Within-host community dynamics of the vaginal microbiota in young adult women

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Résumé

We analyzed data from the PAPCLEAR cohort that followed 189 women aged from 18 to 25 in the area of Montpellier with 974 on-site visits and a total of 1,619 months of follow-up. Building on a first metabarcoding analysis, we performed metagenomics sequencing on a selection of 658 samples from 123 participants.

In our analysis, we leverage this new shotgun metagenomics data to cluster our samples into a finer, new classification of communities with 27 classes known as mgCST (metagenomics CST). We first use this new information to better understand VM stability using a multi-state model.
Second, we investigate the evolution of Lactobacillus crispatus, one of the most frequent species in the human VM. By combining VIRGO2, a gene catalog for VM organisms, and breseq, a software package designed for identifying mutations in longitudinal settings, we look for within-host genetic variation and estimate L. crispatus evolutionary rates.

This represents one of the few studies looking into the evolution of the VM over a long time. A future goal is to get an even finer resolution, going beyond mgCSTs, to understand changes in VM communities over time. Furthermore, for "stable" strains, which remain the dominant species over time in our follow-ups, we will identify substitutions associated to specific effects at cellular and molecular level.
This approach will then be extended to other organisms from the VM, offering a framework to better understand the stability and shifts in vaginal microbiome.

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