P433. Genome-scale metabolic model of the human pathogen *C. albicans*: aiming the identification of promising new drug targets

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Candida albicans is the most common cause of invasive candidiasis, partly due to its ability to acquire drug resistance. With the rise in frequency of multidrug resistant clinical isolates, therapeutic options are running low. The identification of new drug targets and new drugs is crucial to overcome the increase in therapeutic failure. Currently, genome-scale metabolic models can be considered established tools for drug targeting.
In this study, we propose the first genome-scale metabolic model for *Candida albicans*, iRV1930. The model consists of 1556 reactions, 1344 metabolites, 1053 genes, and 5 compartments. This model, currently under validation, proved accurate when predicting the capability of utilizing different carbon and nitrogen sources when compared to experimental data. This model was reconstructed using open source software tool, merlin 3.9.6, and is provided in the well-established systems biology markup language (SBML) format, thus, it can be used in most metabolic engineering platforms, such as OptFlux or Cobra.
Altogether, this model provides a promising platform for global elucidation of the metabolism of *C. albicans*, currently being used to guide the identification of new drug targets to tackle human candidiasis.