

TITLE: Characterization and comparison of intestinal bacterial microbiomes of *Piezodorus guildinii* collected in Brazil and the United States

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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 red-banded stink bug *Piezodorus guildinii* collected in Brazil and the United States. Since the species *P. guildinii* co-occurred in both Brazil and the US, we further explored the association between its intestinal microbiome and the country of origin. The NMDS analysis (Fig. 4B) showed distinct groups of bacterial species in insects from Brazil and the US with a p-value of 0.0107. According to the number of observed OTU (p-value = 0.015) and the richness estimator Chao1 (p-value = 0.0087), *P. guildinii* sampled from Brazil were richer in intestinal bacterial species than insects from the US (Fig. 4C). The Deinococcaceae family occurred only in stink bugs collected from Brazil, and the Sinobacteraceae occurred only in insects collected from the US (Fig. 4D). The families Acetobacteraceae, Bradyrhizobiaceae, and Moraxellaceae were significantly more abundant in *P. guildinii* from the United States than Brazil, and the family Rhodocyclaceae was more abundant from Brazilian insects (Supplemental Fig. 5). Enterobacteriaceae, the most abundant bacterial family in both countries, constituted about 80% of the gut microbiome of both countries and showed no significant difference. 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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