BRC Science Highlight

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).

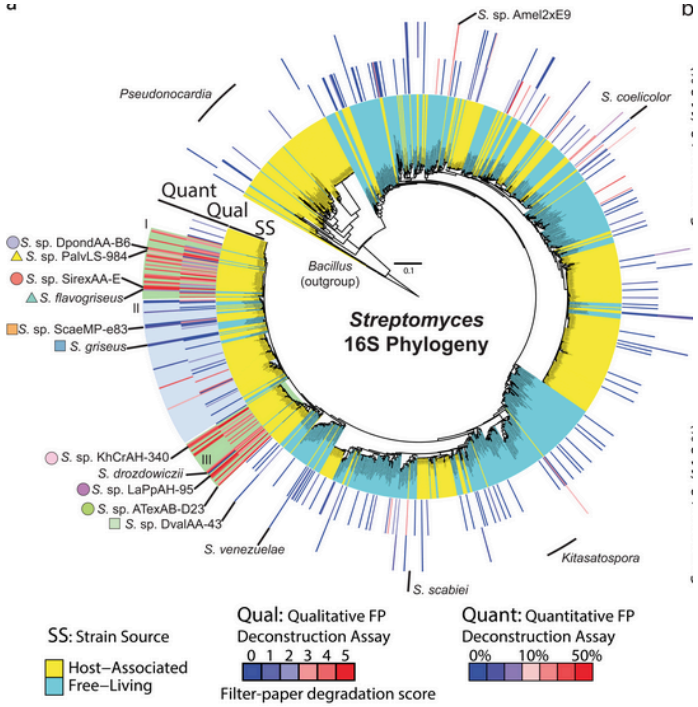

Figure 1. Distribution of cellulolytic ability in the genus *Streptomyces*.

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.

Book AJ, Lewin GR, McDonald BR, Takasuka TE, Wendt-Pienkowski E, Doering DT, Suh S, Raffa KF, Fox BG, Currie CR "Evolution of High Cellulolytic Activity in Symbiotic *Streptomyces* through Selection of Expanded Gene Content and Coordinated Gene Expression". *PLOS Biology.* 55 (12), 14(6): e1002475 (2016) [DOI: 10.1371/journal.pbio.1002475]