

The vaginal microbiome of women residing in Amsterdam: association with ethnicity

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Conclusion

Dysbiotic vaginal microbiome compositions are significantly increased in women of non-Dutch ethnic origin. Therefore, these women may be at increased risk of STI acquisition and adverse reproductive health outcomes.

Introduction

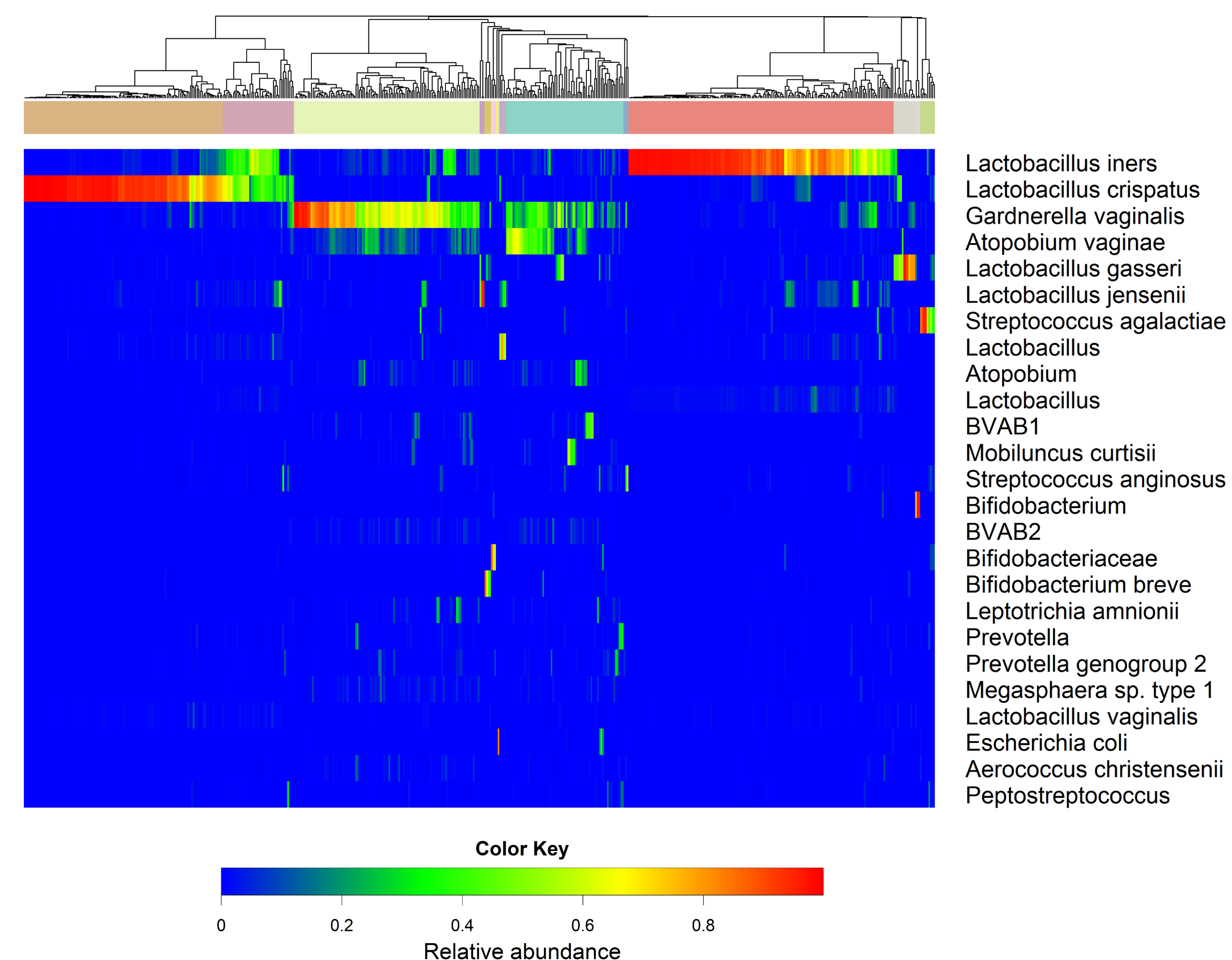
American women of African or Hispanic ancestry have increased risk of vaginal microbiome dysbiosis compared to women of European or Asian ancestry. However, the association between vaginal microbiome composition and ethnicity within Europe is largely unknown.

Methods

Non-pregnant women (18-34 years, n=614) representing six ethnic origins were cross-sectionally selected from the ongoing HELIUS multi-ethnic cohort study in Amsterdam for vaginal microbiome analysis. Extracted DNA from self-sampled vaginal swabs was sequenced targeting the V3V4 region of the 16S rRNA gene using double-indexing and paired-end Illumina MiSeq sequencing. OTUs (97% similarity) were assigned to taxonomy using pplacer, and clustered using hierarchical clustering.

Microbiome composition

Clustering of 525/614 samples with a read count of ≥ 100 (median read count 2.6×10^4) resulted in microbiome clusters dominated by *Lactobacillus crispatus* (n=118), *L. iners* (n=160), *L. crispatus* and *L. iners* (n=43), *L. gasseri* (n=13), *Gardnerella vaginalis* (n=111), a mixture of anaerobes (n=70), aerobic bacteria (n=14), and *Bifidobacterium* spp. (n=7), respectively. 10 women were clustered in small or singleton clusters ('other').



Microbiome and ethnicity

Microbiome composition was significantly associated with ethnic origin ($P=0.002$). Women of Dutch ethnic origin had the highest prevalence of *L. crispatus*-dominated microbiome, the lowest prevalence of *L. iners*-dominated microbiome, and the lowest prevalence of clusters dominated by *G. vaginalis* or a mixture of anaerobes (dysbiosis). Turkish women and South-Asian/Indonesian Surinamese women had the highest prevalence of *L. iners*-dominated microbiome, and women from African descent (African Surinamese and Ghanaian women) the highest prevalence of clusters dominated by *G. vaginalis* or dysbiosis.

Prevalence of vaginal microbiome compositions

