DNA Sequencing of Soil Microbiota from Mulching: A Novel Rotational Fragment Farming for Efficient Agriculture

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Purpose: Weeds in agriculture compete for energy resources, decreasing yields and increasing labor costs. Herbicides to kill weeds are toxic to human health, environment and most importantly to the soil microbiota. Mulching materials prevent growth of weeds by covering the soil and may alter the microbiota. Therefore, in this unique research study using DNA sequencing, I analyzed the effect of mulching on the composition of soil microbiota from various organic & conventional farms and gardens. Procedure: Collected 30 soil samples with & without mulching, and analyzed bacterial & fungal communities. Results: There was a statistically significant increase ($P<0.000001$) in Actinobacteria & Proteobacteria, Ascomycota & Basidiomycota upon straw mulching, while herbicide-using farms significantly decreased them. Alpha diversity analysis showed straw mulched soils have highest bacterial & fungal diversity with high Chao1 and Shannon values ($P<0.001$). Linear Discriminate Analysis showed significant increase in several beneficial microbes like nitrogen-fixing bacteria ($P<0.008$). However, Principal Coordinate Analysis (Beta diversity) showed uniqueness of bacterial & fungal community composition in straw mulching compared to other mulching materials. Conclusion: This research study shows straw based mulching creates a healthy & diverse soil microbiota in both bacteria & fungi, increasing decomposition of organic matter & nutrient availability to plants. Straw mulching is a sustainable method applicable for small & large industrial farms through my “Rotational Fragment Farming (RFF)” model. This research offers solutions to agricultural challenges of weeds, chemical contamination, Bioremediation, droughts, global warming, labor & fertilizer costs, and growing food demands.

Awards Won:
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