scientific reports

Check for updates

OPEN

Genomic, morphological, and biochemical analyses of a multi-metal resistant but multi-drug susceptible strain of *Bordetella petrii* from hospital soil

Urmi Halder[1], Raju Biswas[1], Ashutosh Kabiraj[1], Rajendar Deora[2], Moitri Let[1], Rajendra Kr Roy[1], Annapurna Chitikineni[3,4], Krishnendu Majhi[1], Shrabana Sarkar[1], Bhramar Dutta[1], Anubhab Laha[1], Arunava Datta[1], Dibyendu Khan[1], Rajeev K. Varshney[3,4], Dipnarayan Saha[5], Saswati Chattopadhyay[6] & Rajib Bandopadhyay[1]✉

Contamination of soil by antibiotics and heavy metals originating from hospital facilities has emerged as a major cause for the development of resistant microbes. We collected soil samples surrounding a hospital effluent and measured the resistance of bacterial isolates against multiple antibiotics and heavy metals. One strain BMCSI 3 was found to be sensitive to all tested antibiotics. However, it was resistant to many heavy metals and metalloids like cadmium, chromium, copper, mercury, arsenic, and others. This strain was motile and potentially spore-forming. Whole-genome shotgun assembly of BMCSI 3 produced 4.95 Mb genome with 4,638 protein-coding genes. The taxonomic and phylogenetic analysis revealed it, to be a *Bordetella petrii* strain. Multiple genomic islands carrying mobile genetic elements; coding for heavy metal resistant genes, response regulators or transcription factors, transporters, and multi-drug efflux pumps were identified from the genome. A comparative genomic analysis of BMCSI 3 with annotated genomes of other free-living *B. petrii* revealed the presence of multiple transposable elements and several genes involved in stress response and metabolism. This study provides insights into how genomic reorganization and plasticity results in evolution of heavy metals resistance by acquiring genes from its natural environment.

Development of drug and heavy metal resistance in bacteria, particularly resulting in reduction of antibiotic efficacy has intensified in last few decades. Hospital activities like byproducts discharges are generally a big source of antibiotics and heavy metals[1–4]. Health care facilities from different geographical locations are getting contaminated with ~ 1.5–310 g/day due to the uncontrolled and extensive use of drugs. Over the past few years, in different countries hospital effluents have resulted in the discharge of multiple antibiotics; erythromycin (13–7545 ng/L), azithromycin (113–7351 ng/L), clarithromycin (10–14,000 ng/L), spiramycin (40–2200 ng/L), josamycin (12–15 ng/L), roxithromycin (140–2189 ng/L), clindamycin (31–1465 ng/L), lincomycin (7–48,400 ng/L), ofloxacin (662–37,000 ng/L), ciprofloxacin (11–101,000 ng/L), lomefloxacin (313–1162 ng/L), levofloxacin (150–750 ng/L), enoxacin (450–480 ng/L), norfloxacin (100–44,000 ng/L), sulfadiazine (19.2–6640 ng/L), and

[1]Microbiology Section, Department of Botany, The University of Burdwan, Burdwan, West Bengal 713104, India. [2]Department of Microbial Infection and Immunity, The Ohio State University, Columbus, OH 43210, USA. [3]Center of Excellence in Genomics and Systems Biology, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad 502324, India. [4]State Agricultural Biotechnology Centre, Centre for Crop and Food Innovation, Murdoch University, Murdoch 6500, Australia. [5]Biotechnology Unit, Division of Crop Improvement, ICAR-Central Research Institute for Jute and Allied Fibres, Barrackpore, West Bengal 700121, India. [6]Department of Microbiology, Burdwan Medical College, Burdwan, West Bengal 713104, India. ✉email: rajibindia@gmail.com