



Correlation of microflora with the presence of dengue virus in *Aedes aegypti* and *Aedes albopictus* in endemic areas of Panama

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BACKGROUND

The association of insects with disease and pestilence has been recognized as the critical point to develop control strategies.

Aedes aegypti and *Aedes albopictus* are the main vectors of dengue virus. The close relationship between bacteria in the mosquito midgut with the immune response against pathogens has been studied and described in a few mosquito vectors.

In addition, microbes have been recognized to play an important role in limiting dengue virus infection in mosquitoes.

AIM

This project aims at taking advantage of the antagonistic effect of bacteria on dengue virus infection by assessing the correlation between bacterial diversity in *Ae. Aegypti* and *Ae. albopictus* and dengue virus infection through time and geographical localization.

METHODS

Mosquitoes were collected in 3 dengue-endemic areas of Panama: Rio Abajo, San Miguelito, and Chiriquí. For the isolation and characterization of bacteria from mosquito guts, at least 10 mosquitoes per site were pulled. Primers for 16s RNA gene were used for PCR and sequencing. RNA was extracted from individual mosquito heads and subjected to RT-PCR and RFLP for specific dengue virus serotype identification.

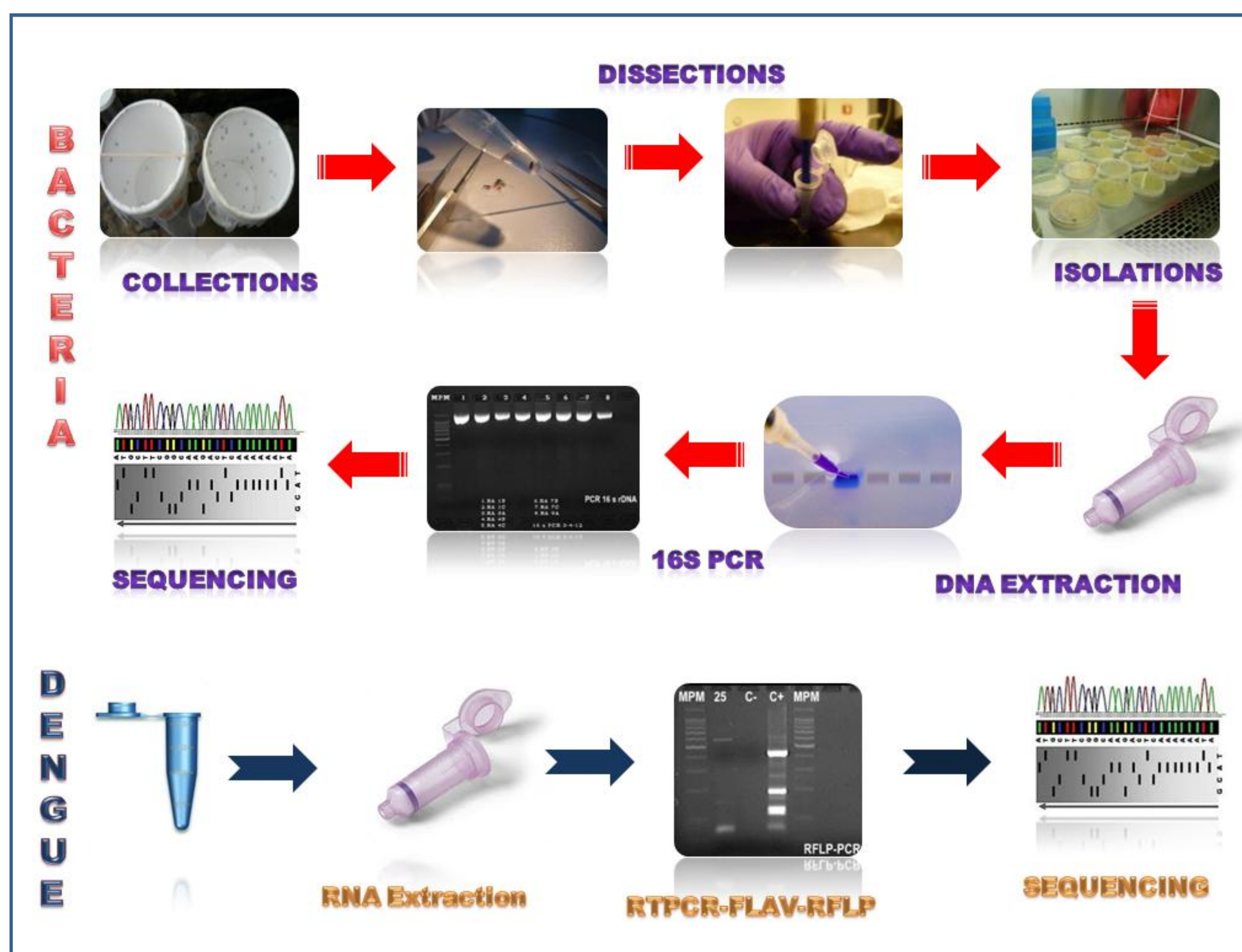


Fig. 1. Lab Workflow for the isolation and characterization of bacteria and dengue virus from field-collected mosquitoes

RESULTS

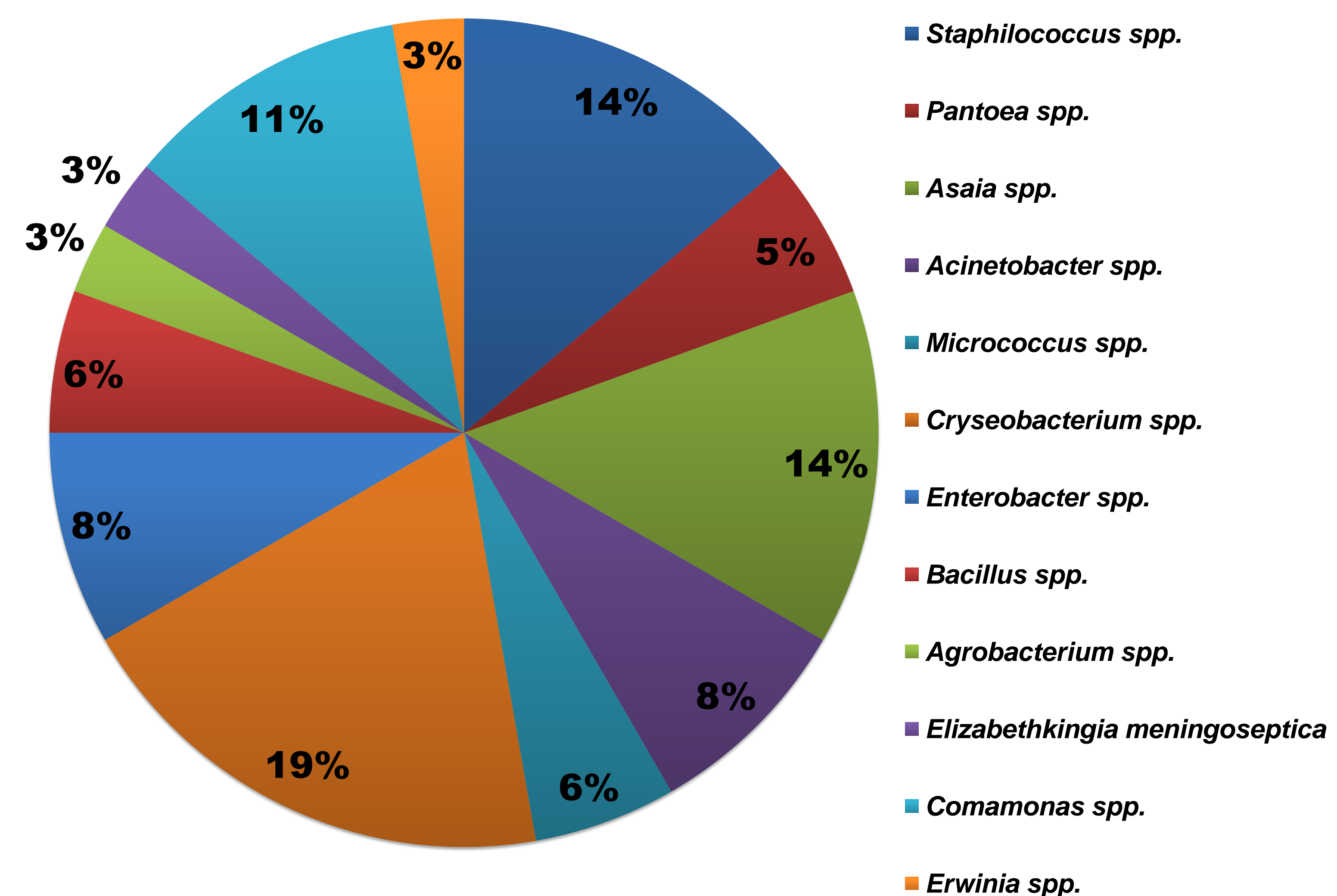


Fig. 2. Genera composition of bacteria isolated from the gut of field-collected mosquitoes.

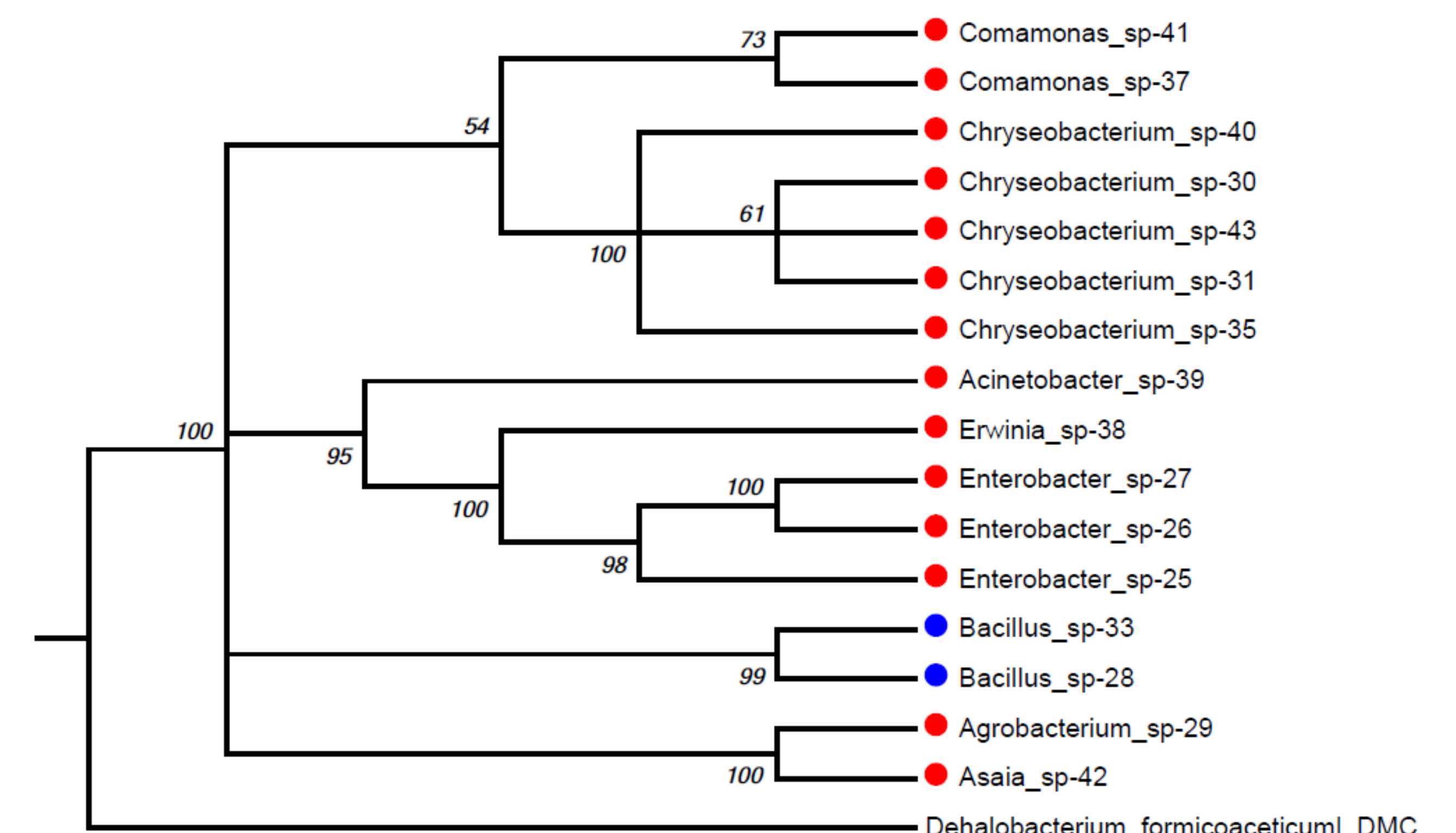


Fig. 3. Phylogenetic tree of bacterial strains isolated from the mosquito gut (red dot: Gram (-) bacteria; blue dot : Gram (+) bacteria)

CONCLUSION

Studying the vector biology of the mosquito is key for a better interpretation and understanding of dengue epidemiology.

Here we present a preliminary survey of bacteria from the gut of field-collected *Ae. aegypti* and *Ae. albopictus* from regions with reported dengue fever and dengue hemorrhagic fever. Our preliminary results show a diverse mosquito microbiome that most likely influences dengue virus infection of the mosquito.

FUTURE WORK

We are currently conducting infection assays to assess the effect of the isolated bacteria on dengue infection of the mosquito midgut.

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