Microbes on the Margins

Fungi and Bacteria on the Edges of Kansas Rivers

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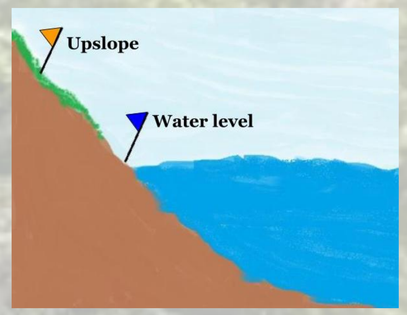
Background

Fungi and bacteria are essential to decomposition, nutrient flow, and regulation of greenhouse gases (GHGs). Drying and wetting (D/W) cycles have major effects on soil microbes, especially on how they store and emit GHGs. Climate change will impact the frequency and intensity of D/W cycles. Microbes on the edges of rivers and streams already experience more frequent and intense D/W cycles than those living on dry land or in aquatic environments.

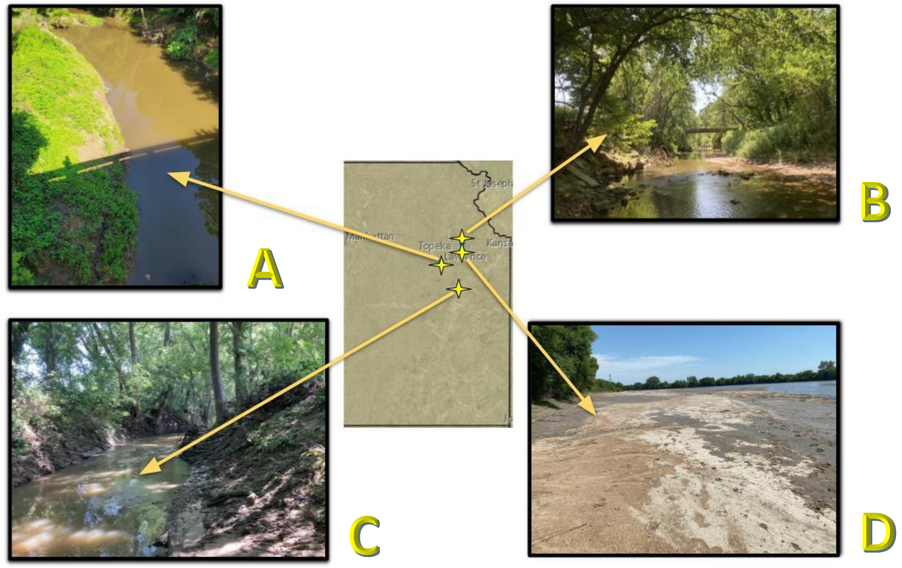
Research Question

How do microbial communities at the edges of rivers differ with proximity to the water level?



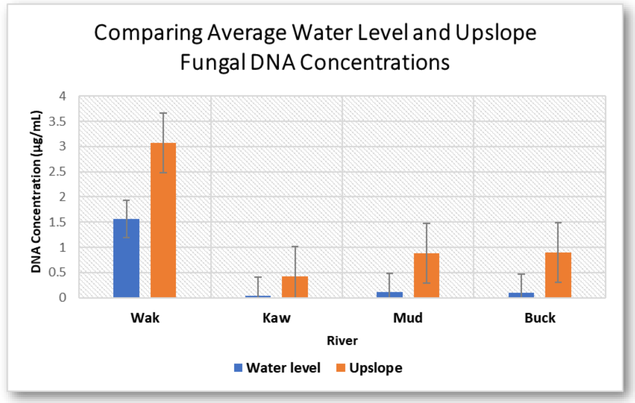
Methods and Materials

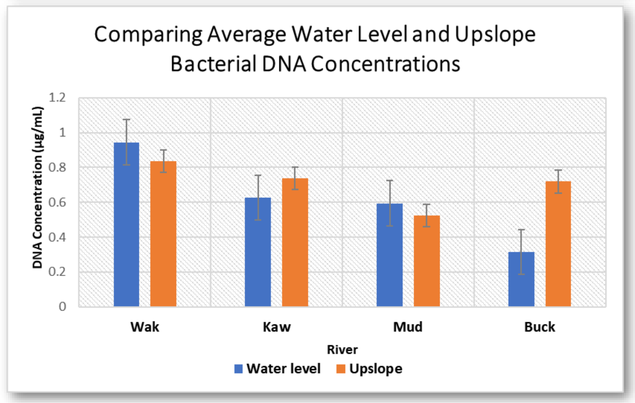
- **24 samples from 4 eastern Kansas rivers: Wakarusa (A), Buck Creek (B), Mud Creek (C), Kaw (D)**
- **Soil at water level and upslope collected in plastic tubes; 3 pairs per river**
- **Fungal and bacterial DNA amplified using polymerase chain reaction (PCR)**
- **DNA quantified using Qubit 2.0 Fluorometer**



Results

- **Fungal DNA counts higher for upslope samples than corresponding water level samples ($F_{1,8}$=12, p=0.008)**
- **Bacterial DNA counts not affected by proximity to the water ($F_{1,8}$=0.26 p=0.62)**
- **Total DNA concentration affected by distance from water, with river-specific effects ($F_{3,8}$=5.5, p=0.026)**
- **High variance in total DNA concentrations among rivers (p=1.7e-06)**





Findings

- **Fungi were more abundant upslope and so may be more sensitive to dry/wet cycles at the water's edge.**
- **Bacteria did not vary with slope so may be more resilient.**
- **Variation among rivers shows that characteristics of each impacted both microbial groups.**

Discussion and Future Work

Differences in fungal and bacterial biology may explain their different, river-specific responses to hydrology. Future work will identify species (DNA sequencing), compare to purely terrestrial/aquatic communities, and quantify microbial genes related to greenhouse gas emissions (dd PCR).

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