Aug 09, 2017
Poster #13
Abstract #68933

Soil bacterial diversity in response to stress from farming system, climate change, weed diversity, and wheat streak virus.

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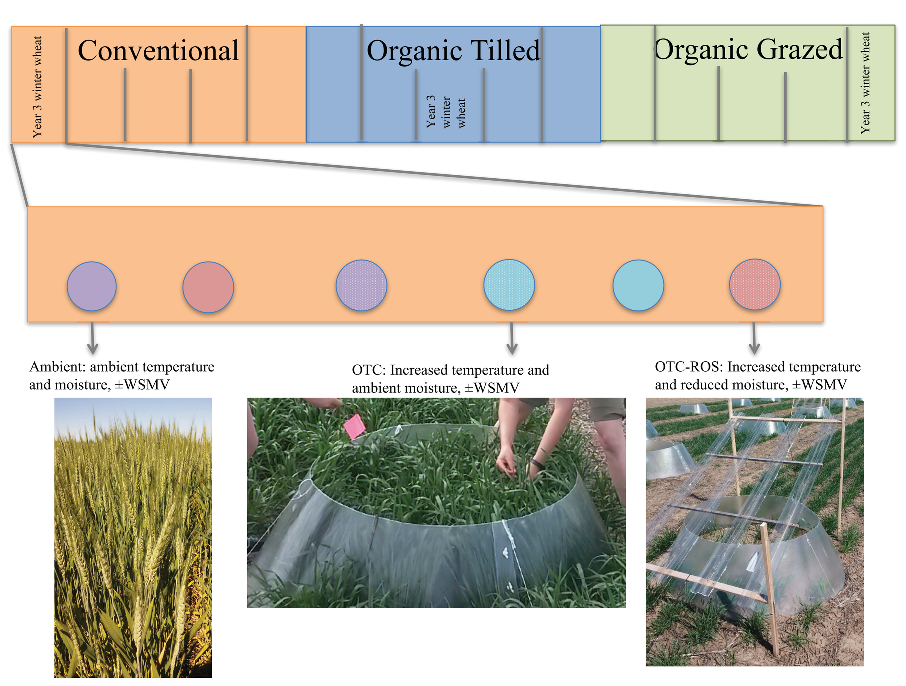
Background

Farming system (i.e. conventional or organic) has previously been shown to affect microbial diversity and density [1-6]. Within systems, chemical applications for pest control, types of fertilizer, tillage, livestock grazing, and crop rotation each select for different microbial ecosystems (reviewed in [1,7]). Organic farming can increase bacterial density and diversity [2-6], but all agriculture has shifted microbial diversity away from the communities that are seen in natural pasture or rangeland [8].

Likewise, changes in precipitation/soil moisture, atmospheric gas concentration, soil salinity, and soil temperature can also shift microbial diversity, often reducing it [9-12]. Increasing ambient temperature can increase plant biomass, but this effect can been temporary and may strip soil of nutrients faster than microbial nutrient cycling can replace them [13-16]. Drought has also been shown to change which microorganisms plants will interact with, shifting their resources from bacteria to fungi [17]. A number of studies have shown that adverse growing conditions, as seen in changing climate scenarios, have reduced the nutritional content of plants [18-20], possibly due to soil nutrient stripping or reduced microbial-produced products [16].

We hypothesized that different farming systems would dampen or amplify the effect of climate and wheat streak mosaic virus on soil bacterial communities.

Methods



Farming system (3 field replicates).
Plots were in year 3 of 5-yr rotation: y1: safflower + clover, y2: clover, y3: winter wheat, y4: lentil, y5: w.w.

i. no-till with chemical input (CC) as needed
ii. organic + tillage (OT) for weed control pre-planting and crop termination
iii. organic + sheep grazing (OG) for crop residue termination and weed management

Climate treatments:
i. Ambient
ii. Hotter; open-top chambers (OTCs)
iii. Hotter and drier climate; OTCs + rain-out shelters (ROS)

Virus (sprayed early May)
i. Control
ii. Wheat streak mosaic virus

Subplot soil was sampled monthly. 16S rRNA gene V3-V4 region sequenced by Illumina MiSeq, primers 341F/806R. Data were analyzed w/ PANDAseq, MOTHUR, R, PRIMER. Information on wheat and weed yield can be found in abstract #: 68884. Effect of weed diversity, treatment interactions still under investigation.

References

1. Brussard et al. (2007) Agric Ecosyst Environ 121:233-44.
2. Chaundhry et al. (2012) Microb Ecol 64:450-60.
3. Pershina et al. (2015) PLoS One 10:e0145072.
4. Flohre et al. (2011) Agric Ecosyst Environ 141:210-4.
5. Hartmann et al. (2015) ISME J 9:1177-94.
6. Ishaq et al. (2017) Microb Ecol 73:417-34.
7. Ishaq (2017) AIMS Microbiol 3:335-53.
8. Fierer et al. (2013) AAAS 342:621-4.
9. Biederbeck et al. (2005) Soil Biol Biochem 37:1775-84.
10. Biederbeck and Campbell. (1973) NRC Research Press 53:363-76.
11. Barcenas_Moreno et al. (2009) Glob Chang Biol 15:2950-7.
12. Alster et al. (2016) J Geiphys Res Biogeosci 121:1420-33.
13. Robinson et al. (1995) Oikos 74:503.
14. McHale et al. (1998) Can J For Res 28:1365-72.
15. Luo et al. (2011) Nature 413:622-5.
16. Gschwendtner et al. (2017) PLoS One 9:e114278.
17. Fuchslueger et al. (2014) New Phytol 201:916-27
18. Myers et al. (2014) Nature 510:139-42.
19. De La Puente et al. (2000) Agrochimica 44:506.
20. Poorter et al. (1997) Plant, cell Environ 20:472-82.

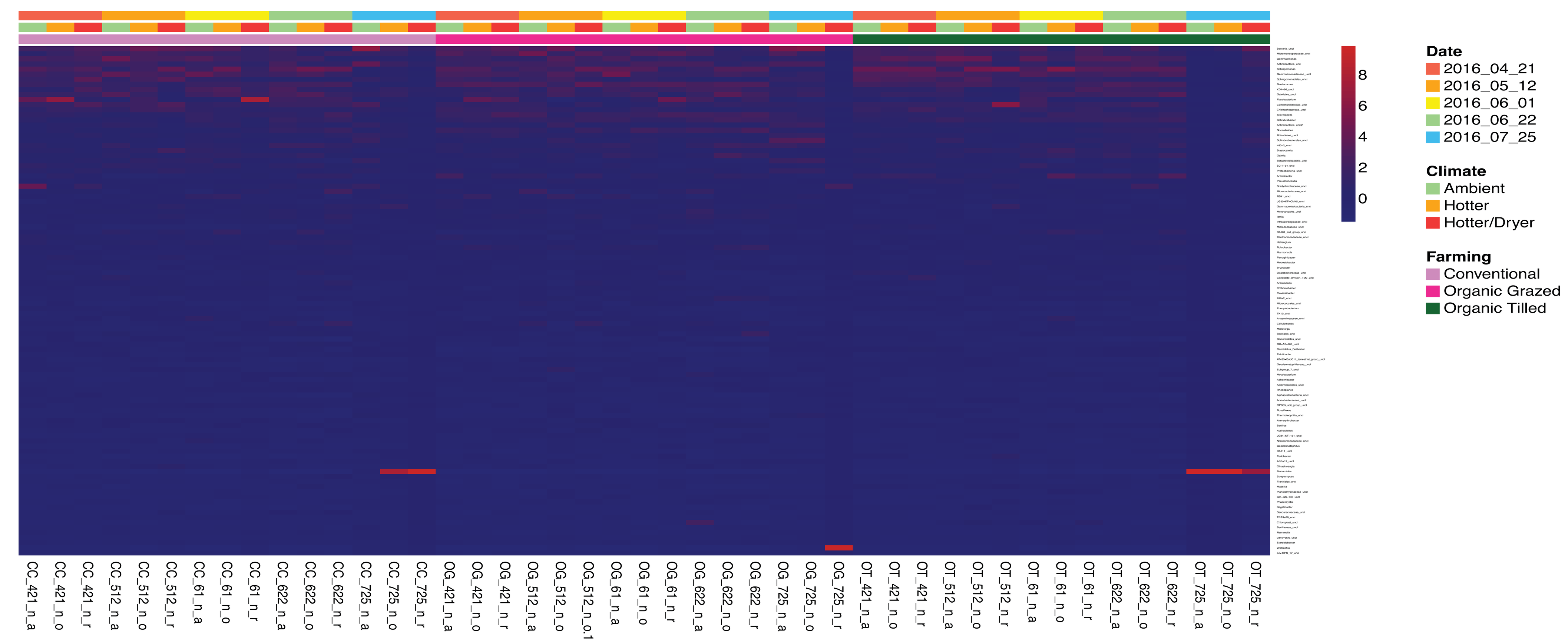


Fig 1 Heatmap of top 100 most relative abundant genera.

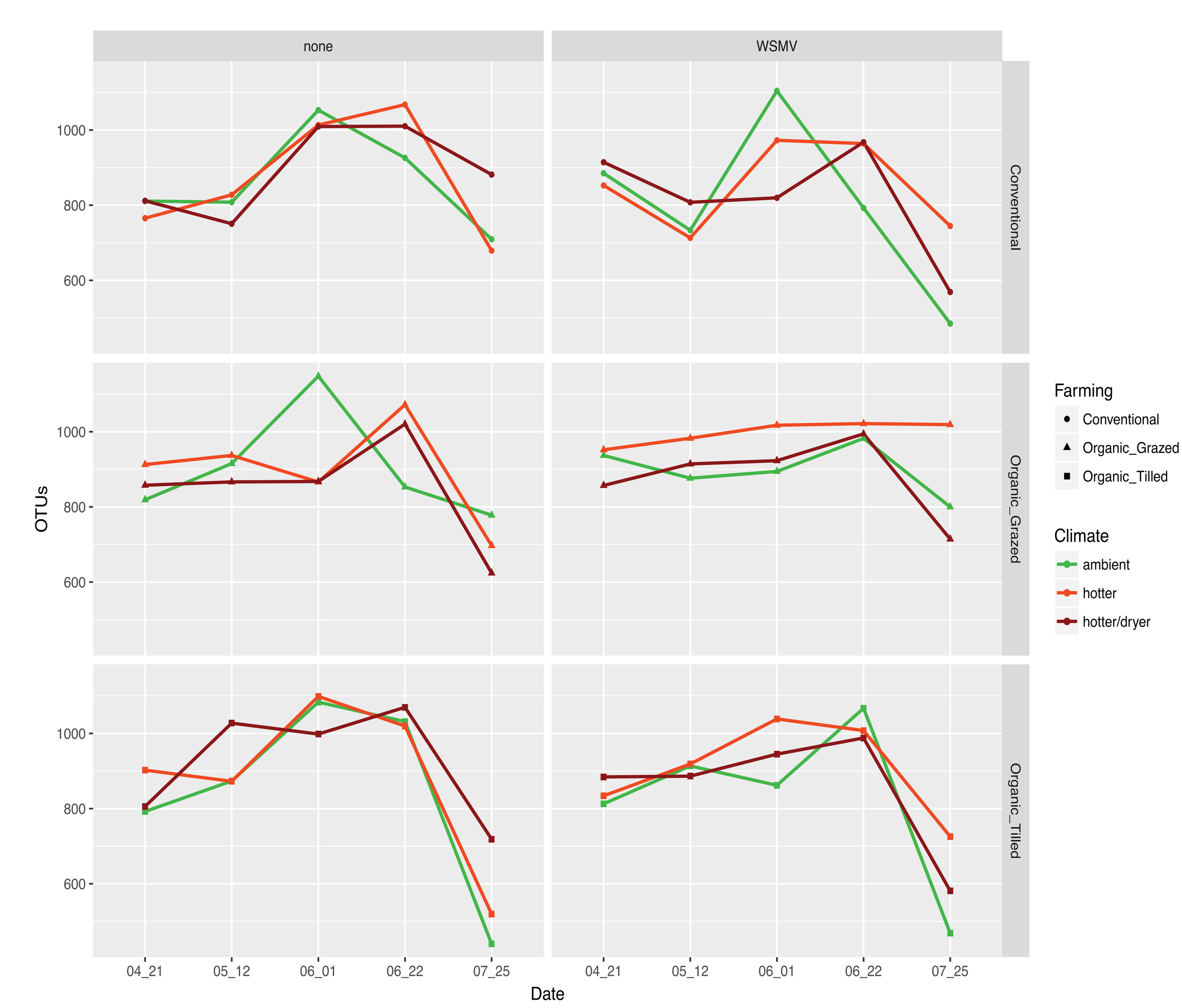


Fig 2 Genus-level OTUs over time for all treatment.

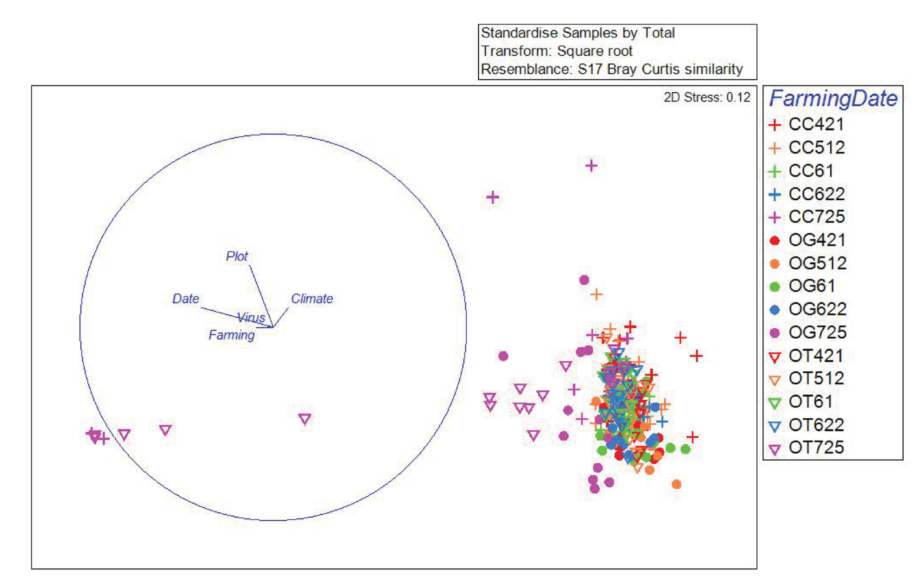


Fig 3 nMDS with Spearman's Rank correlation vectors of treatment factors.

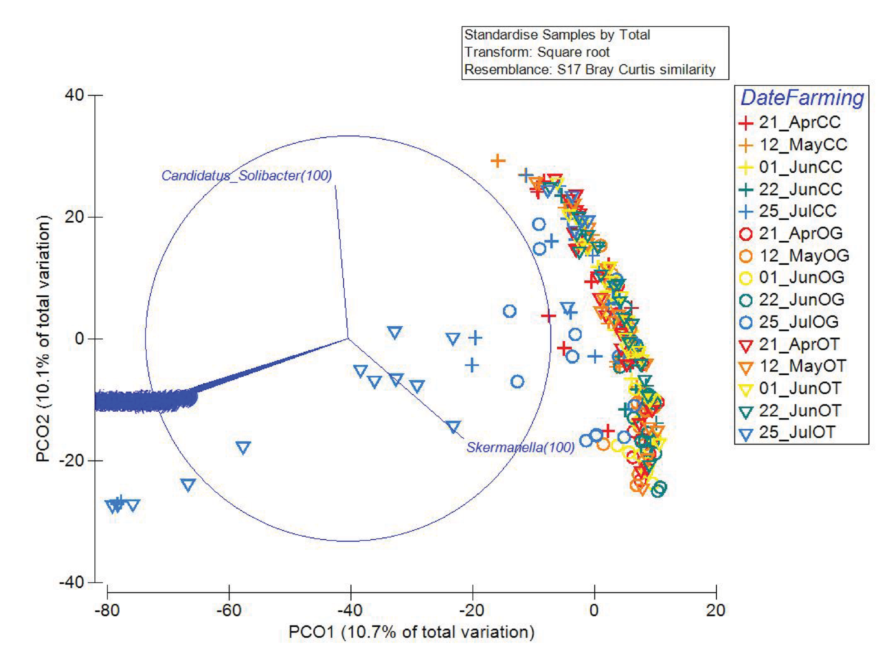


Fig 4 PCoA with vectors >0.85 Spearman's Rank correlation vectors to taxa.

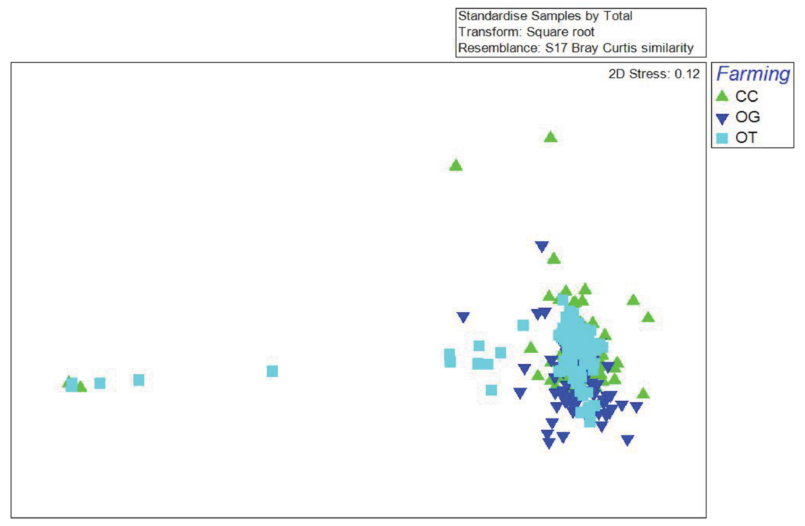


Fig 5 nMDS colored by farming system.

Season and Farming System

Seasonal effect within the growing season was a factor in determining community diversity and driving sample clustering (Fig. 1-4).

i. PERMANOVA Pseudo-F = 3.67, $p = 0.001$ MC. The July samples were the most variable, but even when July samples were removed date was significant (PERMANOVA Pseudo-F = 1.84, $p = 0.001$ MC).

i. ANOSIM date: R = 0.14, $p < 0.001$

ii. There were 177 genus-level OTUs discriminatory to time (LDA > 2, $p < 0.05$), especially in the July samples (Fig. 1, 3), though total diversity was reduced at that time (Fig. 2).

iii. Diversity increased in all plots until June, then sharply dropped in July (Fig. 2).

Farming system significant affected community (Fig. 1, 5).

i. PERMANOVA Pseudo-F = 5.9, $p = 0.001$ MC; farm x day Pseudo-F = 1.5, $p = 0.001$ MC

ii. ANOSIM farming: R = 0.08 - 0.15, $p < 0.001$

iii. Genus-level discriminatory OTUs to farming system (LDA > 2, $p < 0.05$): conventional, 68; organic grazed, 89; organic tilled, 42

iv. Organic grazed plots with WSMV experienced a more stable number of OTUs across season (Fig 2).

Climate Change

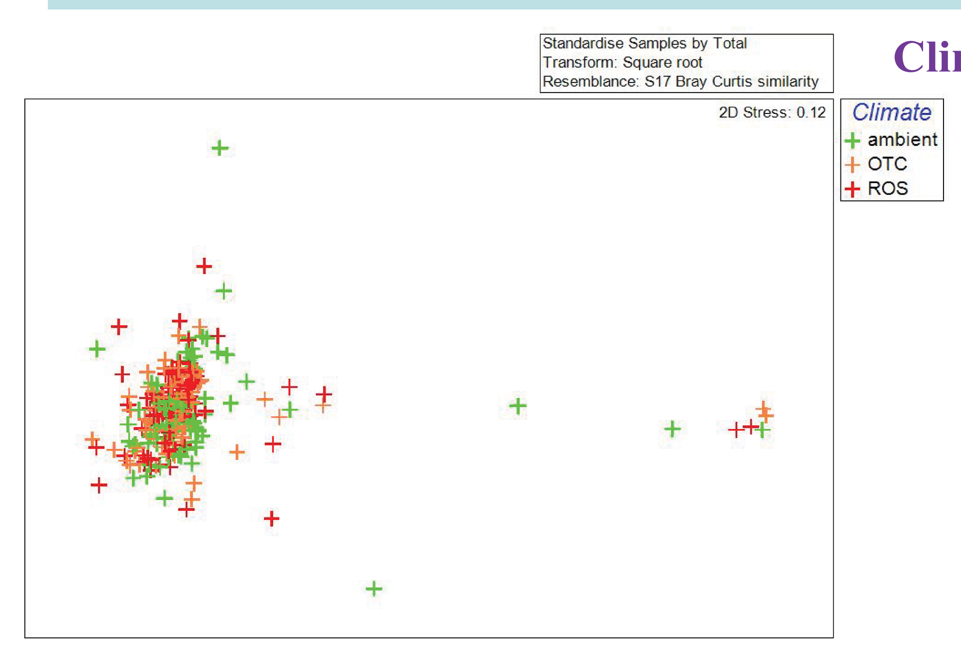


Fig 6 nMDS colored by climate treatment. X-axis has been flipped to clarify visibility.

Climate change, within Date, affected community structure (Fig. 1-3, 6).

i. Climate was significant from April to late June (PERMANOVA Pseudo-F = 1.5, $p = 0.014$ MC), but not from April to July (PERMANOVA Pseudo-F = 1.3, $p = 0.075$ MC), indicating the hot/dry summer climate of was enough to homogenize climate treatment effects.

ii. ANOSIM climate: R = 0.14, $p < 0.001$

iii. Genus-level OTUs discriminatory to climate (LDA > 2, $p < 0.05$): ambient, 11; hotter, 18; hotter and drier 15

iv. Hotter, and hotter/drier climates increased the number of OTUs for CC and OT farming systems, while it decreased slightly in OG, however CC and OT also saw a larger drop in diversity in July (Fig. 2).

Viral Treatment

Overall, wheat streak mosaic virus was not a significant driver of diversity on its own, but there were virus x climate interactions.

i. ANOSIM: ns; PERMANOVA: ns

ii. PERMANOVA virus x climate: Pseudo-F = 1.5, p = 0.012 MC

iii. Virus plots had lower average OTUs, except for OG hotter, OG hotter/drier, and OT hotter (Fig. 3).

iv. Diversity was reduced in Conventional plots 1-wk post inoculation (Fig. 2).