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 albicansis 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-scaleC. albicansmetabolic model to investigatebacterial-fungal metabolic interactions in the gut as determinants of fungal abundance. We optimized the predictive capacityof our model using wild type and mutantC. albicansgrowth 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 modulatingC.albicanscolonization levels. Among the studied microbes,Alistipes putrediniswas predicted to negatively affectC. albicanslevels. We confirmed thesefindings by metagenomic sequencing of stool samples from 24 human subjects and by fungalgrowth experiments in bacterial spent media. Furthermore, our pairwise simulations guided us to specific metabolites withpromoting or inhibitory effect to the fungus when exposed in defined media under carbon and nitrogen limitation. Our studydemonstrates that in silico metabolic prediction can lead to the identification of gut microbiome features that cansignificantly affect potentially harmful levels ofC. albicans.

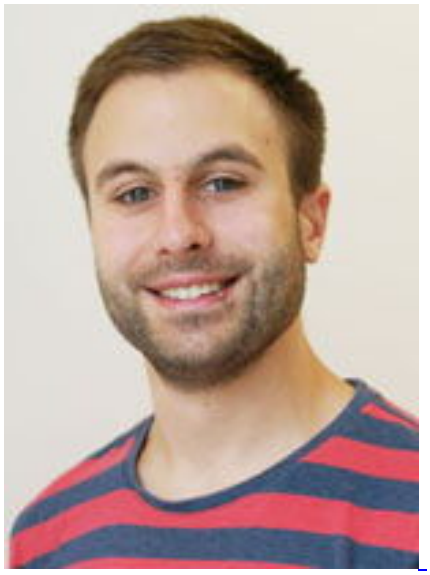
Involved units

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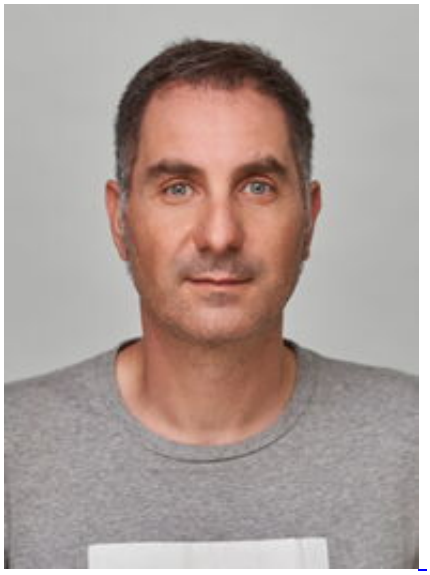
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Topics

Synthetic Ecology

Host-Pathogen Interactions

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