


Genomics reveal hybridization between deeply-diverging South American grasshopper species of the genus *Orotettix* (Orthoptera: Acrididae)

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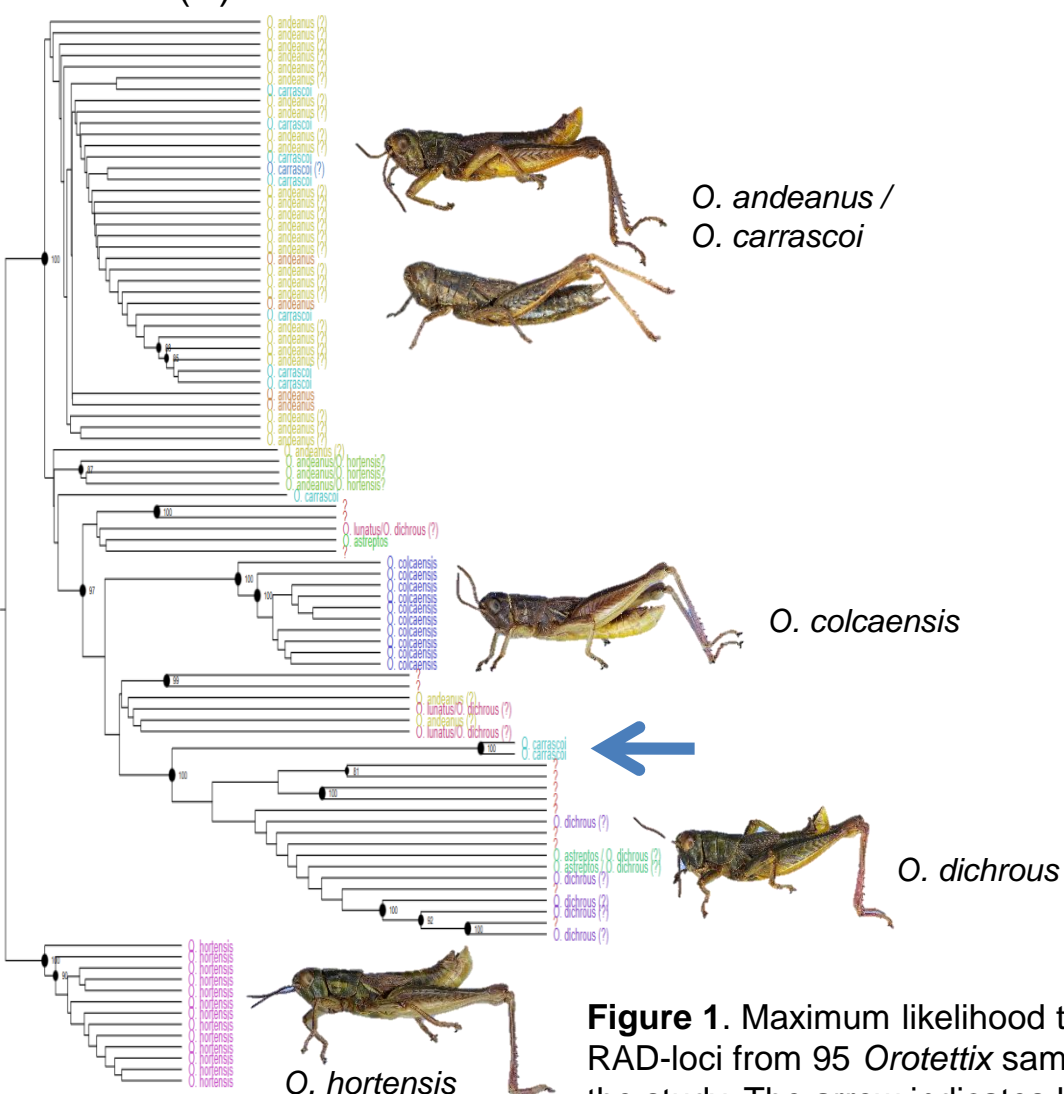
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INTRODUCTION & AIM

The Andes are among the world's most significant hotspots of species richness and have acted both as a barrier and a conduit for biotas with diverse geographic origins. The grasshopper genus *Orotettix*, with its ten species endemic to the Central Andes, offers a compelling opportunity to study diversification mechanisms. In this study, we performed the first genomic approach to analyze the phylogenetic relationships and the population structure of *Orotettix* species, to ultimately have an insight on the strength of species limits and the role altitude in speciation and adaptation.

METHOD

We conducted a RAD-Seq procedure to analyze 95 samples representing seven *Orotettix* species. We obtained a final matrix of 1239 RAD-loci (one SNP per locus) using the software STACKS (denovo_map.pl). A Maximum Likelihood phylogenetic analysis using IQ-TREE was performed, assessing statistical node supports with 1000 bootstrap pseudo replicates. A population analysis using STRUCTURE was also carried out, inferring the optimal number of clusters (K) with the Evanno method.



RESULTS & DISCUSSION

The phylogenetic inference (Figure 1) and the population structure analysis (Figure 2) yielded congruent results. The optimal number of clusters is five, which differentiate samples at the species level (Figure 2). The sister species *O. andeanus* and *O. carrascoi* were found within a single cluster, suggesting ongoing gene flow between them (Figures 1, 2). Additionally, two individuals had mixed ancestry, with 50% genetic contribution from both *O. andeanus* and *O. dichrous*, indicative of hybridization between these deeply diverged species (2 Ma) (pointed with arrows in Figures 1 and 2).

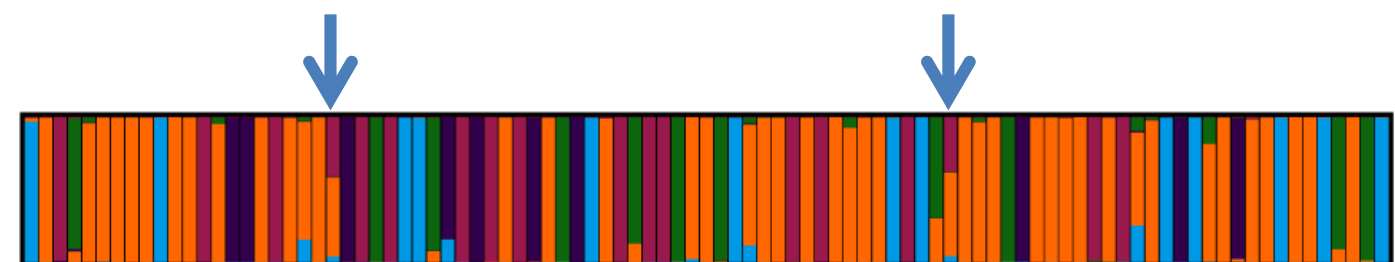


Figure 2. Admixture plot of K = 5 optimal clusters obtained with STRUCTURE. The arrows indicates hybrid individuals.

The results presented herein, together with the fact that they share significant geographic and ecological niche overlap, underline the need for revising the taxonomic status of *O. andeanus* and *O. carrascoi*. It is also remarkable that *O. dichrous* also displays significant niche overlap with these two species, confirming the critical role of ecological niches in hybridization.

CONCLUSION

The genomic approach used in this study revealed that the species boundaries within the genus *Orotettix* might be blurrier than previously believed.

FUTURE WORK / REFERENCES

The next steps involve identifying outlier loci that may indicate adaptation in pairs of allopatric sister species, as well as detecting selective signatures in genes that influence the development of the male phallic complex, which is often the primary diagnostic characteristic between species in the genus.