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Identification of a Photoarsenotrophic and Sulfur-Oxidizing *Rhodoplanes* sp.: Implications for Arsenic and Sulfur Biogeochemistry

NATSUKO HAMAMURA, SAKI YURIOKA AND MELODY C. CABRERA OSPINO

Faculty of Science, Kyushu University

Microbial arsenic and sulfur metabolism play crucial roles in shaping Earth's elemental cycles, influencing environmental chemistry and ecosystem dynamics. Among these, photoarsenotrophs, anoxygenic phototrophic bacteria that oxidize arsenite [As(III)] to arsenate [As(V)], contribute to arsenic transformation in natural and contaminated environments. While photoarsenotrophy may have originated in early Earth's anaerobic environments, few cultured representatives exist, and their phylogenetic and metabolic diversity remain poorly understood.

Here, we report the isolation of a novel photoarsenotrophic and sulfur-oxidizing bacterium, *Rhodoplanes* sp. strain TS-1, from heavy metal-contaminated environments. This strain TS-1, a purple non-sulfur bacterium, grew photoheterotrophically using both arsenite and thiosulfate as electron donors, demonstrating its metabolic flexibility. Genomic analysis revealed genes involved in sulfur oxidation (*sox* system) and an arsenite oxidase gene (*aioBA*) with 68% amino acid identity to that of the recently described photoarsenotrophic *Rhodobacter* sp. strain CZR27[1].

Notably, the strain TS-1 exhibited photoarsenotrophy independent of sulfur oxidation, oxidizing As(III) to As(V) under light even in the absence of thiosulfate. This confirms that TS-1 can utilize arsenite as a primary electron donor, futher supporting the hypostheis that phototrophic arsenite oxidation is a widespread metabolic strategy in anoxygenic bacteria. In the presence of thiosulfate, complete oxidation of 1 mM As(III) occurred within 8 days. This dual arsenic-sulfur metabolism suggests the ecological significance of phototrophic bacteria in both arsenic detoxification and sulfur cycling. This study provides the first evidence of photoarsenotrophy in the genus *Rhodoplanes*, expanding the diversity of phototrophic arsenite oxidizers and supporting the role of light-driven arsenic oxidation in microbial redox transformations in natural and contaminated environments.

[1] Wu Y-F., et al. (2023), *Environ Microbiol*, 25, 1538-1548.