**Correlating Flavonoid Exudation and Microbiome of *Medicago truncatula***

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Symbiotic nitrogen fixation in legumes provides a sustainable nitrogen source for agriculture. However, the symbiosis is often not optimal. A potential method to improve the symbiosis is by modifying the exudation of flavonoids, a family of metabolites that signal the symbiotic infection of rhizobia. This poster reports on an experiment that utilised metabolomic and metagenomic methods to test for a correlation between the microbiome in three spatial compartments at different distances from the root of a null segregate *Medicago truncatula* (2HA) and an isoflavone synthase overexpression transgenic line (IFS:OE), which showed different flavonoid exudation when grown on media (Liu *et al.* 2017). Plants were grown in a mixture of sand and field soil, and nodulated with native soil rhizobia, with significant increases in total shoot N in the IFS:OE line compared to the control. The compartments harvested were bulk soil, rhizosphere soil and root tissue. The experiment successfully identified differences in the microbiome of the compartments, with the diversity of microbes decreasing with proximity to the root. However, the differences in flavonoid exudation observed when 2HA and IFS:OE were grown in media were not observed when grown in soil, with a difference in flavonoid accumulation only observed within the root. This result meant a correlation between flavonoid exudation and microbiome could not be made, as there was no difference in either flavonoid profile or microbiome outside of the root when comparing plant lines. These results suggest a greater understanding of the root exudation mechanism is necessary to manipulate nodulation through flavonoid exudation.

***References:***

*[1] Liu Y.* *et al, Ethylene signaling is important for isoflavonoid mediated resistance to Rhizoctonia solani in Medicago truncatula. Molecular Plant-Microbe Interactions vol. 30: 2017, p. 691-700*