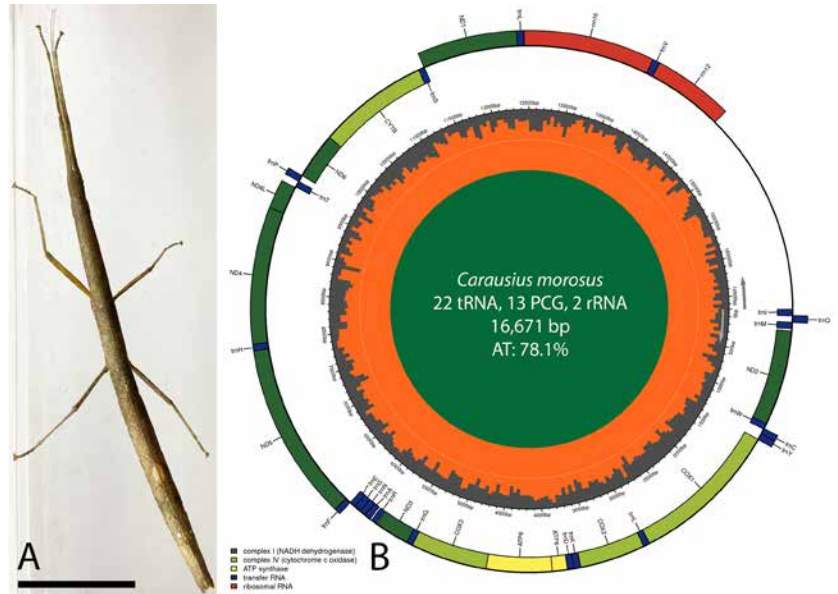


Complete mitochondrial genome of the introduced Indian walking stick *Carausius morosus* (Lonchodidae, Insecta) from California

Mentor: Dr. Jeffrey R. Hughey

ONLINE STUDENTS:

Mariana Aguirre Linares, Taym Al-Zuhairi, Yareli Alfaro Maldonado, Layla Alvarez, Elizabeth Anguiano, Hailey B. Nava, Christian B. Trujillo, Mateo Brambila, Javier C. Diaz, Flavio C. Mora, Gladys Cabrera Luis, Aniyah Chambers, Pearl Chenevert, Aiden Clarke, Caitlin Collins, Audri Contreras, Benny Cuevas, Emily D. Alcaraz, Jenny Do, Soledad Duran, Lacey E. Prescott, Angelica G. Fernandez, Roberto Garcia Velazquez, Mariah I. Marquez-Gonzalez, Maria J. Velasquez-Moreno, Mia J. Windham Cortes, Konnor L. Barrett, Claudia L. Dominguez-Trejo, Steven L. Meza, Phoebe Lewis, Jessica Lopez, Victor M. Padilla, Andres Mandujano, Lizbet Merino Juarez, Henry N. Huynh, Eduardo Pantoja-Garcia, Michael Perez, Felipe Rodriguez, Juan Pablo Rodriguez Cortes, Jesus Rosas, Areli Ruiz Nunez, Jeriel S. Sevilla, Samantha Santos, Stephanie Solis, Froylan Tinoco Rivera, Alice Trujillo, Natalie Trujillo, Maximiliano Villa, Reema Y. Mubarz



Carausius morosus, the Indian walking stick, is a large polyphagous species originally described from specimens from Shembagonor and Trichinopoly, Madura Province, southern India. It was introduced to Australia, Azores, Madagascar, Madeira, South Africa, United Kingdom, and United States, likely due to the escaping of captive *C. morosus* and the accidental discarding of eggs. *Carausius morosus* was first reported from San Diego county, California in 1991 and has since spread to ten counties where it is a pest on ornamental plants. Here, we analyzed the complete mitochondrial genome of *C. morosus* from Salinas, California. The mitochondrial genome of is circular, AT rich (78.1%), and 16,671 bp in length. It consists of 13 protein-coding, 22 transfer RNA, and 2 ribosomal RNA genes and is identical in gene content to *Carausius* sp. from China. These data contribute to the bioinformatics of *C. morosus* and future studies on the phylogenomics of Phasmatodea.

†All authors contributed equally to the analysis and writing of this paper. Author order was determined alphabetically. – Research mentor, Jeffery R. Hughey.

