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## **Harnessing the Cannabis sativa plant's ability to recruit microbes in search of a developmentally specific rhizosphere microbiome**

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**Abstract:** A plant's nutritional needs are different over the course of growth and development, and Cannabis is no stranger to this phenomenon. Recent studies have shown that plants may actively recruit differential microbiomes throughout growth to aid in nutrient uptake to meet these changing nutritional needs. Microbes are attracted to the plant's roots through root exudation, and can also assist their hosts with uptake of certain nutrients. Further, the types of exudates deposited by plants have been shown to change over growth and development, presumably to attract differentially functional microbiomes to their rhizospheres to meet their developmental needs mediated by nutrition transfer. While the changing root exudation profile of Cannabis requires further investigation, here we aim to show how the rhizobacterial microbiomes of cannabis are differential based on the vegetative, transition, and blooming stages of maturation. We have and are still collecting rhizosphere soil samples from hemp to observe similarities in bacterial taxa across multiple production regions in the US. We intend to observe these communities with next generation sequencing, and annotate how they are changed over hemp's major developmental stages (Vegetative, Transition, and Blooming). The observation of overlapping bacterial communities in the rhizosphere of hemp, across multiple production regions, will move forward the scientific notion of the hemp core bacterial microbiome. The annotation of a core bacterial community (or core functional bacterial community), associated with the cultivation of hemp will assist growers nationwide by providing information about these communities and how to manage production with consideration of the soil microbiome.

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