Applicant: Dan Thomas

Abstract:

The plant microbiome, with its collective abundance of microbial genetic resources, may represent an important and adaptive addition to the host plant genome. Here we propose to undertake sampling for the functional microbiome of a host tree species, *Eugenia nesiotica*, across the extent of the BCI forest dynamics plot. Endophytes from both leaf and root tissue of *Eugenia* will be surveyed for the presence of biosynthetic gene clusters, using metabarcoding with primers targeting two of the largest families of microbial secondary metabolites, polyketides and nonribosomal peptides. We predict that stressors faced by the host plant will predict the relative abundance of "useful" secondary metabolites synthesized in the microbiome. These data will paint a general picture of the metabolic potential of the tree microbiome, and its responsiveness to environmental challenges. The results of the proposed survey are readily extensible to food plant systems in the current time of rapid environmental changes, and also contribute fundamentally to the STRI's ongoing work on the Janzen-Connell hypothesis of tree diversity created by conspecific negative density dependence.

Methods:

We will sample the functional plant microbiome of E. nesiotica using Illumina MiSeq platform sequencing of amplicons from two broad classes of microbial metabolite pathways. We will emphasize the detection of key metabolic steps in the microbial (non-plant) biosynthesis of anti-herbivory and pathogen response, coupled with micro-site data, estimates of disease and herbivory load, and the proximity of conspecific trees. We will undertake both community-level analyses of these data, and also be mine them for specific secondary metabolites of interest, such as ergot alkaloids, or unknown gene clusters that may appear be acting to control disease. Leaf and root tissue will be collected at 36 locations within the plot according to a spatial grid with a grain of 100m. Epiphyte and endophyte microbial populations will be sampled. Aerial plant tissues will be sampled at upper and lower canopy sites, to test micro-site variability in microbiome expression due to position in the canopy.