Comparing in-situ, individual bacterial community growth rates in cropped and successional soils using a 16S rRNA internal standard

Cassandra Wattenburger[1*], Daniel Buckley[1]

(1) Soil and Crops Science Section, Cornell University, Ithaca, NY

*cjw259@cornell.edu @CJWattenburger

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Background

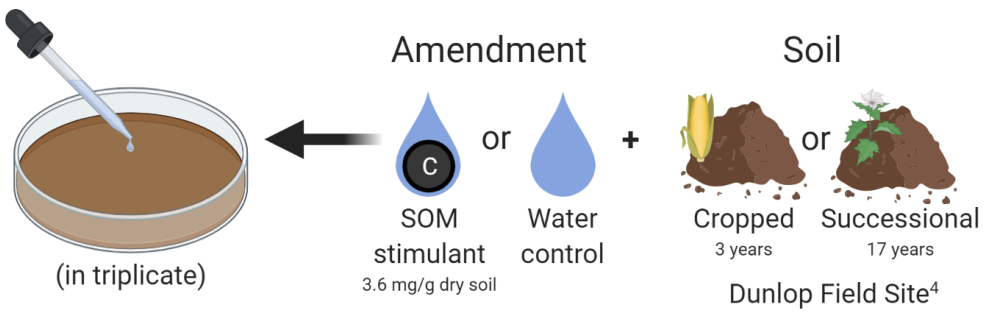
- Soil bacteria drive biogeochemical cycles via their metabolic activities, **growth is driven by metabolism**
- Growth is a metric that combines evolutionary, ecological, and environmental factors[1,2]
- Community **growth dynamics may inform ecosystem processes**, such as carbon cycling[3]

Hypotheses

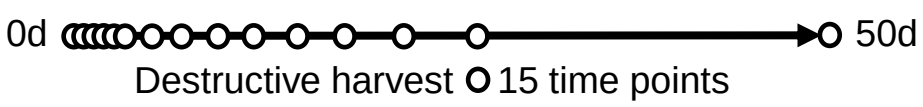
1. Soil bacterial communities consist of a dynamic spectrum of fast and slow growing species
2. 16S rRNA copy number is positively correlated with in-situ growth rate
3. Soil habitat and resource availability modify in-situ community growth rates, with faster growth in more disturbed or higher resource environments

Experimental design

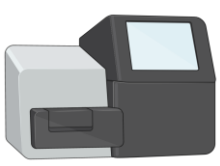
Microcosms



Incubation



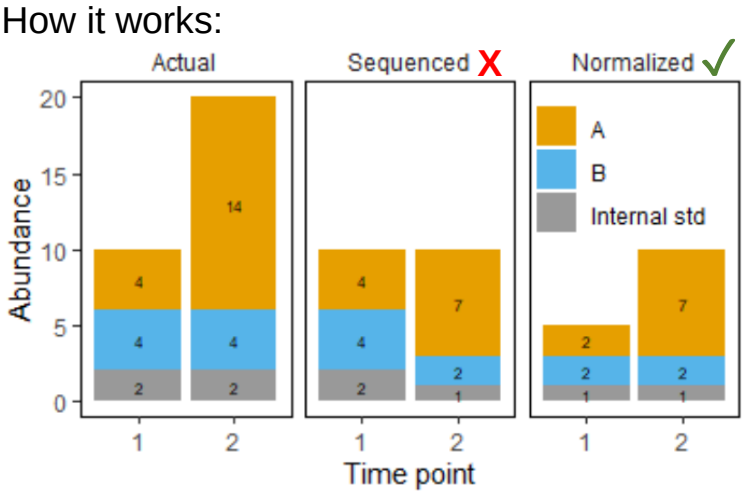
Sequencing



16S V4 rRNA amplicon sequencing with internal standard

Internal standard

How it works:

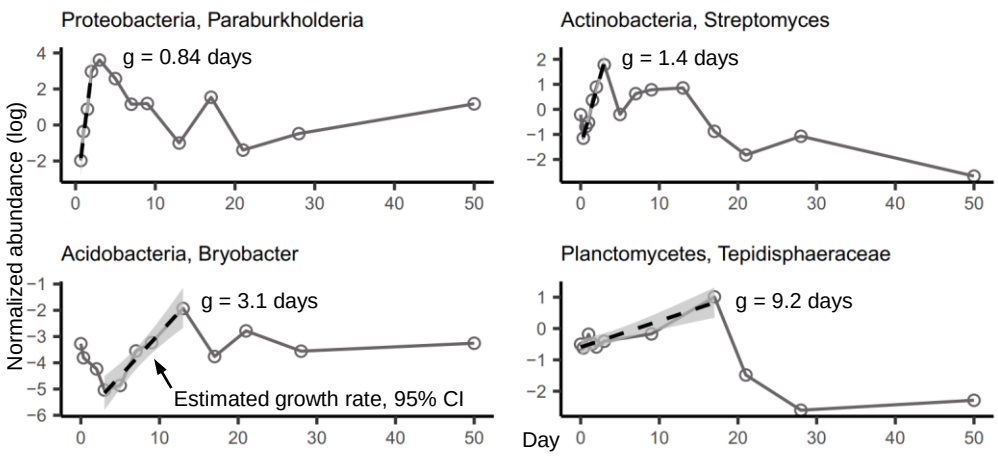


Compositional data corrected[5]

16S rRNA oligo, *Aquifex aolicus*

10 pg in soil DNA extraction

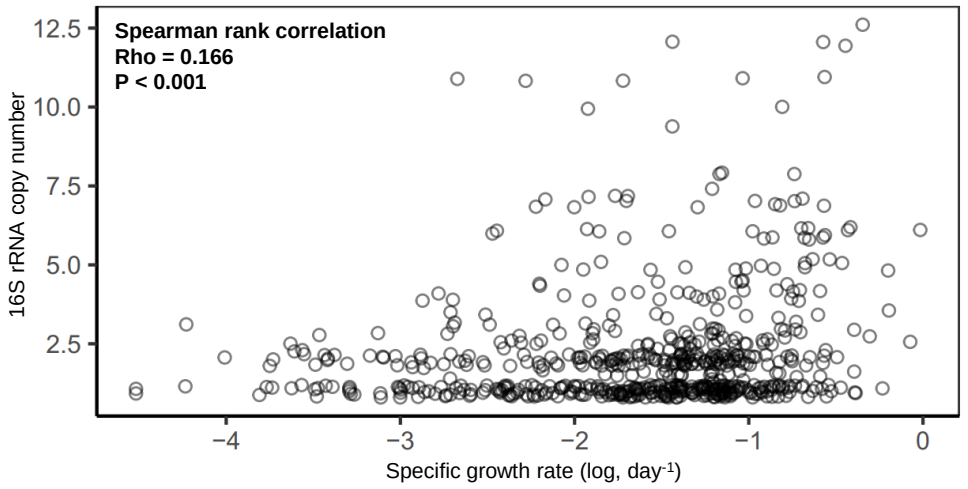
In-situ growth rate estimates



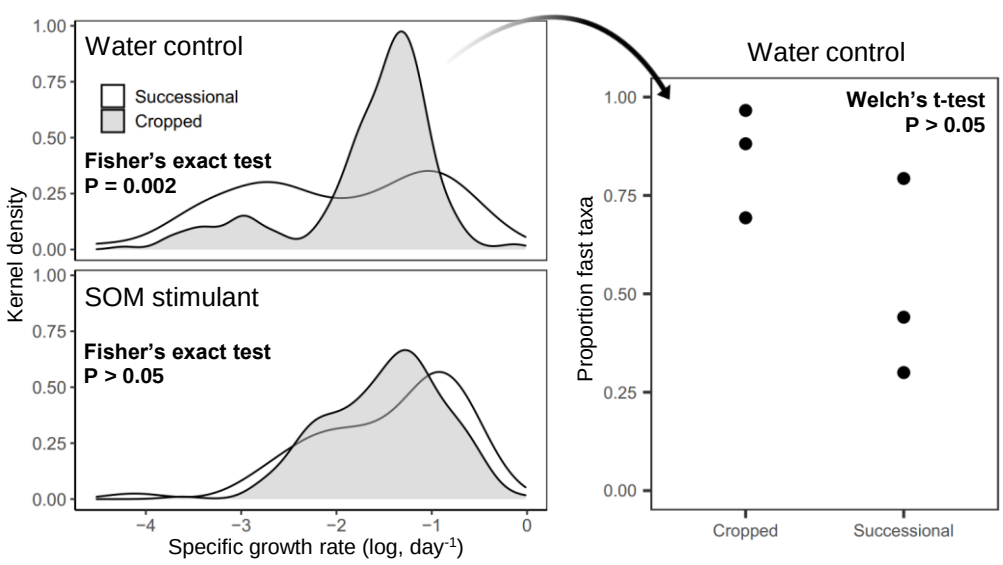
Estimated growth rates for 453 taxa in total
Generation times (g), min: 0.7; max: 64; mean: 5 days

Growth rates had a weak, positive correlation with 16S rRNA copy number

16S rRNA copy number estimated using PAPRICA[6]



Land use and resource availability affected growth rate distributions



Conclusions

In-situ growth rates in bacterial communities are altered by soil history and resource availability. They are weakly correlated with 16S rRNA copy number.

References: 1. Koch et al., 2018. Ecosphere 9. doi:10.1002/ecs2.2090; 2. Li et al., 2019. The ISME Journal 13, 2162–2172. doi:10.1038/s41396-019-0422-z; 3. Blazewicz et al., 2020. The ISME Journal. doi:10.1038/s41396-020-0617-3; 4. Howard et al., 2018. Oecologia 187, 547–559. doi:10.1007/s00442-018-4088-4; 5. Lin et al., 2019. Applied and Environmental Microbiology 85, e02634-18, doi:10.1128/AEM.02634-18; 6. Bowman & Ducklow, 2015. PLOS ONE 10, e0135868. doi:10.1371/journal.pone.0135868