UNTANGLE

Understanding the role of transposons as novel forces in genomic landscapes

DURATION
1/09/2022 – 1/12/2026

BUDGET
246 771 €

PROJECT DESCRIPTION

Context
The possible effects of transposable elements (TEs) on evolution and adaptions of the non-marine ostracod Darwinula stevensoni (Crustacea) will be investigated. This species has a wide geographic and ecological distribution. It is also one of the few remaining examples of putative ancient asexuals, having lost sex and recombination at least 20 million years ago. How D. stevensoni can survive and adapt in the apparent absence of sex, remains an evolutionary puzzle. There are indications that TEs could be one of the major factors shaping evolution of D. stevensoni. TE activity might in part compensate for the absence of meiosis and sex, which are generally the main generator of genetic variation for selection to act on.

General objectives and underlying research questions
UNTANGLE will test the hypothesis that TEs have played a major role in the evolution and adaptation. Results will significantly contribute to the understanding of rapid evolutionary processes in the living world, including current and future adaptations to climate change. UNTANGLE will generate an annotated, reference genome (objective 1). This will provide the required large-scale genomic data to study frequency, diversity, and insertion sites of different TE families in the reference genome (objective 2A) and estimate the frequency of horizontal TE transmission (objective 2B). Objective 3 will be assessing the relevance of TEs for host adaptations and evolution with different statistical approaches. This will also show if stochastic rather than adaptive processes have shaped the transposon landscape of the target species.

Methodology
UNTANGLE will generate a high-quality reference genome at the chromosome level for D. stevensoni by using cutting edge sequencing technologies. Patterns of TEs will be assessed in the reference genome, including tests for horizontal transmission of TEs and genes from other metazoans. Ostracod genomes from five additional populations will be re-sequenced with long read technologies to test for adaptive effects of TEs to different environmental conditions; this is the first time that such an approach is used in a population genetic framework of non-model organisms.

Potential impact of the research
UNTANGLE will have an important impact on three levels: the FSI, the Belgian and the international research landscape going well beyond the state of the art. UNTANGLE will contribute significantly to our understanding of rapid adaptation and evolution in natural. Knowledge of such processes is imperative as the ability for fast adaptations will be crucial for natural populations and ecosystems to survive the increasing pace of climate change and its impacts. The generated genomic data will provide important resources for future research at the FSI and beyond.
Estimating frequencies of horizontal transfer of genes and TEs in natural populations is crucial for decisions on safety and use of genetically modified organisms. UNTANGLE will thus also contribute to policy and public services concerning biosafety and health. UNTANGLE will further develop future capacities and skills in genomics. The fascination of the public for unusual examples of evolution and adaptation is expected to create a wide interest in the results of this project and create an impact on civil society, heritage, and culture. This includes two of the Sustainable Developmental Goals of the UN (https://www.un.org/sustainabledevelopment/), “Life below water” and “Life on land” and the goal “Good Health and Well-being”.

UNTANGLE

Description of the expected final research results and valorisation perspectives at short and medium term.

The results of UNTANGLE will be valorised for different target audiences, mainly focusing on national and international scientific communities, but also on science policy managers and the general public. The scientific target audience will include evolutionary biologists, molecular biologists, bioinformaticians, and ecologists who are interested in the mechanisms that allow natural populations of higher organisms to adapt fast to changing environments.

Workflows and bioinformatic scripts will be made freely available, molecular datasets with their metadata will be published in open access on suitable platforms, and results and their impacts will be disseminated in international, peer-reviewed scientific journals and presentations at various scientific workshops and conferences. During the project, results will be communicated to the general public by press communiques, blogs, and tweets, and in a popular scientific magazine.

For the end-project meeting, a wide range of stakeholders, including scientists and (non-scientific) managers and policy makers, both national and international, will be invited. The novel results of UNTANGLE for our understanding of the adaptative mechanisms of natural populations to climate change and for biosafety will be explained and made public.

CONTACT INFORMATION

Coordinator

Isa Schön
Royal Belgian Institute of Natural Sciences (RBINS)
OD Nature, Freshwater Biology
ischoen@naturalsciences.be

LINKS

https://www.naturalsciences.be/en/science/do/98/scientific-research/research-projects/project/22315