

FIRST CHARACTERIZATION OF THE MICROBIOME OF THE JOINTED PUMPKIN FLY, *DACUS VERTEBRATUS* BEZZI (DIPTERA: TEPHRITIDAE)

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Introduction

The Jointed Pumpkin Fly, *Dacus Vertebratus* is among the economically important pests of horticultural crops in Africa. The pest attacks mainly cucurbits causing 25% to 100% losses. While its impact on agriculture is well documented, little is known about the microbial communities associated with this pest. This study presents the first characterization of the gut microbiome of *D. vertebratus*.



Methodology

Sites were established at Sokoine University of Agriculture (SUA) in Morogoro Tanzania. Third instar larvae were collected from infested watermelon (*Citrullus lanatus*) at two different sites and across four plots subject to agroecological or conventional pest management. A subset of 43 samples of *D. vertebratus* was subjected to 16S rRNA metabarcoding. We also considered an extended set of samples including cucurbit-feeding fruit flies from the Morogoro area.



Agroecological farm at SUA and laboratory experiments at RMCA

Results and Discussion

The analysis of the microbial communities of larvae of *D. vertebratus* produced 2,552 filtered ASVs assigned to 22 phyla, 212 families, and 465 genera of bacteria. More than 99.8% of ASVs belonged to 10 phyla (Figure 1). On the other hand, the 10 most abundant bacterial families (Figure 2) contributed to 88.4% of the ASVs, while more than 75.4% of the ASV belonged to 10 genera (Figure 3). When *D. vertebratus* was compared with samples of other tephritids feeding on watermelon collected in the Morogoro area, it was found that it significantly differed from *D. bivittatus*, *D. ciliatus*, and *Z. cucurbitae* (Figure 4). The results align with other studies that reported Proteobacteria, Bacteroidota, and Firmicutes as the most dominant phyla in tephritidae.

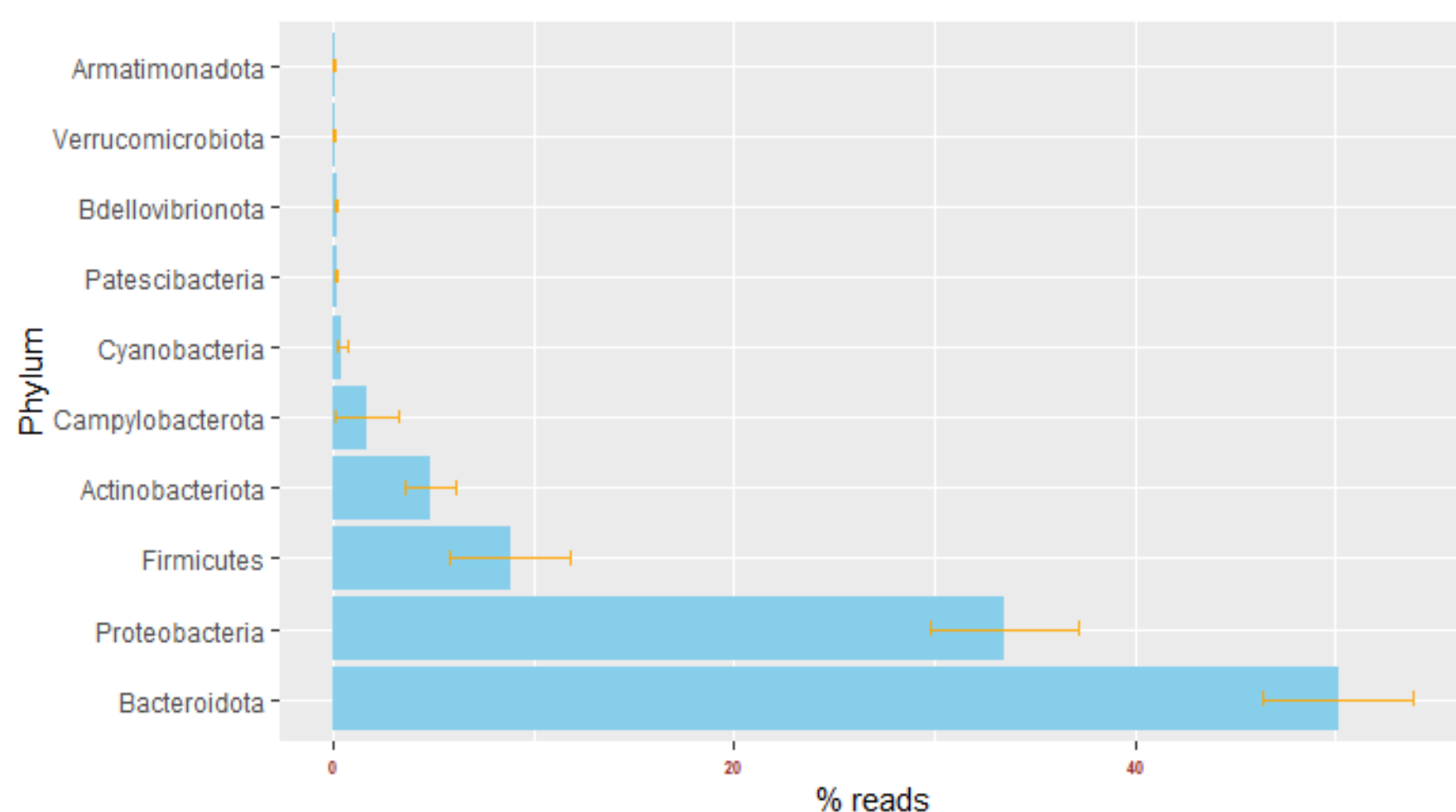


Fig 1: Bacterial phyla in *D. vertebratus*

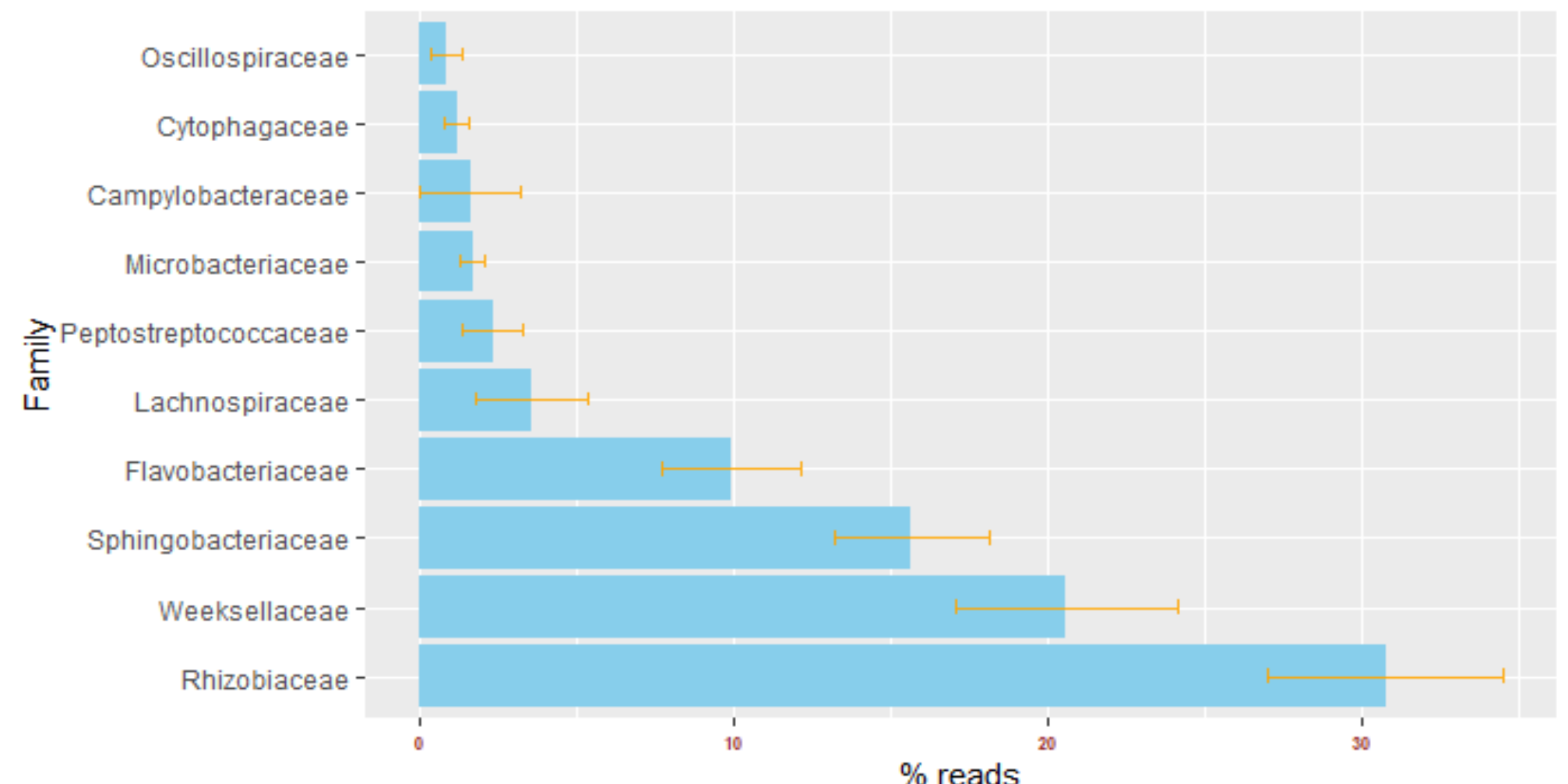


Fig 2: Bacterial families in *D. vertebratus*

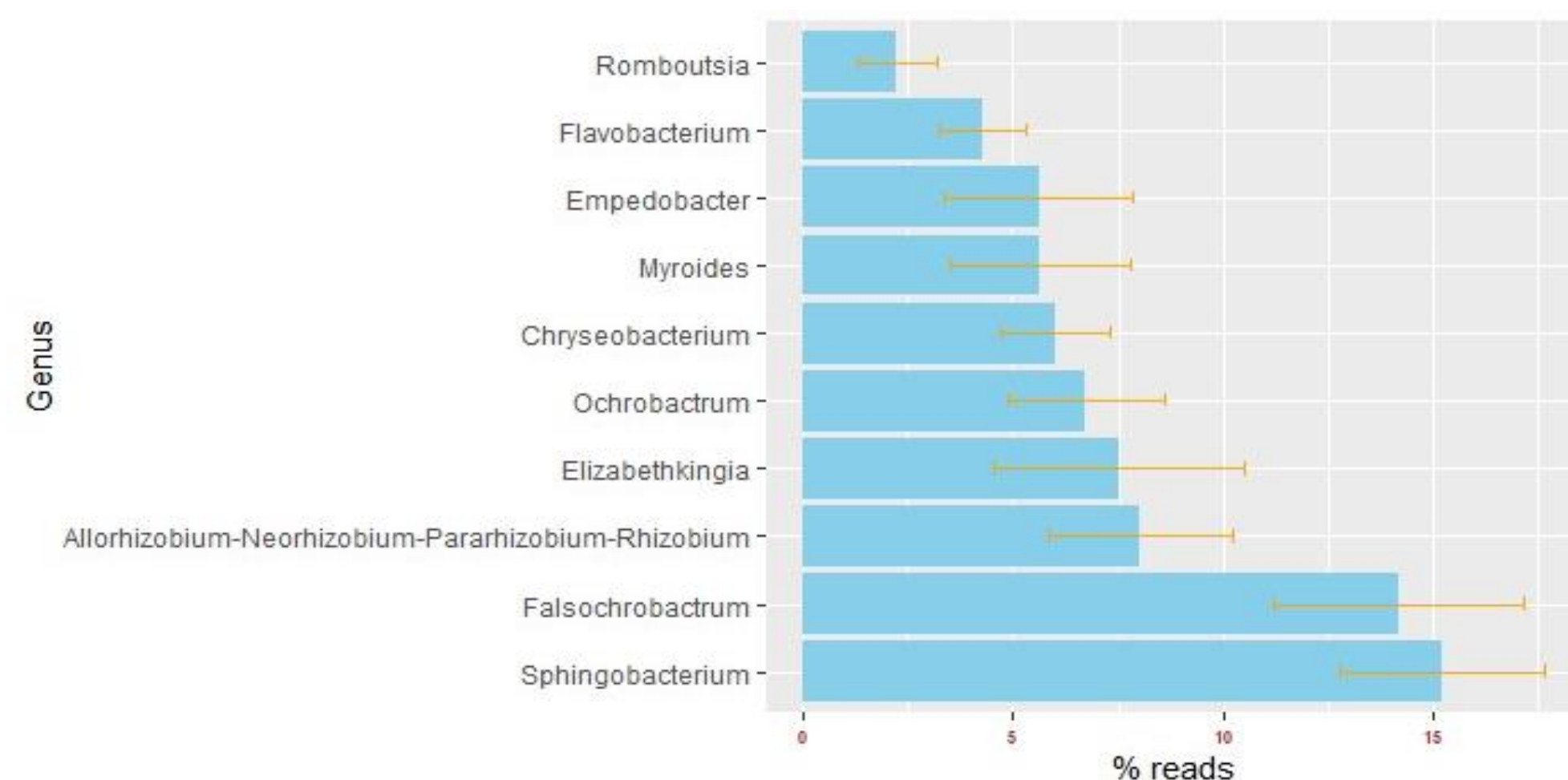


Fig 3: Bacterial genera in *D. vertebratus*

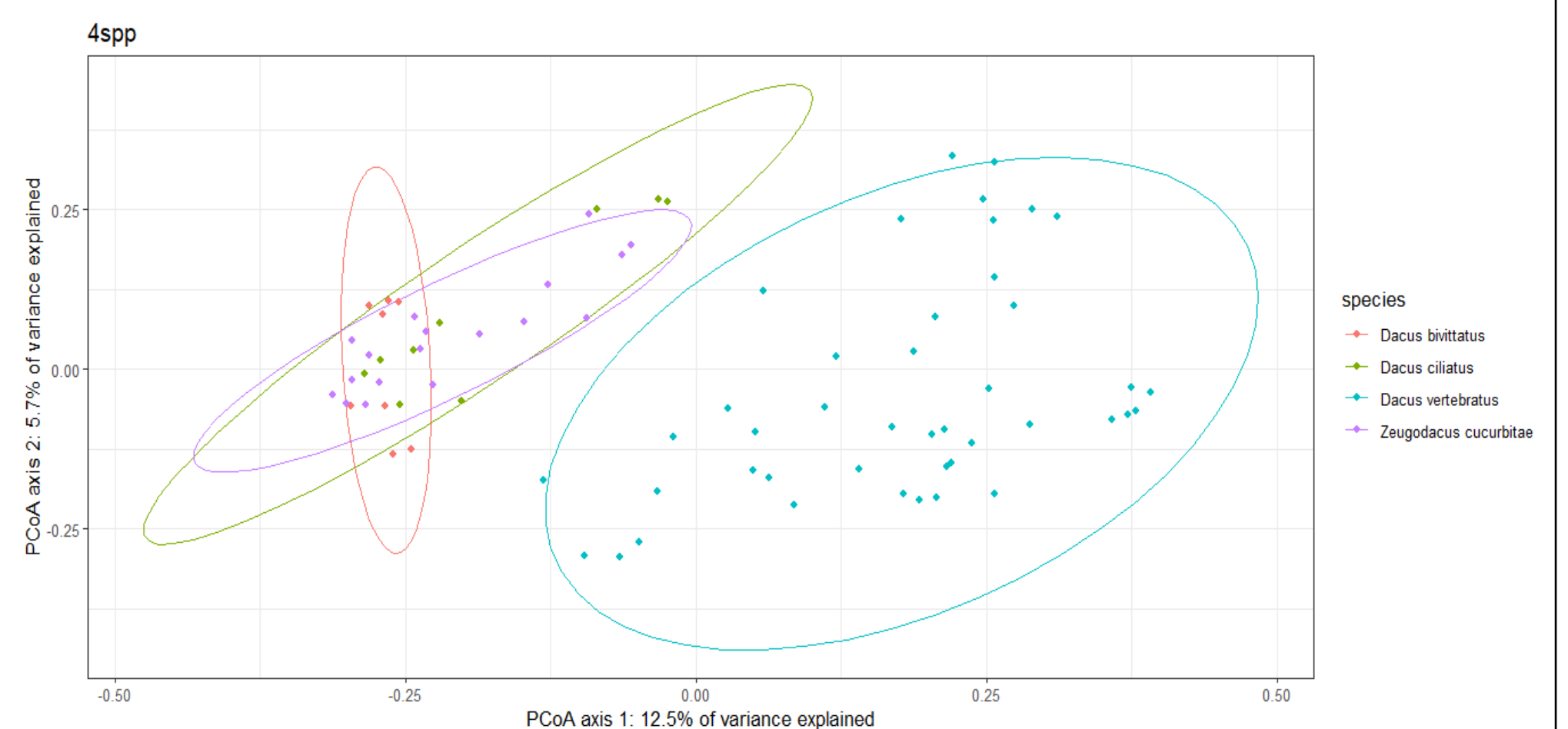


Fig 4: Relationship between *D. vertebratus* and fruit flies from Morogoro region

Conclusion

This study marks the initial step to more studies on *D. vertebratus* microbial communities. These data will contribute to a better understanding of the drivers of microbial diversity in cucurbit-feeding Tephritidae and, in the longer term, the development of microbial approaches to insect pest management.

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