

**TITLE:** Characterization and comparison of intestinal bacterial microbiomes of *Euschistus heros* collected in Brazil

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**ABSTRACT:**

Herbaceous insects are one of the main biological threats to crops. One such group of insects, stink bugs, are extremely damaging to the quality of the seed yield as they feed directly on green developing seeds leading to poorly marketable harvests. In addition to causing physical damage to the seed during feeding, the insects can also transmit microbial pathogens, leading to even greater yield loss. Conducting surveys of the insect intestinal microbiome can help identify possible pathogens, as well as detail what healthy stink bug digestive systems have in common. We used the conserved V4 region of the 16S rRNA gene to characterize the bacterial microbiome of the neotropical brown stink bug *Euschistus heros* collected in ten regions in Brazil. Recent discoveries indicated that *E. heros* from the north and the south of Brazil were composed of two distinguished lineages. Thus, we performed analyses to investigate the relationships between the intestinal microbiome and the proposed lineages: north, south, and hybrids. The NMDS analysis showed that the bacterial species clustered significantly by stink bug lineages. The species richness is higher in samples from the north lineage than the south lineage, and the hybrids have an intermediate species richness. The species diversity is bigger on the north and hybrid lineages of *E. heros*. Analyzing the relative abundance of the 10 most abundant bacterial families in each group, the hybrids had more bacterial families and their proportion is more evenly distributed than in pure lineages. The family Bacillaceae is unique in the hybrids and the Acetobacteraceae family is unique in the south lineage. Comparing the bacteria families, the family Bradyrhizobiaceae was the most abundant in hybrids *E. heros* than either of the pure lineages. The family Hyphomicrobiaceae was the most abundant in hybrid *E. heros* than north lineages. The families Moraxellaceae and Sphingomonadaceae were the most abundant in the hybrid than south lineages and the Enterobacteriaceae family was the most abundant in both pure lineages than hybrids. The diversity and abundance of intestinal bacteria vary among the lineages. This variability allows individuals to perform different functions to better adapt to the environments in which they live. Some families may be related to providing nutrients, break down cellulose, detoxify phytochemicals, and degrade organic compounds.

**Keywords:** Distribution, Glycine max, insect pests, microflora, stink bugs

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