

Metagenome-based identification of EPS degraders in a Shark Bay pustular mat

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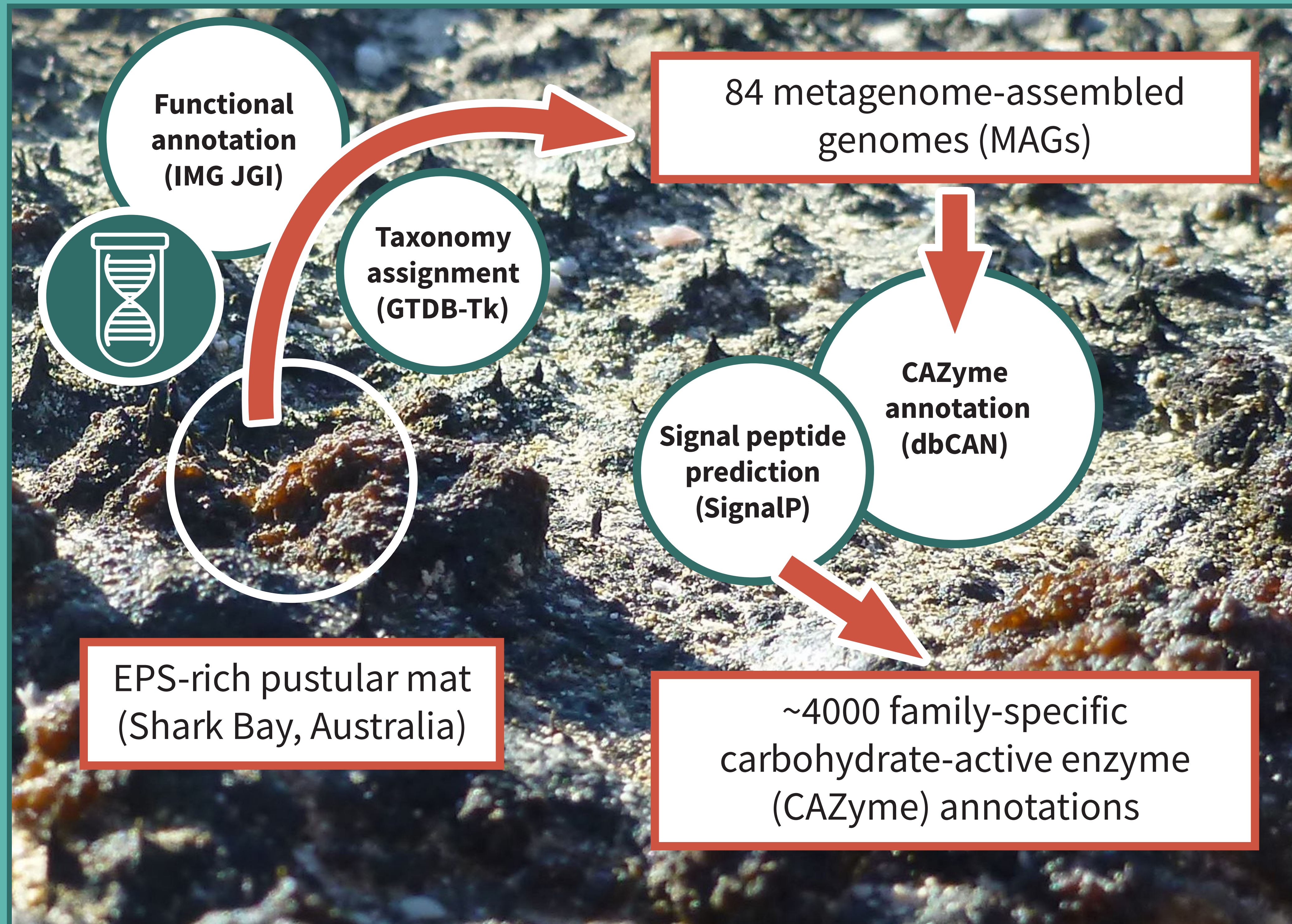
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Context

- Polysaccharide-rich **exopolymeric substances (EPS)** are the major structural component of microbial mats
- Anionic groups in EPS (ex. uronic acid, sulfate) bind cations like Ca²⁺
- EPS degradation** raises carbonate alkalinity and alters the properties of the EPS matrix, impacting **CaCO₃ saturation and nucleation**
- Taxa responsible for EPS degradation not known despite importance for **mat mineralization**

Goal: Determine which taxa degrade EPS in marine microbial mats based on genetic potential for polysaccharide degradation.

Bacteroidetes, Verrucomicrobia, and Anaerolineae likely degrade EPS in marine mats



Results

- >4000 degradation-related CAZymes from >100 families, ~25% extracellular
- Bacteroidetes**: high total and extracellular CAZyme variety
- Anaerolineae, Verrucomicrobia, and Cyanobacteria**: high total but low extracellular CAZyme variety
- Alpha- and Gammaproteobacteria**: low variety with single high-variety outliers
- Planctomycetes and Myxococcota**: “in the middle” with total and extracellular CAZyme variety in 3rd quantile.
- Large gap between top 9% and bottom 91% of extracellular CAZyme varieties

Conclusions

- Bacteroidetes**: perform first steps of EPS polysaccharide degradation using large suites of extracellular CAZymes
- Verrucomicrobia and Anaerolineae**: high intracellular CAZyme variety for “downstream” carbohydrate degradation
- Cyanobacteria**: intracellular CAZymes for metabolizing their own carbohydrates
- Alpha- and Gammaproteobacteria**: most likely not major players in EPS degradation, with few exceptions having high total/extracellular CAZyme variety

References & Images

Dupraz et al., *Earth-Sci. Rev.*, 2009. 96, 141–162
 Wong et al., *ISME*, 2018. 12, 2619–2639
 Decho & Gutierrez, *Front. microbiol.*, 2017. 8
 Braissant et al., *FEMS Microbiol. Ecol.*, 2009. 67, 293–307
 Gallagher et al., *Geobiology*, 2012. 10, 518–530
 tube by ibrandify from the Noun Project, Bacteria by Maxim Kulikov from the Noun Project, calcite by Rodri from theNoun Project

