

1 **Reconstruction of *Drosophila* Symbiotic Bacterial Genomes Using**  
2 **Metagenomic Data**

3

4 María Alejandra Ulloa<sup>1-2</sup>, Laura Carolina Camelo Valera<sup>1-2</sup>, Alejandro Reyes<sup>1-2</sup>,  
5 Angela Viviana Peña.

6

7 <sup>1</sup> Department of Biological Sciences, Universidad de los Andes, Bogotá, Colombia

8 <sup>2</sup> Max Planck Tandem Group in Computational Biology, Universidad de los Andes,  
9 Bogotá, Colombia

10

11 **Abstract**

12 The reconstruction of complete high-quality genomes from metagenomic data has  
13 been one of the great advances brought by new bioinformatics tools. *Drosophila* is  
14 emerging as a valuable model for studying the microbiota-host interaction, so  
15 knowing and understanding the composition of its microbiota is relevant. This project  
16 used metagenomic data taken from twenty-four different species of *Drosophila* to  
17 reconstruct complete high-quality bacterial genomes with the purpose of determining  
18 how accurate they were to represent the complexity and diversity of *Drosophila*  
19 endosymbiont communities. To do this, we followed a bioinformatic workflow that  
20 integrated various assembly and binning strategies that made it possible to recover  
21 more than sixty high-quality genomes of the most abundant taxa like  
22 *Acetobacteraceae* and *Morganellaceae*, families that were widely noted, among  
23 others. In conclusion, we sustain that the *Drosophila* microbiota is taxonomically  
24 restricted as has been discussed in previous works and raise the possibility for future  
25 projects to perform phylogenomic analyzes with the reconstructed genomes.

26