

THE IMPACT OF BIOINOCULANTS ON MICROBIAL COMMUNITIES IN FINGER MILLET

In order to transform agroecosystems to become resilient to climate change there is an urgent need to undertake the study of microbial interactions with plants in the rhizosphere, a region of soil characterized by its close proximity to the plant roots. Accumulating evidence suggests that increased efforts to use the next generation techniques to identify microorganisms for empowering crop production and sustaining agriculture by eliminating our reliance on chemical inputs so as to minimise environmental degradation is a huge challenge.

In a study Rohini Mattoo et al. have used finger millets to identify the microbial communities in its rhizosphere using high throughput sequencing of bacteria to compare and contrast the abundance of different functional groups. The study revealed that incorporating chemical fertilizers increased the relative abundance (~95.70 % and ~75.89 %) of opportunistic pathogens and caused reduction in beneficial ones. The use

of bioinoculants leads to an increase in plant growth during the flowering stage and microbes involved in important biogeochemical cycles (e.g., nitrogen cycle). Bioinoculants did not result in instant improvements as compared to the chemical fertilizer but have been demonstrated to benefit soils in the long run. In addition, the results revealed that inclusion of Agro-chemicals induced major shifts in the bacterial species, reduced the bacteria involved in biogeochemical cycling of essential nutrients and enriched the opportunist pathogens. This work has laid ground for future studies to obtain direct evidence as to how the beneficial and functionally relevant microorganisms maintain healthy ecosystem by engineering the soil rhizosphere.

Reference:

Mattoo, Rohini et al. "Contrasting rhizosphere microbial communities between fertilized and bio-inoculated millet." *Rhizosphere* 17 (2021): 100273

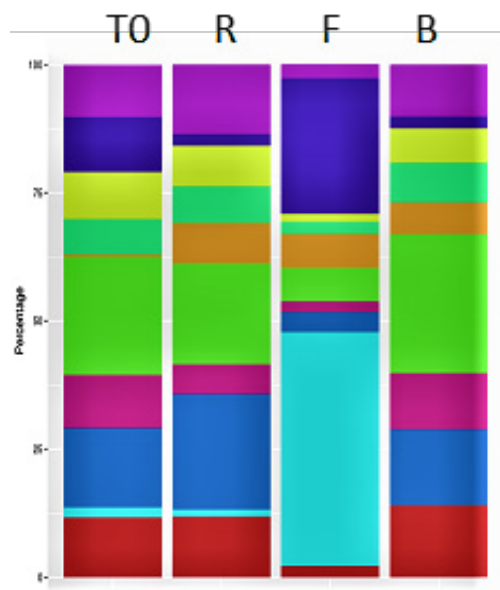


Figure: Comparison of the relative abundance of microorganisms at bacterial species level obtained from high throughput genome sequencing.