

Isolation and characterization of two novel halotolerant Catechol 2,3-dioxygenases from a halophilic bacterial consortium

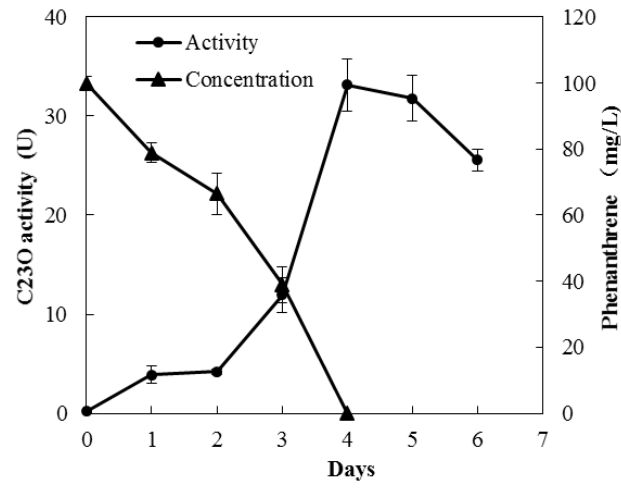
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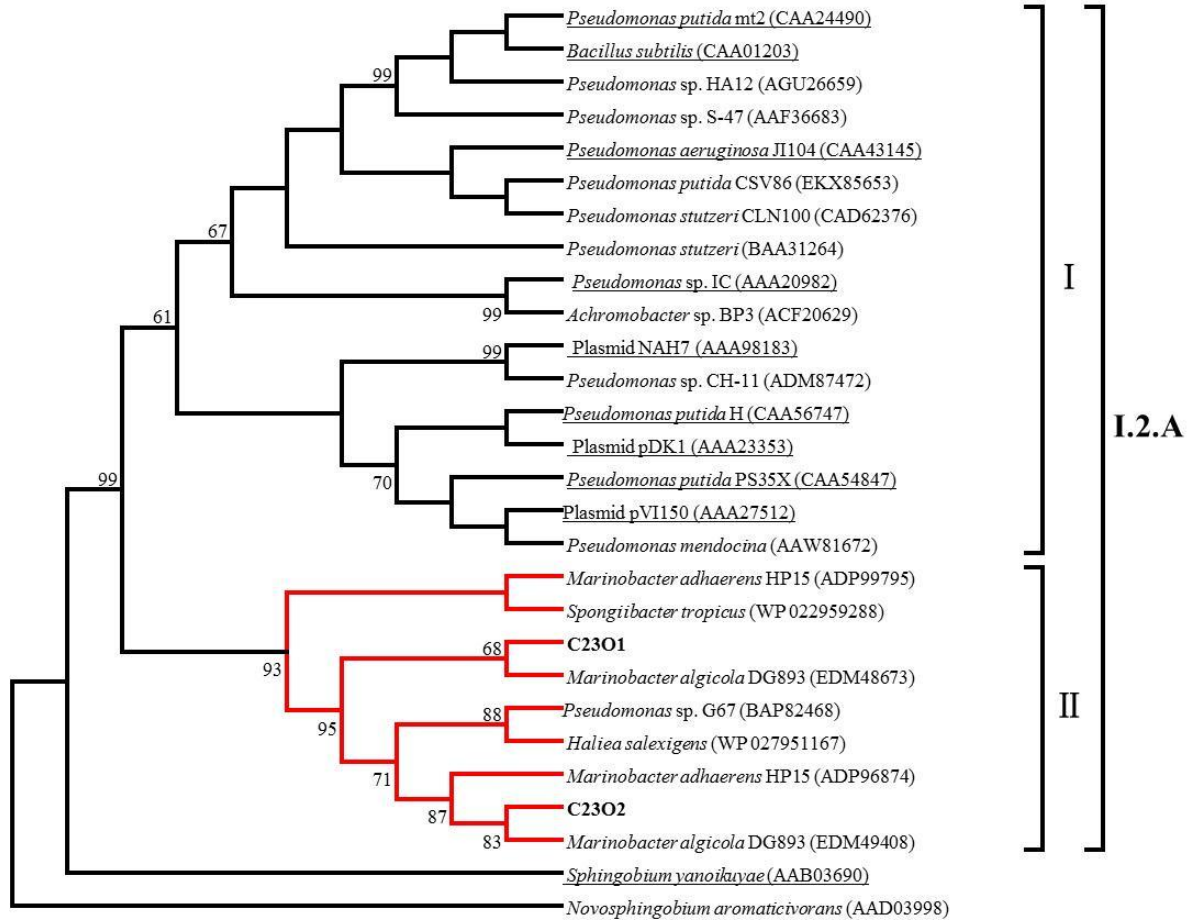
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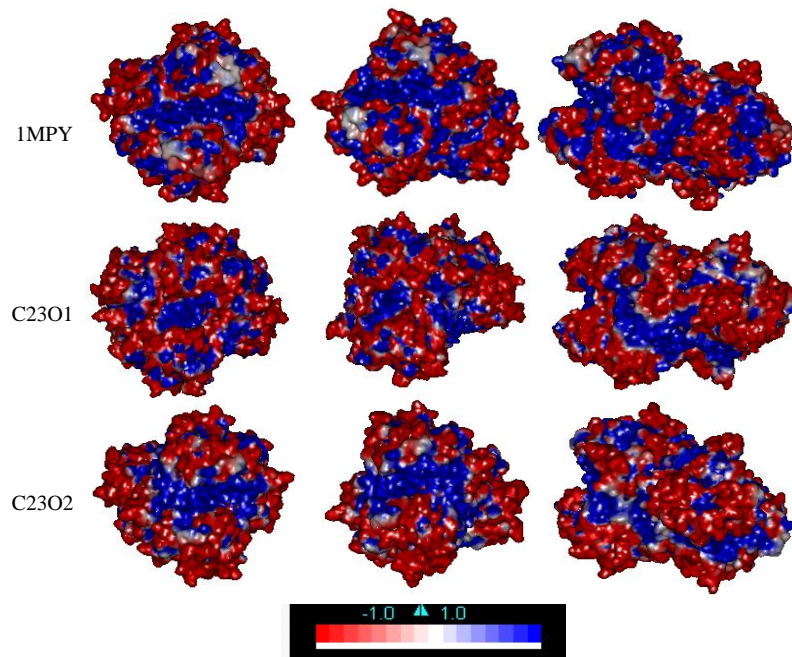
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Supplementary Figure S1 C23O activity during phenanthrene degradation by the halophilic bacterial consortium at an initial concentration of 100 mg/L



Supplementary Figure S2 Phylogenetic maximum-parsimony tree based on the C23O amino acid sequences. The clones isolated in this study are indicated with boldface type. The sequences with the underline are classic C23Os which were classified by Eltis and Bolin. The C23O amino acid sequences of *Sphingobium yanoikuyae* (AAB03690) and *Novosphingobium aromaticivorans* (AAD03998), two members of subfamily I.2.B were used as an outgroup. Bootstrap values (>60) expressed as percentages of 1000 replications are indicated at the branch points.



Supplementary Figure S4 Surface electrostatic potentials of C23O1, C23O2 and C23O from *Pseudomonas putida* mt2 (PDB no. 1MPY) obtained using Discovery Studio 2.5 software. The first, second and third column were seen from the right, top and front of the structures, respectively, with the red color corresponding to negatively charged residues and the blue surface corresponding to positively charged residues (color figure line).

Supplementary Table S1 Sequence similarity between selected C23O reference sequence^a and C23O1 or C23O2

Reference sequence	C23O1	C23O2
Group 1		
<i>Pseudomonas putida</i> mt2 (CAA24490)	79%	79%
<i>Pseudomonas</i> sp. HA12 (AGU26659)	79%	79%
<i>Bacillus subtilis</i> (CAA01203)	79%	79%
<i>Pseudomonas</i> sp. S-47 (AAF36683)	79%	79%
<i>Pseudomonas stutzeri</i> (BAA31264)	81%	79%
<i>Pseudomonas stutzeri</i> CLN100 (CAD62376)	80%	79%
<i>Pseudomonas aeruginosa</i> JII104 (CAA43145)	80%	79%
<i>Pseudomonas putida</i> CSV86 (EKX85653)	80%	79%
<i>Pseudomonas</i> sp. IC (AAA20982)	78%	78%
<i>Achromobacter</i> sp. BP3 (ACF20629)	79%	79%
Plasmid NAH7 (AAA98183)	78%	77%
<i>Pseudomonas</i> sp. CH-11 (ADM87472)	77%	76%
Plasmid pDK1 (AAA23353)	78%	76%
<i>Pseudomonas putida</i> H (CAA56747)	78%	79%
<i>Pseudomonas putida</i> PS35X (CAA54847)	77%	76%
Plasmid pVI150 (AAA27512)	78%	77%
<i>Pseudomonas mendocina</i> (AAW81672)	79%	77%
Group 2		
<i>Spongiibacter tropicus</i> (WP 022959288)	83%	81%
<i>Marinobacter adhaerens</i> HP15 (ADP99795)	90%	87%
<i>Marinobacter algicola</i> DG893 (EDM48673)	93%	90%
<i>Pseudomonas</i> sp. G67 (BAP82468)	91%	92%
<i>Haliea salexigens</i> (WP 027951167)	91%	92%
<i>Marinobacter adhaerens</i> HP15 (ADP96874)	87%	91%
<i>Marinobacter algicola</i> DG893 (EDM49408)	88%	95%

^aThese reference sequences corresponded to the ones in Figure 3.