

Genomic architecture of speciation: the role of chromosomal rearrangements - additional Support for Europe

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How reproductive barriers between populations emerge originating new species has been one of the most debated questions in evolutionary biology. Theoretical models suggest that chromosomal rearrangements (CRs) can play a role in speciation by suppressing recombination, fostering the accumulation of genetic incompatibilities between populations connected by gene flow. Despite the plausibility of these models and their well-defined predictions (i.e. higher sequence divergence, stronger signatures of positive selection, and enrichment for loci involved in isolation within CRs when compared to collinear regions), empirical evidence supporting them is still scarce. Benefiting from the recent advances in sequencing technologies and associated bioinformatics tools, this research proposal aims to provide new insights on the impact of CRs in accelerating genome-wide divergence during speciation under different geographic scenarios and across two very distinct taxonomic groups (great apes and marine gastropods). Building on previous collaborations and joining research lines and ongoing projects, this study will deliver important knowledge on the main mechanisms of adaptive divergence and speciation.

Projektbeteiligte

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