WA- IsoC_NAG.1.0

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IAREC, WA 16S Sequencing (fastq.gz)

1. 180215 [2.47 GB; 659 items]
2. 180317 [1.90 GB; 321 items]
3. 180428 [1.69 GB; 321 items]
4. 180529 [2.02 GB; 481 items]

IAREC, WA ITS Sequencing (fastq.gz)

1. 180217 [1.14 GB; 659 items]
2. 180423 [2.81 GB; 641 items]

Data Header Naming Key

Fastq sequence **file folder format** represents collection year, month, and day (yymmdd).

EX: 16S Folder 180215 = data collected on 2018 February 15th

Fastq sequence **file header format** labeling represents collection location, incubation condition, serial dilution, and replicate assignments.

EX: WAlq10e-1RepA = Prosser WA, liquid incubation, $10e^{-1}$ dilution, replicate A

WA	soil was collected from Prosser, Washington
lq	incubated using liquid
s	incubated using soil
$10e^{-x}$	serial 10× dilution of native soil microbiome abundance ($10e^{-1}$ up to $10e^{-4}$)
A-H	replicate designation (8 total)
Control	sample not inoculated with soil and gamma sterilized (negative control)
Chitin	incubated using chitin as a carbon source
NAG	samples show N-acetyl glucosamine

Supplemental Material Descriptions

- **FIG S1:** The most abundant bacterial (A) and fungal (B) phyla are plotted for the native soil (labeled as “n”) and the 6-week-chitin-enriched soil (labeled as “c”). The alpha diversities of bacteria (C) and fungi (D) were estimated using species richness and Simpson’s evenness.

- **FIG S2:** Rate of respiration varies over time based on dilution and physical environment. The respiration rate was plotted for both liquid (top) and soil (bottom) for NAG enrichment cultures from weeks 2 through 7 to avoid the light spike in CO_2 released immediately after inoculation. Respiration was monitored three times a week with a PP Systems (Amesbury, MA) EGM-4 environmental gas monitor. The gas analyzer was set up in static mode to measure CO_2 and monitor respiration in each sample at periodic intervals. To measure CO_2, a 10-ml gas aliquot was taken from the incubation container using a sterile plastic syringe with a control valve.

- **FIG S3:** Bacterial OTUs observed from 16S rRNA gene amplicon products in uninoculated controls. The most abundant OTUs shown in the controls were also found in the other samples.

- **FIG S4:** Patterns of variation within sample groups and within replicates. (A) Beta dispersion (within sample group variation) varies among time points as shown by the pairwise permutation test for homogeneity of multivariate dispersion at each time. Pairwise comparisons of the observed *P* values are tabulated for both the 16S and ITS for liquid and soil treatment conditions and indicate significant difference of within group dispersion. (B) A linear regression fit to the pairwise distance between replicates also shows changes in dispersion over time. The different dilutions are shown in separate facets and are used as strata during the permutation testing of beta dispersion.

- **TABLE S1:** Final richness significantly varies between dilutions. Tukey's honestly significant difference (HSD) test was performed to compare the richness between dilutions, and the *P* values are shown here.

- **TABLE S2:** The Adonis test (permutational multivariate analysis of variance using distance matrices) was used to partition variation associated with dilution in the final time points from each treatment condition. The R2 column reports the percentage of weighted Unifrac distance that can be attributed to differing dilution.

- **TABLE S3:** Outputs from the tests for homogeneity of multivariate dispersions performed with respect to each treatment.