

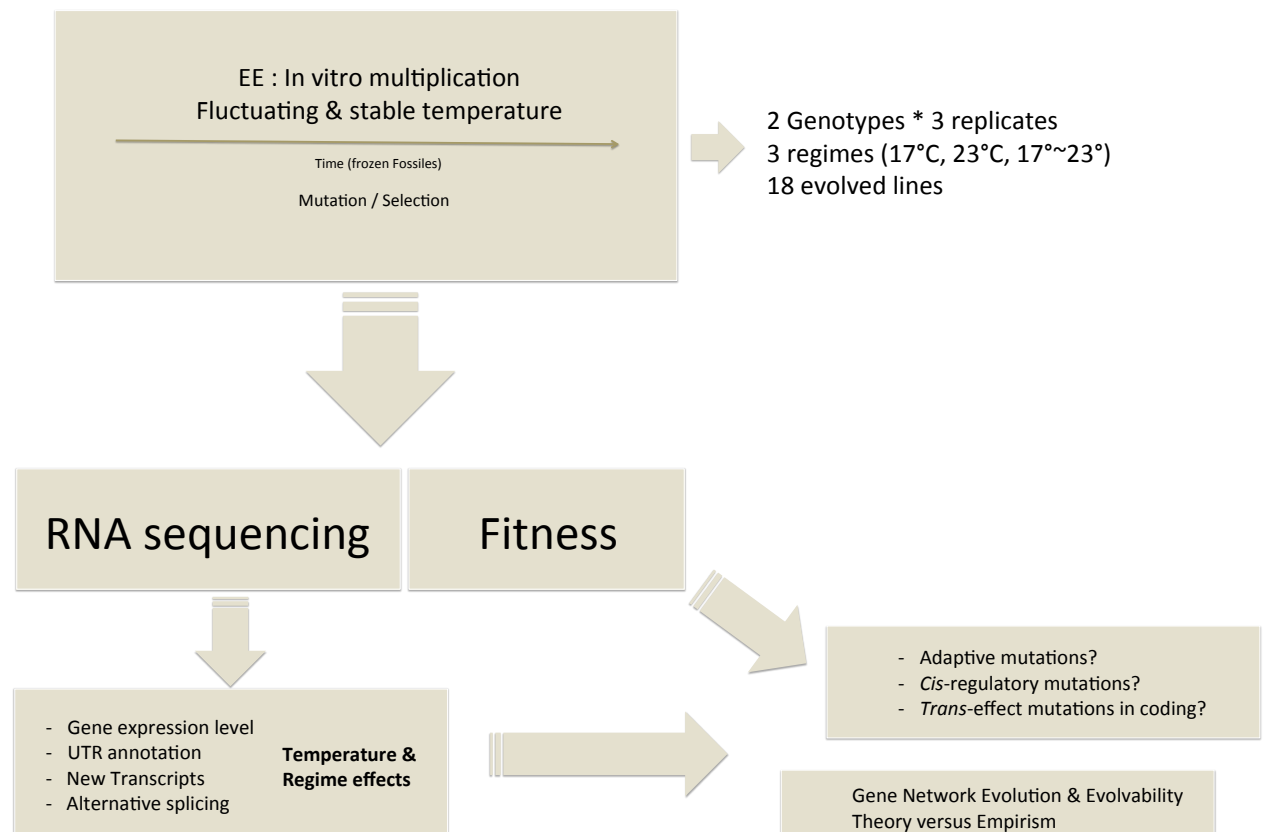
Project EVOFUNGI

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

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One main question in Biology is to understand how organisms in our agroecosystems adapt to environmental changes. One main challenge to reach this goal is to carry out empirical approaches that are relevant, in order to understand the nature of the molecular mechanisms associated with this adaptation.

The project EVOFUNGI aims at addressing challenging questions regarding the capacity of a plant pathogen to evolve and respond to abiotic factor changes, with a focus on adaptation to fluctuating selection. The originality of this project is based on combining empirical and theoretical approaches, using evolutionary transcriptomics and modelling of gene networks. We performed an evolve and re-sequencing approach in the fungus *Zymoseptoria tritici*, the main species responsible for the Septoria Tritici Blotch disease. Our goal is to (1) understand the role of transcription evolution in adaptation and (2) track down gene functions and gene interactions that are responsible for adaptation to fluctuating selection.



❖ Main achievements of the project so far include: (1) an experimental evolution (EE) in the fungal *Zymoseptoria tritici* (first EE with this model to our knowledge); (2) and RNA-sequencing and analysis of transcriptional differences of evolved lines between temperatures and selection regimes.

❖ This collaboration is now reinforced with two PhD projects that emerged from Evofungi: two doctoral grants were obtained last June (ED567: A. Jallet and ED577: A. Odorico).

