qPCR-based quantification of Gardnerella spp. in vaginal and penile samples: insights into partner dynamics

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Résumé

 ${\it Gardnerella\ spp.}$ is a natural bacterial component of the vaginal microbiome. However, its

overabundance is linked to bacterial vaginosis (BV), a shift in the vaginal microbial environ-

associated with an increased risk of infertility, perinatal complications and sexually transmitted

infections (STI). Although BV is not currently classified as an STI, Gardnerella spp. has been

detected in the penile anatomy. Reliable detection of *Gardnerella spp.* in vaginal and penile samples is therefore crucial for understanding its potential transmission dynamics, the role of

male partners in BV onset and recurrence, and its broader implications for sexual health. We

implemented and validated a quantitative polymerase chain reaction (qPCR) assay targeting the elongation factor Tu gene of $Gardnerella\ spp$. We applied this method to 163 vaginal fluid

and penile skin samples from 22 heterosexual couples in Switzerland. This is intended to explore potential links between microbial patterns and factors such as partner dynamics, sexual practices, e.g. use of barrier contraceptives, and broader questions around the transmission and classification of *Gardnerella spp.* as a sexually associated pathogen. Our results show low to moderate positive correlations of *Gardnerella spp.* loads between sexual partners samples across three timepoints (Spearman's $\rho = 0.38, 0.76, 0.51$). No association was found between bacterial load and frequency of sexual intercourse. Condom use was linked

to significantly lower *Gardnerella spp.* loads in penile skin samples, but not in vaginal fluid. Improved understanding of these patterns may support more effective treatment strategies and

reduce stigma surrounding vaginal and sexual health by making this knowledge more accessible to the public.

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