

Metabolic modeling predicts specific gut bacteria as key determinants for *Candida albicans* colonization levels.

Mirhakkak M, Schäuble S, Klassert T, Brunke S, Brandt P, Loos D, Uribe R, de Oliveira Lino FS, Ni Y, Vylkova S, Slevogt H, Hube B, Weiss G, Sommer M, Panagiotou G[#] (2021) Metabolic modeling predicts specific gut bacteria as key determinants for *Candida albicans* colonization levels. *ISME J* 15(5), 1257-1270.

[Details](#)

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Abstract

Candida albicans is a leading cause of life-threatening hospital-acquired infections and can lead to candidemia with sepsis-like symptoms and high mortality rates. We reconstructed a genome-scale *C. albicans* metabolic model to investigate bacterial-fungal metabolic interactions in the gut as determinants of fungal abundance. We optimized the predictive capacity of our model using wild type and mutant *C. albicans* growth data and used it for in silico metabolic interaction predictions. Our analysis of more than 900 paired fungal-bacterial metabolic models predicted key

gut bacterial species modulating *C. albicans* colonization levels. Among the studied microbes, *Alistipes putredinis* was predicted to negatively affect *C. albicans* levels. We confirmed these findings by metagenomic sequencing of stool samples from 24 human subjects and by fungal growth experiments in bacterial spent media. Furthermore, our pairwise simulations guided us to specific metabolites with promoting or inhibitory effect to the fungus when exposed in defined media under carbon and nitrogen limitation. Our study demonstrates that *in silico* metabolic prediction can lead to the identification of gut microbiome features that can significantly affect potentially harmful levels of *C. albicans*.

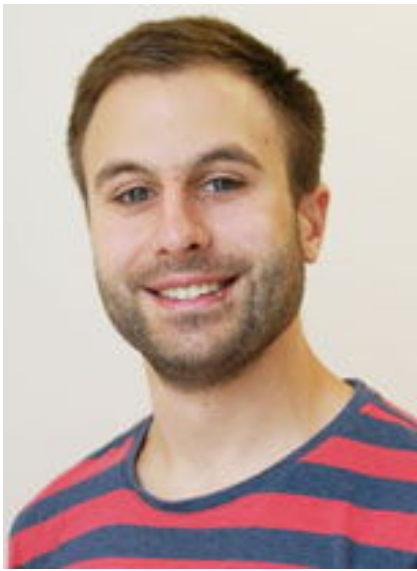
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