

What’s in Spud Soil?

Findings from Soil Functional Analysis

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Abstract:

Soil DNA sequencing technology is a powerful tool for the in-depth understanding of soil microbiome, biodiversity, and overall soil health. Technology has great utility in sustainable soils research programs to assess the impact of various soil treatment programs on natural soil, bacterial and fungal populations, and their associated functions. In summer of 2021, a small plot study was conducted in a commercial potato field to assess the impact of fumigant alternative treatment programs on soil microbiome, *Verticillium Wilt* control, and yield/grade of potatoes. Soil samples for microbiome analysis were collected early in the season (before and immediately after planting) in various treatments, including fumigant check and untreated plots. Genetic analysis yielded interesting results in terms of biodiversity in various treatments with over 500 different species belonging to various bacterial and fungal phyla identified. Interesting insights into soil nutritional status through microbial mobilization were also observed in certain study treatments. The objective of this poster presentation is to discuss, in detail, the findings from this soil functional analysis.

Introduction:

The rhizosphere microbiome plays an important role in overall soil and crop health. Various soil management practices including but not limited to nutrient/organic soil amendments, cover crop(s), crop rotation, use of soil chemical control measures such as fumigation can influence the composition of microbiome. Studies in crops such as potato are underway to understand and optimize microbiome to improve plant health and productivity (1). A comprehensive review of literature suggests that plant genotype, growth stage, and fumigation practices alter/effect composition of soil bacterial communities (2). Frequent usage of fumigants such as Chloropicrin and Vapam changes the microbial biomass and enriches certain microbe populations capable of degrading the fumigants (3&4). This study evaluates the effect of alternative soil treatment programs including biological inputs on the changes in the natural soil microbiome, its functions, and soil-borne plant pathogens in a potato cropping system.

Materials and Methods:

Soil samples for genome analysis were collected from a study conducted during the year 2020-21, designed to evaluate the efficacy of fumigant alternative treatment programs for the control of *Verticillium Wilt* in potatoes. Fumigant alternative programs involve H₂O₂/PAA-based formulations (SaniDate® HC and OxyFusion®) that are either EPA-registered (SaniDate HC) or in the experimental stage (OxyFusion) as a pre-plant bactericide/fungicide in soil. The study site was a commercial potato field located near Park Rapids, MN, with a sandy loam soil type. Each treatment plot was 25’ x 25’, replicated four times but due to limitations with the field layout, replicated plots were not completely randomized. Fumigation treatment (Vapam) was applied during Fall of 2020, after potatoes were harvested. SaniDate HC (1,000 PPM PAA equivalent) or OxyFusion (1,000 PPM PAA equivalent) were applied during Spring of 2021, as a pre-plant soil drench immediately before planting followed by application of Bacillus-based biological product (TerraGrow, 1.5 lbs./acre) immediately post planting. A total of eight soil samples were collected for microbiome analysis from different treatments that represent the untreated check (UTC), the fumigated check (VPM), before and after soil drenches with SaniDate HC (SD HC), OxyFusion (OF), and post TerraGrow treatments. Each soil sample is a pool of multiple sub-samples collected in a ‘W’ pattern from replicated plots to a depth of eight inches. Soil samples were immediately frozen after collection and sent to Biome Makers based in CA for DNA sequencing and further analysis of treatment effects using Gheom technology.

Table 1. List of Soil Samples Collected for Microbiome Analysis

- Sample 1: Untreated check (UTC)
- Sample 2: Fumigated check (VPM)
- Sample 3: Before SD HC soil drench (SHC21-Before)
- Sample 4: Immediately after SD HC soil drench (SHC21-After)
- Sample 5: 2 weeks after SD HC + TerraGrow (SHC21-After 14)
- Sample 6: Before OF soil drench (OF21-Before)
- Sample 7: Immediately after OF soil drench (OF21-After)
- Sample 8: 2 weeks after OF soil drench + TerraGrow (OF21-After 14)

Results:

Microbial Species Distribution:

Over 500 different bacterial and fungal species were identified from the soil samples collected from various treatments. Among fungal species, majority (>75.0%) belonged to Phylum Ascomycota (Ex. *Cladosporium macrocarpum.*, *Coniothyrium* sp.). Other major fungal phyla include Basidiomycota (Ex. *Amanita muscaria*, *Bolbitius demangei*) and Mortierellomycota (Ex. *Mortierella alpina*, *Mortierella clonocystis*). Among bacterial species, majority (>35%) belonged to Phylum Proteobacteria (Ex. *Acidicadlus* sp., *Acidiphilus* sp.). Other major bacterial phyla include Actinobacteriota (Ex. *Ferethrix* sp., *Lamia* sp.), Acidobacteriota (Ex. *Acidicapsa* sp., *Acidobacterium* sp.) and Bacteroidota (Ex. *Dysgonomonas* sp., *Petrimonas* sp.). Overall, soil samples were ranked “Medium” in terms of richness, evenness, and equilibrium of microbial species. Plant pathogen populations in soil were very low and detection is limited primarily to *Verticillium* and *Fusarium*.

Impact of Treatments on Soil-borne Plant Pathogens:

Soil-borne plant pathogen population is naturally very low in these soils. Reductions in pathogen populations were observed twenty-four hours after applications of SaniDate HC and OxyFusion suggesting an immediate and partial suppression but populations rebounded to pre-application levels in the sample taken fourteen days later (Figures 1 and 2).

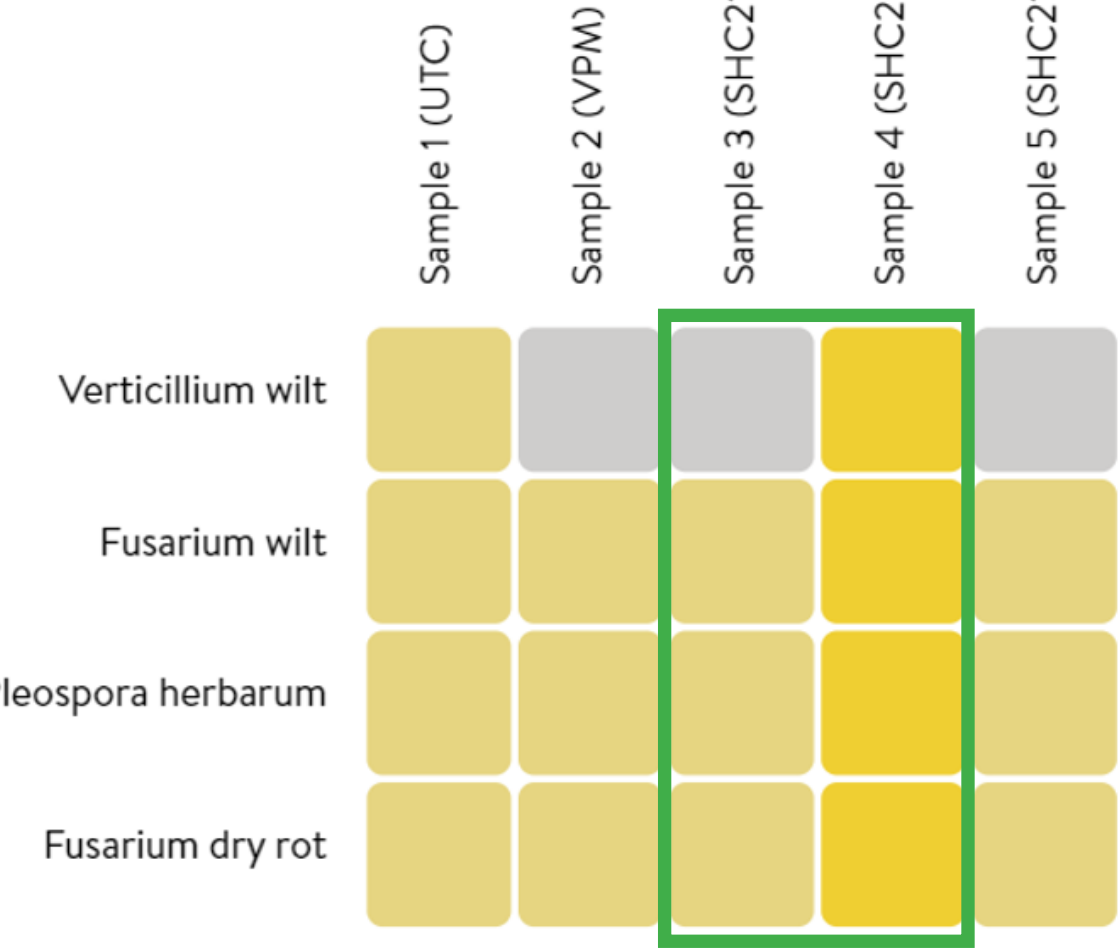


Figure 1.

Soil-borne Pathogen Population Before and After Treatment with SaniDate HC (Green Border-Light Yellow (Higher-Before Treatment) to Bright Yellow (Lower-After Treatment))

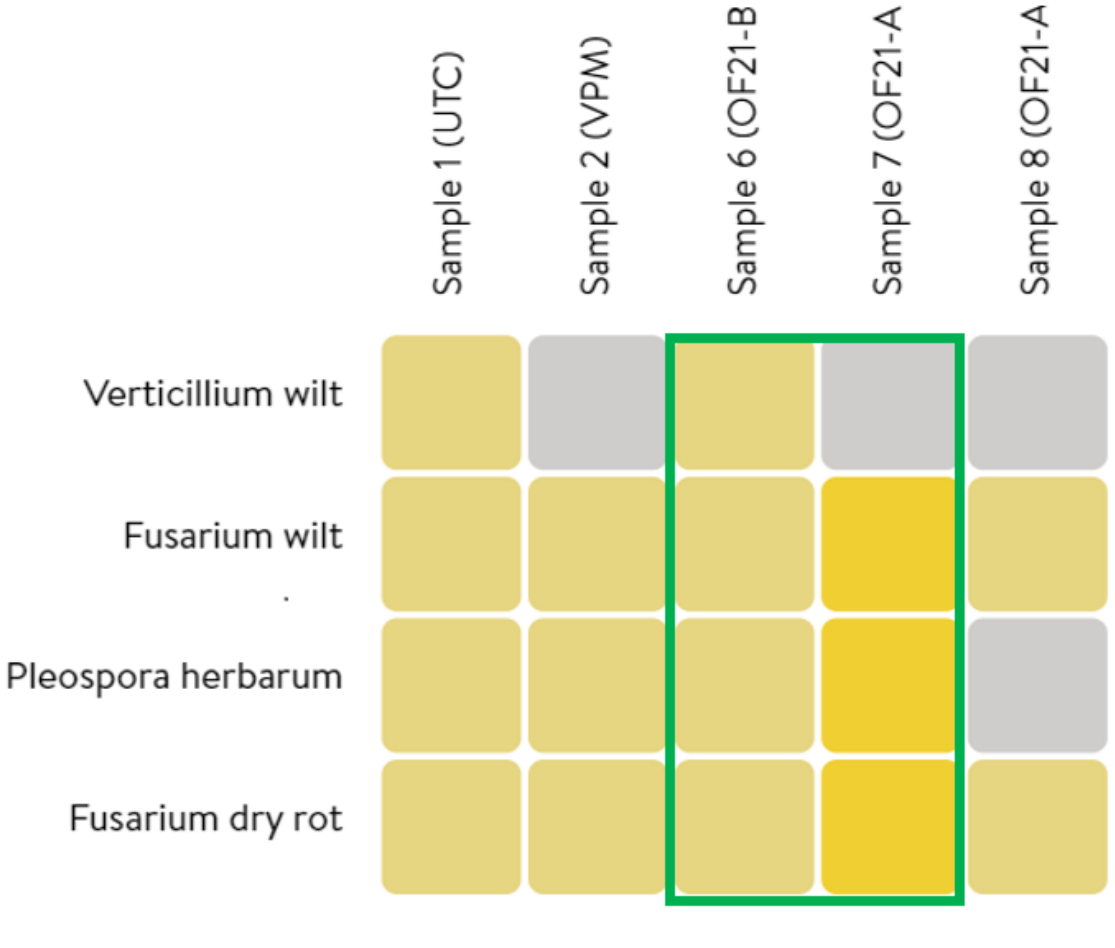


Figure 2.

Soil-borne Pathogen Population Before and After Treatment with OxyFusion (Light Yellow = Higher to Bright Yellow=Lower)

Impact of Treatments on Microbiome Resistance and Biodiversity:

Resistance (ability of communities/populations to remain unchanged when stressed by disturbance) levels decreased twenty-four hours after application of SaniDate HC and OxyFusion but increased fourteen days after application (Figures 3 and 4) suggesting a temporary shift and possible rejuvenation from TerraGrow application. Biodiversity (richness, evenness, and equilibrium of microbial species) seem to have improved after application of SaniDate HC when compared to pre-treated sample that showed slightly low in biodiversity (Figure 3).

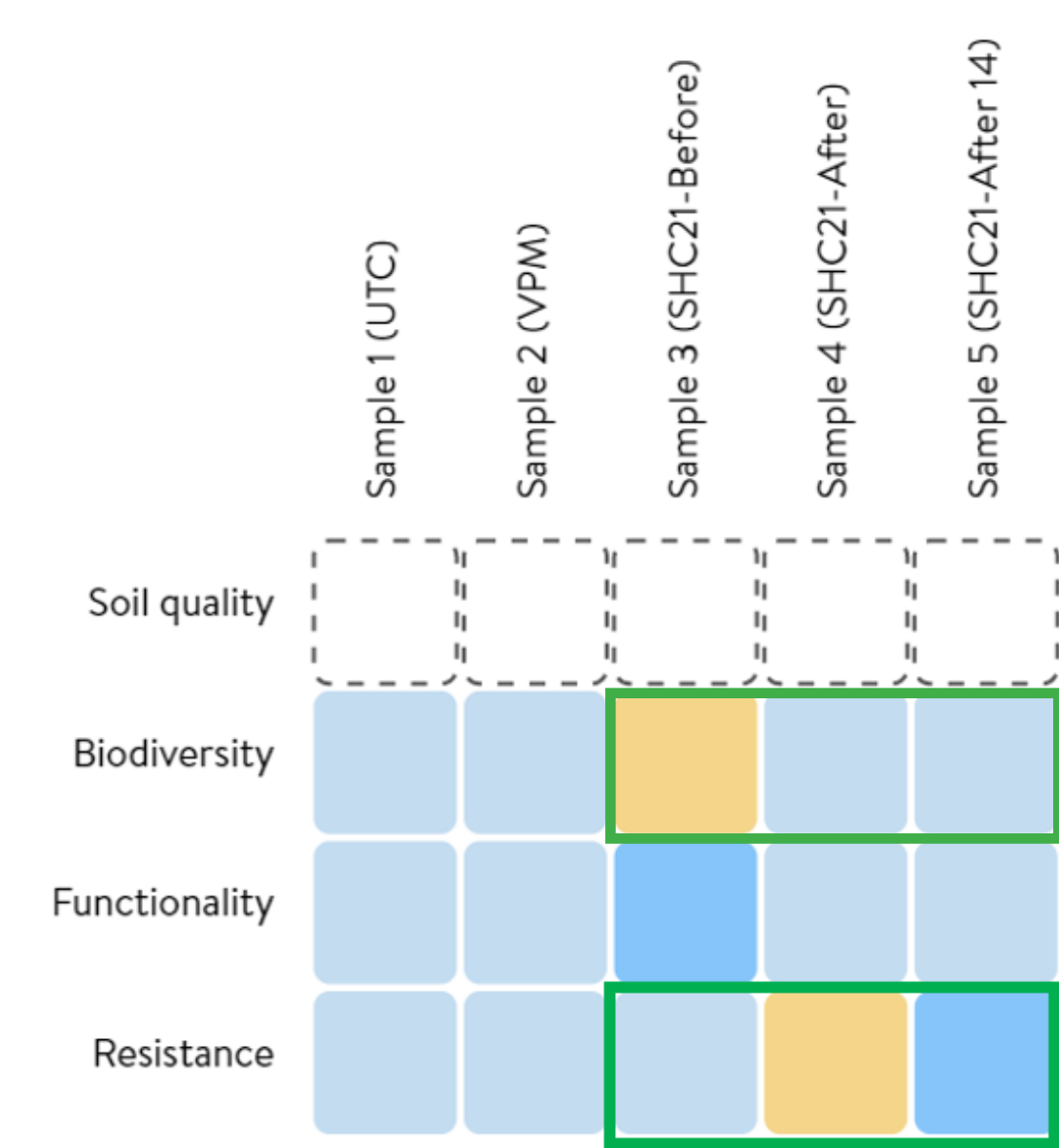


Figure 3.

Changes in Microbiome Biodiversity (Yellow-Blue-Blue) and Resistance (Blue-Yellow-Dark Blue) Before and After Treatments with SaniDate HC and TerraGrow

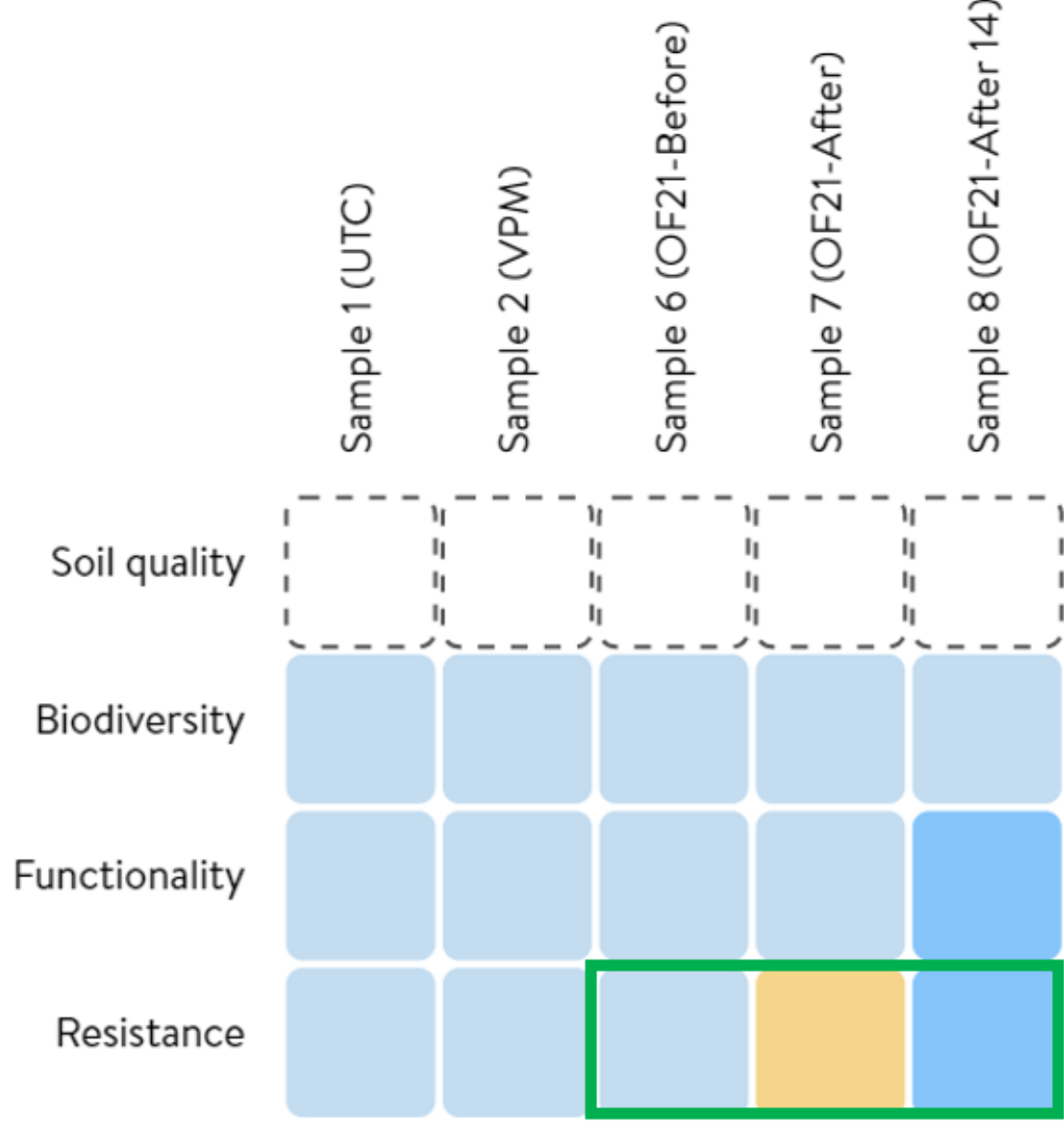


Figure 4.

Changes in Microbiome Resistance (Blue-Yellow-Dark Blue) Before and After Treatments with OxyFusion and TerraGrow

Impact of Treatments on Nutritional Pathways in Soil:

Shifts in nutritional status were observed with the treatments, especially with microbial mobilization of phosphorus and potassium. Certain phosphorus and potassium pathways in the soil seem to have been impacted immediately after treatment with SaniDate HC and OxyFusion but levels increased in the samples collected fourteen days after application, suggesting a temporary shift and possible rejuvenation from biological (TerraGrow) application (Figures 5 and 6). Similar effects were observed on organic matter release (Figures 6 and 7).

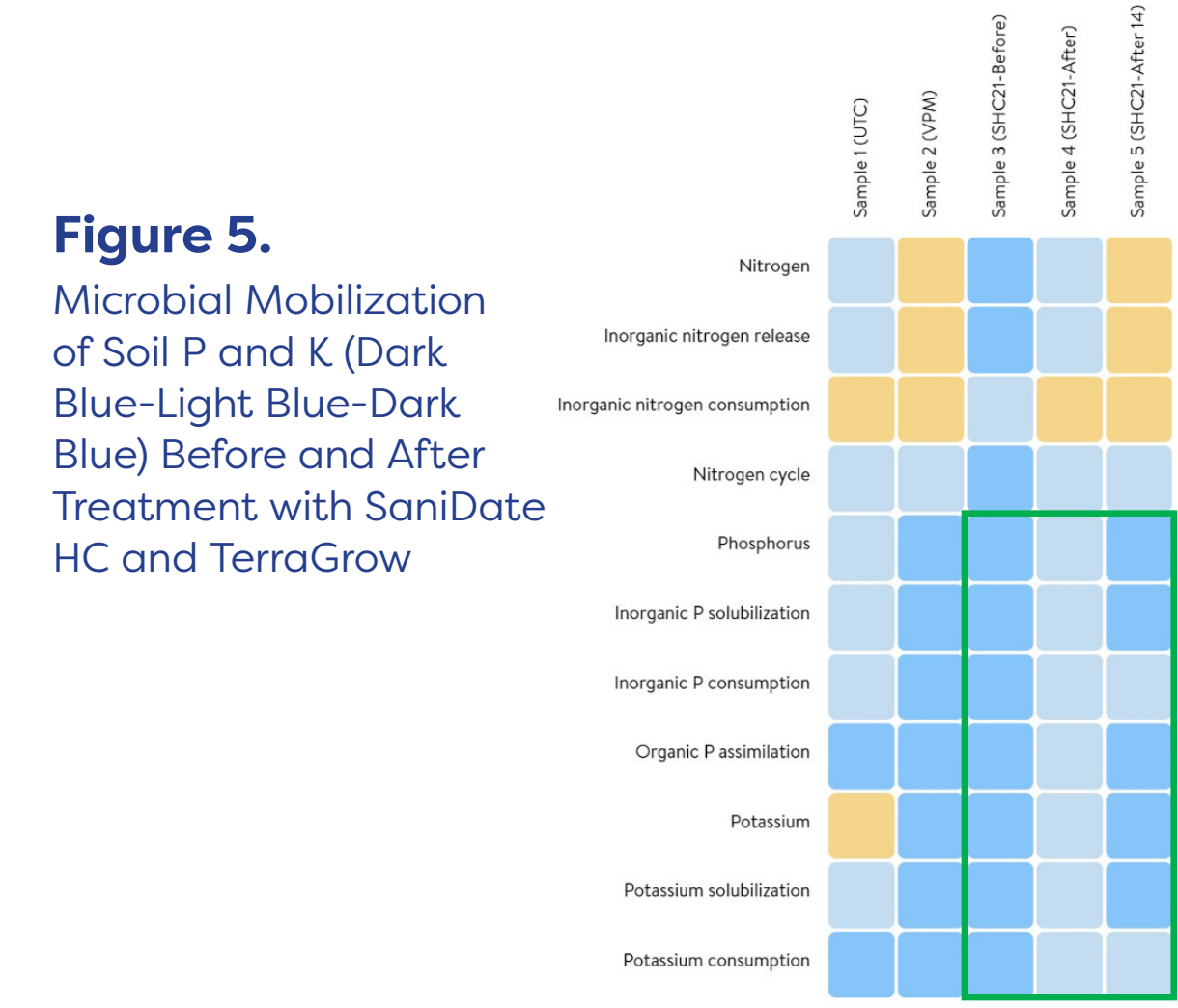


Figure 5.

Microbial Mobilization of Soil P and K (Dark Blue-Light Blue-Dark Blue) Before and After Treatment with SaniDate HC and TerraGrow

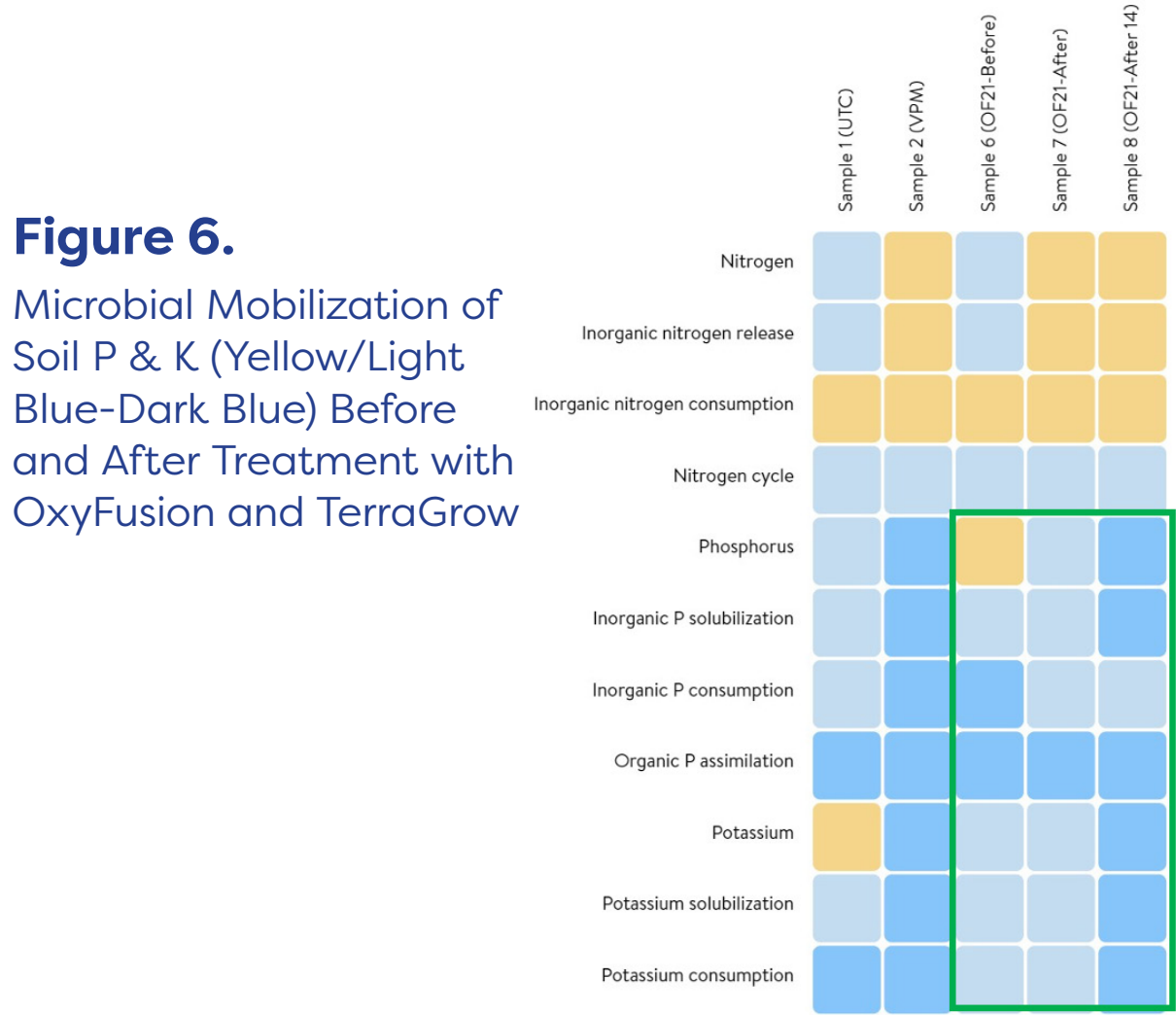


Figure 6.

Microbial Mobilization of Soil P & K (Yellow/Light Blue-Dark Blue) Before and After Treatment with OxyFusion and TerraGrow

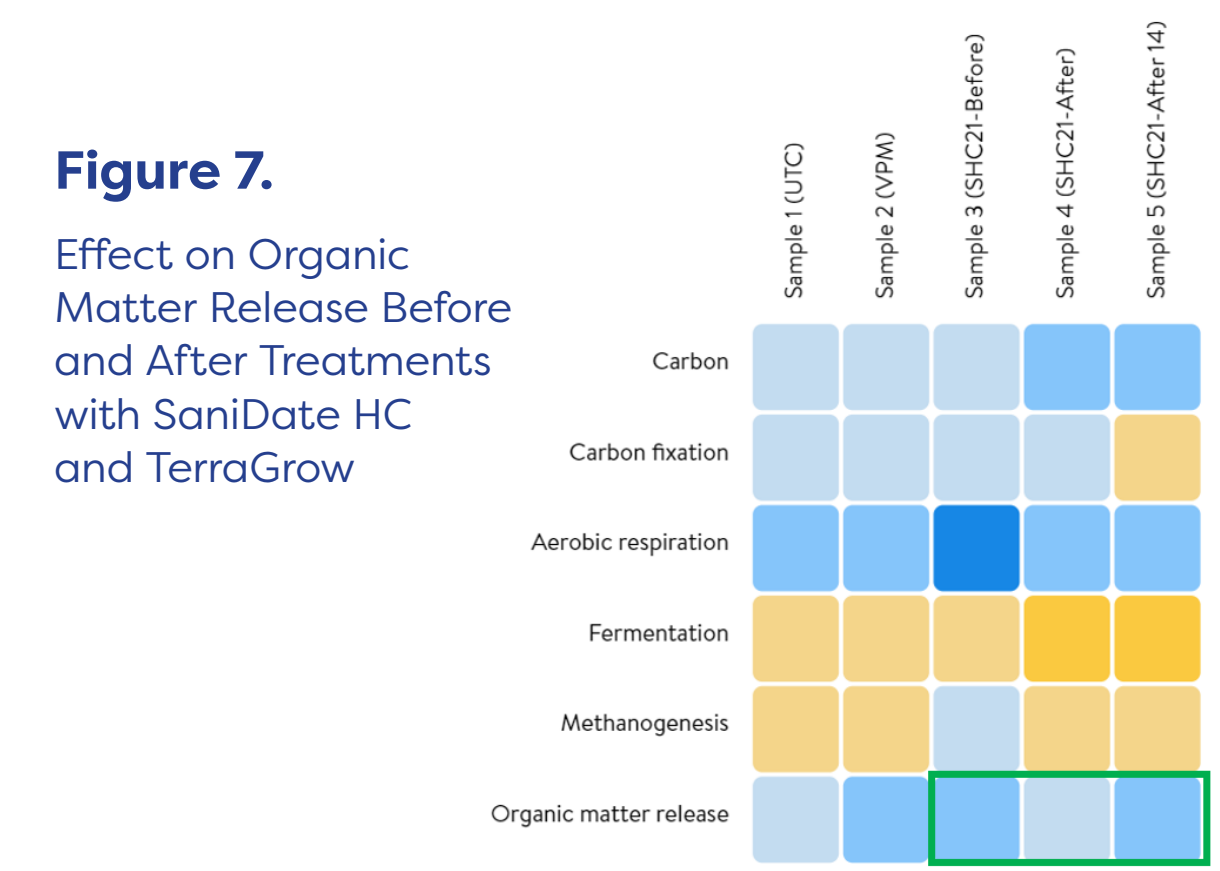


Figure 7.

Effect on Organic Matter Release Before and After Treatments with SaniDate HC and TerraGrow

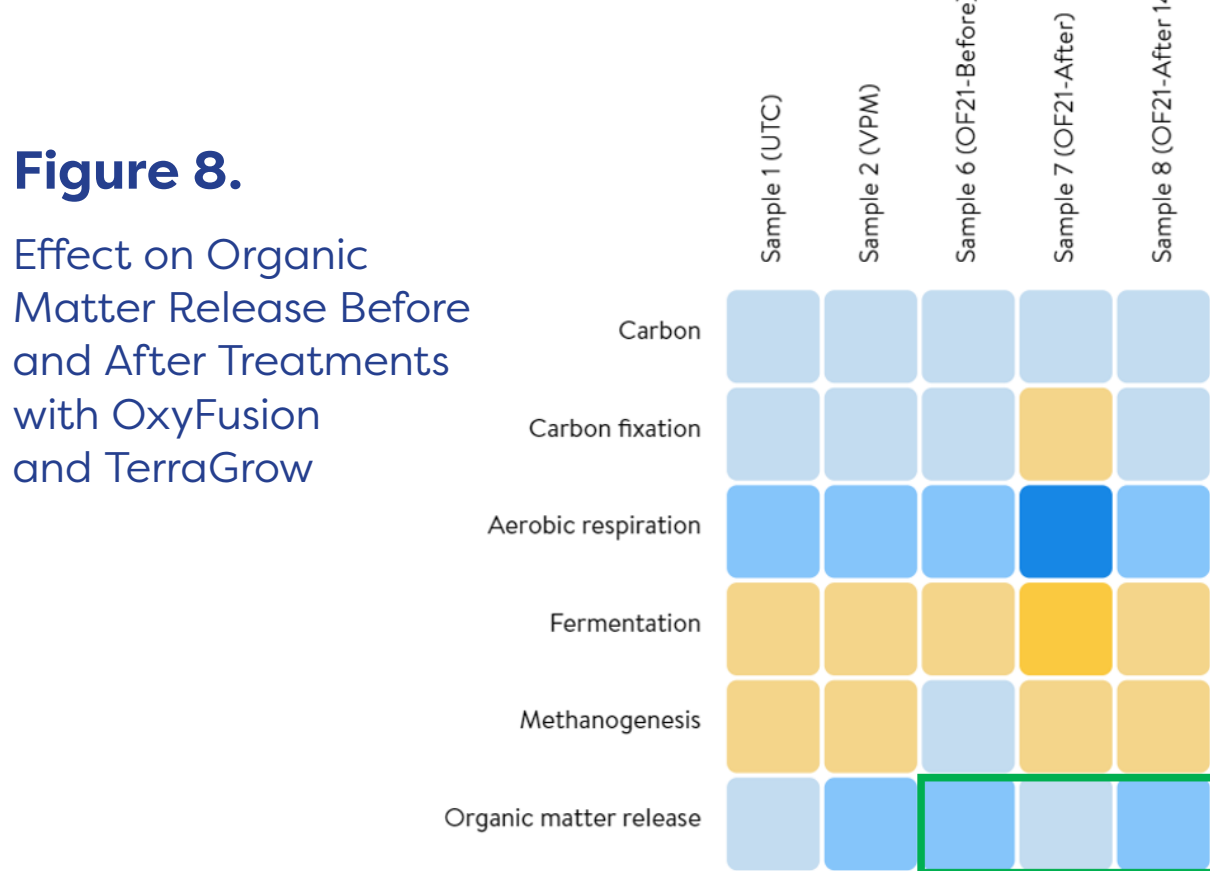


Figure 8.

Effect on Organic Matter Release Before and After Treatments with OxyFusion and TerraGrow

Discussion:

Despite limitations with the study design (small plots and not randomized), the study overall presented interesting findings in terms of microbiome diversity, composition, functionality, and nutritional status of the soil with a history of potato production. Since fumigant (Vapam) was applied in late Fall and soil analysis was not conducted before and immediately after fumigant was applied, the effect of fumigation on soil microbiome parameters is not known. Even though some suppression of soil pathogens such as *Fusarium* and *Verticillium* was observed immediately after treatment with SaniDate HC and OxyFusion, soil pathogen population is very low to offer any conclusive evidence. While no clear trends were observed as far as impact of alternative treatments on other test parameters (biosustainability, health and nutrition of soil), evidence in certain areas were stronger, especially with microbial mobilization of phosphorus (P) and potassium (K) pathways in the soil. Studies on a larger scale and in a more controlled environment may provide better insights into the overall effects of these alternative programs on soil microbiome and its functions. DNA sequencing technology can be a great tool to utilize for these evaluations.

References:

Enhancing Soil Health in U.S. Potato Production Systems. USDA Specialty Crops Research Initiative Coordinated Agricultural Project (CAP) # 2018-51181-28704.

Smart, Trevor Blake, “Microbial Community Response to Fumigation in Potato Soils” (2018). Theses and Dissertations. 7355. <https://scholarsarchive.byu.edu/etd/7355> Microbial Community Response to Fumigation in Potato Soils (byu.edu).

Rokunuzzaman M, Hayakawa A, Yamane S, Tanaka S & Ohnishi K (2016) Effect of soil disinfection with chemical and biological methods on bacterial communities. Egyptian Journal of Basic and Applied Sciences 3: 141-148.

Di Primo P, Gamliel A, Austerweil M, Steiner B, Beniches M, Peretz-Alon I & Katan J (2003) Accelerated degradation of metan-sodium and dazomet in soil: characterization and consequences for pathogen control. Crop protection 22: 635-646.

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