Assessing the evolvability of a pathogenic fungus in the context of global change

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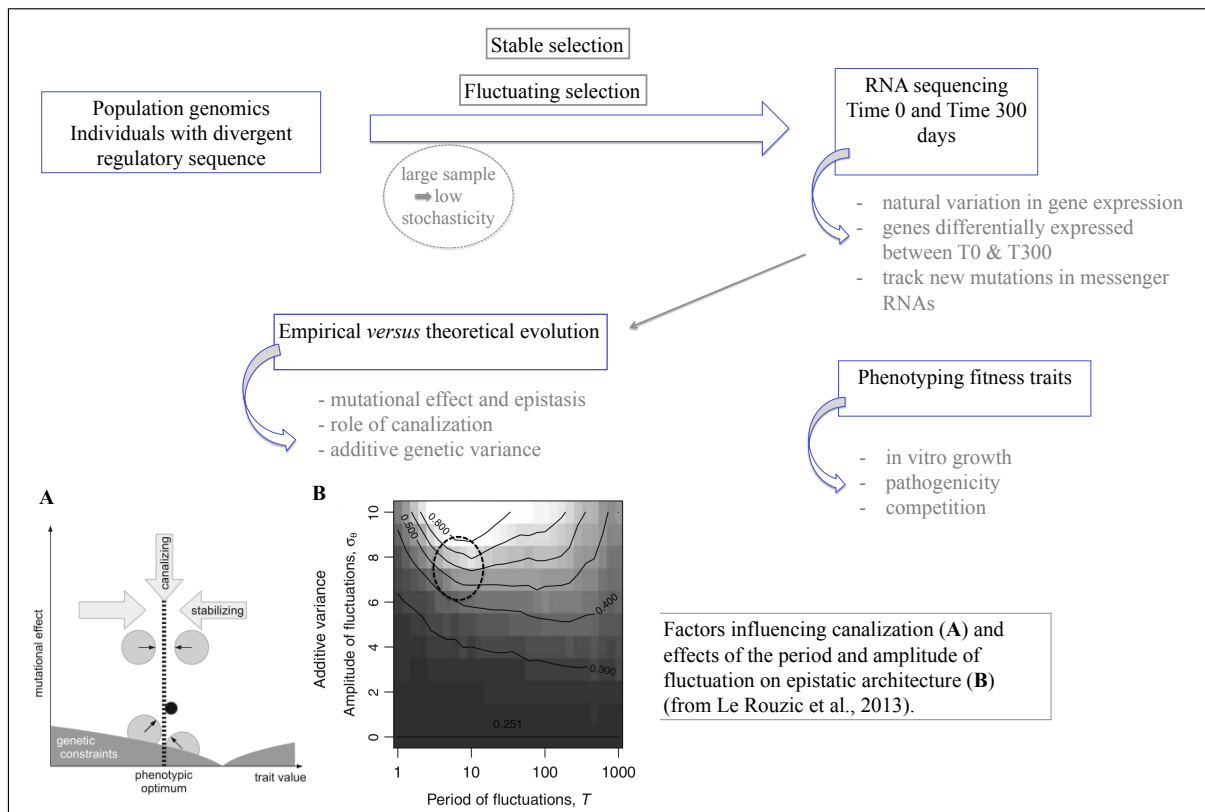[@] CNRS LEGS, UPR 9034 , 91190 Gif-sur-Yvette.

In the context of global change it is fundamental to understand how species in our agroecosystems can adapt to **modifications of their environment**. As a first attempt towards this goal, we want to estimate the **evolvability** (the capacity to evolve) of a plant pathogen (*Mycosphaerella graminicola*) in response to **temperature fluctuations**. We consider that regulatory regions of the genome play a major role in adaptation and thus want to examine transcription changes that occur during fluctuating selection. Towards this goal, we will perform experimental evolution, under stable and fluctuating temperatures. Our first objective is two tiered: -1 to sequence the transcriptome of fungal lines submitted to selection and -2 to measure some fitness-related traits. Our second objective is to confront empirical data to theoretical models to better understand the process of evolution and the nature of the genetic basis associated with the response to the selection.

Questions

What are the modes and tempo of genome regulation during the selection?
How does the genetic architecture evolve?
Which components will contribute to evolution?
    Plasticity of gene expression (disclosed hidden variation)?
    Mutational effects in *cis*-regulatory regions or *trans*-regulatory regions?
Does fluctuating environment 'increase' the evolvability of the individuals?
What is the fitness of individuals undergoing different selection regimes?
Does this selection regime have an impact on the pathogenicity?
Is there any antagonistic effect on other major life history traits?

Methods

Factors influencing canalization (**A**) and effects of the period and amplitude of fluctuation on epistatic architecture (**B**) (from Le Rouzic et al., 2013).

Bibliography. Le Rouzic A., J.M. Alvarez-Castro and T. Hansen 2013 *Evol. Biol.* 40: 317-340.