



Comparative and functional genomics of *Roseovarius*

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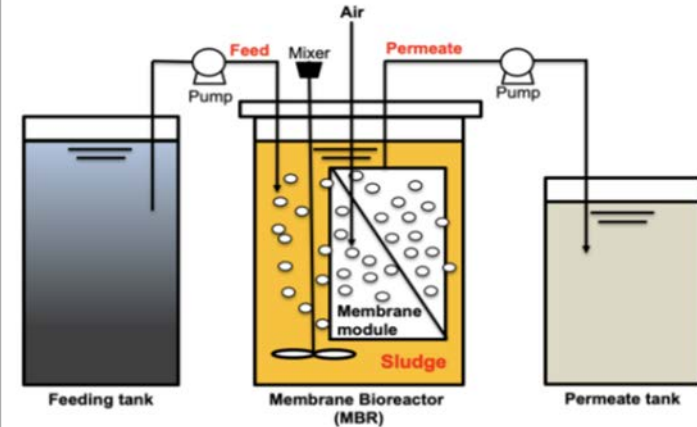
Mentor

- **Oil extraction => wastewater**
 - 600 billion liters of PW in 2017 in the U.S. alone¹
 - Not easy to clean
- **Using Microbes to clean = bioreactor**
 - Increased salinity past marine
- **Roseovarius genus prevalent**



Collaboration with
Colorado School of Mines

Membrane Bioreactor

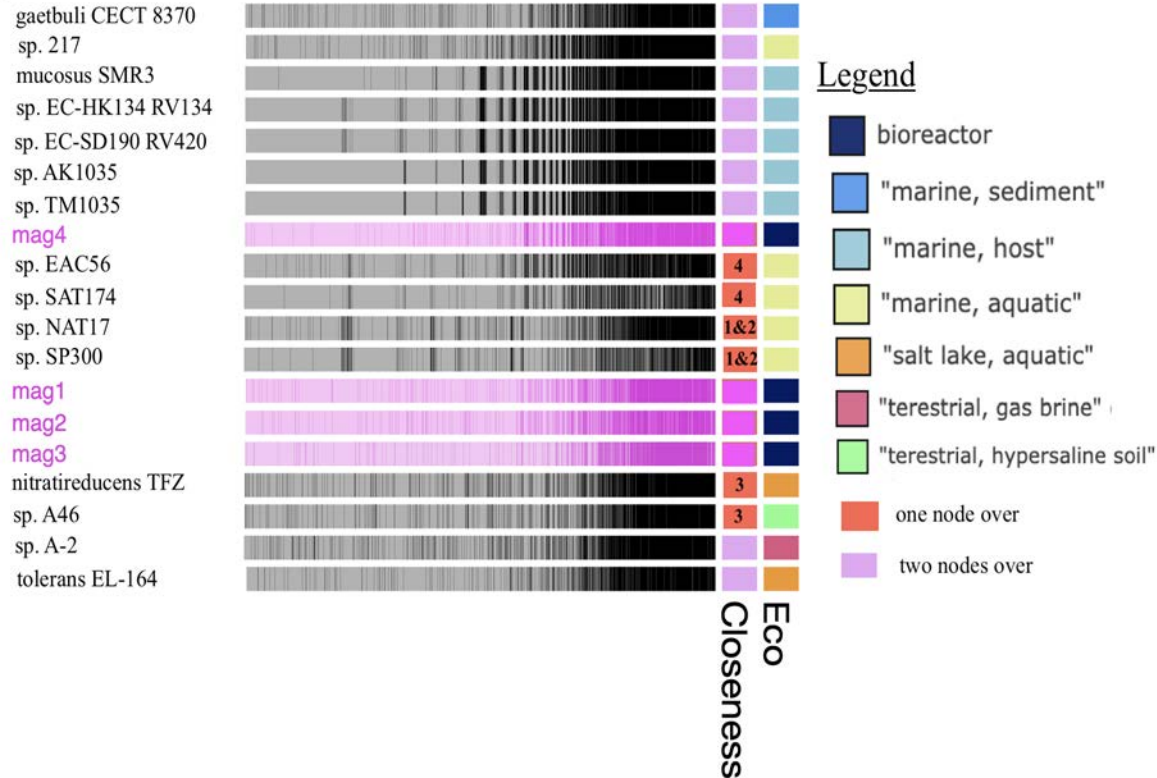


PW source: Denver-Julesburg basin
Reactor volume : 70 L, aerated
Inoculum: Activated sludge from conventional wastewater facility

- **KBase**
 - Data Analysis: Phylo-trees, Pangenomes, Annotation, and Building of Metabolic Models
- **KEGG Pathway Database**
 - Collections metabolic processes
- **COG NCBI Database**
 - Cluster of Orthologous Genes

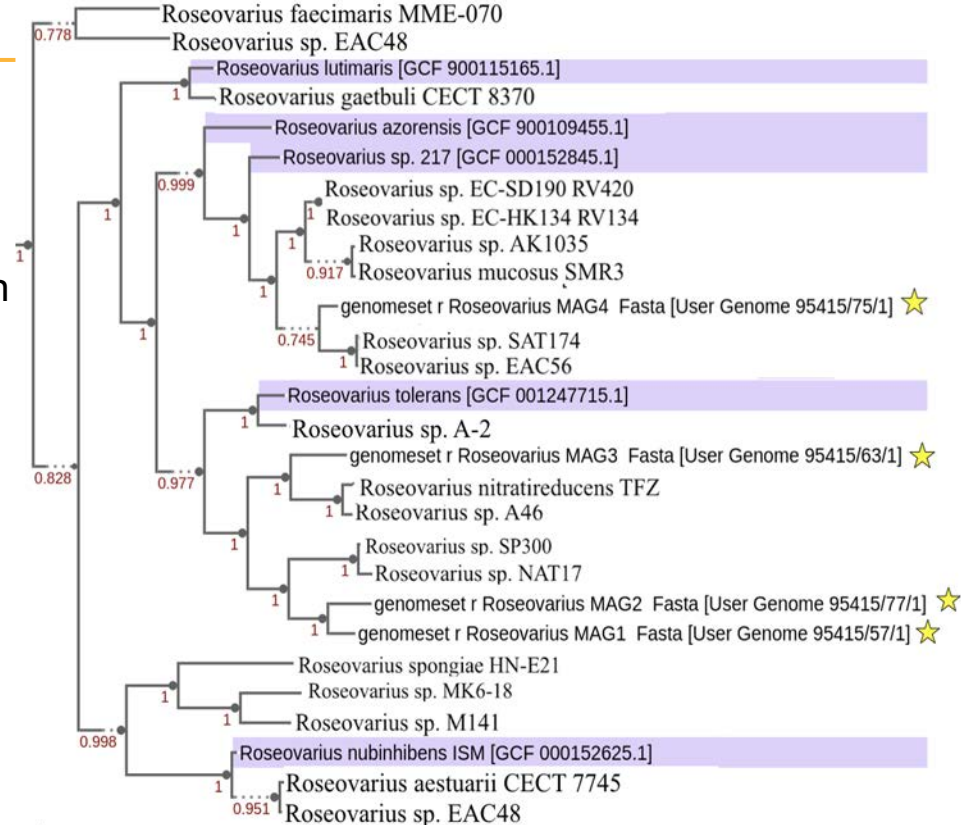
MAG name	Completeness	Contamination
MAG1	98.77	0.06
MAG2	95.18	1.58
MAG3	97.63	0.3
MAG4	98.32	0.17

Potential ID of Roseovarius MAGs



Enriched Function

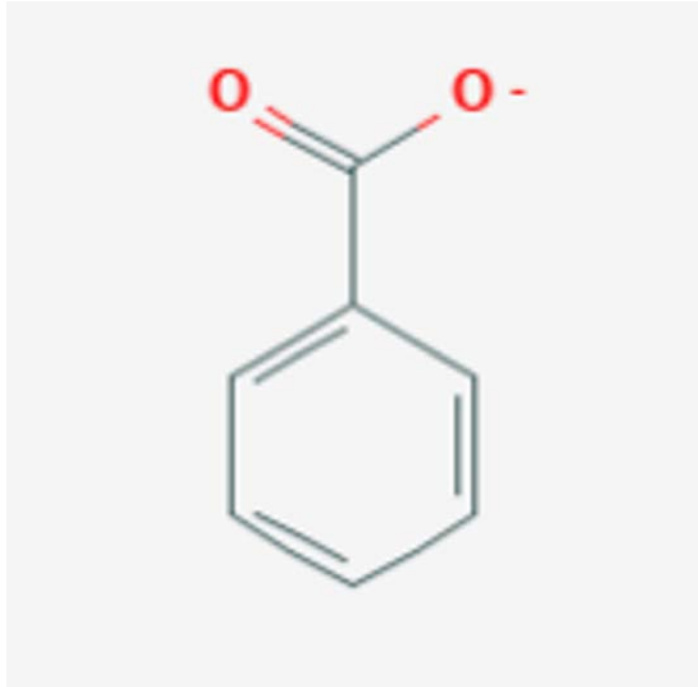
- **Phylogenetic Closeness**
 - 2 nodes out had the most in common
- **By Environment/habitat**
 - Marine, Plastic Surface had most in common [shared functions, not enriched ones]



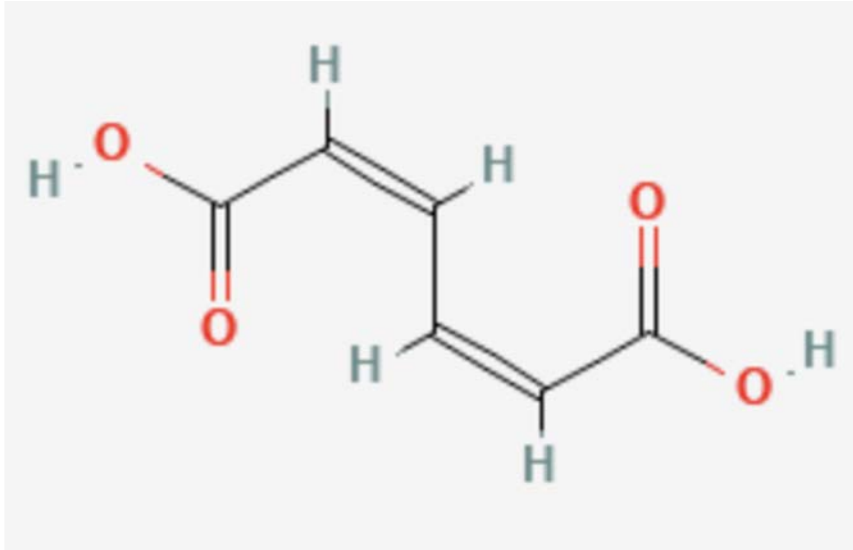
Unique Functions Theorized Role

- **ABC-type sulfate transport system, permease component** [PDB 3d31]
 - Transports molybdate/tungstate² natural, inorganic metal salts³
- **Tetraheme cytochrome c subunit NapC of nitrate or TMAO reductase (NapC)**
 - Transmembrane electron acceptor in Q-Cycle⁴
- **Predicted esterase of the alpha/beta hydrolase fold** [PDB:1UXO]
 - Hydrolase, predicted to work on hydrophilic esters/thioesters⁵
- **Serine protease, subtilisin family (AprE)** [PDB:1SCJ]
 - Predicted thermal-stability function⁶
- **p-Aminobenzoyl-glutamate transporter AbgT**
 - Transport polycyclic aromatic hydrocarbon aminobenzoate⁷

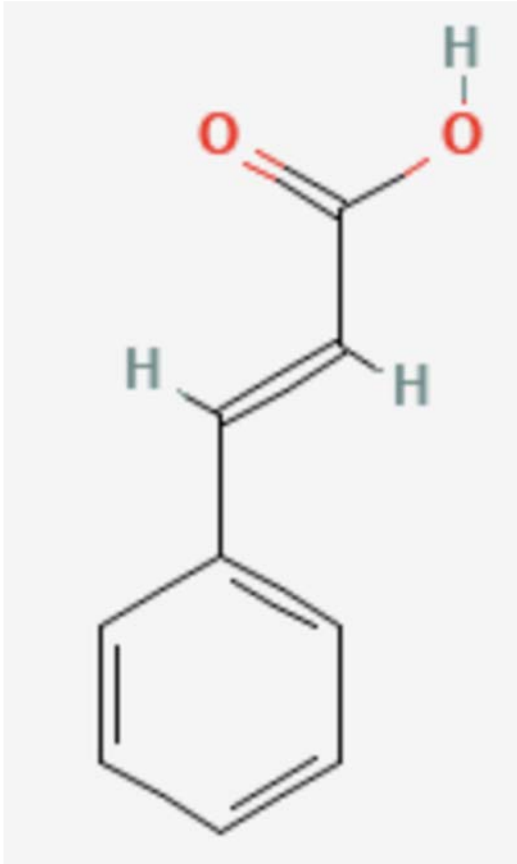
Hydrocarbon Degradation



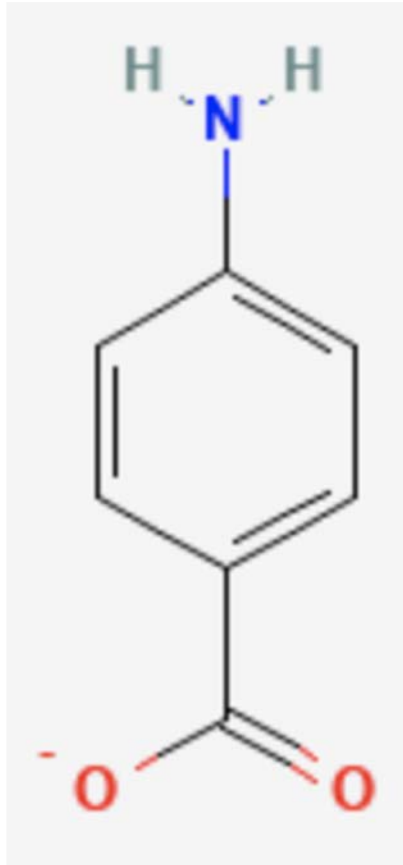
- 8/36
- Has a complete path for
- Excluding MAG3
- benzoate => catechol



- 10/36
- Excluding MAG3



- 34/36
- Cinnamaldehyde turns into this with exposure to light



- Partial path

- **Benzoate, Muconic Acid, Cinnamic Acid**
 - additives to fracking water
- **Xylene, Dioxin, Caprolactam, Polycyclic aromatic Hydrocarbon**
 - Only has a 1-2 enzymes from the entire pathway
 - Unsure if preforms

Unique Function

- **Common to 3**

- MAG3 only has one
 - Biopolymer transport protein ExbD/ToIR [1,2,3]
 - Iron uptake⁸
- MAGs 1, 2, and 4 have four in common
 - Transcriptional regulator, AcrR family
 - Can have a role in biofilm formation/stress response⁹

- **Common to 2**

- Range of enzymes & transporters & specific subunits
- MAGs 1 & 2 share the most
- MAG 3 shares the least

- **Might have a role in the actual**
 - Hydrocarbon Degradation
 - Inorganic metal metabolism

- **Things to further explore**
 - Looking for things the MAGs don't have compared to the other
Roseovarius
 - Iodide oxidation

Acknowledgements



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Any Questions?

Background

1. Scanlon BR, Reedy RC, Xu P, et al. Can we beneficially reuse produced water from oil and gas extraction in the U.S.? *Science of The Total Environment*. 2020;717:137085. doi:10.1016/j.scitotenv.2020.137085
2. Procko E, O'Mara ML, Bennett WF, Tieleman DP, Gaudet R. The mechanism of ABC TRANSPORTERS: General lessons from structural and functional studies of an Antigenic PEPTIDE TRANSPORTER. *The FASEB Journal*. 2009;23(5):1287-1302. doi:10.1096/fj.08-121855
3. The Editors of Encyclopedia Britannica. Molybdate and tungstate minerals. *Encyclopædia Britannica*. <https://www.britannica.com/science/molybdate-mineral>. Accessed July 29, 2021.
4. Brondijk TH, Fiegen D, Richardson DJ, Cole JA. Roles of NAPF, Napg and NapH, subunits of the Escherichia Coli periplasmic nitrate reductase, IN UBIQUINOL OXIDATION. *Molecular Microbiology*. 2002;44(1):245-255. doi:10.1046/j.1365-2958.2002.02875.x
5. Sukul P, Lupilov N, Leichert LI. Characterization of ml-005, a novel metaproteomics-derived esterase. *Frontiers in Microbiology*. 2018;9. doi:10.3389/fmicb.2018.01925
6. DiTursi MK, Kwon S-J, Reeder PJ, Dordick JS. Bioinformatics-driven, rational engineering of protein thermostability. *Protein Engineering Design and Selection*. 2006;19(11):517-524. doi:10.1093/protein/gz1039
7. Delmar JA, Yu EW. The AbgT Family: A novel class Of antimetabolite transporters. *Protein Science*. 2015;25(2):322-337. doi:10.1002/pro.2820
8. Biopolymer transport protein ExbD/ToIR. Interpro. <https://www.ebi.ac.uk/interpro/entry/InterPro/IPR003400/>. Accessed July 29, 2021.
9. Colclough AL, Scadden J, Blair JM. TetR-family transcription factors in Gram-negative BACTERIA: CONSERVATION, variation and implications For efflux-mediated antimicrobial resistance. *BMC Genomics*. 2019;20(1). doi:10.1186/s12864-019-6075-5

Programs/Tools [In addition to those used in the Midterm Presentation]

- Arkin AP, Cottingham RW, Henry CS, Harris NL, Stevens RL, Maslov S, et al. KBase: The United States Department of Energy Systems Biology Knowledgebase. Nature Biotechnology. 2018;36: 566. doi: 10.1038/nbt.4163 <https://www.nature.com/articles/nbt.4163>
- KEGG PATHWAY Database. KEGG: Kyoto Encyclopedia of genes and genomes. <https://www.genome.jp/kegg/>. Accessed July 29, 2021.
- COG - NCBI. National Center for Biotechnology Information. <https://www.ncbi.nlm.nih.gov/research/cog>. Published 2014. Accessed July 29, 2021.