

Title: The opportunist: How the human pathogen *Salmonella* has adapted to the tomato host

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While little is known about the mechanisms that allow *Salmonella* to multiply in tomatoes, even less is understood about how interactions of this human pathogen with phytobacteria contribute to its survival in alternate hosts such as plants. It is now known that bacterial soft rot contributes to an increased fitness of *Salmonella enterica* sv. Typhimurium in tomato fruits. The goal of this research is to understand the underlying mechanisms involved in this phenomenon. The hypothesis is that a change in the tomato environment caused by *Pectobacterium* provides an overall benefit for *Salmonella*. In order to determine the full complement of functions that may be vital for the success of *Salmonella* in soft rots, we employed high throughput transposon sequencing (Tn-seq). Libraries of mutants made via transposon mutagenesis were seeded into tomatoes inoculated with fully virulent *Pectobacterium*, less virulent *Pectobacterium*, and no *Pectobacterium*. As a result, pathways involved in nitrogen metabolism, motility, and other regulatory pathways have been identified as potentially playing a role in these interactions. We conclude that a variety of metabolic changes do in fact contribute to the increased growth of *Salmonella* in tomatoes. The research presented here contributes to furthering our understanding of how human pathogens interact with environmental bacteria, an area which is not well studied. Furthermore, if we can understand the means by which *Salmonella* is able to benefit from bacteria present in the tomatoes, we can take steps toward predicting and preventing outbreaks of *Salmonella* in fresh produce.

Characterization of Microbial Communities within Tropical and Sub-Tropical Peatlands

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Wetland soil microbial communities are highly complex and interconnected assemblages of bacteria, archaea, and fungi that drive many biogeochemical processes, including those regulating carbon (C) sequestration and greenhouse gas emissions. These communities can be influenced by many environmental factors, such as pH, C quality, and nutrient availability. In this study, we analyze how prokaryotic and fungal community composition changes within tropical and sub-tropical peatlands to investigate the fundamentals of peatland microbial community assembly. We used next generation sequencing to analyze prokaryotic and fungal community structure within two peatlands: the Everglades Water Conservation Area-2A (WCA-2A) of South Florida and San San Pond Sak (SSPS) of Panama. Both sites are characterized by well-studied phosphorus (P) gradients that have led to documented changes in vegetation communities and biogeochemical cycling. We sampled soils at sites along both gradients, ranging from low-P to high-P sites, and isolated DNA from these soils, and assessed differences in prokaryotic and fungal community composition with relative nutrient availability. We found that dominant prokaryotic taxa remained consistent along both gradients, while dominant fungal taxa shifted along both gradients, suggesting that fungi are more responsive to environmental changes within this system. The co-occurrence of certain taxa, such as Eurotiomycetes and Cyanobacteria, suggest that there may be coupled prokaryotic-fungal interactions occurring within these two peatlands. Additionally, many of the microbial classes identified, whether prokaryotic or fungal, have been previously described as important C cyclers within freshwater wetlands, highlighting the role that these organisms, and their potential interactions, play in regulating peatland C cycling. This work is an initial step to further our understanding of prokaryote-fungal dynamics within peatlands, and can provide future insights into potential interactions between these essential organisms, and how they may regulate peatland biogeochemical cycling.

Drivers of Peatland Soil Carbon Composition and Potential Greenhouse Gas Production: A Global Perspective

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As humans continue to transform the global landscape and climate, identifying the drivers of terrestrial carbon (C) cycling is crucial to effective management of C dense ecosystems. Peatlands store up to 20% C (~529 Pg C) of the global terrestrial soil. Variability in peatland soil organic matter (SOM) composition may influence its stability and production of greenhouse gasses (GHG). We used ¹³C Solid State Nuclear Magnetic Resonance to quantify SOM composition from 115 freshwater peatlands across the globe. Redundancy Analysis constrained 52% of data variation along axis 1 representing a decomposition and stability gradient from least decomposed (O-alkyl C) to highly decomposed (methoxyl, carboxyl, alkyl, and aromatic C) SOM. The model showed statistical significance of the dominant drivers –temperature, vegetation inputs, land use, and C to nitrogen (N) ratio, but not pH. Land use accounted for the most variation (9.8%) suggesting that long-term degradation may control SOM chemical composition regardless of other environmental drivers. To determine the effect of chemical composition on SOM decomposition, we incubated select peatland soils under aerobic and anaerobic conditions and measured potential carbon dioxide and methane production. Stepwise regression analysis showed that increased O-alkyl C is the most significant driver of GHG production. Aromatic and alkyl C corresponded to a decrease in aerobic and anaerobic CO₂ production. Therefore, global patterns of peatland SOM composition driven by land use, C/N ratio, temperature, and vegetation are key to modeling SOM stability with respect to C loss to GHG production.

Impact of floating aquatic vegetation suppression on canal sediment properties in the Everglades Agricultural Area

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A significant portion of phosphorus (P) loads discharged from the Everglades Agricultural Area (EAA) in south Florida is in the form of organic particulates from biological sources during farm drainage events. This study was initiated on four treatment-control farm pairs over a five year period to investigate the role of suppressing floating aquatic vegetation (FAV), such as water lettuce (*Pistia stratiotes*), on the formation of more recalcitrant inorganic P forms in farm canal sediments. Treatment canals implemented aggressive FAV suppression, while control canals operated under normal management practices. It is hypothesized that with FAV suppression, co-precipitation of P with calcium and magnesium (Ca-Mg) into less labile, more recalcitrant minerals is increased due to more light penetrating the water column, while P sorption with iron and aluminum increases with higher dissolved oxygen and redox potential. Phosphorus fractionation was used to measure labile and recalcitrant P pools in the eight farm canal sediments at the 0-2.5 cm depth, as well as particulates exported with drainage water during pumping events. On most farms, sediment residue and Ca-Mg-bound P pools had the highest percent of total P ranging from 23.6 to 73.4% for Ca-Mg-bound and 6.1 to 63.6% residue P, while labile P had the lowest between 0.5 to 5.5%. In the discharged particulates, Ca-Mg-bound-P had the highest percentage (28.2 to 61.0%) and labile P was the lowest (0.9 to 19.1%). While labile P was the smallest pool, it was higher in the discharged particulates than canal sediments. The generation of denser inorganic mineral P may reduce P transport out of farm canals and reduce P loads into the downstream Everglades ecosystem.

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SOIL SALINITY UNDER SEEPAGE IRRIGATION AND IRRIGATION DRAINAGE TILE IN NORTHEAST FLORIDA

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Salinity of irrigation water has been a concern for growers in the Tri-County Agricultural Area (TCAA) for many years. This issue becomes most apparent during low rainfall years when salts can become concentrated in the soil due to evaporation and reduced leaching. In an effort to reduce water use and nutrient loading to the Lower St. Johns River, alternative irrigation practices, including Irrigation Drainage Tile (IDT), are being evaluated in the TCAA; however, IDT drainage has also been hypothesized to reduce saline soils by improved leaching of salts from the soil profile. This research was conducted to evaluate whether IDT irrigation and drainage could reduce soil salinity as compared to conventional seepage irrigation (SI) and drainage. Soil samples were collected from SI and IDT fields on six farms between 2013 and 2015. For both SI and IDT fields, soil samples were collected at three distances from the water furrow or IDT pipe. At each sampling location, 30cm composite samples were collected from four sample depths below the surface. This was replicated at three different zones in the field representing areas of water inflow, outflow, and center of field. Soil salinity was assessed using the saturated paste method. Overall results indicated that IDT field soils were significantly lower in salinity than SI fields in five out of six farms. Overall reduction in soil salinity by IDT for all six farms was **32.1%** and **39.2%** in 0-30 and 30-60 cm depths respectively in Fall 2014, and **6.6%** and **30.1%** in Summer 2015. In conclusion, IDT has the potential to significantly lower soil salinity compared with SI systems.

List of Abbreviations

Irrigation Drainage Tile (IDT)

Seepage Irrigation (SI)

Tri-County Agricultural Area (TCAA)