

Hybridization in late stages of speciation: strong but incomplete genome-wide reproductive isolation and “large Z-effect” in a moving hybrid zone

Guilherme Caeiro Dias¹, Alan Brelsford², Mariana Meneses-Ribeiro³, Pierre-Andre Crochet⁴, and Catarina Pinho³

¹University of New Mexico College of Arts and Sciences

²University of California Riverside

³Universidade do Porto Centro de Investigacao em Biodiversidade e Recursos Geneticos

⁴Centre d’Ecologie Fonctionnelle et Evolutive

December 19, 2022

Abstract

In organisms reproducing sexually, speciation occurs when increasing divergence results in pre- or post-zygotic reproductive isolation between lineages. Studies focusing on reproductive isolation origin in early stages of speciation are common. Many rely on indirect measures of introgression providing limited information on the genomic architecture of reproductive isolation maintenance in the long term. This study focuses on direct measures of introgression between two species in a late stage of speciation. We used ddRADseq genotyping in a natural hybrid zone between *Podarcis bocagei* and *P. carbonelli* to examine admixture extent, estimate effective selection, analyse hybrid zone stability, and assess variation in selection against introgression across the genome. Hybridization was confirmed the narrow and bimodal hybrid zone demonstrating the existence of strong mechanisms of reproductive isolation. Simulations suggested that simple premating barriers were not enough to explain the observed distribution of admixture classes, pointing out the role of post-mating isolation. A geographic cline approach confirmed strong reproductive isolation and high effective selection preventing extensive introgression outside of the contact zone; and detected a signal of hybrid zone movement towards *P. bocagei* distribution. Genomic cline analysis revealed heterogeneous patterns of introgression among loci within the syntopy zone, but most of the loci do not introgress more or less than the genomic average maintaining a strong association with the genomic background of origin. However, genomic clines can be driven by confounding effects resulting in incongruences between both cline approaches. Importantly, overall patterns of introgression seem to result from strong intrinsic barriers across the genome, without clear “islands of differentiation”. Last, an important role of the Z chromosome in reproductive isolation is suggested.

Hosted file

MolEcol_introgression_late_stages_speciation.docx available at <https://authorea.com/users/509863/articles/613840-hybridization-in-late-stages-of-speciation-strong-but-incomplete-genome-wide-reproductive-isolation-and-large-z-effect-in-a-moving-hybrid-zone>