

## Linking microbial communities to ecosystem function:

what we can learn from genotype-phenotype mapping in organisms

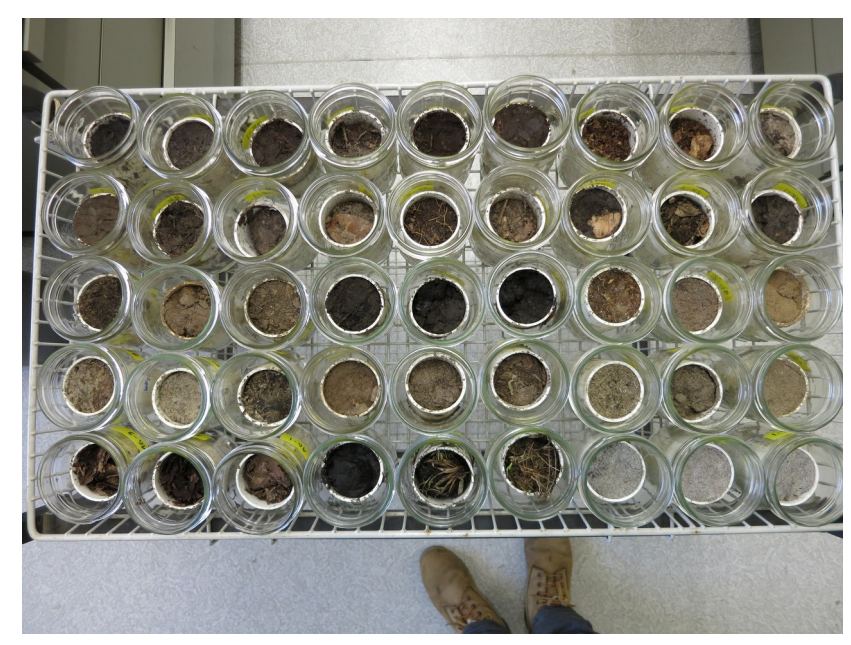
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### INTRO

- Most of the natural variation in atmospheric methane is due to microbial communities in tropical wetlands.
- It is unclear which microbes drive this variation so we used methods typically used to connect genes to traits in organism by treating the ecosystem as an “organism” and bacterial species as “genes.”
- We wanted to know: Which members of the microbial community in these ecosystems best predict methane dynamics?

### METHODS

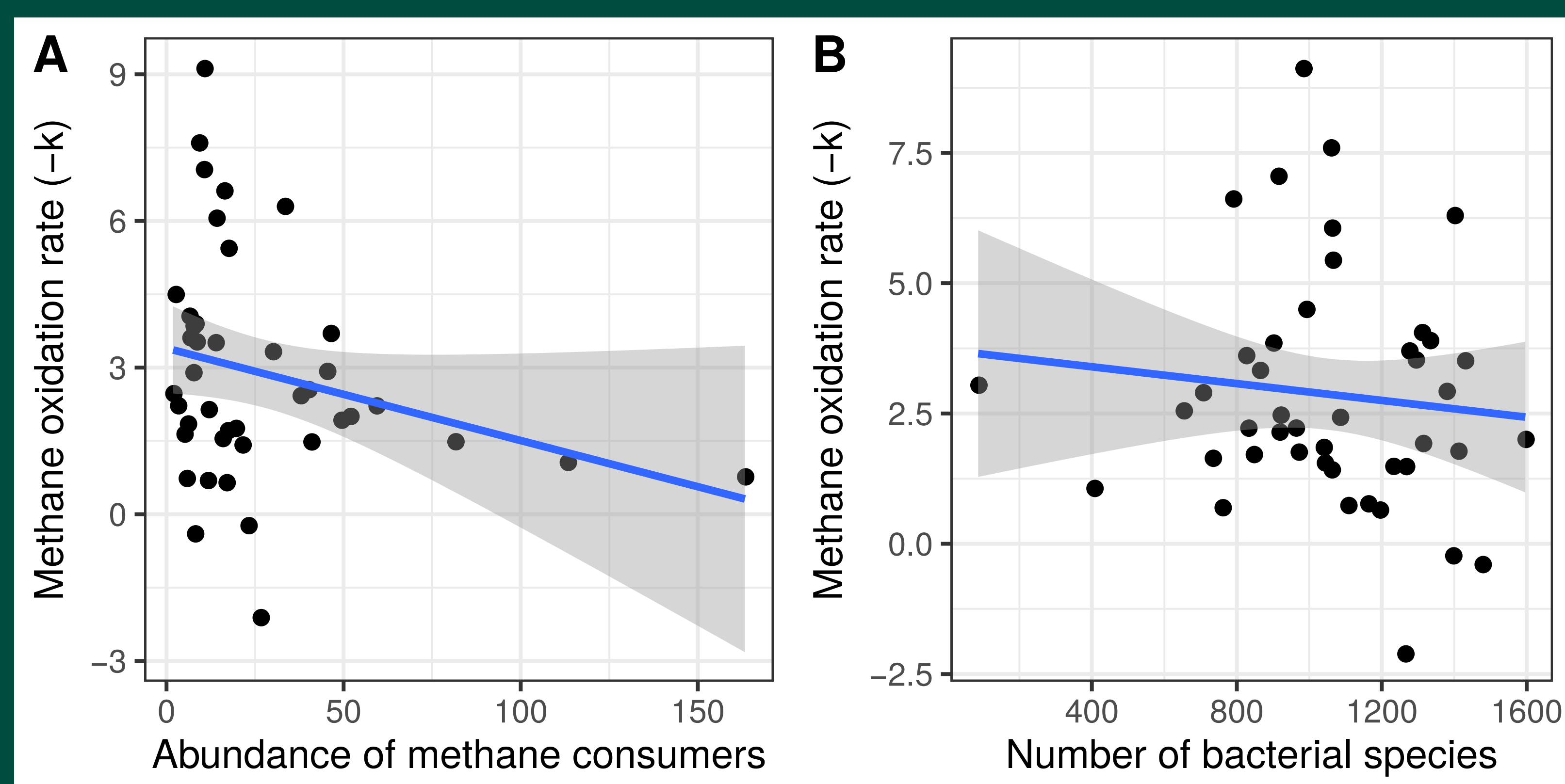
1. Collected soil cores from various ecosystems in the Congo Basin of Gabon, Africa
2. Measured rates of methane oxidation and production
3. Sequenced the 16S rRNA gene from bacteria and archaea in the soil to identify microbial taxa
4. Correlated microbial relative abundances with the rate of methane oxidation while accounting for similarities in location, environment, and community composition



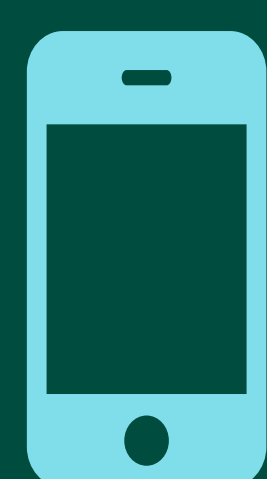
### RESULTS

- Abundance of methane oxidizers did not correlate with methane oxidation.
- Soil communities exhibited considerable spatial and environmental structure.
- Six taxa not known to consume methane were strongly predictive of methane oxidation rates.

# Abundance of methane-cycling bacteria may not be the best predictor of methane emissions from ecosystems

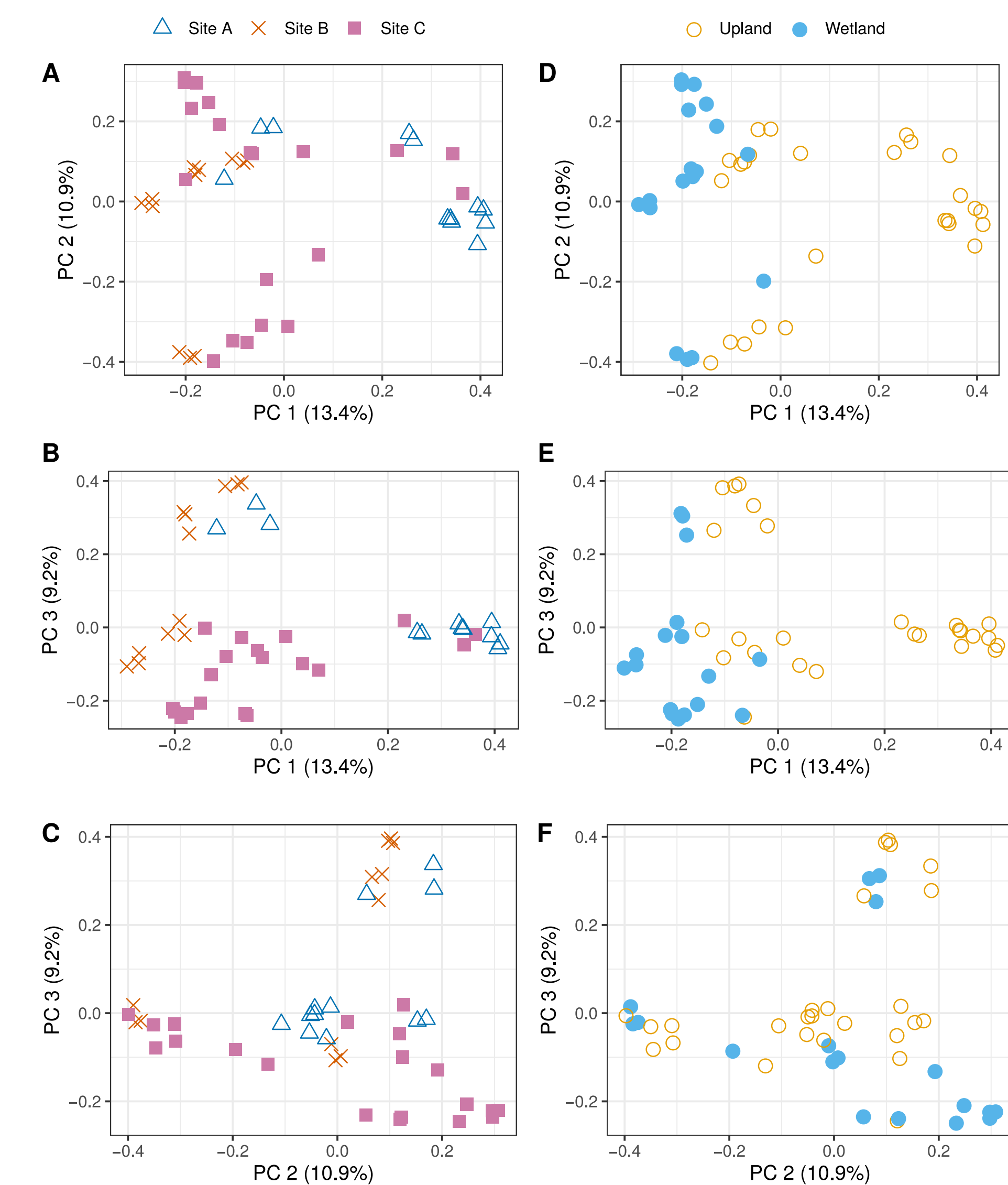
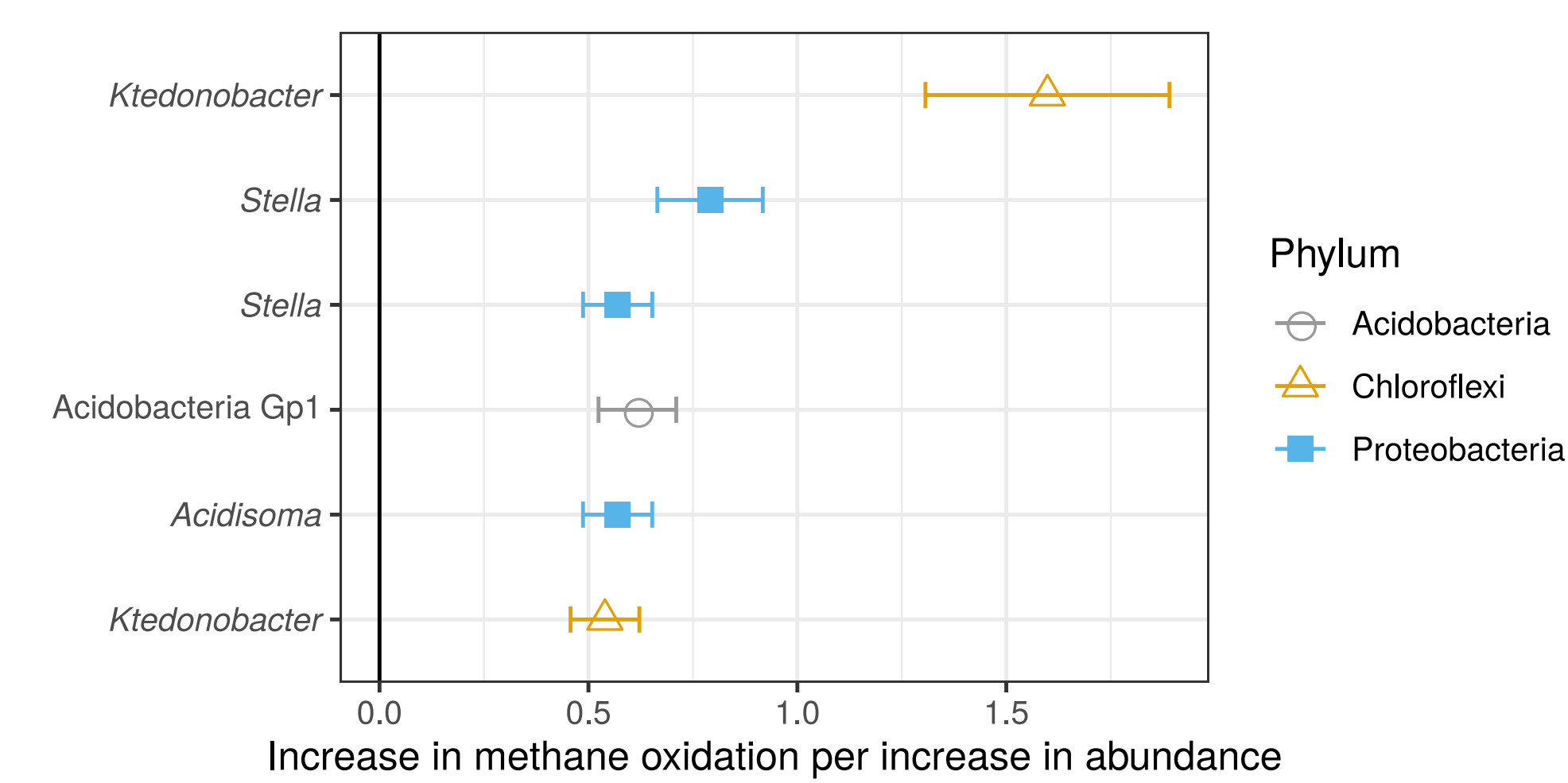


*Methane oxidation rate is not correlated with the abundance of methane consumers nor the number of bacterial species.*



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### SUMMARY

Atmospheric methane, a potent greenhouse gas, varies from year to year due to the activity of microorganisms in tropical wetlands. Here we used methods from population genetics to link specific microbial species to the rate of methane production and consumption. We found that the abundance of methane consumers did not correlate with methane oxidation. Instead, six bacterial taxa not known to consume methane were significant predictors of methane oxidation rate. This suggests that broader patterns of microbial community composition are important to understand ecosystem functioning.

