Genome studies of a soil bacterium, a potential candidate for removing arsenic from contaminated water

Worldwide various human activities such as mining, chemical industries, use of arsenic-based pesticides, and natural occurrences result in contamination of soil and water with heavy metals and cause severe environmental and health problems. Millions of people are exposed to directly or indirectly to the toxic metals including arsenic (As). Long-term exposure to As leads to several skin diseases, such as hyper- and hypo-pigmentation, hyperkeratosis and melanosis, as well as gangrene, skin cancer, lung cancer and bladder cancer. Poisoning occurs through drinking of contaminated water and/or consumption of foods produced on cultivated lands irrigated with As-contaminated water. It is therefore important to develop efficient, yet affordable technologies to remove As from water by any means. Use of microorganisms such as bacteria is one of the possibilities. In fact, the bacteria have developed several metabolic processes and strategies to convert As to various forms including respiratory arsenate reduction, cytoplasmic arsenate reduction and arsenite methylation. Furthermore, certain bacteria have developed the necessary genetic components that make the bacteria resistant to As toxicity, allowing them to survive and grow in an As contaminated environment where other organisms can hardly exist.

This report concerns a bacterial strain, *Lysinibacillus sphaericus* B1-CDA as potential candidate for removal of heavy metals from the contaminated sources. The strain was isolated from a cultivated land in the Chuadanga district of Bangladesh, where soil, sediment, and ground water were contaminated with As for many years. The genetic composition and evolutionary history of this bacterium were investigated by using massively parallel sequencing and comparative analysis with other known *Lysinibacillus* genomes. The summary of the genome with nucleotide content and gene count levels are presented in Table 1. All genes of B1-CDA predicted to be involved in its resistance to As and/or other heavy metals were annotated. Annotation of all genes predicted to be metal responsive was manually curated, with a particular focus on genes responsive to As. The presence of As responsive genes was verified by PCR *in vitro* conditions. PCR amplification confirmed that B1-CDA is harboring *acr3, arsR, arsB* and *arsC* arsenic responsive genes.

Attribute	Value	% of total
Genome size (bp)	4 509 276	100,00
DNA GC content (bp)	1 690 719	37,49
DNA coding region (bp)	3 911 574	86,75
Number of replicons	1	
Total genes	4 601	100,00
rRNA genes	11	0,24
tRNA genes	77	1,67
Protein coding genes	4 513	98,09
Genes assigned to RAST functional categories	2 671	58,05
Genes assigned Gene Ontology terms by Blast2GO	3 050	66,29

Table 1. Summary of the genome of B1-CDA with nucleotide content and gene count levels

Based on results obtained by using several bioinformatics tools it was confirmed that *L. sphaericus* B1-CDA contains many specific metal resistant genes, such as arsenic, nickel, cobalt, iron, manganese, chromium, cadmium, lead and zinc. These results also revealed that B1-CDA genome consists of many proteins that catalyze binding and transport of metal ions. Therefore, the findings in this study may be useful in bioremediation of the toxic metals from the polluted environment. This study also demonstrates that it is possible to speed up molecular biology research by using bioinformatics tools.

Publication

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