

Antibiotics create a shift from mutualism to competition in human gut communities with a longer-lasting impact on fungi than bacteria.

Seelbinder B, Chen J, Brunke S, Vazquez-Urbe R, Santhanam R, Meyer AC, de Oliveira Lino FS, Chan KF, Loos D, Imamovic L, Tsang CC, Lam RP, Sridhar S, Kang K, Hube B, Woo PCY, Sommer MOA, Panagiotou G (2020) Antibiotics create a shift from mutualism to competition in human gut communities with a longer-lasting impact on fungi than bacteria. *Microbiome* 8(1), 133.

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Abstract

Background

Antibiotic treatment has a well-established detrimental effect on the gut bacterial composition, but effects on the fungal community are less clear. Bacteria in the lumen of the gastrointestinal tract may limit fungal colonization and invasion. Antibiotic drugs targeting bacteria are therefore seen as an important risk factor for fungal infections and induced allergies. However, antibiotic effects on gut bacterial-fungal interactions, including disruption and resilience of fungal community

compositions, were not investigated in humans. We analysed stool samples collected from 14 healthy human participants over 3 months following a 6-day antibiotic administration. We integrated data from shotgun metagenomics, metatranscriptomics, metabolomics, and fungal ITS2 sequencing.

Results

While the bacterial community recovered mostly over 3 months post treatment, the fungal community was shifted from mutualism at baseline to competition. Half of the bacterial-fungal interactions present before drug intervention had disappeared 3 months later. During treatment, fungal abundances were associated with the expression of bacterial genes with functions for cell growth and repair. By extending the metagenomic species approach, we revealed bacterial strains inhibiting the opportunistic fungal pathogen *Candida albicans*. We demonstrated in vitro how *C. albicans* pathogenicity and host cell damage might be controlled naturally in the human gut by bacterial metabolites such as propionate or 5-dodecenoate.

Conclusions

We demonstrated that antibacterial drugs have long-term influence on the human gut mycobiome. While bacterial communities recovered mostly 30-days post antibacterial treatment, the fungal community was shifted from mutualism towards competition.

Involved units

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