

## Uncovering the Composition and Function of the Aquatic Microbiome for Duckweeds

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**Abstract:** Duckweed is a family of aquatic plants that are the fastest flowering plants in the world. They are capable of quickly converting wastewater into an easily harvestable, low lignin content biomass. Recent research has demonstrated the potential of duckweed to be used as a sustainable source of renewable biomass for biofuel. For us, this system is very attractive because scaling-up duckweed farming does not require the use of arable land that are being used for other crops. However, realizing this fast-growth potential, and making it economically viable depends on our ability to create a reliable biomass production pipeline through a knowledge-based approach. The studies proposed here would define the role for the microbiome to increase duckweed biomass and extract carbon, nitrogen, and phosphate from its environment. For these studies, we have a set of duckweed growth-promoting bacterial isolates for identification of the targeted host pathways resulting in plant growth. To define the "core", "genotype-specific", and "environment-specific" microbiomes, we will perform a series of 16S rRNA surveys on 6 duckweed accessions grown in 2 different aquatic environments. Finally, we will examine how "pre-association" of the growth-promoting strains under controlled conditions impacts microbiome composition and function to extract carbon, nitrogen, and phosphate from the duckweed aquatic environment. The facilities at EMSL will allow us to determine if our set of duckweed growth promoting bacteria are actually endophytes, and if they affect the ability of duckweed to extract organic carbon from its environment. The facilities at JGI will allow us to define the relevant microbes present in the duckweed microbiome and begin to understand the functions that these microbes provide in plant growth and carbon, nitrogen, and phosphate cycling. Lastly, testing selected strains of microbes from duckweed on growth of a model land-plant *Arabidopsis* should reveal potential opportunities for discovering new tools to characterize the pathways involved. The results from these studies will provide us with a platform to move forward with the functional deployment of defined microbial amendments for the optimal farming of different species of duckweed in the future.