

Relationship Ancestor Descendants of Stingless Bees

Vargas Romero J.M.¹, Luna Rodríguez L.^{1*}, Losada Custardoy H.R.¹, Cortes Zorrilla J.¹, Alemán López V.¹, Vieyra Durán J.E.¹, Pérez Martínez S.², Chico Jiménez L.², Landeros Díaz L.A.³

¹Departamento de Biología de la Reproducción, Universidad Autónoma Metropolitana, Unidad Iztapalapa

²Lic. en Producción Animal, Universidad Autónoma Metropolitana, Unidad Iztapalapa

³Lic. en Biología, Universidad Autónoma Metropolitana, Unidad Iztapalapa

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*Corresponding author: Luna Rodríguez L.

Departamento de Biología de la Reproducción, Universidad Autónoma Metropolitana, Unidad Iztapalapa

Abstract

Stingless bees are a group of eusocial insects, they inhabit tropical and subtropical areas of the world and approximately 500 species are reported. In the pre-Hispanic era in Mesoamerica, vestiges of meliponiculture are reported; the relationship between the people of the civilizations of this time and the stingless bees had an important value in social, economic, and religious aspects. The objective of this study was to perform an ancestor-descendant bioinformatic analysis with molecular data (mtDNA) of the Meliponines. Nucleotide sequences of the COI-COII fragments of mtDNA were obtained from the Nucleotide sequence database at the National Center for Biotechnology Information (NCBI), using the search and Entrez functions. The fragments the sequences were aligned with cluster and then a phylogenetic analysis of the native bee species reported for Mexico in the NCBI was carried out. Based on the COI-COII mtDNA fragments, it was possible to build a phylogenetic tree, finding evolutionary relationships between the species, allowing to demonstrate that species of the Meliponini Tribe diverge from a more recent common ancestor to a less recent one.

Keywords: Meliponini, bioinformatics, phylogenetics, tribe, relationships, species.

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INTRODUCTION

In the world there are approximately 20,000 species of bees (Gennari, 2019; Martínez, *et al.*, 2014) and according to their behaviour we could differentiate three main groups of bees: solitary, parasites, and social; in the latter is the Meliponini tribe, they are commonly known as stingless bees, they live in tropical and subtropics areas of the world and approximately 500 species are reported (Real *et al.*, 2022). In the American continent (Mexico, Central America, and South America) there are data on the use of these species in the prehispanic era and vestiges of meliponiculture have been documented. The place of greatest roots and development was in the region called Mesoamerica (southern half of Mexico, the territories of Guatemala, El Salvador, and Belize, as well as western Honduras, Nicaragua, and Costa Rica) (Arnold *et al.*, 2018), the relationship between the people of the civilizations of this era and the stingless bees had an important value in social, economic, and religious

aspects (Vásquez *et al.*, 2021). The identification of species has been carried out using: a dichotomous key and morphometric indicators (Figueroa *et al.*, 2016), although they classify species efficiently, they have limitations. Due to the above the molecular approach is considered the most appropriate.

In this context, international databases will make it possible to investigate the genetic sequences of the Meliponini tribe, the different genera and species are classified from the tribe. Therefore, the objective of this study was to perform an ancestor-descendant bioinformatic analysis with molecular data (mtDNA).

EXPERIMENTAL SECTION

A search of the Nucleotide sequence database at the National Center for Biotechnology Information (NCBI) <http://www.ncbi.nlm.nih.gov/BLAST/>, using the search and functions Entrez. The sequences were

nucleotides of COI-COII fragments of mitochondrial DNA from different species of native bees.

Subsequently, a sample of those species reported in our country was obtained and a data crossing was carried out, for the selection of the sequences that were used for the phylogenetic analysis of the native bee species reported in the database for Mexico.

Each selected sequence was entered into a MEGA program file (v.4.0), along with a sequence out of group. Then, the alignment of the sequences was carried out with the ClustalW included in the MEGA program (v.4.0).

For the phylogenetic tree construction, the discrete method of maximum parsimony with 5,000 repetitions bootstrap was used.

RESULTS AND DISCUSSION

Phylogeny is the determination throughout evolutionary history in which groups of related organisms they have a common ancestor. The phylogeny of the group of species of the Meliponini Tribe, in various studies has been have used data derived primarily from morphology and comparative anatomy, and from the sequences of the genes to reconstruct ancestor-descendant relationships.

The phylogeny or graphic representation of the evolutionary history of a group of organisms of the Meliponini tribe is shown in Figure 1. This pattern of

relationships is reconstructed as a phylogeny, using homologous characters or homology, which is a key concept in evolution and in the recreation of relationships between species, since only it adequately reflects the common ancestry of organisms.

The phylogenetics of the Meliponini Tribe was investigated by cluster alignment (González *et al.*, 2016) of nucleotides based on fragments of the COI-COII mtDNA sequences extracted from the NCBI, the phylogenetic tree was built in which *Apis mellifera* was found to be outside the Meliponini group (they have a common ancestor less recent).

Stingless bees are found to be decreasingly related based on nest building, starting by *Scaptotrigona hellwegeri*, to the other end of the taxon *Melipona becheii*.

The species of *Scaptotrigona* more related to *Plebeia frontalis* having an ancestor in common. The species *Lestrimelitta* derived from a node of the previous group, are further away from the species of *Scaptotrigona*, they have a less recent ancestor. *Friesseomelitta nigra* and *Trigona fulviventris* are closer because they converge from a more recent common ancestor. *Partamona bilineata* derivates from common ancestors of the above species groups analogous to *Lestrimellita*. *Melipona collimana* is found less related to *Partamona bilineata*, but more related to *Melipona fasciata* deriving from a most recent common ancestor.

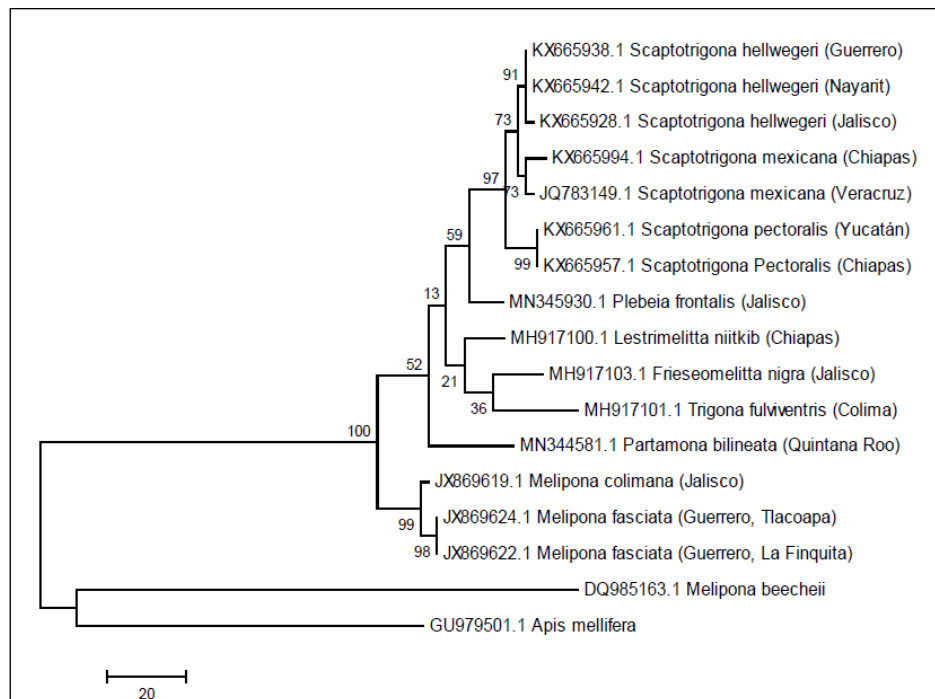


Figure 1: Phylogenetic tree of the species of the tribe Meliponini, based on the COI-COII fragments of mtDNA. The maximum parsimony method was used, with 5,000 replicates

CONCLUSION

Build a phylogenetic tree was possible based on the mtDNA COI-COII fragments, finding evolutionary relationships between species, allowing to demonstrate that species of the Meliponini Tribe diverge from a more recent common ancestor to a less recent one.

It allowed us to order the species in descending order *Scaptotrigona*, *Plebeia*, *Lestrimelitta*, *Frieseomelitta*, *Trigona*, *Partamona*, *Meliponas* and the species that is separated from the rest of the Meliponini Tribe is *Apis mellifera*.

With the mtDNA COI-COII tools, complement which species are far away, which species are from the Meliponini Tribe and close to its root (common ancestor).

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CONFLICTS OF INTEREST

The authors declare no conflict of interest.

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