

## ESCAPES

Project title: Effects of Secondary Contacts and Admixture on a Pathogen Epidemiological Success  
Acronym: ESCAPES

Project duration: 36 months – Start date: 2/11/ 2016 - End date: 31/10/2019

Key-words: Epistasis, hybridization, fungal pathogen, secondary contact, quantitative genomics, QTL mapping, Dobzhansky-Muller Incompatibilities

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Total cost of the project: Total cost of the project: 120 770 € (Do not include salaries others than those of the people hired for the project: PhD or post-doc)

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### Summary:

- Context

Secondary contacts with gene flow between divergent populations of pathogens dramatically increase risks of producing new combinations of genes leading to changes in epidemiological properties. Such an outcome however depends on the number and nature of genetics barriers to gene flow as well as the distribution of effects of interaction between loci (epistasis) in hybrids. Ecological barriers will condition the fitness of hybrids according to ecology (e.g. host). Conversely non-ecological barriers mainly depend on negative epistasis in new combinations of loci in hybrids. At last, positive epistasis would increase fitness of hybrids. Our project will focus on the secondary contact between populations of the apple scab, *Venturia inaequalis*, in wild and anthropized habitats of Kazakhstan that diverged 7,000 years ago. We previously identified phenotypic differences between these populations and genomic regions associated to genetic barriers to gene flow.

- Goals

Our PhD project will be a first attempt to understand the complex factors at work that determine the outcome of a contemporary hybridization in a fungal pathogen. This project is structured around two main objectives:

- First the PhD student will identify ecological and non-ecological genetic barriers to gene flow between strains of wild and anthropized habitats of Kazakhstan.

- Second, the project aims at evaluate the impact of hybridization on traits relevant for epidemiological efficiency. We particularly search for the distribution of epistasis effects in hybrids.

- Methodology

The biological material is composed of i) 90 strains already sampled in wild habitats of Tien-Shan mountains in Kazakhstan where hybrids have been found on the base of 181 quasi-diagnostic SNPs and ii) 200 offspring of an in vitro cross (to be available at the beginning of the PhD) between a strain from wild and a strain from anthropized habitats. Phenotypic measures will be performed on all natural and offspring strains on mycelial growth, sporulation rate, spore size, and pathogenicity on *M. sieversii* and *M. x domestica*. Detection of genetic barriers to gene flow will be performed thanks to full genome sequencing and association analyses using phenotypic classes previously identified. At last, analysis of quantitative genetics models parameter will be used to characterize the distribution of epistatic effects in hybrids.