**Hydrological conditions influence soil and methane-cycling microbial populations in seasonally saturated wetlands**

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Supplemental Tables

**Supplementary Table 1:** Mean water level (cm), saturation duration (days), and saturation frequency (# of events) for the 2018 water year (09/30/2017 – 09/29/2018, total observations = 365 days) and the month samples were collected (November 2017). Negative (-) values indicate the water table fell below the soil surface and positive (+) values indicate inundation. Statistical model results presented; an asterisk denotes significant models (p < 0.05). Tukey HSD letters indicate significant differences among the mean comparisons across the transect. Hydrology values collected from wetland 1A were removed from analysis since soil samples were not collected from these sites.

**Supplementary Table 2:** Rank abundance of the 8,113 amplicon sequence variants (ASVs), also commonly referred to as operation taxonomic units (OTUs), classified by phyla. The five *Archaea* phyla are italicized and shaded.The two horizontal lines demark the boundary between dominant (>10%), common (>1 to <10%) and rare (<1%) phylotypes.

**Supplementary Table 3**: Edaphic and microbial community diversity properties for five seasonally saturated wetland sites. Duplicate cores were collected from the upper soil horizons (0-30 cm) of five hydrologic zones across five seasonally saturated wetlands and then homogenized into a single representative sample (n = 24). Summary statistics include the mean (± standard error of the mean) for soil pHCaCl2, soil organic matter (SOM) content (g OM g-1 soil), and microbial community diversity (Richness and Shannon’s Diversity Index). Transformed variables are marked with a hashtag (#). Statistical model results are presented for the one-way ANOVA used to test for mean differences among hydrologic zones (r2, F statistic, and p-value); an asterisk denotes a significant model (alpha = 0.05).

Supplemental Figures

**Supplementary Figure 1:** Rarefaction curves showing OTU richness as a function of sequencing depth. Rarefaction analysis shows that sequencing depth sufficiently captured OTU richness. Paired-end reads were rarified to the minimum sequence depth (20,135 reads).

**Supplementary Figure 2:**. Non-metric multidimensional scaling plot showing separation of the soil microbiome based on Bray-Curtis dissimilarities across the five selected wetland sites. Microbial community composition did not statistically differ by site (PERMANOVA = F4,19 = 1.198, p > 0.05).

**Supplementary Figure 3**: Mean relative abundance of dominant bacterial phyla across each of the five hydrologic zones.

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| **Hydrologic Characteristics** | **Model Statistics** | **Hydrologic Zone** |
| r2 | F-value | p-value | A(Basin Edge Area) | B | C | D | E(Upland Area) |
| **Annual Summary Statistics (October 2017 – October 2018)** |
| Mean Water Level (cm) | 85.4% | F4, 20 = 27.8 | < 0.05\* | +4.5 ± 6.6 A | -11.2 ± 4.5 AB | -33 ± 6.4 BC | -53 ± 6.8 CD | -75.6 ± 5.4 D |
| Sat. Duration (days) | 88.7% | F4, 20 = 37.3 | < 0.05\* | 311 ± 17 A | 260 ± 26 AB | 182 ± 18 BC | 122 ± 19 C | 17 ± 9 D |
| Sat. Frequency(# of events) | -- | χ2 = 2.39df = 4 | > 0.05 | 2.5 ± 0.5 | 2.8 ± 0.5 | 3.8 ± 0.7 | 4.0 ± 1.0 | 3.8 ± 1.7 |
| **Sample Month Statistics (November 2017)**  |
| Mean Water Level (cm) | -- | -18.8 ± 3.4 | -32.6 ± 5.4 | -54.4 ± 9.3 | -75.2 ± 11.0 | -98.0 ± 9.9 |
| Duration (days) | -- | 27 ± 2 | 11 ± 7 | 3 ± 3 | 0 ± 0 | 0 ± 0 |
| Frequency (# of events) | -- | 1.0 ± 0.0 | 0.6 ± 0.2 | 0.2 ± 0.2 | 0.0 ± 0.0 | 0.0 ± 0.0 |

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| **Supplementary Table 2:** Rank abundance of the 8,113 amplicon sequence variants (ASVs), also commonly referred to as operation taxonomic units (OTUs), classified by phyla. The five *Archaea* phyla are italicized and shaded.The two horizontal lines demark the boundary between dominant (>10%), common (>1 to <10%) and rare (<1%) phylotypes. |
| Phylum | Taxa Count | Relative Percent (%) |
| Acidobacteria | 1305 | 17.55 |
| Chloroflexi | 1301 | 17.49 |
| Proteobacteria | 1217 | 16.36 |
| Planctomycetes | 993 | 13.35 |
| Verrucomicrobia | 576 | 7.75 |
| Actinobacteria | 341 | 4.59 |
| *Thaumarchaeota* | *214* | *2.88* |
| Patescibacteria | 191 | 2.57 |
| Cyanobacteria | 183 | 2.46 |
| Chlamydiae | 137 | 1.84 |
| Bacteroidetes | 130 | 1.75 |
| WPS-2 | 119 | 1.60 |
| Nitrospirae | 91 | 1.22 |
| Firmicutes | 75 | 1.01 |
| *Euryarchaeota* | *74* | *1.00* |
| Elusimicrobia | 66 | 0.89 |
| Gemmatimonadetes | 66 | 0.89 |
| Armatimonadetes | 62 | 0.83 |
| *Crenarchaeota* | *50* | *0.67* |
| GAL15 | 46 | 0.62 |
| FCPU426 | 44 | 0.59 |
| Dependentiae | 42 | 0.56 |
| *Nanoarchaeaeota* | *30* | *0.40* |
| Rokubacteria | 24 | 0.32 |
| Spirochaetes | 21 | 0.28 |
| *Diapherotrites* | *20* | *0.27* |
| Dadabacteria | 8 | 0.11 |
| Omnitrophicaeota | 8 | 0.11 |
| Tenericutes | 3 | 0.04 |

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| **Supplementary Table 3**: Edaphic and microbial community diversity properties for five seasonally saturated wetland sites. Duplicate cores were collected from the upper soil horizons (0-30 cm) of five hydrologic zones across five seasonally saturated wetlands and then homogenized into a single representative sample (n = 24). Summary statistics include the mean (± standard error of the mean) for soil pHCaCl2, soil organic matter (SOM) content (g OM g-1 soil), and microbial community diversity (Richness and Shannon’s Diversity Index). Transformed variables are marked with a hashtag (#). Statistical model results are presented for the one-way ANOVA used to test for mean differences among hydrologic zones (r2, F statistic, and p-value); an asterisk denotes a significant model (alpha = 0.05). |
| **Hydrologic Characteristics** | **Model Statistics** | **Wetland Site** |
| r2 | F-value | p-value | 1 | 2 | 3 | 4 | 5 | Grand Mean |
| ***Sample Size (n)*** | -- | -- | -- | 4 | 5 | 5 | 5 | 5 | 24 |
| ***Edaphic Properties*** |
| Soil pH-(CaCl2) | 47.0% | F4,19 = 4.22 | < 0.05\* | 3.6 ± 0.1AB | 3.6 ± 0.1A | 3.3 ± 0.1AB | 3.6 ± 0.1A | 3.2 ± 0.1B | 3.4 ± 0.0 |
|  #Soil Organic Matter | 21.2% | F4,19 = 1.28 | > 0.05 | 12.0 ± 3.3 | 7.3 ± 0.9 | 7.5 ± 1.4 | 6.6 ± 1.2 | 5.7 ± 0.7 | 7.7 ± 0.8 |
| ***Microbial Diversity*** |
| Richness | 23.6% | F4,19 = 1.47 | > 0.05 | 715 ± 116 | 876 ± 25 | 896 ± 72 | 939 ± 112 | 970 ± 23 | 886 ± 36 |
| Shannon (H’) | 32.5% | F4,19 = 2.29 | > 0.05 | 5.53 ± 0.32 | 6.06 ± 0.07 | 6.08 ± 0.12 | 6.15 ± 0.21 | 6.22 ± 0.07 | 6.08 ± 0.08 |

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