Evolution of gene repertoire during a major environmental transition

Background

Species' gene repertoires exhibit a very high degree of evolvability[1]. Although the construction of these gene repertoires often depends on historical contingencies[2,3], changes in gene repertoires have clear eco-evolutionary implications for organisms fitness and ecosystem processes (e.g. the recycling of organic matter). Despite their importance, the evolutionary factors and processes that govern gene gain or loss are still relatively poorly understood. Taking into account the gene repertoire of microbial communities living in association with their host further complicates our understanding: it is therefore the holobiont's gene repertoire that must be considered to better understand its evolution[4]. The aim of this PhD project is to gain a better understanding of the factors that govern the evolution of gene repertoires by addressing two understudied aspects: complementarity with the gut microbiota and gene loss following the loss of function. These two aspects will be investigated through a major ecological transition observed on numerous occasions in Asellidae isopods: the shift from surface to ground water. Studying several pairs of surface-dwelling and groundwater Asellidae species (Fig. 1) allows to assess the impact of a striking ecological contrast on a large number of species that acquire and lose traits in a convergent manner[5]. The Asellidae model is therefore a powerful biological model for understanding how the gene repertoire responds to ecological constraints and, in particular, to changes in diet and composition of the gut microbiota, and to the loss of phenotypic traits.

By developing an evolutionary genomics approach on an original ecological model, we aim at addressing two **fundamental questions in trophic ecology and evolutionary genomics**: (1) do trophic changes modulate the holobiont's gene repertoire, and (2) do trait losses lead to gene losses, and if so, are they adaptive?

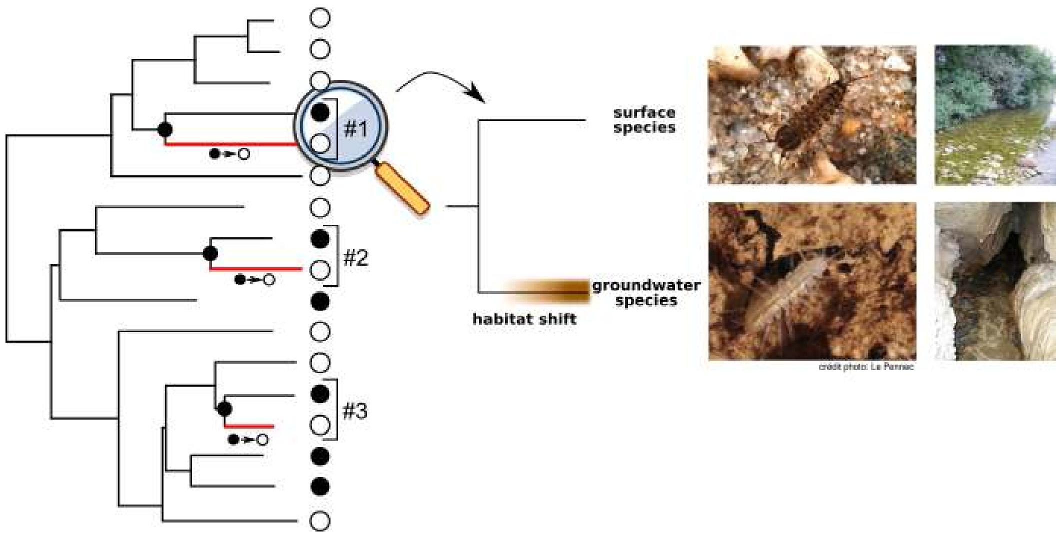

Figure 1 : Example of three pairs of Asellidae species: groundwater (white circle) and surface-dwelling (black circle) species, with photographs of the organisms and their habitats. In each pair of species, the transition from the surface to the groundwater occurs along the red branch.

Objectives and methodology

Part 1: Evolution of gene repertoire and trophic ecology

Given its functional significance, the impact of a change in diet on gene repertoires has already been studied (e.g. the transition to myrmecophagy in mammals[6]), however, these studies generally focused on a single gene. A more comprehensive approach, looking at taxa involved in key ecosystem processes, has yet to be developed.

Following the transition to ground water, subterranean Asellidae shifted from a detritivorous diet consisting mainly of leaf litter to a diet based on groundwater microbial biofilms, which constitute the primary food source in these environments[7,8]. This trophic change has significant implications, as the acquisition of nutrients and energy from decomposing leaves in surface streams requires the action of specific enzymes (**CAZymes**) to break down lignocellulosic compounds. The transition to a diet dominated by microbial biofilms therefore implies a significant relaxation of the selective pressure on these CAZymes, making them a prime target for studying the **dynamics of the metazoan gene repertoire during a drastic change in diet**. To this end, the **genomes and transcriptomes** of 10 pairs (Fig. 1) of surface-dwelling and groundwater species (already acquired, see below) will be analysed to characterise the repertoire of lignocellulose-degrading genes, as well as their expression, and to assess the influence of isopod habitat and diet.

The gene repertoire of Asellidae is not the only factor determining their nutrient assimilation efficiency. It has now been acknowledged that the **gut microbiota** plays a central role in digestion and nutrient uptake[9], and that the composition of this microbiota changes depending on the host's diet[10]. It is therefore necessary to take gut communities into account to understand how constraints on digestion and assimilation capabilities affect the host genome during a shift in habitat and diet. Potential losses in the host genome could, for example, be compensated by changes in the composition of gut communities. For a subset of the 10 species pairs, the repertoire of lignocellulose-degrading genes encoded in the **metagenome** of the gut microbiota will be characterised to estimate the level of **complementarity and redundancy** between the functional repertoires of the host and its microbiota.

The overall aim of this first research axis is therefore to determine the extent to which a change in diet will affect the gene repertoire of a metazoan, and how this process is modulated by concomitant changes in the functional composition of its gut microbiota.

Part 2 : Evolution of gene repertoire and loss of function

Evolutionary biology has focused on the development and optimisation of traits, and less frequently on the loss of traits. Yet the question of the processes involved in trait loss is a very old one[11] and remains the subject of much debate[12]. For example, it is still unclear whether trait loss and gene non-functionalisation are adaptive processes or the result of neutral processes (mutation and genetic drift). With the widespread development of genomics, the study of trait loss has once again become a central topic in evolutionary biology[13] and, in particular, the role of gene loss in the evolution of phenotypes[14].

Groundwater populations of teleosts are powerful models for studying the loss of functions, but they are nevertheless limited by the small number of contrasts studied and the recent age of the groundwater populations[15]. The Asellidae model is therefore particularly relevant for investigating how the loss of functions associated with the transition to a groundwater environment (such as vision, pigmentation, female guarding, etc.) is linked to gene loss. Using phylogenetic approaches, for the 10 pairs of surface-dwelling and groundwater species and their genomes, we will estimate the rates of gene gain and loss, and test whether an increase in gene loss is observed in the functions that have regressed. A similar analysis will also be carried out on gene expression. Finally, using polymorphism data, we will test whether genes undergoing nonfunctionalisation show signatures of positive selection that would indicate that these losses are adaptive.

Project environment

The PhD project will take place in Lyon, at the LEHNA laboratory (Ecology of Natural and Man-impacted Hydrosystems (https://umr5023.univ-lyon1.fr/).
This project builds heavily upon and complements the ANR JCJC DIET project (led by C. François), which investigates the influence of detritivores' gut microbiota on the decomposition of leaf litter in aquatic ecosystems (2023–2028). Sequencing of the gut microbiota of Asellidae is being carried out as part of this ANR project. This project also draws on data acquired as part of the ANR NeGA project (led by T. Lefébure), which has already generated genome and transcriptome assemblies, as well as polymorphism data, for the 10 pairs of Asellidae. The sequencing datasets that will underpin this PhD project have already been acquired or are currently being acquired, and, when combined, will allow to address new research questions.
The successful candidate will work in close collaboration with the bioinformatics engineer and the postdoctoral researcher recruited as part of the DIET project. The platforms of the FR BioEEnViS research federation, together with the IN2P3 computing centre, provide access to computing clusters for the bioinformatics analyses at the core of this project.

PhD supervision

This PhD project will be co-supervised by Clémentine François (https://umr5023.univ-lyon1.fr/lehna/annuaire/profile/642-clementine-francois) and Tristan Lefébure (https://umr5023.univ-lyon1.fr/lehna/annuaire/profile/573). The successful candidate will also work alongside researchers from the UMR LEHNA and other laboratories at Lyon 1 University. Supervisors will provide expertise in bioinformatics, evolutionary genomics and trophic ecology[7,8,16], as well as an in-depth knowledge of the Asellidae biological model.

Skills / candidate profile

- Concepts in evolutionary biology and genomics
- Proficiency in molecular evolutionary methods (homology search, alignment, phylogeny, …)
- Skills in bioinformatic analysis of sequencing data, development and implementation of reproducible analysis pipelines
- Proficiency in one or more programming languages
- Rigour and autonomy (work organisation)
- Writing and communication skills
- Ability to work as part of a team

How to apply

Please send a cover letter, a CV and the contact details of a reference to:

Clémentine FRANCOIS : clementine.francois@univ-lyon1.fr

Tristan LEFEBURE : tristan.lefebure@univ-lyon1.fr

Applications will be assessed on a rolling basis until the position is filled. The successful candidate is expected to be **selected by the end of July**, with the contract due to **start in November 2026**.

Références

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