Correction to: Genome analysis of *Thauera chlorobenzoica* strain 3CB-1^T, a halobenzoate-degrading bacterium isolated from aquatic sediment

Tiffany S. Louie¹ · Elizabeth Jane Pavlik¹ · Max M. Häggblom¹

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In the original article, there are few errors in the figure 5. The correct description is given below.

Figure 5 shows that based on phylogenetic analysis of amino acid sequences of CRE, strain 3CB-1^T contains three genes that group with the beta subunits of similar benzoyl-CoA reductases. Three major groups can be seen in this tree; benzoyl-CoA reductase, 4-hydroxybenzoyl-CoA reductase and methylbenzoyl-CoA reductases. Ga0104426_101109 grouped with beta subunits of 4-hydroxybenzoyl-CoA reductase from *T. aromatica*, *Magnetospirillum* sp. SS-4, and *Magnetospirillum kuznetsovii*. Of the BCR beta subunits, Ga0104426_101325 groups with the BcrBs from *T. phenylacetica*, *T. aromatica* and a Rhodocyclaceae bacterium. Ga0104426_1343, is more distantly related to the above. It groups with the class I BCRs, but does not group closely with either the conventional class I BCRs or the methylbenzoyl-CoA reductases. The MBR homologues in strain 3CB-1^T have low percent identities to the BCR genes within its own genome, which makes sense since Tiedt et al. (2018) suggested they are in a separate subclass of the ATP-dependent BCRs. The MbdQ homologue had a 50% identity to BcrA. The beta, gamma, and delta subunits had only 34% identities or less to the Bcr genes. Ga0104426_13413, the putative chlorobenzoate-CoA ligase gene in 3CB-1^T, had low percent identities to the other CLEs in the genome ranging from 35 to 49%. Perhaps this is an indication that they

have different substrate specificities than the other BCRs and BCLs.

Fig. 5 Molecular phylogenetic analysis of related amino acid sequences from the genome of *Thauera chlorobenzoica* strain 3CB-1^T and known beta subunits of benzoyl-CoA reductases. The evolutionary history was inferred by using the Maximum Likelihood method based on the JTT matrix-based model (Jones et al. 1992). The tree with the highest log likelihood – 4800.77) is shown. The percentage of trees (> 93%) in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 11 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 310 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 (Kumar et al. 2016)

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✉ Max M. Häggblom
haggblom@rutgers.edu

¹ Department of Biochemistry and Microbiology, School of Environmental and Biological Sciences, Rutgers, The State University of New Jersey, New Brunswick, NJ, USA