Supporting Information for

Trait-based patterns of microbial succession in dormancy potential and heterotrophic strategy: case studies of resource-based and post-press succession

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Supporting Methods

For the Centralia metagenomes, DNA was extracted using a phenol-chlorofom method (Cho et al., 1996) and purified with the MoBio DNEasy PowerSoil Kit (MoBio, Carlsbad, CA, USA) following the manufacturer's instructions. Metagenomic sequencing was performed by the Department of Energy's Joint Genome Institute (DOE JGI) on an Illumina HiSeq 2500. Assembly and processing of raw reads were processed following JGI's standard operating procedures (http://www.**jgi**.doe.gov). Annotated dormancy genes were retrieved from IMG using KO identifiers K07699 (*spo0A*), K10715 (*rpfC*), K07154 (*hipA*), K03830 (*yafP*), K07172 (*mazE*), K06218 (*relE*), K01451 (*hipO*), K07473 (*dinJ*), K07171 (*mazF*), and K00951 (*relA*). tRNA and dormancy gene abundance were normalized to the single copy house-keeping gene *rplB*. Centralia metagenomes are available at JGI IMG (GOLD Study ID Gs0114513) and computational workflows are available on GitHub (https://github.com/ShadeLab/Centralia_operons_dormancy).

Supplemental Figures

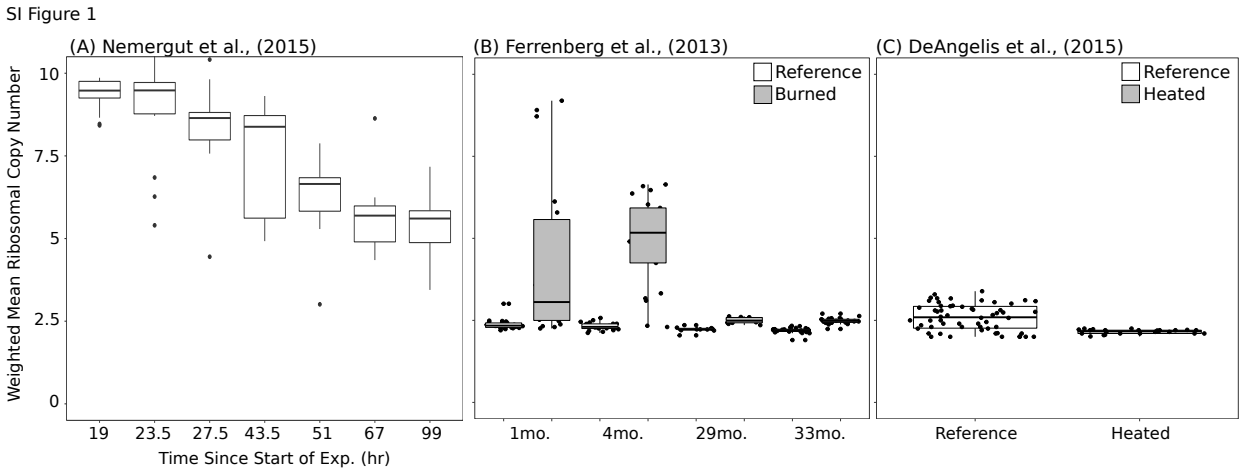

Figure S1. As a community-level microbial trait linked to heterotrophic strategy, weighted mean community ribosomal copy number decreased over time in a nutrient-rich mesocosm experiment (A), increased relative to reference soils during resource-based succession (B), and decreased relative to reference soils during post-press succession (C). Weighted mean ribosomal gene copy number was calculated from 16S rRNA gene surveys for nutrient-based succession studies (A) Nemergut et al., (2015) and (B) Ferrenburg et al., (2013) and for the post-press succession study from DeAngelis et al., (2015) (C).

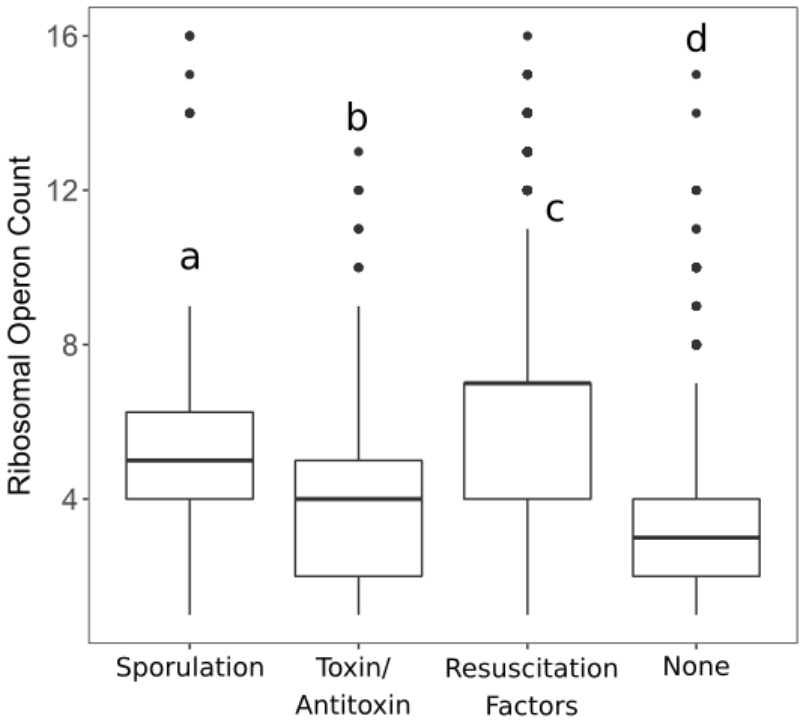

Figure S2. The number of ribosomal operons in cultivated bacteria is higher for taxa with dormancy strategies. Ribosomal operon counts for genomes in NCBI. The category 'none' refers to taxa without a significant BLASTn hit for any of the three dormancy strategies examined here. Letters indicate groups that are significantly different based on a Kruskal-Wallis test with a Dunn Test for multiple comparisons.

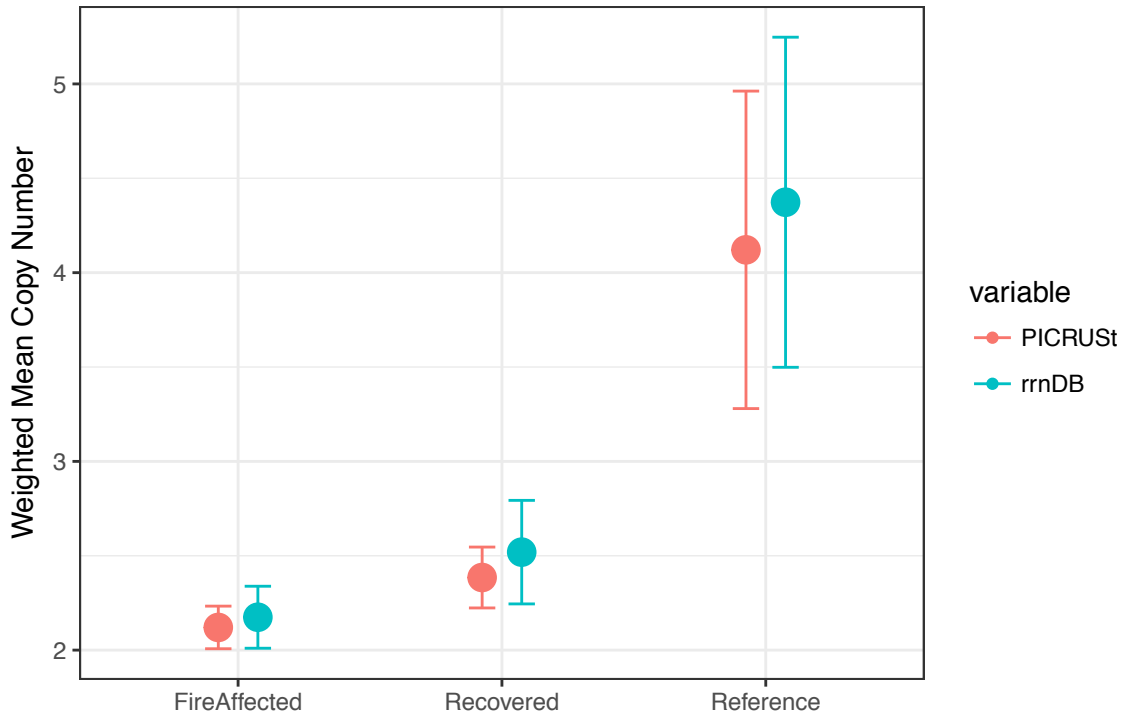

Figure S3. There is agreement between methods to estimate ribosomal operon count based on 16S rRNA amplicon data. Biplot of weighted mean ribosomal operon count estimated using PICRUSt and the ribosomal operon database. Datasets display a strong correlation (ϱ=0.86, p<0.01).

Supporting Tables

Table S1- Case studies analyzed in this piece.

	Ferrenberg et al., (2013)	Nemergut et al., (2015)	DeAngelis et al., (2015)	Lee and Sorensen et al., (2017)
Major driver of succession	Resource availability and changes	Resource availability and changes	Modest temperature increase driving biogeochemical changes	Extreme temperature increase driving biogeochemical changes
Succession Type	Endogenous heterotrophic, nutrient-based, (primary, post-sterilization)	Endogenous heterotrophic, nutrient based, (primary, "blank slate")	Post press disturbance (secondary)	Post press disturbance (secondary)