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Extending the genomic toolbox to decipher lineage-wide parallel wing evolution

DURATION
15/01/2017 - 15/04/2019

BUDGET
149 580 €

PROJECT DESCRIPTION

Context

The recurrent and rapid evolution of identical but complex traits during the time course of evolution has puzzled evolutionary biologists since Darwin. Recent developments in molecular and developmental biology enabled evolutionary biologists to gain some preliminary insight into how molecular mechanisms might underly trait gain and loss at small evolutionary timescales. However, we still lack a comprehensive view on how these mechanisms are playing over longer evolutionary timescales. The difficulty to trace back the genomic basis of the same phenotypic trait in distantly related species as well as difficulties to reconstruct the entire sequence of the genomic region of interest strongly hampered such insights.

General objectives

In the proposed project, we will tackle these issues by investigating the genomic basis underlying the repeated evolution of wing development across the insect linage of carabid beetles. Across this beetle family, species are found with either fully developed wings (macropterous species), species with reduced wings (brachypterous species) and species with individuals possessing either fully developed wings and reduced wings (wing-dimorphic species). This wing dimorphism evolved repeatedly across the entire family of carabids and will allow us to (i) unravel how a single genomic element might underly the development of such a complex trait and (ii) if the same or different genomic region is involved in the repeated evolution of wing-dimorphism across this beetle family.

Methodology

In this project, we will take full advantage of the unique property of wing-dimorphic species in showing this profound intraspecific variation in wing development. This allows us to associate phenotypic (wing-size) variation with genetic variation at a genome-wide scale and, thus, to trace back the genomic region underlying this trait in multiple species distributed across the lineage. Next, we will implement a recently developed medical genomics tool, i.e. Targeted Locus Amplification (TLA), to reconstruct the entire sequence of this region. Combining these approaches will add an important layer of insight into the recurrent evolution of complex traits, and the genomic basis of adaptive evolution in general

Nature of interdisciplinarity

Investigating the genomic basis underlying trait variation strongly builds on genomic and bioinformatic tools developed within the field of medical genetics. The proposed TLA methodology will be conducted in tight collaboration with a spin-off of the University of Utrecht. This methodology has so far only been used within the field of medical genetics.

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Potential impact

Humans have an overwhelming impact on our natural environment. The ability of organisms to genetically adapt to these changes remains at present poorly understood and is hypothesized to strongly depend on (i) the genetic variation underlying ecologically important traits and (ii) the genetic architecture underlying these traits. Investigating the molecular basis underlying traits that strongly determine species extinction rates (i.e. dispersal traits in the current project) will have a strong impact on our predictive capacities on the rate and propensity of species to rapidly adapt to human-induced environmental change.

Finished products

Results of this research will be published in scientific journals, wherein we aim for high-impact journals, and be disseminated to a larger audience that includes non-specialists through news outlets and popular scientific journals.

CONTACT INFORMATION

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