

Genetic Analysis of the Upper Phenylacetate Catabolic Pathway in the Production of Tropodithietic Acid by *Phaeobacter gallaeciensis*

Martine Berger,¹ Nelson L. Brock,² Heiko Liesegang,³ Marco Dogs,¹ Ines Preuth,¹ Meinhard Simon,¹
Jeroen S. Dickschat,² and Thorsten Brinkhoff^{1*}

Institute for Chemistry and Biology of the Marine Environment (ICBM), University of Oldenburg, D-26111 Oldenburg, Germany, ¹ *Institute of Organic Chemistry, Technical University of Braunschweig, Braunschweig, Germany,* ² *and Göttingen Genomics Laboratory, Georg-August-University Göttingen, D-37077 Göttingen, Germany* ³

Running title: Phenylacetate catabolic pathway in *P. gallaeciensis*

*Corresponding author. Mailing address: Institute for Chemistry and Biology of the Marine Environment (ICBM), University of Oldenburg, P.O. Box 2503, D-26111 Oldenburg, Germany.
Phone: +49-441-7983269. Fax: +49-441-7983438. E-mail: t.brinkhoff@icbm.de.

Figure S1

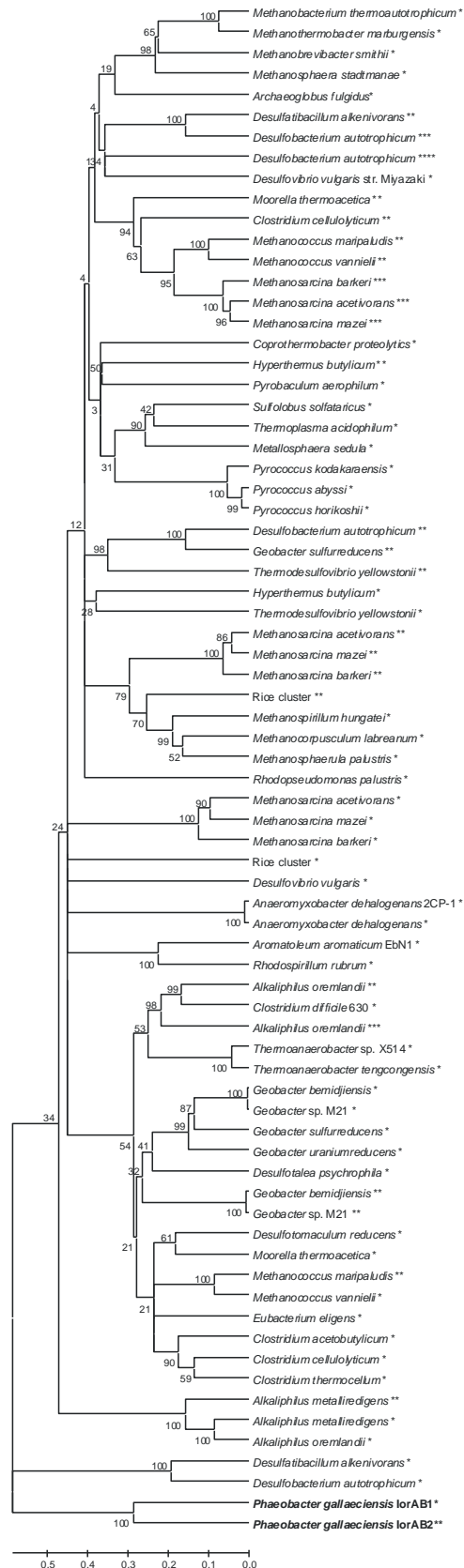


Figure S1: Evolutionary analysis of 74 proteins of the anaerobic IorA family from 46 different taxa (sequences available at UniProt using access keys in list S1L). Corresponding subsequences of Ior1 and its paralogue Ior2 from this study are bold. Paralogous proteins are indicated by a corresponding number of asterisks. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches. The relative evolutionary distance of the nodes is represented by the scale.

List S1L, Organisms and access keys of *iorA* protein sequences for Figure S1.

Alkaliphilus metalliredigens (tr|A6TNS0), Alkaliphilus metalliredigens (tr|A6TTE3), Alkaliphilus oremlandii (tr|A8MEE8), Alkaliphilus oremlandii (tr|A8MEG9), Alkaliphilus oremlandii (tr|A8MGP3), Anaeromyxobacter dehalogenans (tr|B8J7S4), Anaeromyxobacter dehalogenans (tr|B4UKJ6), Archaeoglobus fulgidus (sp|O28783|), Aromatoleum aromaticum (tr|Q5P920), Clostridium acetobutylicum (tr|Q97HL0), Clostridium cellulolyticum (tr|B8I7C3), Clostridium cellulolyticum (tr|B8I1E5), Clostridium difficile (tr|Q181W5|), Clostridium thermocellum (tr|A3DD19), Coprothermobacter proteolyticus (tr|B5Y9N4), Desulfatibacillum alkenivorans (tr|B8FL36), Desulfatibacillum alkenivorans (tr|B8FDS9), Desulfobacterium autotrophicum (tr|C0QLS9), Desulfobacterium autotrophicum (tr|C0QDI1), Desulfobacterium autotrophicum (tr|C0QMA9), Desulfobacterium autotrophicum (tr|C0QCB9), Desulfotalea psychrophila (tr|Q6ANT1), Desulfotomaculum reducens (tr|A4J9D8), Desulfovibrio vulgaris (tr|Q72F41), Desulfovibrio vulgaris (tr|Q72AP1), Eubacterium eligens (tr|C4Z4K7), Geobacter bemidjensis (tr|B5EDL0), Geobacter bemidjensis (tr|B5EIS3), Geobacter sp. (tr|C6E897), Geobacter sp. (tr|C6E209), Geobacter sulfurreducens (tr|Q74CD5), Geobacter sulfurreducens (tr|Q74BI8), Geobacter uraniumreducens (tr|A5G3F5), Hyperthermus butylicus (tr|A2BMR8), Hyperthermus butylicus (tr|A2BN79), Metallosphaera sedula (tr|A4YH50), Methanobacterium thermoautotrophicum (sp|O27880), Methanobrevibacter smithii (tr|A5UK69), Methanococcus maripaludis (tr|Q6M0F5), Methanococcus maripaludis (tr|Q6LZB6), Methanococcus vanniellii (tr|A6URV2), Methanococcus vanniellii (tr|A6USK8), Methanocorpusculum labreanum (tr|A2SQ01), Methanosarcina acetivorans (tr|Q8TPD1), Methanosarcina acetivorans (tr|Q8TQ25), Methanosarcina acetivorans (tr|Q8TRY9), Methanosarcina barkeri (tr|Q46GE4), Methanosarcina barkeri (tr|Q46A68), Methanosarcina barkeri (tr|Q467Q9), Methanosarcina mazei (tr|Q8PV81), Methanosarcina mazei (tr|Q8PTS8), Methanosarcina mazei (tr|Q8PTC8), Methanosphaera stadtmanae (tr|Q2NFH6), Methanosphaerula palustris (tr|B8GFY5), Methanospirillum hungatei (tr|Q2FSL3), Methanothermobacter marburgensis (tr|P80910), Moorella thermoacetica (tr|Q2RJY7), Moorella thermoacetica (tr|Q2RG75), Phaeobacter gallaeciensis (tr|A9GES2), Phaeobacter gallaeciensis (tr|A9FQI0), Pyrobaculum aerophilum (tr|Q8ZT17), Pyrococcus abyssi (tr|Q9UZR8), Pyrococcus horikoshii (tr|O58865), Pyrococcus kodakaraensis (tr|Q5JIU3), Rhodospseudomonas palustris (tr|Q6NAG1), Rhodospirillum rubrum (tr|Q2RSW7), Rice cluster (tr|Q0W0I6), Rice cluster (tr|Q0W1P9), Sulfolobus solfataricus (tr|Q97WQ2), Thermoanaerobacter sp. (tr|B0K5X1), Thermoanaerobacter tengcongensis (tr|Q8R837), Thermodesulfovibrio yellowstonii (tr|B5YGU6), Thermodesulfovibrio yellowstonii (tr|B5YK60), Thermoplasma acidophilum (tr|Q9HJF7)

Figure S2

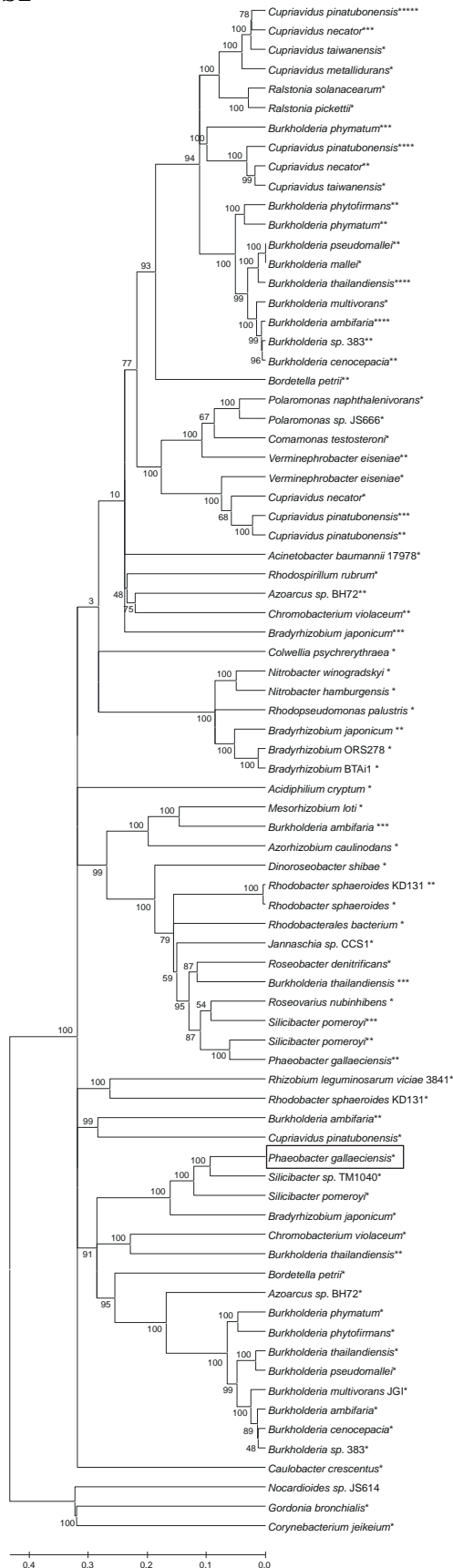


Figure S2: Evolutionary analysis of 79 proteins of the aerobic Ior1 family from 47 different taxa (sequences available at UniProt, using access keys from list S2L). The Ior1 from this study is framed. Paralogous proteins are indicated by a corresponding number of asterisks. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches. The relative evolutionary distance of the nodes is represented by the scale.

List S2L, Organisms and access keys of *ior1* protein sequences for Figure S1.

Acidiphilium cryptum (tr|A5G199), Acinetobacter baumannii (tr|A5G199), Acinetobacter baumannii (tr|B7I3D9), Acinetobacter baumannii (tr|B7I3D9), Acinetobacter sp (tr|D0C4Y2), Azoarcus sp. (tr|A1K6Z2), Azoarcus sp. (tr|A1K868), Azorhizobium caulinodans (tr|A8IPU9), Bordetella petrii (tr|A9I170), Bordetella petrii (tr|A9I206), Bradyrhizobium BTAi1 (tr|A5ELH2), Bradyrhizobium japonicum (tr|Q89RP0), Bradyrhizobium japonicum (tr|Q89JE5), Bradyrhizobium japonicum (tr|Q89D54), Bradyrhizobium ORS278 (tr|A4YVY9), Burkholderia ambifaria (tr|Q0BJ75), Burkholderia ambifaria (tr|Q0BBC9), Burkholderia ambifaria (tr|Q0B246), Burkholderia ambifaria (tr|Q0B1J4), Burkholderia cenocepacia (tr|Q1BT28), Burkholderia cenocepacia (tr|Q1BT28), Burkholderia mallei (tr|Q62GP9), Burkholderia multivorans (tr|A9AE30), Burkholderia multivorans (tr|A9AE30), Burkholderia phymatum (tr|B2JKE7), Burkholderia phymatum (tr|B2JKE7), Burkholderia phymatum (tr|B2JKE7), Burkholderia phytofirmans (tr|B2SWP8), Burkholderia phytofirmans (tr|B2SWP8), Burkholderia pseudomallei (tr|Q63Y33), Burkholderia pseudomallei (tr|Q63Y33), Burkholderia sp. (tr|Q39KJ6), Burkholderia sp. (tr|Q39KJ6), Burkholderia thailandensis (tr|Q2T4P2), Burkholderia thailandensis (tr|Q2T1R3), Burkholderia thailandensis (tr|Q2STZ6), Caulobacter crescentus (tr|Q9A3M6), Chromobacterium violaceum (tr|Q7P1B0), Chromobacterium violaceum (tr|Q7P1B0), Colwellia psychrerythraea (tr|Q483G1), Comamonas testosteroni (tr|D0J7M3), Corynebacterium jeikeium (tr|Q4JVL8), Cupriavidus metallidurans (tr|Q1LHV8), Cupriavidus necator (tr|Q0JZR2), Cupriavidus necator (tr|Q0JZR2), Cupriavidus necator (tr|Q0JZR2), Cupriavidus pinatubonensis (tr|Q46W90), Cupriavidus pinatubonensis (tr|Q46NV1), Cupriavidus pinatubonensis (tr|Q46QD7), Cupriavidus pinatubonensis (tr|Q46MH2), Cupriavidus pinatubonensis (tr|Q46MU8), Cupriavidus taiwanensis (tr|B3R7X6), Cupriavidus taiwanensis (tr|B3R7X6), Dinoroseobacter shibae (tr|A8LMF9), Gordonia bronchialis (tr|D0L683), Jannaschia sp. (tr|Q28SR3), Mesorhizobium loti (tr|Q98CF1), Nitrobacter hamburgensis (tr|Q1QLC6), Nitrobacter winogradskyi (tr|Q3SRT5), Nocardioides sp. (tr|A1SHR1), Phaeobacter gallaeciensis (tr|A9ERV7), Phaeobacter gallaeciensis (tr|A9ERV7), Phaeobacter gallaeciensis (tr|A9ERV7), Phaeobacter gallaeciensis (tr|A9GES2), Polaromonas naphthalenivorans (tr|A1VU55), Polaromonas sp. (tr|Q122L2), Ralstonia pickettii (tr|C6BGH6), Ralstonia solanacearum (tr|Q8XYC9), Rhizobium leguminosarum (tr|Q1M4S9), Rhodobacter sphaeroides (tr|Q3J275), Rhodobacter sphaeroides (tr|Q3J275), Rhodobacter sphaeroides (tr|Q3J275), Rhodobacterales bacterium (tr|B6AVD9), Rhodobacterales bacterium (tr|B6AVD9), Rhodopseudomonas palustris (tr|Q6NAG1), Rhodospirillum rubrum (tr|Q2RSW7), Roseobacter denitrificans (tr|Q163W1), Roseobacter litoralis (tr|A9GZI3), Roseovarius nubinihibens (tr|A3SNT4), Silicibacter pomeroyi (tr|Q5LVX7), Silicibacter pomeroyi (tr|Q5LVX7), Silicibacter pomeroyi (tr|Q5LVX7), Silicibacter sp. (tr|Q1GHL3), Verminephrobacter eiseniae (tr|A1WJB0), Verminephrobacter eiseniae (tr|A1WJB0),