Impact of Microalgal Addition on the Soil Microbiome

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Background

Microalgae, often overlooked but immensely significant, inhabit diverse environments across our planet. From the depths of oceans to the surfaces of freshwater bodies their ability to adapt to a wide array of conditions and their rapid growth make them an intriguing subject for research and innovation. While the majority of research involving microalgae has been focused on biofuel production, the impact of utilizing them as a soil treatment remains largely unknown. The rapid loss of soil carbon with intensive agriculture is leading to soils that will not be able to support sustainable cropping. It is estimated that the majority of soil C in the midwest will be lost in approximately 15-20 years. In addition, fertilizer application results in runoff leading to environmental pollution while the majority of fertilizer N is lost via numerous pathways. Thus, it is important to develop methods to increase soil C and N in cropping systems in order to support sustainable agriculture.

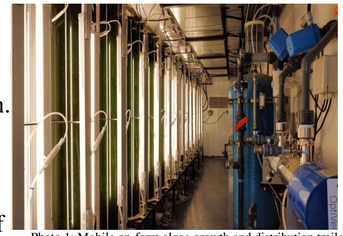

Photo 1: Mobile on-farm algae growth and distribution trailer

To address both C loss and the negative impacts of fertilizer addition, this research project focuses on the impact of the addition of microalgae on the soil microbiome, particularly on the abundance and activity of nitrogen-fixing bacteria (diazotrophs) within the soil. These bacteria perform a critical process that impacts both soil fertility and plant growth. Overall, our hypothesis is that algae addition will enhance the recruitment of N fixers and increase soil C which can potentially reduce the need for synthetic N fertilizers while enhancing soil C, thus promoting sustainable agriculture.

Methods

In this research, soil DNA was extracted using a DNeasy® PowerLyzer® PowerSoil® Kit and quantitative PCR (qPCR) was utilized to assess the abundance of the soil microbial community using 16S rRNA gene-targeted primers and primers for the *nifH* gene for nitrogen-fixing bacteria. The qPCR assays were calibrated using standard curves generated from known quantities of E. coli K12 plasmids containing the target gene sequences.

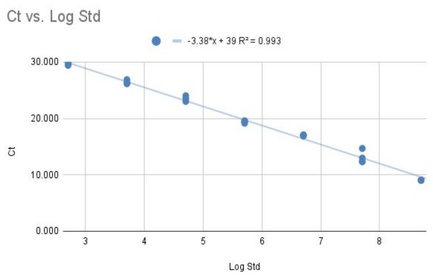

Figure 1. Standard curve a dilution series of a known standard, is crucial as it establishes a relationship between the known concentrations of the standard and the corresponding fluorescence intensity. This allows for the accurate quantification of the unknown samples by comparing their fluorescence to the standard curve, ensuring precise and reliable results.

Methods

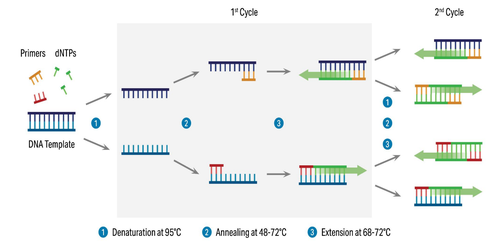

Figure 2. qPCR used to amplify and simultaneously quantify a targeted DNA molecule. The process involves using specific primers to amplify the DNA of interest, with a fluorescent marker that increases in intensity as the DNA is amplified. This fluorescence is measured in real-time during each cycle of the PCR, providing a quantitative measurement of the initial amount of the target DNA.

Results

The abundance of soil microbial communities and diazotrophs increased in the algae-treated fields from the initial to the final sampling.

Depth (cm)	Organic N	Inorganic N	Organic N Reserve	Available N	Total P	Available P	Water Extract TOC	TOC
0-15	0.8%	-2.8%	15.5%	-2.6%	-7.7%	-8.8%	2.5%	10.9%
15-30	23.3%	16.4%	47.0%	16.5%	21.6%	20.6%	23.1%	18.6%
30-60	12.6%	11.0%	68.7%	7.0%	27.3%	27.1%	5.2%	-1.0%
24-36	-6.00%	51.8%	-10.9%	50.8%	62.8%	67.0%	8.1%	2.1%

Table 1. Soil props following the percent change in soil nutrients with the application of algae across various depth after one cropping season.

- Organic N / inorganic N both show increases with algae application as well as with P.
- Total organic C also increases across most depths.

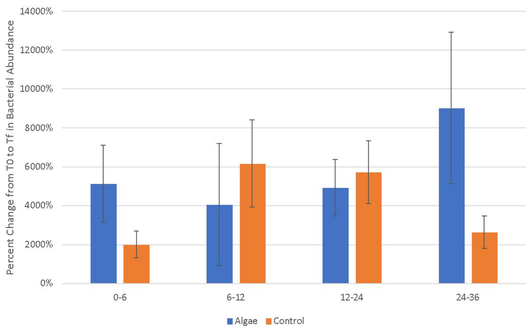

Figure 3. Percent change from T0 to Tf (initial sampling to harvest) of the abundance of the total soil microbial community in the algal supplemented fields (blue) and control fields (orange).

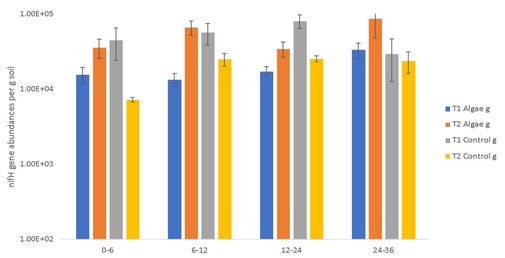

Figure 4. *NifH* gene abundance of the soil bacterial community increased with time for both the controls in the algae fields.

- Likely due to the impact of root risophere (during crop growth).
- Seen in surface layer 0-6 and at 24-36 the agal fields had a significant higher increase over time.
- Hypothesized due to the increase of feeding the algae at this level.

Results

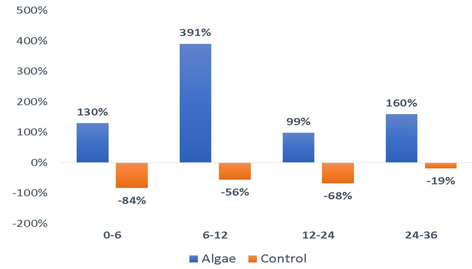

Figure 5. Percent increases or decreases in the abundances of N fixing populations over the cropping period in the algae and control treatments by depth.

Discussion and Conclusions

Our results generated thus far indicate that the addition of microalgae to soil can positively influence the soil microbiome by increasing the abundance of N-fixing bacteria. This is also reflected in increases in soil N. We hypothesize that algal exudates serve as a labile C source that supports the growth of nitrogen-fixing bacteria. Thus, algae addition may enhance N fixation in the soil, though *in-situ* measurements of N fixation are needed to confirm these data. Conversely, the decrease in N-fixing bacteria in control plots indicate the well-known inverse relationship between fertilizer N addition and N fixation. This study also shows that soil organic carbon increased over one cropping season with algae addition. Future research will focus on the stability of this new soil C to indicate whether algae addition can increase soil C over long periods, thus serving as a C sink. This could potentially provide farmers with an additional income source via C credits.

Figure 6. Hypothetical benefits of microalgae addition to agricultural soils. Note that the majority of these benefits have not been measured to date.

Acknowledgements

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