GENESORT

Is evolution repeatable? Introducing novel tools to unravel the genetics of parallel radiations

DURATION
01/10/2013 – 31/12/2015

BUDGET
149.978 €

PROJECT DESCRIPTION

A most intriguing feature of adaptive radiation within island archipelagos is that morphologically similar species can apparently evolve independently along similar environmental gradients on the different islands. This remarkable observation appeared pivotal to demonstrate the non-randomness and repeatability of evolutionary trajectories, showed that ecological and evolutionary processes can affect island communities within similar time windows and proved that niche evolution within a lineage is much less conserved as generally assumed.

Yet, the extent to which such replicated patterns can be considered as independent evolutionary pathways is currently poorly understood. In this project, this claim is challenged by testing the hypothesis if the apparent recurrent evolution of similar phenotypes within archipelagos could be the result of a complex process of low levels of migration and gene exchange between different islands combined with higher levels of gene flow between ecologically and morphologically different species living on the same island. First, low levels of gene exchange among different islands may lead to introgression of adaptive genetic variation, which can be expected to strongly facilitate evolution towards identical endpoints. Second, dispersal of species into suitable habitats found on different islands, a process called ‘species sorting’, could be followed by introgression of neutral genetic variation among the ecologically divergent species of the same island, leading to a spurious phylogeny of repeated adaptive radiation on each island separately.

Under both scenario’s, it is expected that genes involved in adaptation will be distributed across the islands, but only retained by natural selection in their respective habitat. Topological relationships of neutral genes will in contrast primarily be influenced by the rate of inter- and intra-island gene exchange and as such be a poor reflection of the adaptive divergence process. Hence, in this project, it will be tested if parallel radiation is a process of ‘gene-sorting’ of adaptive genes throughout an archipelago. If this hypothesis holds, this would have strong implications on our current understanding on the genesis of island communities as it can be considered a process being intermediate between ecological (‘species dispersal’) and evolutionary (‘independent evolution’) processes, which were previously assumed to be mutually exclusive.

GENESORT

To achieve this, it is evident that there is a need to obtain the evolutionary histories of both neutral and non-neutral genes on a genome wide level, which was previously hampered by technological constraints. However, recent advances in sequencing technology and efficient library preparation techniques that reduce genome size and complexity currently allows to obtain genomic information from several thousand targets in the genome, hereby opening new avenues to unravelling the genetic basis of adaptive divergence.

In this project, we will make use of a recently developed molecular tool – Restriction Associated DNA (RADseq) – that allows to screen approximately 5000 regions throughout the genome. Bioinformatic tools will be developed to reconstruct gene genealogies from these regions in order to compare the evolutionary relationships between neutral and putative non-neutral gene fragments.

This technique will be applied on a most unique repeated speciation gradient of Calosoma caterpillar hunter beetles from the Galapagos. Here, apparent repeated ecotypic divergence as a function of island age occurred on multiple islands under (historic) levels of gene flow.

Hence, understanding the evolutionary history of this adaptive variation will strongly enhance our insight to what extent the interplay between ecological and evolutionary dynamics affects community assemblies on islands.

CONTACT INFORMATION

Coordinator

Frederik HENDRICKX
Royal Belgian Institute of Natural Sciences (RBINS)
Operational Direction Taxonomy and Phylogeny
Frederik.hendrickx@naturalsciences.be