
Inferring the genomic variation in introgression rates

Camille Roux*¹, Christelle Fraïsse², Yoann Anciaux³, Jonatha Romiguier³, Simon Martin⁴, Chris Jiggins⁴, Nicolas Galtier³, and Nicolas Bierne³

¹Université de Lille – CNRS, Université de Lille – France

²IST – Austria

³Institut des Sciences de l'Évolution [Montpellier] (ISEM) – Université de Montpellier, Institut de recherche pour le développement [IRD] : UR226, Centre National de la Recherche Scientifique : UMR5554 – Place E. Bataillon CC 064 34095 Montpellier Cedex 05, France

⁴University of Cambridge – United Kingdom

Abstract

Speciation results from the progressive accumulation of barriers in genomes. The speciation genomic literature, however, is mainly a collection of case studies, each with its own approach and specificities, such that a global view of the gradual process of evolution from one to two species is currently lacking. Of primary importance is the prevalence of gene flow between diverging entities, which is central in most species concepts and has been widely discussed in recent years. Here, we explore the continuum of speciation thanks to a comparative analysis of genomic data from 61 pairs of populations/species of animals with variable levels of divergence. Gene flow between diverging gene pools is assessed under an approximate Bayesian computation (ABC) framework. We show that the intermediate "grey zone" of speciation, in which taxonomy is often controversial, spans from 0.5% to 2% of net synonymous divergence, irrespective of species life history traits or ecology. Thanks to appropriate modeling of among-locus variation in genetic drift and introgression rate, we clarify the status of the majority of ambiguous cases and uncover a number of cryptic species. Our analysis also reveals the high incidence in animals of semi-isolated species and highlights the intrinsic difficulty of delineating species.

*Speaker