Single-cell Genomics Reveals Metabolic Strategies for Microbial Growth and Survival in the Subsurface

Objective

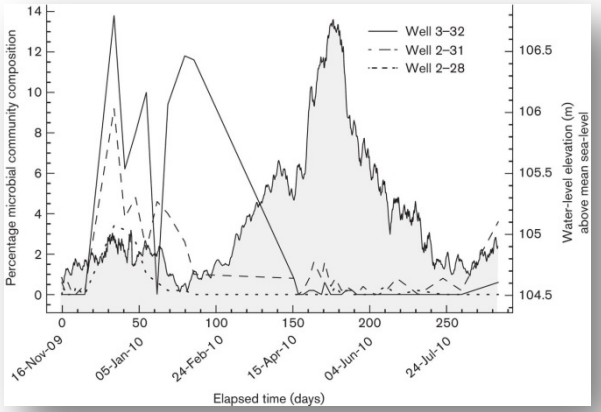
- Infer metabolic function of important subsurface microbial taxa using single-cell genomics.

Approach/Results

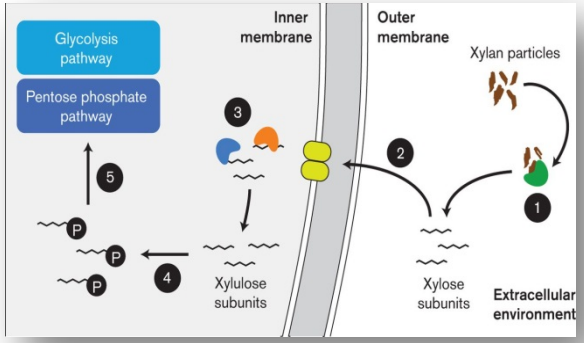
- Isolated four *Pedobacter* single cells from Hanford aquifer sediments using flow cytometry, and undertook whole genome amplification, sequencing.
- Genome assembly enabled functional potential to be inferred, revealing a potential role for these species in the Hanford subsurface in metabolizing recalcitrant organic carbon.

Significance and Impact

- Cultivation-independent single-cell sequencing identified versatile lifestyle for *Pedobacter* within the Hanford aquifer, with roles in carbon cycling and colonization of microaerophilic habitats.
- Biogeochemical shifts (e.g. nutrients, carbon influx) associated with Columbia river water intrusion into the subsurface had a deleterious effect on *Pedobacter* populations.
- Mixing of groundwater and river water in the Columbia River subsurface interaction zone can result in community shifts that may impact carbon cycling.



Temporal abundances of *Pedobacter* 16S rRNA gene pyrotag sequences recovered from groundwater at the Hanford 300 Area.



Inferred mechanism for extracellular xylan degradation and subsequent uptake in Hanford *Pedobacter* SAGs.

Wilkins, M. J., Kennedy, D. W., Castelle, C. J., Field, E. K., Stepanauskas, R., Fredrickson, J. K., and Konopka, A. E., 2014. "Single-cell genomics reveals metabolic strategies for microbial growth and survival in an oligotrophic aquifer." *Microbiology-(UK)* 160, 362-372. 10.1099/mic.0.073965-0