Complete genome of *Pandoraea pnomenusa* RB-38, an oxalotrophic bacterium isolated from municipal solid waste landfill site

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**Abstract**

*Pandoraea pnomenusa* RB-38 is a bacterium isolated from a former sanitary landfill site. Here, we present the complete genome of *P. pnomenusa* RB38 in which an oxalate utilization pathway was identified. The genome analysis suggested the potential of this strain as an effective biocontrol agent against oxalate-producing phytopathogens.

*Pandoraea pnomenusa* are gram-negative, non-sporeulating, rod-shaped bacteria which are mostly recovered from sputum of cystic fibrosis patients and contaminated soil environment (Chen et al., 2009). Biotechnological potential of this species is currently confined to a handful of previously documented activities due to the lack of genomic data, namely polychlorinated biphenyls (PCBs) and dichloromethane (DCM) degradation capability (Pham et al., 2012; Yu et al., 2014). Similarly, there is also a limited understanding on the biotechnological potential of other *Pandoraea* species, to date, the metabolic activities discovered are oxalate, thiosulfate, lignin and malachite green utilization (Anandham et al., 2010; Chen et al., 2009; Sahin et al., 2011; Shi et al., 2013).

Previously, we reported the isolation of *P. pnomenusa* RB-38 from a non-operational municipal solid waste landfill site in Malaysia (Ee et al., 2014). We sequenced the complete genome of *P. pnomenusa* RB-38 with the objective to provide insights into metabolic pathways in this species which could be of significant industrial values.

Genomic DNA of *P. pnomenusa* strain RB38 was extracted using Masterpure\textsuperscript{TM} DNA Purification Kit (Epicentre). Quality assessment of the gDNA was determined by using Qubit 2.0 fluorometer (Life Technologies) and Nanodrop spectrophotometer (Thermo Fisher Scientific). A 10 kb SMRTbell\textsuperscript{TM} template library was prepared and sequenced using Pacific Biosciences (PacBio) RSII sequencer. *De novo* assembly was subsequently performed using Hierarchical Genome Assembly Process (HGAP) assembly pipeline Version 2 (190 fold coverage). The circularity of the assembled genome was examined using Gepard dotplot tool followed by genome circularization via removal of one of the duplicated sequence to produce a blunt end circular genome. Quiver algorithm was subsequently used to polish the circularized genome. Multi-platform gene predictions were performed using RAST, Integrated Microbial Genomes-Expert Review (IMG-ER), RNAmmer, tRNAscan-SE and Prokka pipeline.

*P. pnomenusa* RB38 genome consists of a circular chromosome with 5,378,872 bp and a G+C content of 64.76%. A total of 4766 genes, inclusive of 4640 protein coding sequences and 79 RNA genes (12 rRNA and 67 tRNA genes) were predicted (Table 1). Furthermore, 3634 protein coding genes were clustered into 24 clusters of orthologous groups (COGs). Annotation performed revealed a complete putative oxalate degradation operon: oxalate-formate antiporter (PROKKA: position: 1880801–1879455), succinyl-coenzyme A:oxalate CoA-transferase (DA70_00945; EC: 2.8.3.2), oxalyl-CoA decarboxylase (DA70_08450; EC: 4.1.1.8); formyl-CoA transferase (DA70_08435; EC: 2.8.3.16). Similar oxalate-degrading properties were discovered in the other four *Pandoraea* species suggesting that this activity is potentially a homogenous phenotype within the *Pandoraea* genus (Ee et al., 2015; Jin et al., 2007; Sahin et al., 2011). Moreover, we also identified a microcystin degradation protein encoding gene (MlrC...
gene) (DA70_157770) and various heavy metal resistance genes for chromium, cobalt, zinc, cadmium, nickel, arsenic in this genome.

In conclusion, the complete genome sequence of _P. pneumonia_ RB38 revealed the potential of this isolate as an oxalotrophic bacteria and provides a fundamental groundwork to further study its biotechnological potential. The oxalate degradation capacity of this strain will be valuable as a biocontrol agent in protecting crops against oxalic acid-producing phytopathogenic fungi (Schoonbeek et al., 2007). Moreover, the heavy metal resistance properties of this strain would strengthen its potentiality as a biocontrol agent by rendering survival advantage against agrochemicals. Furthermore, in biotechnological terms, the oxalate-degrading enzymes of this strain could be used to develop transgenic crops with heightened resistance towards phytopathogens.

### Nucleotide sequence accession numbers

This whole-genome project has been deposited at DDBJ/EMBL/GenBank under the accession number CP007506.1. This isolate has been deposited in Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ) culture collection centre with the accession number of DSM 100868.

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### References


Ee, R., Yong, D., Lim, Y.L., Yin, W.F., Chan, K.G., 2015. Complete genome sequence of oxalate-degrading bacterium Pandoraea vervacti DSM 23571T. J. Biotechnol. 204, 5–6.


<table>
<thead>
<tr>
<th>Table 1</th>
<th>Genome features of <em>Pandoraea pneumoniaa</em> RB38.</th>
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<tbody>
<tr>
<td>Features</td>
<td>Value</td>
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<tr>
<td>Genome size (bp)</td>
<td>5,378,872</td>
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<tr>
<td>GC content (%)</td>
<td>64.76</td>
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<tr>
<td>Total number of genes</td>
<td>4,766</td>
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<tr>
<td>Protein coding genes (CDSs)</td>
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<tr>
<td>rRNAs (5S, 16S, 23S)</td>
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<td>tRNAs</td>
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<td>ncRNA</td>
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