Evolution of gene expression plasticity in Zymoseptoria tritici

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Résumé

Organisms inhabit continuously changing environments and are faced with the challenge of optimizing their fitness in these novel environments. This adaptation is facilitated through a variety of mechanisms including genetic modulation, behavioral modifications, and transient physiological adjustments. The evolution of plasticity has long intrigued scientists who have tried to uncover the intricate mechanisms governing these phenotypic modifications; however, it remains largely unexplored. Here, we use experimental evolution tools to study the evolution of gene expression plasticity in strains of *Zymoseptoria tritici* exposed to stable and fluctuating environmental conditions. Theoretical models posit that phenotypic plasticity is likely to evolve in response to fluctuating environments. Nonetheless, empirical evidence from various studies presents a mixed picture, with some studies supporting this prediction while others do not. In our study, we aim to study the evolution of transcriptome after exposure to variable environments for over 200 generations (_~ six months). The experimental conditions will comprise of a combination of temperature and media treatments. We expose these strains to two different temperatures (17℃ and 23℃) and two different media (Yeast Potato Dextrose and Potato Dextrose Broth – differing in protein and carbohydrate composition). We will generate a full-factorial combination of these experimental treatments, combined with stable and fluctuating regimes. Our plan is to measure the change in the gene expression after exposure to the environmental treatments for six months and analyze if certain regime (stable or fluctuating) results in evolution of gene expression and gene expression plasticity in the strains. Furthermore, we would assess the changes in gene regulatory networks across replicates and analyze if the evolution of gene expression patterns is repeatable. Delving into the interaction of distinct abiotic factors, such as temperature and media composition, provides us with an opportunity to understand how strains respond to environmental stimuli. This study endeavors to uncover whether these responses may be orchestrated through conserved pathways or divergent mechanisms, thus shedding light on the evolution of gene expression networks in response to environmental cues.

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Mots-Clés: gene expression, plasticity, gene networks, differentially expressed genes, transcriptome