**Methods**

*Sequence data processing*

*Statistical analyses of sequence data*

**Results**

*Summary of sequence data pre-processing*

Following pre-processing, X% of total raw reads were retained, for a mean sample read depth of 8,020. Dada2 ASV assignments produced 1,337 ASVs. Within sample proportional abundances were calculated as sum of reads assigned to each taxa divided by the total reads for that sample. Upon rarefaction to 1,100 reads, the dataset consisted of 851 ASVs. Rarefaction at 1,100 reads sufficiently captured richness as demonstrated in by plots of rarefaction curves (figure S1). For subsequent analyses, we report independent 69 samples in the rarefied dataset and 72 for the within sample proportional abundances dataset.

*Alpha (α) diversity*

ANOVA showed sampling location to be a significant predictor of species richness, Shannon diversity (H`), and Chao1 (p < 0.05, F < 2.702) (Figure S2). The interaction of sampling timepoint x sampling location was a significant of species richness and Chao1 (p < 0.05, F < 2.871), while sampling location x treatment was significant for Shannon diversity (H`) (p < 0.05, F < 2.718). No clear trends in directionality were observed for alpha diversity metrics across sampling locations, treatments, or sampling timepoints.

*Beta (β) diversity*

When examining the entire dataset, we show sampling location to be the dominate predictor of β-diversity for both weighted and unweighted unifrac distances (p < 0.001, R2 = 0.31, F5,36 = 8.149, p < 0.001, R2 = 0.15, F5,36 = 2.768, respectively) (Figure 2). When controlling for variability within sampling locations (e.g., strata = sampling location), we show sampling timepoint (e.g., before and after treatment) to be a significant predictor of community composition (p < 0.05, R2 = 0.03, F1,36 = 4.256, p < 0.001, R2 = 0.03, F1,36 = 2.959, respectively). Additionally, we show that treatment was a significant predictor of unweighted unifrac distance (p < 0.05, R2 = 0.029, F2,36 = 1.269) but not for weighted unifrac (p > 0.3, R2 = 0.016, F2,36 = 1.096).

To better understand the effect of miticide treatment on the bee bread microbiome, we subset our dataset to include only those samples collected after application. When sampling location variability was controlled for (e.g., srata = sampling location), we report no significant predictors of β-diversity at sampling time 2.

*Core bee bread microbiome*

Core membership assigned as XX and XX revealed XX

Figures:

Figure 1. Descriptive map of sampling locations

Figure 2. 4 panel, 3 ordinations and a plot of beta disper

Figure 3. Prevalence and abundance histogram

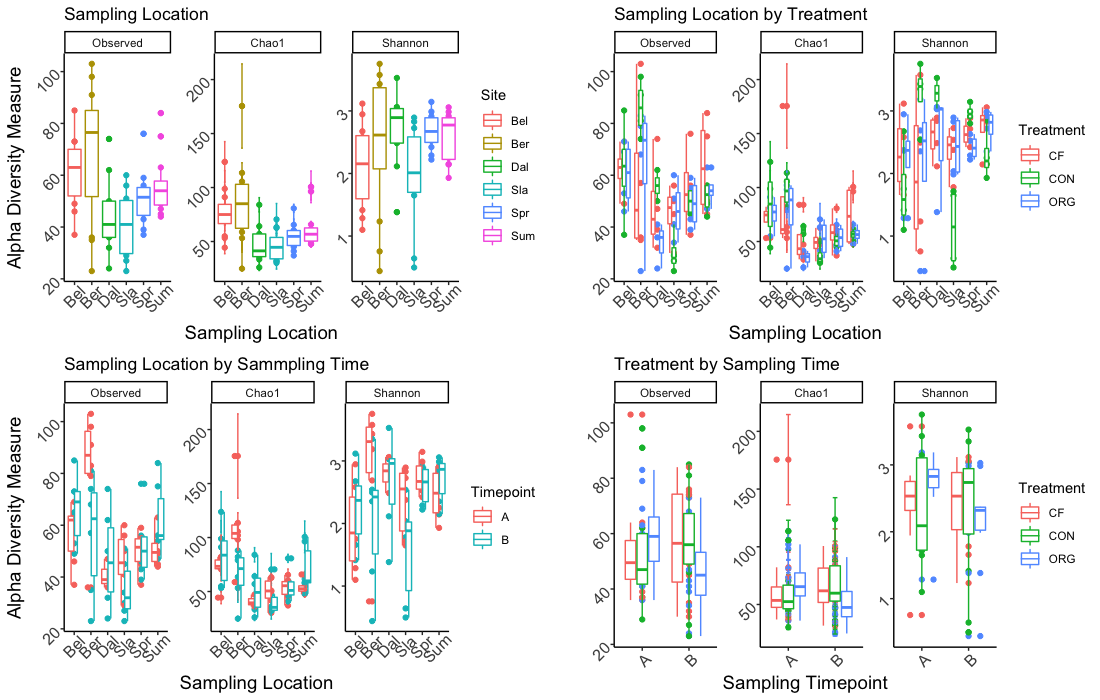
Supplementary Figures:

SFigure1. Rarefaction curves depicting leveling off at approximately 1,000 reads.

A picture containing diagram

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SFigure2. Boxplots of alpha diversity metrics.

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