RESEARCH AREA III
HIGHLIGHT

01
TITLE OF THE WORK

Microbiota restauration in dysbiotic mice by intranasal application of individual bacterial strains

02
SOME BACKGROUND

An increasing body of evidence shows that the host microbiota strongly influences lung diseases. Microbiota-targeting therapies like fecal microbiota transfer and probiotic treatment confer health-benefits to humans suffering from intestinal diseases. However, it is still unclear how the beneficial effects are accomplished mechanistically. It also remains to be established whether probiotics can also confer beneficial effects in lung diseases.

03
WHAT DID SCIENTISTS DISCOVER?

We investigated microbiota alterations in mice that underwent antibiotic treatment followed by intranasal application of bacteria that had originally been isolated from lungs of wild mice. As expected, mice developed profound dysbiosis after antibiotic treatment. Surprisingly, application of isolates of the genus Lactobacillus, Corynebacterium, and Actinobacillus to antibiotic-pretreated mice diversified the entire host caecum microbiota, including increased α-diversity and convergence to homeostatic pretreatment microbiota.

04
WHY IS IT IMPORTANT?

Microbial dysbiosis contributes to the development of a multitude of diseases and syndromes and is a sustaining factor in certain disease states. Probiotic treatments can confer health benefits to such patients. Host and microbiota coexist in an evolutionary established equilibrium, and our study suggests that self-renewal forces exist which correct states of dysbiosis. This process can be promoted by intranasal application of certain bacterial strains. A deeper insight into the function of probiotics can lead to rational development of microbiota-targeting medication. These might be more effective and cover a broader range of diseases than today's probiotics.

05
WHO DID THE RESEARCH?

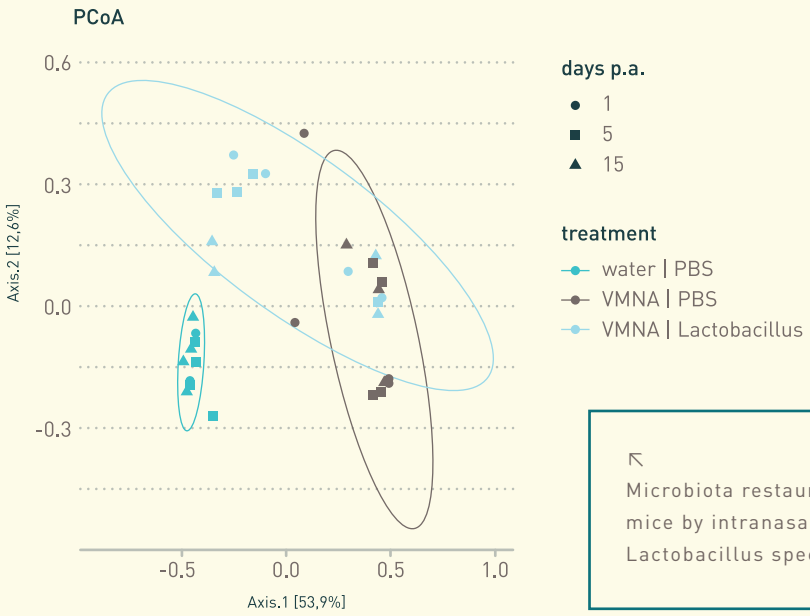
Matthias Hauptmann, Lisa Lübbe,
Jessica E. Ojong, Ulrich E. Schaible
Cellular Microbiology,
Research Center Borstel, Germany

06
WHY DID THEY CHOOSE THE DESCRIBED METHODS?

The rationale of our experiments was to replace the microbiota of certain mouse strains by other bacteria to investigate the effect of genotype-specific microbiota on host susceptibility towards tuberculosis. While we could not set up a simple microbiota-replacement model, which might have served our initial research question, a new research project was initiated based on the described findings. Our model of antibiotic treatment of mice mimics severe dysbiosis. 16S sequencing is an established and accepted way to characterize microbiota compositions.

07
DETAILS FOR SCIENTISTS – PUBLICATION

A manuscript describing our observations is currently being prepared.



↖ Microbiota restauration in dysbiotic mice by intranasal application of a Lactobacillus spec.

Mice were first treated with an antibiotic cocktail to induce dysbiosis. Six days later, mice received Lactobacillus spec. or PBS by intranasal administration. Caecum microbiota were characterized by 16S rRNA-gene sequencing. PCoA plot shows Bray-Curtis dissimilarities between groups of mice.