

Genetic diversity reveals a complex evolutionary history for the white-fringed weevils (Coleoptera, Curculionidae)

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INTRODUCTION & AIM

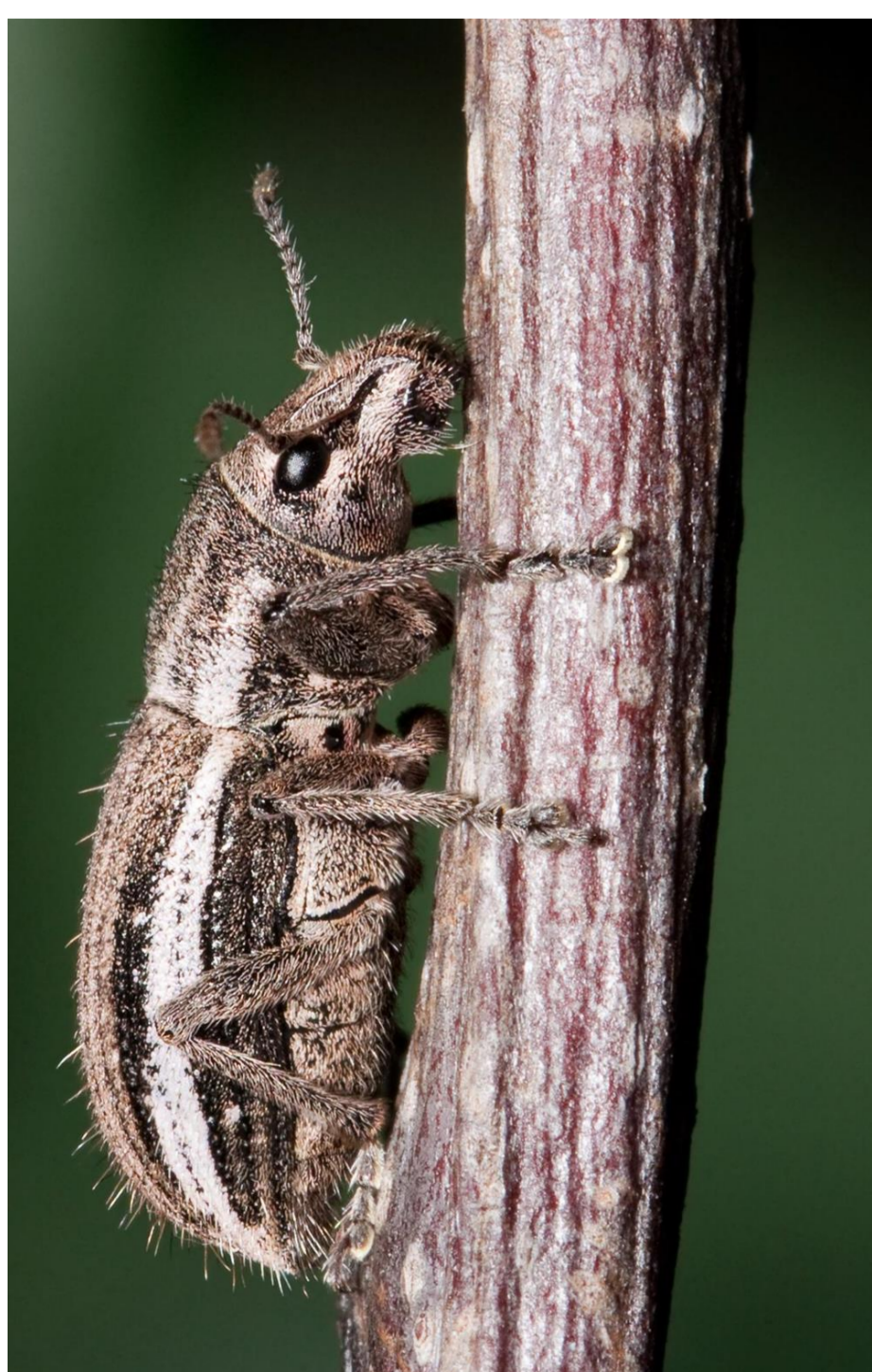
- The closely related Naupactini species *Naupactus leucoloma*, *Naupactus peregrinus* and *Naupactus minor*, known as "white-fringed weevils," form the monophyletic "leucoloma group."
- Naupactus leucoloma* and *N. peregrinus* reproduce via parthenogenesis, with males occasionally observed, while *N. minor* shows no evidence of sexual reproduction.
- These species overlap geographically in the Argentinean Mesopotamia. This, the intermediate morphology of *N. minor* between the other two and the absence of males led to postulation of the hybrid origin of this



Recently, after several decades, males have been found that could belong to *N. leucoloma* or *N. minor*.

- The aim of the present work is to unravel the evolutionary history of the white fringed weevils and to identify the taxonomic status of these elusive males.

METHOD

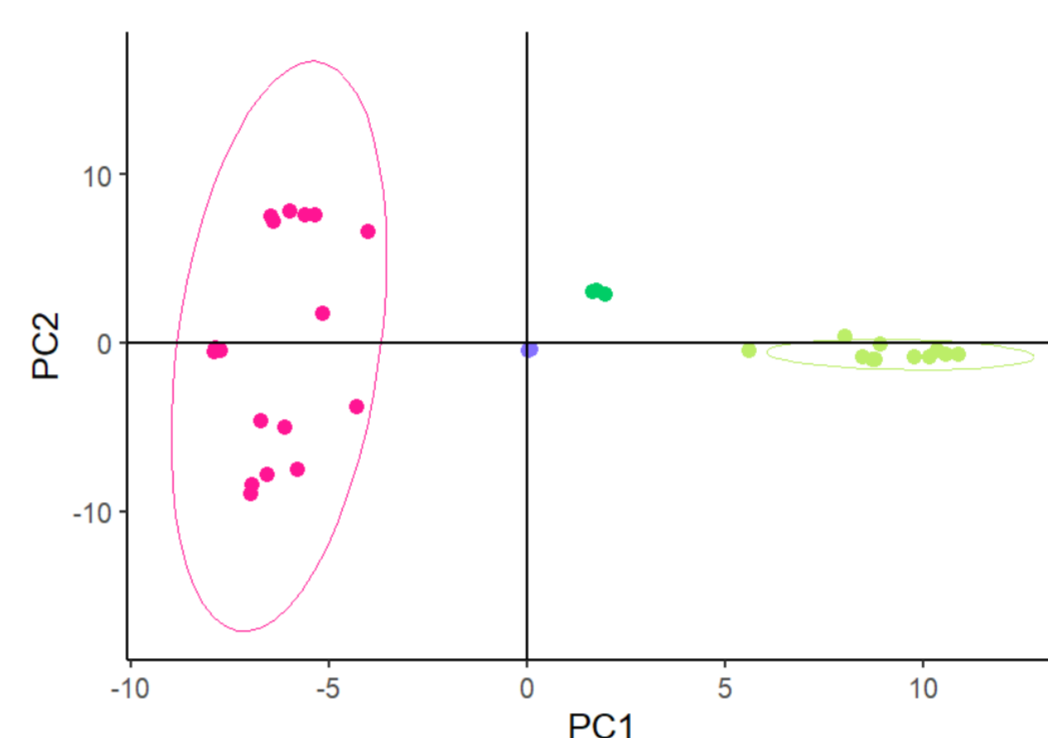


Individuals from the species of the leucoloma group were sampled in several localities from Northeastern and Central Argentina. In addition, *N. leucoloma* samples from Australia and Chile were included.

Three datasets were obtained: mitochondrial (COI) and nuclear (ITS1) DNA sequences and SNPs (acquired through the dd-RAD-Seq method)

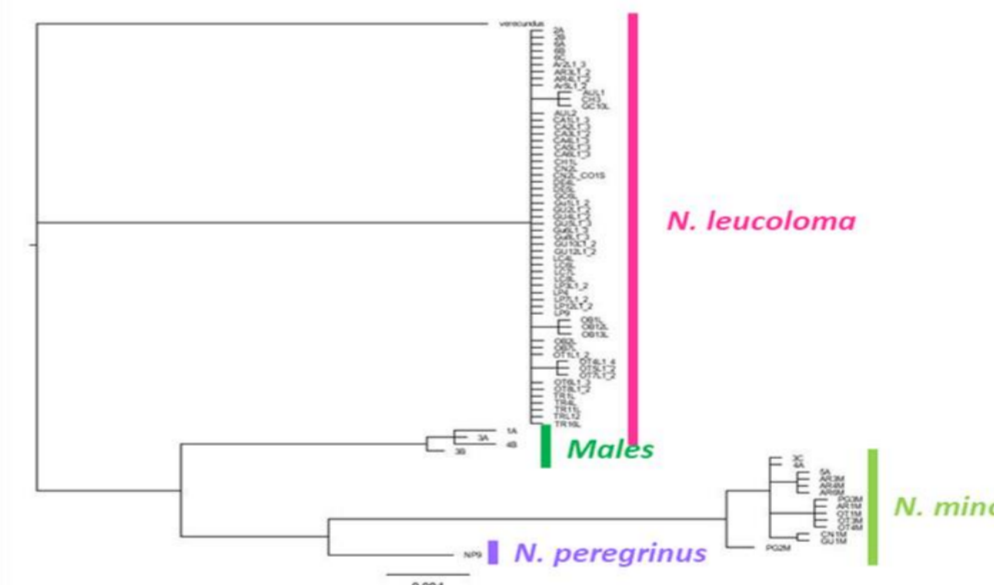
Programs like MrBayes, Stacks, Aegenet, Tree Mix And SplitsTree were employed to analyze the three datasets with a variety of analytical tools

RESULTS & DISCUSSION

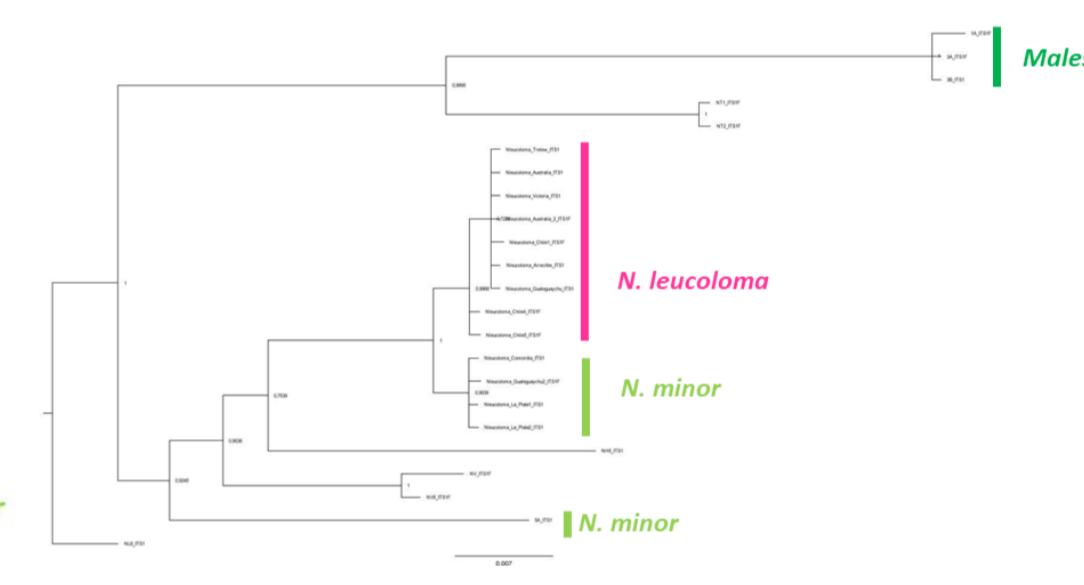


Principal Components Analysis reveal four separate groups within the leucoloma group: *N. leucoloma*, *N. minor*, *N. peregrinus*, and unknown males, which are intermediate between (*N. leucoloma* + *N. peregrinus*) and *N. minor*.

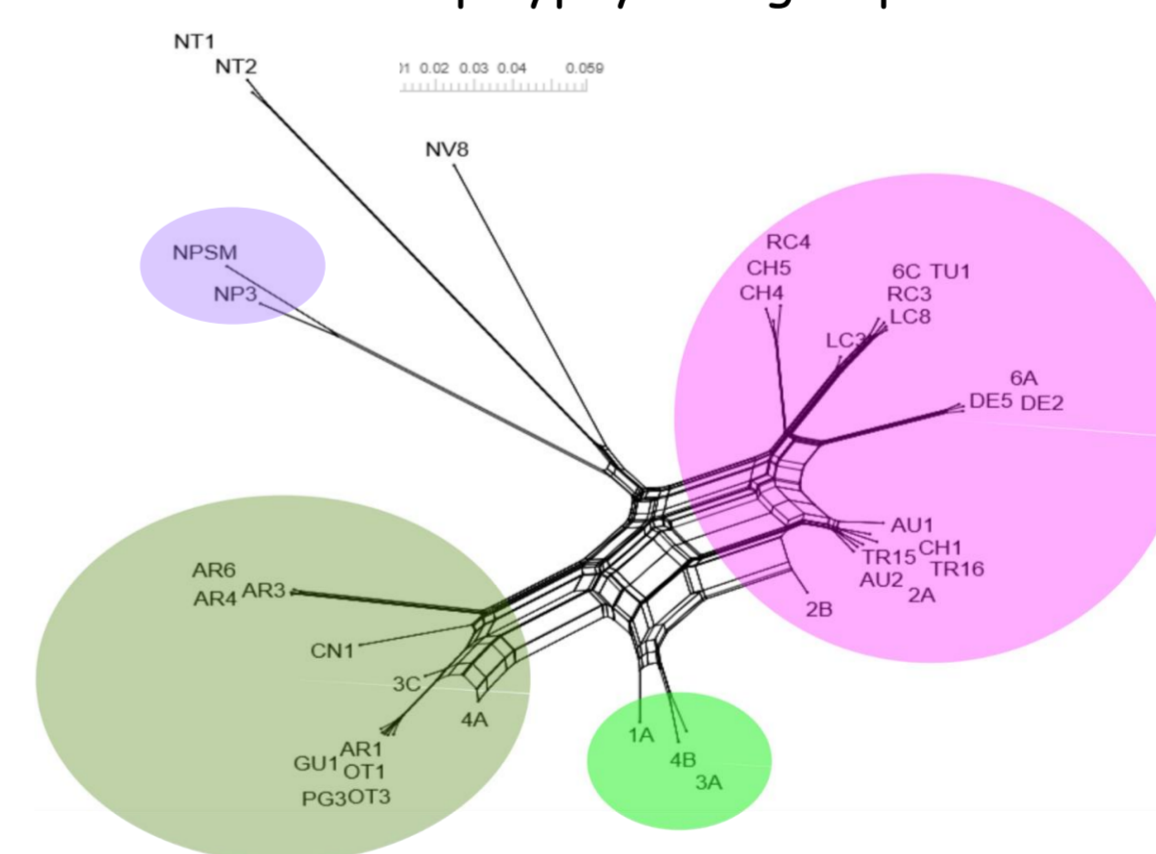
mtDNA



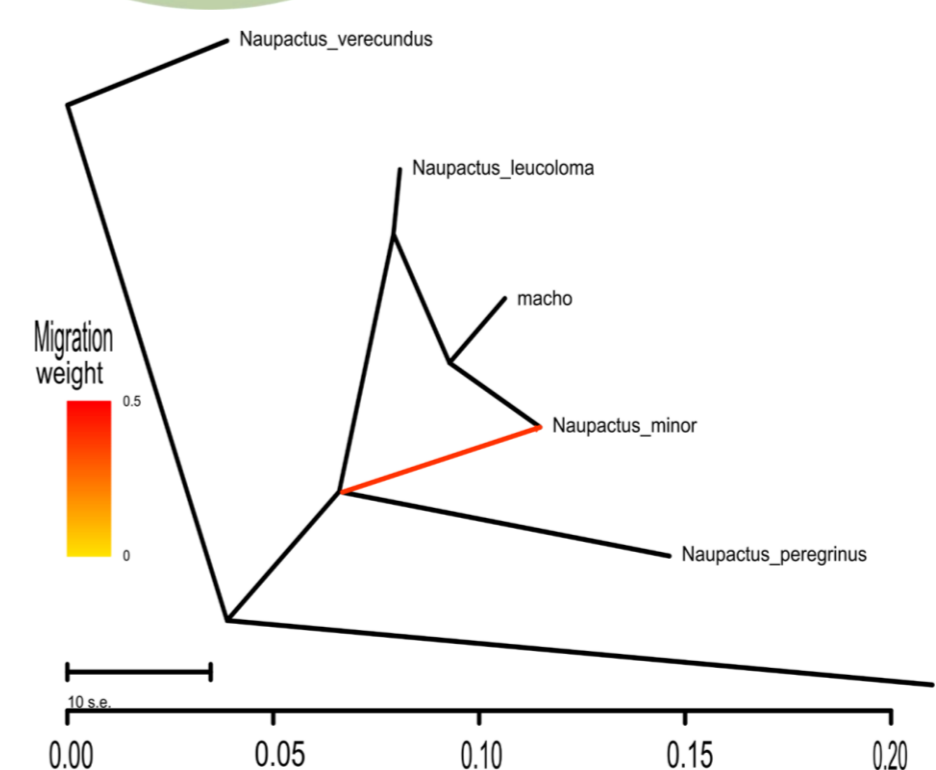
nDNA



Phylogenetic reconstructions based on mitochondrial and nuclear sequences, respectively suggest that unknown males conform a monophyletic group very divergent of any species of the leucoloma group. Strikingly, nuclear sequences reveal *N. minor* as a polyphyletic group.



The SplitsTree network based on ddRADseq data support the distinctiveness of the unknown males and suggests complex evolutionary history within the two parthenogenetic species, with several degrees of divergence and possibly occurrence of hybridization. The colors of the branches correspond to the same groups highlighted in previous figures



Maximum-likelihood tree inferred with treemix shows the most likely migration events, represented as arrows with color intensity corresponding to the migration weight (yellow, low migration to red, high migration).

CONCLUSION

The three datasets yielded consistent results regarding the number of evolutionary groups, indicating that the males of unknown specific status constitute an independent evolutionary unit. Most analyses pointed out possible hybridization within the group

Our results suggest a complex evolutionary history within this group of neotropical weevils.