The coevolution of Rickettsial endosymbionts and their tick vectors

## **Project Summary**

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The genus *Rickettsia* consists of gram-negative bacteria vectored by hematophagous arthropods (Salje et al. 2021). Out of the 1407 known human pathogens, at least 60% are known to have zoonotic origin (Jones et al. 2018). Every year, zoonotic diseases are responsible fro about 1 billion cases and millions of deaths worldwide (Karesh et al. 2012). Between 2004-2016 a total of 491,671 cases of tick-borne diseases were reported in the United States, which is about 76.5% of all vector borne diseases (VBD) ((Karim et al. 2021).

The tick family Ixodidae is the most common vector for vector borne zoonotic diseases, transmitting 40% of emerging vector borne diseases, and are the primary vector of *Rickettsia* (Swei et al. 2020). In addition to the transmission of pathogenic *Rickettsia*, ticks also harbor beneficial species. *Rickettsia monacensis* strain Humboldt, an endosymbiont to Ixodes pacificus was found to have a 100% prevalence, a transmission of efficiency of 100% for both transstadial and transovarial, as well as participate in nutrition based symbiosis with its host (Bodnar et al. 2018; Bodnar et al. 2020). Other endosymbionts have been documented in other tick species including *Ixodes lividus* (*Rickettsia vini*) and *Dermacentor andersoni* (Rickettsia peakcockii) (Simser et al. 2001; Nováková et al. 2018).

Coinfections of pathogenic *Rickettsia* and endosymbionts for ticks may impact the success of pathogen transmission (Paddock et al. 2022). The close association between tick species and their endosymbionts implies the need for codependence. The development of such relationships may reveal the existence of a evolutionary relationship between ticks and certain species of *Rickettsia*.

Using the *ompA*, *gltA*, and or the *16s* rRNA genes I will conduct a phylogenetic analysis of Rickettsial endosymbionts. For the different tick's species, I will conduct a phylogenetic analysis using the *16s* rRNA mitochondrial gene. After tree construction, a comparison of both trees may reveal the coevolutionary history between tick species and their endosymbionts.

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