



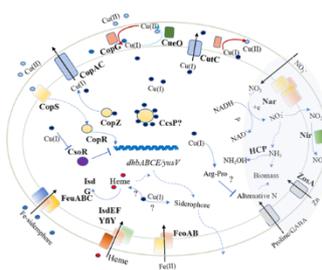
Research Paper

Integrative chemical and omics analyses reveal copper biosorption and tolerance mechanisms of *Bacillus cereus* strain T6Ping Wu^a, Niraj R. Rane^b, Chao Xing^{a,c}, Swapnil M. Patil^b, Hyun-Seog Roh^d, Byong-Hun Jeon^{b,*}, Xiaofang Li^{a,*}^a Hebei Key Laboratory of Soil Ecology, Center for Agricultural Resources Research, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Shijiazhuang 050021, China^b Department of Earth Resources and Environmental Engineering, Hanyang University, Seoul 04763, Republic of Korea^c University of Chinese Academy of Sciences, Beijing 100049, China^d Department of Environmental Engineering, Yonsei University, 1 Yonseidae-gil, Wonju, Gangwon 26493, Republic of Korea

HIGHLIGHTS

- A Cu-resistant *Bacillus cereus* strain T6 was isolated and characterized.
- Chemical and omics tools were integrated to explore its Cu resistance mechanism.
- A cellular view was achieved for T6's Cu sorption and resistance.
- Cell wall structure and intracellular processes are important for T6's Cu binding.
- Cu homeostasis and denitrification pathways were drastically impacted by Cu.

GRAPHICAL ABSTRACT



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ABSTRACT

A comprehensive understanding of the cellular response of microbes to metal stress is necessary for the rational development of microbe-based biosorbents for metal removal. The present study investigated the copper (Cu) sorption and resistance mechanism of *Bacillus cereus* strain T6, a newly isolated Cu-resistant bacterium, by integrative analyses of physicochemistry, genomics, transcriptomics, and metabolomics. The growth inhibition assay and biosorption determination showed that this bacterium exhibited high tolerance to Cu, with a minimum inhibitory concentration of 4.0 mM, and accumulated Cu by both extracellular adsorption and intracellular binding. SEM microscopic images and FTIR spectra showed significant cellular surface changes at the high Cu level but not at low, and the involvement of surface functional groups in the biosorption of Cu, respectively. Transcriptomic and untargeted metabolomic analyses detected 362 differentially expressed genes and 60 significantly altered metabolites, respectively. Integrative omics analyses revealed that Cu exposure dramatically induced a broad spectrum of genes involved in Cu transport and iron homeostasis, and suppressed the denitrification pathway, leading to significant accumulation of metabolites for metal transporter synthesis, membrane remodeling, and antioxidant activities. The results presented here provide a new perspective on the intricate regulatory network of Cu homeostasis in bacteria.

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