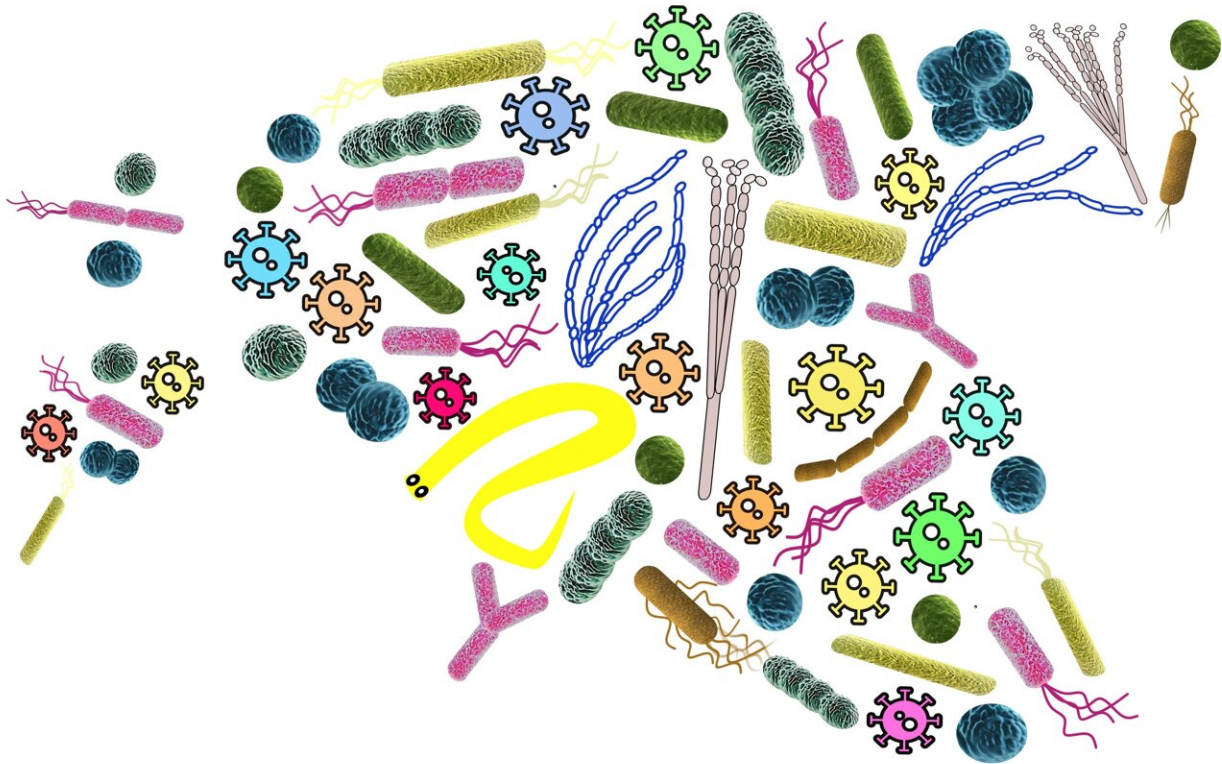



Small country with a great potential for microbiome studies

February 15 2022

ESTONIAN MICROBIOME PROJECT EstMB



The situation is , but it's the fertiliser for our future
Lennart Meri (President of Estonia, 1992-2001)

The scientists from University of Tartu have established the Estonian Microbiome cohort as part of the Estonian Biobank. Credit: Kertu Liis Krigul

The Estonian Microbiome Project, using electronic health data from more than 2500 biobank participants finds long-term antibiotic usage, independent from recent administration, has an impact on the microbiome, partly explaining the common bacterial signatures overlapping between diseases.

Microbiome can have a major impact on [public health](#), including in the identification of [microbiome–drug interactions](#) that are responsible for dose effectiveness and adverse events, management of chronic diseases, and maintenance of one's health. Currently, there are only a few extensive population-based metagenomic cohorts available for studying these microbiome effects on health. The scientists from the University of Tartu have established the Estonian Microbiome [cohort](#) as part of the Estonian Biobank. The cohort includes a stool, oral and plasma samples from 2,509 participants and is supplemented with multi-omic measurements, questionnaires covering participants' dietary preferences, living environment, and various lifestyle choices, and regular linkages to national electronic health records.

"Current microbiome cohorts have mostly used less reliable self-reported diagnoses for detecting microbiome associations, however, our cohort has access to diagnoses and medication prescriptions from electronic health records which are recorded by medical specialists. We have used this data to confirm previously reported microbiome associations as well as extend the understanding of microbiome-host interactions, including the effect of long term antibiotic usage," said Kertu Liis Krigul, one of the first authors of the paper.

The authors demonstrate that the long-term use of [antibiotics](#) has a remarkable effect on microbiome diversity and might partly explain shared dysbiosis between different diseases with diverse

pathophysiologies. They observed significant changes in the composition of the microbiome after the participants had taken only 3–4 courses of antibiotics. "The fact that a shift in the microbial composition is evident with only a few courses of treatment is intriguing, as half of the participants take more than four courses and Estonians are among the lowest consumers of antibiotics in Europe, suggesting an even stronger effect in other populations," said Oliver Aasmets, the first author of the paper. After correcting for the number of antibiotic treatments taken over the last 10 years, continued Aasmets, we identified a clear decline in the number of previously detected microbiome-disease associations, underlining the value of longitudinal health data records in interpreting the results and identifying disease-specific signals.

The Estonian Microbiome cohort is an excellent resource for analyzing the role of fecal microbiota in disease susceptibility, clinical phenotypes, and therapeutic responses using the information on past and future clinical outcomes by linkage to the participants' electronic [health](#) records.

The research was published in *Nature Communications*.

More information: Oliver Aasmets et al, Gut metagenome associations with extensive digital health data in a volunteer-based Estonian microbiome cohort, *Nature Communications* (2022). [DOI: 10.1038/s41467-022-28464-9](https://doi.org/10.1038/s41467-022-28464-9)

Provided by Estonian Research Council

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