

BACTERIAL PROFILE OF THE BROWN DOG TICK *Rhipicephalus sanguineus* sensu lato COLLECTED FROM STRAY AND DOMESTIC DOGS IN NORTHERN MEXICO

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INTRODUCTION

Ticks are obligate hematophagous ectoparasites that parasitize a wide number of animal species in all their life stages, including domestic animals that live closely with humans such as dogs and cats (Saleh et al., 2021). Pathogens of medical and veterinary importance have been detected in the brown dog tick, such as *E. canis*, *E. ewingi*, *E. chaffeensis*, *Borrelia burgdorferi*, *Coxiella burnetii*, *Anaplasma platys*, *Anaplasma phagocytophilum*, and *Rickettsia rickettsii* (Alieva et al., 2020), being *R. sanguineus* s.l. the main vector (Pieracci et al., 2019). In the case of the Comarca Lagunera, TBDs are a recurring problem, and some diseases are considered endemic in the region (Castillo-Martínez et al., 2015).

MATERIALS AND METHODS

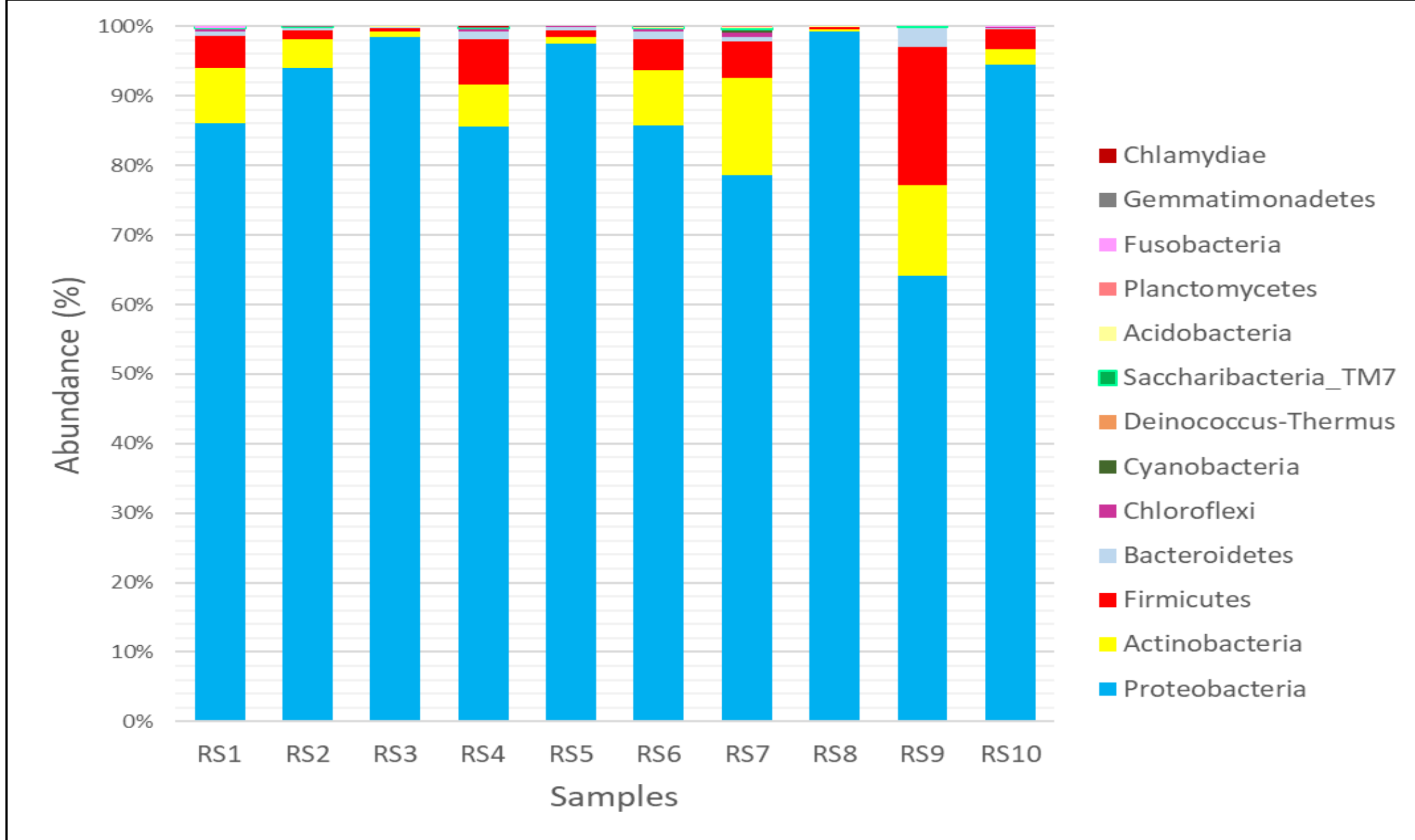
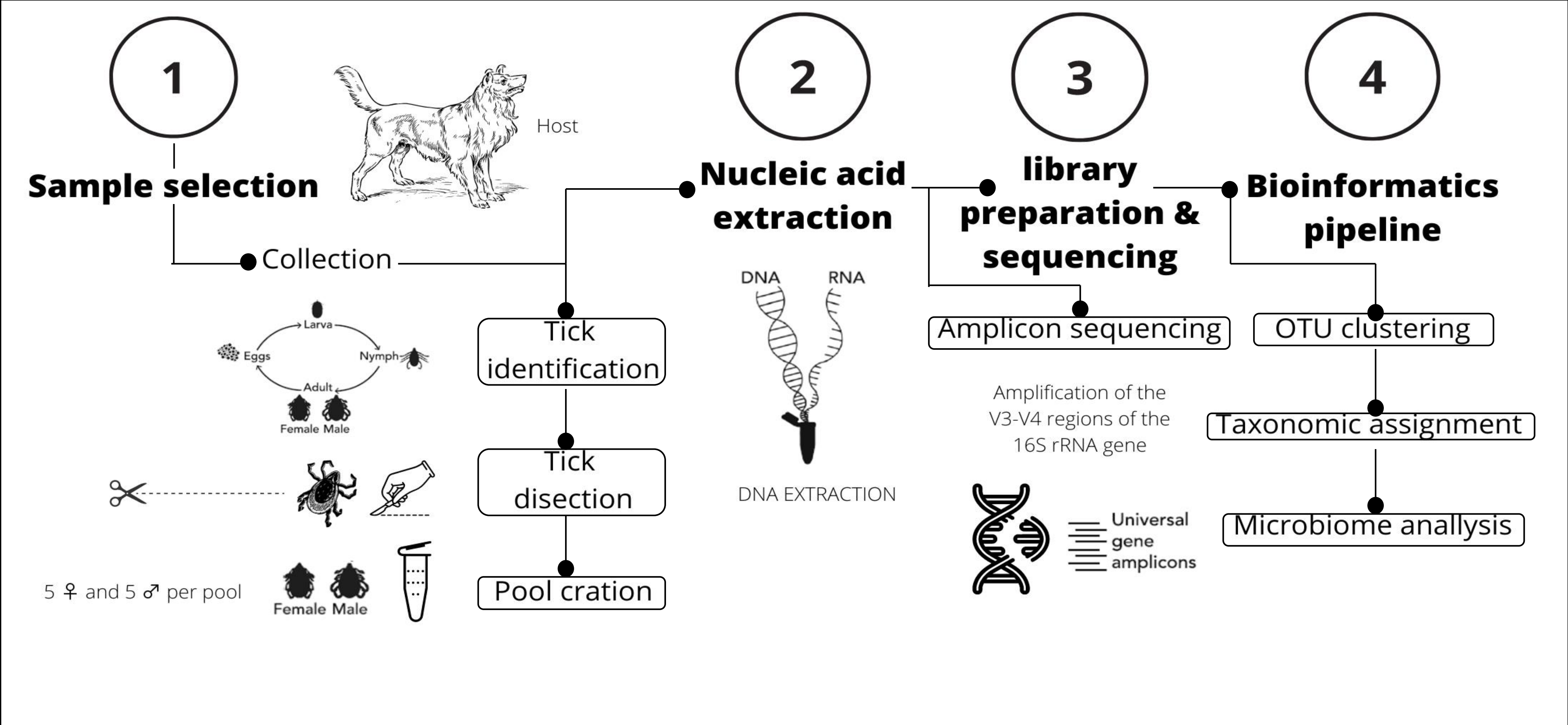


Figure 1. Relative abundance (%) at the phylum level of 10 pools of the internal content of *R. sanguineus* s. l. collected from domestic and stray dogs in the Comarca Lagunera, northern Mexico. Only the first 13 taxa are shown.

RESULTS AND DISCUSSION

The most abundant phyla was Proteobacteria (mean= 88.36; Fig. 1). At the family level, the most abundant taxa were Coxiellaceae (mean= 66.17%), Moraxellaceae (mean= 9.54%), Anaplasmataceae (mean= 3.97%). The most abundant genera were *Coxiella* (mean= 66.16%), *Acinetobacter* (mean= 9.16%), *Ehrlichia* (mean= 3.97%), *Kocuria* (mean= 1.29%) and *Pseudomonas* (mean=1.10%; Fig. 2).

A total of 93 potentially pathogenic species were determined, among which seven are historically considered PTB: *Coxiella burnetii*, *Ehrlichia canis*, *Ehrlichia muris*, *Ehrlichia chaffeensis*, *Ehrlichia minasensis*, *Ehrlichia ewingii* and *Anaplasma platys* (Körner et al., 2021) in decreasing order of relative abundance.

The analyzes of the bacterial composition of ticks at their taxonomic levels were similar to those reported by other studies in different regions of the world (Van Wyk, 2019). *Coxiella* genus was the most abundant in the study with 66.16% on average, unlike other studies where the prevalence of *C. burnetii* has hovered between 5% and 10%. Other relevant TBP found in the present study were Rickettsiales, were the genus *Ehrlichia* was the third most abundant in ticks; *Ehrlichia canis*, *Ehrlichia muris*, *Ehrlichia chaffeensis*, *Ehrlichia minasensis*, *Ehrlichia ewingi* were found. *R. sanguineus* is the main vector of *E. canis* that causes monocytic ehrlichiosis (Groves et al., 1975). This demonstrates that *R. sanguineus* is a reservoir for a mixture of potentially pathogenic ehrlichiosis species and that the 16s rRNA gene-based NGS technique is very effective for analyzing TBD in epidemiological studies. An important finding was *E. minasensis* in the microbiota of *R. sanguineus*. Being a recently discovered species in Minas Gerais, Brazil by Cabezas-Cruz et al. (2016). To our knowledge, this represents the first report of *E. minasensis* in *R. sanguineus* worldwide and the first detection of the species in Mexico.

CONCLUSION

The results obtained contribute to previous studies where the region under study and Mexico in general are recognized as an endemic area of TBP, especially with regard to tick-borne rickettsial pathogens (TBR). On the other hand, it shows that NGS is ideal for the analysis of infections and monitoring of TBD as an epidemiological tool to assess the status of vector-borne zoonotic diseases.

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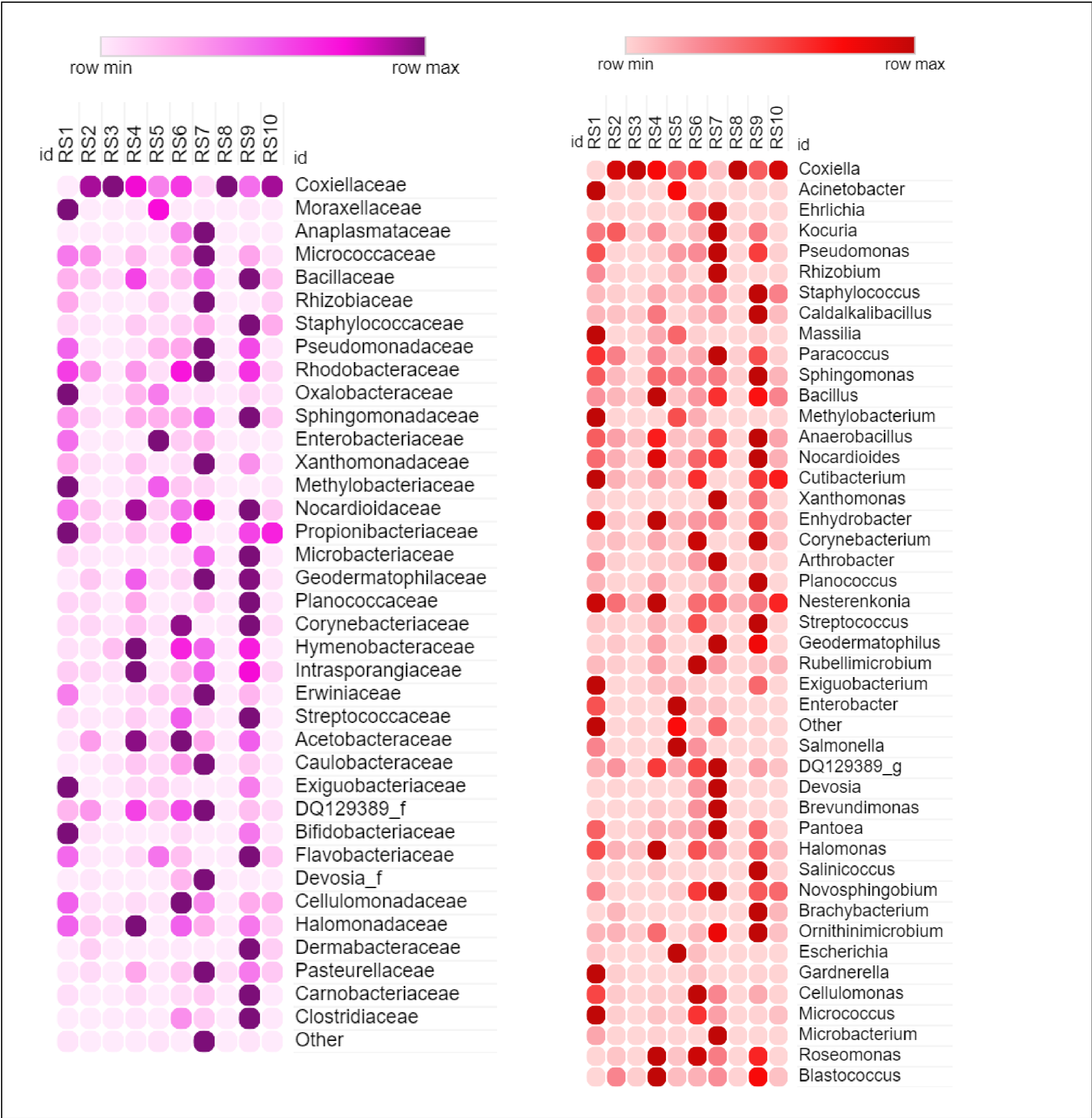


Figure 2. Heatmaps of relative abundance (%) at the family and genus level of 10 pools of the internal content of *R. sanguineus* s. l. collected from domestic and stray dogs in the Comarca Lagunera, northern Mexico. Only the first 45 taxa are shown.