

## Spatial variability of bacterial assemblages associated with the pinon cone beetle *Conophthorus edulis* (Curculionidae: Scolytinae)

Kevin F. Salazar<sup>1</sup>, Rosa María Pineda-Mendoza<sup>1</sup>, Flor N. Rivera-Orduña<sup>2</sup>, Gerardo  
Zúñiga<sup>1</sup>

<sup>1</sup>Instituto Politécnico Nacional, Escuela Nacional de Ciencias Biológicas, Departamento de  
Zoología-Laboratorio de Variación Biológica y Evolución. <sup>2</sup>Departamento de Microbiología-  
Laboratorio de Ecología microbiana. Prolongación de Carpio y Plan de Ayala, Casco de Santo  
Tomás, Miguel Hidalgo, 11340, CDMX, México.  
E-mail: ksalazaro0900@alumno.ipn.mx

Beetles of the genus *Conophthorus* attack the cones of the pinyon pine *Pinus cembroides*, causing significant economic losses, since the pinyon pine is a human food resource. Their distribution is in patches ranging from Arizona in the United States to central Mexico. The composition of the microbial communities associated with the bark beetles *Dendroctonus* and *Ips* is known; however, it has not been explored in *C. edulis*, making this study pioneering in this field. In the present study, the composition of the bacterial assemblages associated with *C. edulis* in localities in central Mexico was determined, persistent and dominant taxa were identified, as well as the geographic impact on the composition of the assemblages, and insect-bacterial association patterns were inferred. Cones infected by *C. edulis* were collected from different localities in Querétaro, Guanajuato, and Hidalgo. The V3-V4 region of 16S rRNA was sequenced by Illumina technology and bioinformatics analysis was done in QIIME2 and R package. The results showed that the dominant phyla were Pseudomonadota, Bacillota, and Bacteroidota. A core bacteriome composed of *Chryseobacterium*, *Anoxybacillus*, *Pedobacter*, *Sphingomonas*, *Rickettsia*, *Stenotrophomonas*, *Sphingobacterium*, and *Pseudomonas* was identified. No significant differences were found in the composition of the bacterial assemblages (measured by beta diversity and FAVA index;  $p > 0.05$ ), indicating that the assemblages are similar across geographic areas. Dirichlet mixture modeling (DMM) suggests that the assembly is influenced by *Pseudomonas*, *Sphingobacterium*, *Stenotrophomonas*, *Rickettsia*, and *Chryseobacterium*. The bipartite network showed high nestedness, connectance, and robustness at both levels, and an intermediate specialization value (NODF = 78.4, C = 0.84, RHL = 0.84, RLL = 0.93, and  $H'2 = 0.41$ , respectively), indicating that abundant bacterial genera have a close association pattern with the insect, suggesting potential specialization. The results obtained show that the bacterial composition is homogeneous across different geographic locations in central Mexico, suggesting a stable association pattern between the insect and abundant bacterial genera and the probable specialization of the core bacteriome. These results allow a better understanding of the ecological dynamics between bacterial communities and the insect *C. edulis* and provide knowledge for developing strategies to mitigate the pest status of this insect in Mexico.