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Gut microbiota-mediated colonization resistance against *Candida albicans*

The opportunistic fungus *Candida albicans* is a common member of the human microbiome and present on different mucosal surfaces of healthy individuals. Changes in gut environment, for example due to antibiotic treatment, can lead to enhanced fungal proliferation, and in combination with immunosuppression result in superficial or systemic infections. Disseminated infections by *C. albicans* have become a major health risk factor over the last decades especially in intensive care units. The fact that antibiotics are a major risk factor and recent research highlights the critical role of the bacterial microbiota in controlling *C. albicans* colonization and translocation. The underlying mechanisms, as well as the types and features of bacteria involved in colonization resistance, are however only incompletely understood.

Aim of the project is to address the influence of the microbiota during the colonization and translocation of *C. albicans* on the host and the clinical outcome of systemic candidiasis. To investigate which members influence *C. albicans* colonization, mouse colonies with different microbiome compositions will be selected and resistance to *C. albicans* colonization will be analyzed. Further, the influence of the microbiome on the susceptibility to the development of systemic candidiasis will be examined. Additionally, the spatial organization of the microbiota in mice, and specifically of bacteria in direct physical contact with *C. albicans*, will be illustrated with the help of different imaging techniques, for example FISH. Thereby, this project will provide new insights into the interaction network of *C. albicans* and the other members of the gut microbiome.

Publications

Krüger W, Vielreicher S, Kapitan M, Jacobsen ID, Niemiec MJ (2019) Fungal-Bacterial Interactions in Health and Disease. *Pathogens* 8(2), Details PubMed

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