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# Genomics of fitness in dynamic environments

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## Résumé

The consequences of genetic mutations on organisms adaptive response are often studied experimentally by applying a single environmental change. However, in nature, environments are dynamic and the contribution of genes to fitness may depend on the timing of the changes, such as their frequency. Genomics, especially in model organisms such as yeast, has been very successful in identifying genes contributing to fitness in various static environmental conditions and genes involved in the response to specific changes. Our ambition is to now extend genomics to the case of dynamic environments, screening for genes that affect growth fitness only at specific frequencies of environmental fluctuations. To do so, we have set up an experimental system to grow cultures over a prolonged period of time while changing the environmental condition periodically. This platform allowed us to screen the systematic Yeast Deletion Library by competitive growth followed by highly-multiplexed NGS sequencing of barcoded mutants. In a preliminary analysis based on a dedicated generalized linear model, we have identified about 20 yeast genes which suppression confers a growth advantage over wild-type cells but only at elevated frequencies of environmental changes. 16 of these were validated by direct cell counting after co-culturing with labeled wild-type cells. The results show that disabling or delaying a normal stress response can be beneficial when normal conditions return fast enough. We are now re-sequencing our populations at higher depth in order to identify milder fitness effects. This work was funded by the E.U. under grant SiGHT nb 281359.

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