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A toolkit for CRISPR-based functional genomics in fungal pathogens

LE JEUDI 20 JUIN 2019 À 12 H 30

Pavillon Charles-Eugène-Marchand, salle Hydro-Québec (1210)

Opportunistic *Candida* pathogens are a leading cause of fungal infections, and new functional genomic tools enable our ability to better study the biology of these important pathogens. Here, we develop a CRISPR-based toolkit for functional genomic analysis in *Candida* species, using CRISPR-based deletions, and strategies for CRISPR-based regulation of gene expression. The first strategy is a CRISPR-Cas9-based 'gene drive' platform for rapid and precise genome editing in *C. albicans*, enabling applications for genetic interaction analysis of fungal pathogenesis. In our gene drive system, a modified DNA donor molecule acts as a selfish genetic element, replaces the targeted site, and propagates to replace any additional wild-type locus. Coupling this approach with mating-competent *C. albicans* haploids, we can rapidly create diploid *C. albicans* strains that are double homozygous deletion mutants, enabling us to create large-scale double-deletion libraries and analyze complex genetic interactions networks in *C. albicans*. In addition, we have developed two powerful technologies, never previously used in fungal pathogens: CRISPR interference (CRISPRi) and CRISPR activation (CRISPRa), for applications in *Candida* species. We demonstrate the ability of these systems to repress or induce gene expression in *Candida*. Since, unlike classic CRISPR systems, these platforms do not require a DNA repair construct, the simplicity of this system lends itself to high-throughput strain generation. Using a highly-efficient, high-throughput cloning strategy, we are able to efficiently and rapidly generate large numbers of fungal mutant strains that over- or under-express any gene of interest, providing a powerful new tool for functional genomic analyses in fungal pathogens.

Lunch et breuvages seront offerts.

SVP confirmer votre présence sur : <https://doodle.com/poll/pehzuakxfs6yvk66>
avant le mercredi 19 juin, 10 h

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