Evolution of cellulolytic activity in *Streptomyces*

**Objective**
- To understand the processes driving the evolution of biomass deconstruction in the *Streptomyces* genus.

**Approach**
- Compared the phylogenetic diversity of over 1,100 strains of *Streptomyces* and used a quantitative filter paper (FP) assay to measure the cellulose degrading activity of 223 diverse strains isolated from free-living and eukaryotic host-associated niches.
- 13% of the strains (29/223) deconstructed cellulose with activity comparable to *Streptomyces* sp. *Sirex*-AA from wood wasps, and 86% of the highly cellulolytic organisms grouped into 2 phylogenetically distinct clades associated with insects that feed on plant biomass (red lines, clades I and III – see Figure 1).

**Result/Impacts**
- Plant biomass degrading enzymes (CAZy) are widespread in *Streptomyces*, but the ability to rapidly deconstruct cellulose is surprisingly rare in this genus (and enriched in strains associated with insect hosts that feed on plant biomass).
- Genomic, transcriptomic, and biochemical analyses identified key changes in gene content and transcriptional control of expression that confer highest cellulolytic activity.
- Genes from naturally evolved cellulolytic *Streptomyces* are a rich new resource for biotechnology research.