

GENBAS

Behavioral and genomic aspects of cichlid speciation

DURATION
 01/12/2013 - 28/02/2018

BUDGET
 1 043 298 €

PROJECT DESCRIPTION

Background

Since Darwin's "The Origin of Species" there has been a continued interest to gain insight in the way species are formed. Initially, the role of geographic isolation in speciation received most attention, as it was believed that the spatial separation of populations formed the most important barrier for reproduction. It is now clear however that other factors than geographic isolation, such as sexual selection or environmental changes, contribute to speciation. Although the external processes influencing speciation have been the subject of many studies, the genetic basis of the speciation process itself remains largely unknown.

The cichlid fishes from the Great African lakes are often cited as the ultimate animal model to investigate adaptive radiation and speciation because of their many independent replicate radiations, phenotypic diversity and wide range of ages. Moreover, several cichlid genomes have recently become available, enabling the use of advanced techniques such as RNA sequencing (RNAseq) and Genotyping By Sequencing (GBS) to address evolutionary changes at the genome level.

Aims

The two main objectives of the GENBAS project are (1) to characterize the genomic differentiation that drives the speciation process, and (2) to verify whether/and to what extent the same genomic changes are maintaining the 'integrity' of the gene pools of the resulting sister species.

These aims will be investigated in the Lake Tanganyika cichlid genus *Ophthalmotilapia* which comprises four species that occur in shallow littoral habitats and have comparable ecological preferences. The four species have different but partially overlapping distribution ranges in Lake Tanganyika. The reproductive behaviour, taxonomy, phylogeny and hybridization of the four members within this genus are well documented. Hybridisation between sympatric species pairs occurs and seems to be unidirectional. As such, *Ophthalmotilapia* forms an ideal system to investigate the genetic basis of speciation.



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Methodology

The GENBAS project comprises four specific building blocks to achieve the main objectives.

First, behavioural and acoustic aspects of mate pairing during con- and hetero-specific interactions among the four *Ophthalmotilapia* species will be experimentally investigated. A comparison of the behavioural response between conspecific and heterospecific fishes will reveal whether mating behaviour and acoustics are different when confronted with a potential sexual partner of the same or a different, but closely related sister species. The results will not only show whether and to what extent the courtship behaviour and acoustics differ among these closely related species, but also which elements of their behaviour and acoustic communication serve as cues for species recognition.

Second, differential gene expression in the female brain associated with pairing behaviour during con- and heterospecific interactions will be assessed using a transcriptome-wide approach allowing us to screen the expression of hundreds to thousands of genes in the brain.

Third, genetic differences within and among relatively recently diverged and hybridizing species will be elucidated at a genome-wide level. We will use genome-wide divergence analysis using Genotyping By Sequencing (GBS) to study populations of four sister species of *Ophthalmotilapia* to pinpoint genomic regions with elevated or decreased differentiation and detect signals of divergent or balancing selection.

Finally, the results of the second and third goal will be integrated by mapping the differentially expressed genes involved in mate pairing and acoustics onto the data obtained for the genome wide screening of genetic variation. This will allow to determine whether the genes involved in mate recognition are situated into regions with an increased variation (diversifying selection) or a decreased variation (balancing selection).

Relevance to society

GENBAS thus integrates the study of behaviour, gene expression and genome wide differentiation and will greatly contribute to our knowledge of the genetic basis of mate choice, sexual selection, mate recognition and eventually speciation. Understanding the mechanisms that yield increased biological diversity is critical because such mechanisms are not only responsible for the generation of extant and future species diversity, they may also influence characteristics of the species, and therefore determine their vulnerability to extinction. In addition, the acoustic information generated in this project can also help to determine how and what kind of anthropomorphic sounds can influence / disturb fish behaviour.

Dissemination of results

The obtained results will be disseminated through annual reports, international peer-reviewed journals and by presentations at annual workshops and international symposia. The genomic data will be added to specific public and international databases such as Genbank. The behavioural data, for which no public databases exist, will be made public as a digital supplement of the scientific publications. All publications and digital supplements will be centralized and made accessible through the projects' website that will be developed. Popular social media (Twitter, Facebook) will also be used to inform the general public on intermediate results.



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Link

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