CONFÉRENCE

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Rewiring of genetic networks in yeast and other organisms

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Abstract:

Phenotypic variation in natural populations is caused by an interplay of genetic determinants. The whole genome sequencing projects have revealed the prevalence of sequence variants and copy number variants in human population.

However, knowledge about how such variants interact to generate phenotypic outcomes is lacking.
It is important to study complex genetic interactions since they represent multiple genes that act to modulate phenotypic variation in natural populations by generating unexpected phenotypic outcomes, which cannot be predicted from the effects of individual mutations.

In our lab we use the budding yeast to study how duplicated genes evolve and contribute to genetic network robustness. We also study the evolution of conditional essentiality—in which certain genes are essential in one species but nonessential in another—often due to genetic interactions.

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