

The gastric caeca as a house for actinomycetes – do they work as an antibiotic factory for stinkbugs?

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Microbes are extensively associated with insects, playing key roles in insect defense, nutrition and reproduction. Most of the associations reported involve *Proteobacteria*. Despite the fact that *Actinobacteria* associated with insects were shown to produce antibiotic barriers against pathogens to the hosts or to their food and nutrients, there are few studies focusing on their association with insects. Thus, we surveyed the *Actinobacteria* diversity on a specific region of the midgut of six species of stinkbugs (Heteroptera: Pentatomidae) known to carry a diversity of symbiotically-associated *Proteobacteria*. A total of 34 phylotypes were placed in 11 different *Actinobacteria* families. *Dichelops melacanthus* held the highest diversity with six actinobacteria families represented by nine phylotypes. *Thyanta perditor* ($n = 7$), *Edessa meditabunda* ($n = 5$), *Loxa deducta* ($n = 5$) and *Pellea stictica* ($n = 4$) were all associated with three families. *Piezodorus guildini* ($n = 3$) and *Nezara viridula* ($n = 4$) had the lowest diversity, being associated with two (*Propionibacteriaceae* and *Mybacteriaceae*) and one (*Streptomyceataceae*) families, respectively. *Corynebacteriaceae* and *Mycobacteriaceae* were the most common families with phylotypes from three different insect species each one. Many phylotypes shared a low 16S rRNA gene similarity with their closest type strains and formed new phyletic lines on the periphery of several genera. This is a strong indicative that stinkbug caeca can harbor new species of actinobacteria, which might be derived from specific associations with the species of stinkbugs studied. Although the well-known role of actinobacteria as a source of biomolecules, the ecological features of these symbionts on the stinkbugs biology remain unknown.