

Gut microbiome

<https://doi.org/10.1038/s41684-025-01661-x>

# Host genetics overrides microbiome normalization

 Check for updates

Co-housing and cross-fostering are experimental strategies that are commonly used to reduce microbiome variability among different groups of mice, allowing for more comparable research findings. However, a new study suggests that these methods only work for genetically identical mice and fail to normalize the microbiomes of mice from different genetic backgrounds.

Although previous studies have explored the influence of host genetics on microbiome composition and normalization, they used specific pathogen-free (SPF) mice with their own established microbiomes, which complicates the interpretation of the results. Here, Lietuvninkas et al. used state-of-the-art approaches involving germ-free (GF) mice colonized with a carefully controlled

microbiome to rule out the influence of prevalent bacterial communities on co-housing and cross-fostering.

First, the investigators tested the effects of co-housing on genetically identical mice. They gavaged GF C57BL/6J (B6J) mice with cecal contents from two sources: either from SPF B6J mice bred in their own facility or from SPF B6J mice purchased from a vendor. After allowing two weeks for the microbiomes to establish, the team co-housed the ex-GF mice—now colonized with two distinct microbiota—for four weeks and then separated them for four weeks. Microbiome analysis showed that co-housing homogenized gut microbial communities, resulting in a unified microbiome across the two groups of B6J mice.

Next, to test whether cohousing would also normalize microbiomes across strains, the team gavaged GF B6J and BALB/c mice with the same input microbiota and co-housed them for four weeks. Unlike previous results in B6J mice, their microbiomes remained distinct after four weeks.

Similarly, the study shows that cross-fostering normalized microbiomes in genetically similar mice, but not in genetically distinct ones. These results suggest that co-housing and cross-fostering can't reliably overcome host genetic effects on microbiomes, and that the impact of these experimental strategies should be confirmed using sequencing methods.

**Alexandra Le Bras**

**Original reference:** Lietuvninkas, H.B. et al. *Cell Rep.* **44**, 116402 (2025)



**MARSHALL**®

*When quality matters*



Marshall Beagle®



Göttingen Minipigs®



Marshall Cat®



Marshall Ferret®



[www.marshallbio.com](http://www.marshallbio.com)

Contact Us

