's groundwater is 3 mg/L. Several blocks in the Murshidabad district, including Bhagobangola I, Bhagobangola II, Jalangi, and Beldanga I, exhibit concerning elevated levels of arsenic in both soil and groundwater. There have been reports of groundwater contamination containing arsenic from every block in the Nadia district. The highest amount of arsenic found in tubewells in the Nadia district has been reported to be 3.2 mg/L.

More than 0.1 mg/L of arsenic is present in the groundwater of the Purbasthali block in the Bardhaman district. An arsenic-contaminated paddy field in Giaghata block, North 24 Pargana, has been found to contain 22.8 mg/kg of arsenic. As a result, millions of people are impacted by arsenic poisoning, and many areas of West Bengal, India, are hotspots for arsenic.

It has been possible to isolate bacteria that are resistant to arsenic from a number of hotspots in West Bengal, India. Numerous of these arsenic-tolerant bacteria demonstrated the ability to promote plant growth and perform arsenic bioremediation. For instance, from arsenic-contaminated groundwater in the Purbasthali block of Bardhaman, West Bengal, Kabiraj et al. isolated strains of *Micrococcus luteus* and *Bacillus pacificus* that were tolerant to arsenic. *Micrococcus luteus* isolated strain was able to withstand 390 mg/L arsenite.

*Bacillus pacificus* strains that are tolerant of arsenic can grow in both 10 mM arsenite and 20 mM arsenate. The genome of *Bacillus pacificus* contained arsenic resistance genes, such as *arsC*, *arsB*, *arsR*, etc. Both types of bacteria have the ability to oxidize arsenic into a less harmful form and adsorb it onto their surfaces. By generating proline, gibberellic acid, and indole acetic acid (IAA), they both accelerated the growth of rice seedlings. The minimum inhibitory concentration (MIC) of *Alcaligenes faecalis* subsp. *phenolicus* DSM 16503 T, which was isolated from the Kulik river in Raiganj, Uttar Dinajpur, West Bengal, was found to be 500 µg/ml for arsenite and 2500 µg/ml for arsenate. The same study area's *Serratia marcescens* NBRC 102204 T isolate revealed MIC values of 600 µg/ml and 1800 µg/ml.

### Conclusion

Arsenic oxidation, adsorption, and bioaccumulation potential were demonstrated by both isolates. According to Roy, the genome of these bacteria revealed the presence of the *arsR*, *arsB*, and *arsC* genes, which are in charge of arsenic tolerance. In bacteria, the *arsRBC*, *arsRABC*, and *arsRDABC* operons contain the genes *arsR*, *arsB*, and *arsC* (Shamim, 2018) [4-10]. Isolated from arsenic-contaminated soil in Bhagobangola I, Murshidabad, West Bengal, *Lysinibacillus* sp. and *Bacillus safensis* demonstrated notable growth in the presence of 76.98 mM and 88.53 mM of arsenite and 560.88 mM and 721.13 mM of arsenate, respectively. Additionally, these bacteria demonstrated the ability to biotransform arsenite into the less toxic form of arsenate as well as bioaccumulate and bioadsorption. Additionally, for 50 ppm of arsenic, they demonstrated more than 30% arsenic bioremediation in

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less than a day hypertolerant faecal arsenic.

#### References

1. Alberti M, Correa C, Marzluff JM, Hendry AP, Palkovacs EP, et al. (2017) Global urban signatures of phenotypic change in animal and plant populations. *Proc Natl Acad Sci* 114:8951-8956.
2. Bearhop S, Fiedler W, Furness RW, Votier SC, Waldron S, et al. (2005) Assortative mating as a mechanism for rapid evolution of a migratory divide. *Science* 310: 502-504.
3. Chamberlain DE, Vickery JA, Glue DE, Robinson RA, Conway GJ, et al. (2005) Annual and seasonal trends in the use of garden feeders by birds in winter. *Ibis* 147: 563-575.
4. Cleary GO, Coleman BR, Davis AD, Jones DN, Miller KK, et al. (2016) Keeping it clean: bird bath hygiene in urban and rural areas. *J Urban Ecol* 2:1-4.
5. Clergeau P and Vergnes A (2011) Bird feeders may sustain feral rose-ringed parakeets *Psittacula krameri* in temperate Europe. *Wildl Biol* 17: 248-252.
6. Cox DT and Gaston KJ (2015) Likeability of garden birds: importance of species knowledge & richness in connecting people to nature. *PLoS ONE* 10:e0141505.
7. Cox DT and Gaston KJ (2016) Urban bird feeding: connecting people with nature. *PLoS ONE* 11:e0158717.
8. Davies ZG, Fuller RA, Dallimer M, Loram A and Gaston KJ (2012) Household factors influencing participation in bird feeding activity: a national scale analysis. *PLoS ONE* 7:e39692.
9. Dhondt AA, Dhondt KV, Hawley DM and Jennelle CS (2007) Experimental evidence for transmission of *Mycoplasma gallisepticum* in house finches by fomites. *Avian Pathol* 36: 205-208.
10. Fuller RA, Warren PH, Armsworth PR, Barbosa R and Gaston KJ (2008) Garden bird feeding predicts the structure of urban avian assemblages. *Diversity Distrib* 14:131-137.