Signals of hybridization in the Trimerotropis pallidipennis complex of andean grasshoppers

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INTRODUCTION & AIM

- This species complex presents challenges in species delimitation and shows signs of hybridization events.
- Climate change and Andean landscape fluctuations may have facilitated hybridization between these phylogenetically related species.
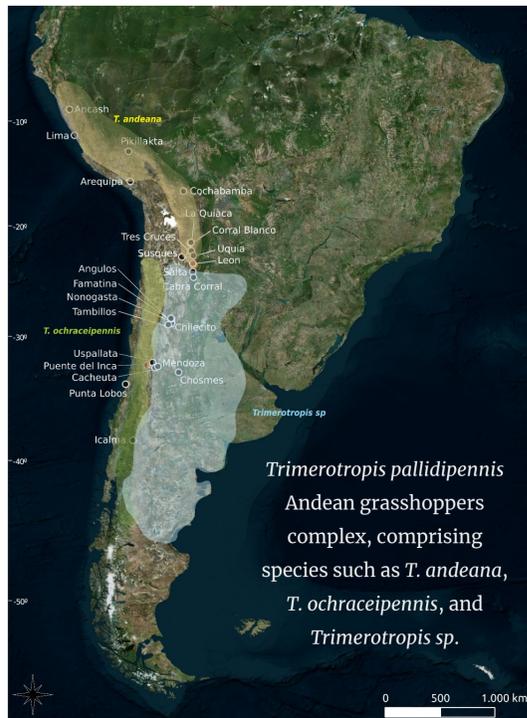
Trimerotropis pallidipennis Andean grasshoppers complex, comprising species such as *T. andeana*, *T. ochraceipennis*, and *Trimerotropis sp.*

Questions

Could the absence of clear morphological differentiation and the difficulty in delimiting species within this group suggest the presence of hybridization events facilitated by topological and climatic changes?
Can we estimate the proportion of genes inherited by hybrid nodes?

METHOD

➡ Individuals from various lineages in southern South America were analyzed using ddRAD-seq loci markers. (Baird *et al.* 2008).

➡ We employed te PhyloNetworks (Solís-Lemus *et al.* 2017), Treemix (Pickrell & Pritchard, 2012)., and fastsimcoal (Excoffier et al. 2013) programs were employed to detect hybridization events and estimate the proportion of genes inherited by hybrid nodes..

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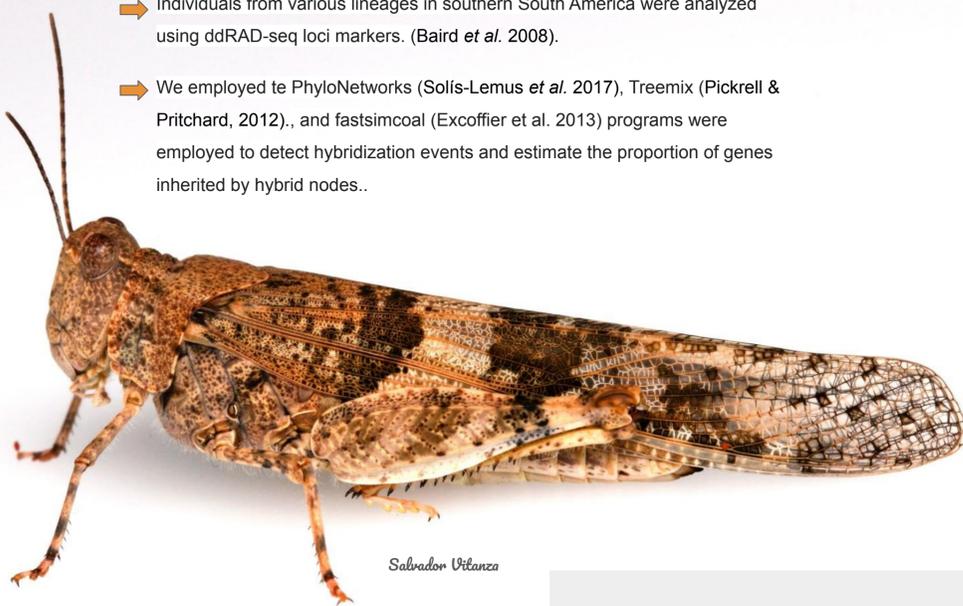
RESULTS & DISCUSSION
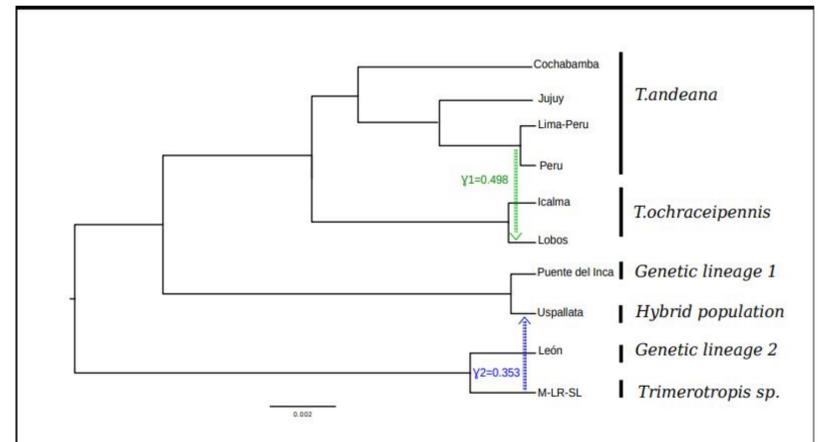
Figure1
Phylonetworks with different species and populations and two hybrid events. Inferred inheritance probabilities (γ_1 and γ_2) for each parent are shown on the phylonetworks tree.
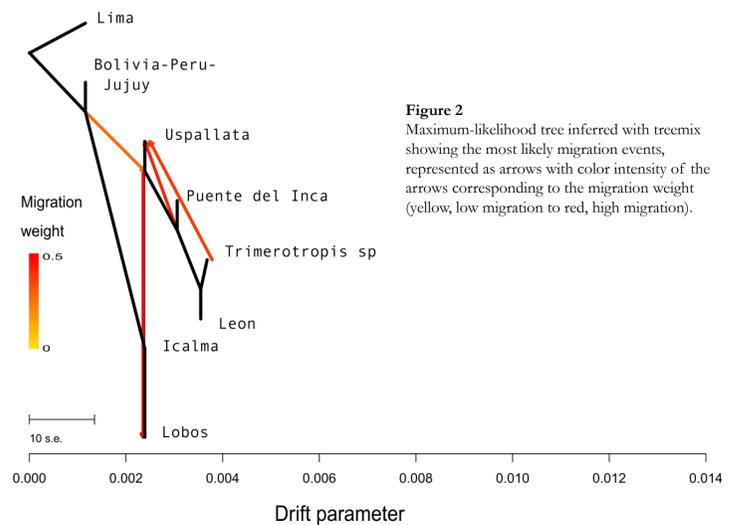
Figure 2
Maximum-likelihood tree inferred with treemix showing the most likely migration events, represented as arrows with color intensity of the arrows corresponding to the migration weight (yellow, low migration to red, high migration).
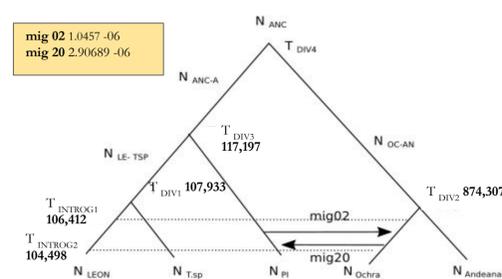
Figure 3
Demographic parameters inferred with fastsimcoal 2 for the most likely species divergence model.Timing of interspecific gene flow (T_{INTROG}) and of species split (T_{DIV}) is given in units of generations.

CONCLUSION

- The analysis revealed the presence of more than one **hybrid event** within this complex.
- This study contribute to understanding the mechanisms of speciation and adaptation in mountainous environments, with implications for conservation and biogeography in the Andean region.

FUTURE WORK / REFERENCES

Further investigation is required to better understand the dynamics and frequency of these events. In particular, additional analyses using *fastsimcoal* will allow us to explore demographic scenarios and estimate parameters such as gene flow and effective population sizes more accurately.

Baird, N. A.et al. (2008). Rapid SNP discovery and genetic mapping using sequenced RAD markers. *PLoS ONE*, 3(10), e3376. https://doi.org/10.1371/journal.pone.0003376
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