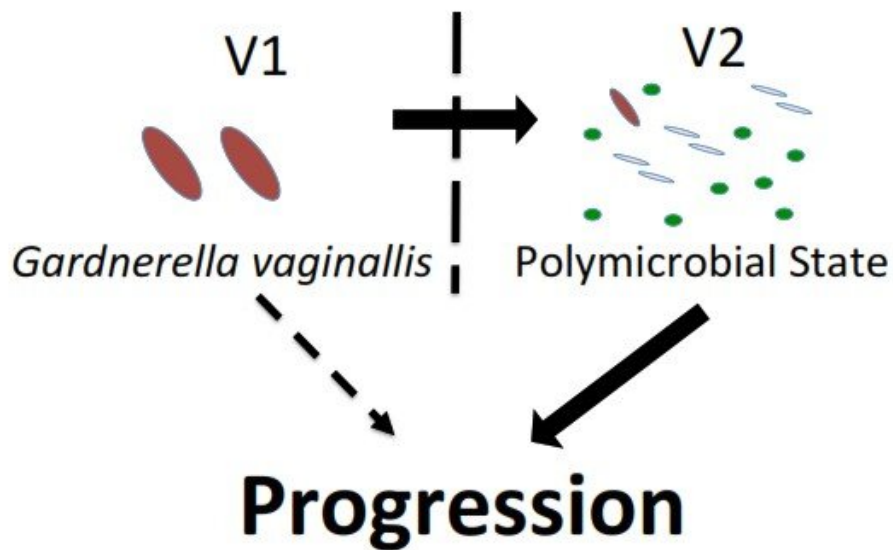


# Microbiome may hold key to identifying HPV-infected women at risk for pre-cancer

March 26 2020

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## Proposed Model of HR-HPV Progression



Model of HPV and microbiome interactions. Credit: Public Library of Science, CC BY 4.0

*Gardnerella* bacteria in the cervicovaginal microbiome may serve as a biomarker to identify women infected with human papillomavirus (HPV) who are at risk for progression to precancer, according to a study published March 26 in the open-access journal *PLOS Pathogens* by Robert Burk and Mykhaylo Usyk of the Albert Einstein College of Medicine, and colleagues. According to the authors, the findings could lead to therapeutic strategies that manipulate the microbiome to prevent disease progression.

HPV [infection](#) is one of the most common sexually transmitted infections and the causal agent of cervical cancer. But it is still not clear why only a small proportion of high-risk HPV infections progress to cervical cancer. To investigate the potential role of the cervicovaginal microbiome, Burk, Usyk and their collaborators evaluated cervical samples from 273 women who had high-risk HPV infection and were participating in the Costa Rica HPV Vaccine Trial.

They found that the abundance of *Lactobacillus iners* was associated with clearance of high-risk HPV infections. By contrast, *Gardnerella* bacteria were the dominant biomarker for progression of a high-risk HPV. Additional analyses revealed that the effect of *Gardnerella* is mediated by increased cervicovaginal bacterial diversity directly preceding the progression of a persistent infection to precancer. The findings suggest that monitoring the presence of *Gardnerella* and the subsequent elevation in microbial diversity could be used to identify women with persistent high-risk HPV infection at risk for progression to precancer. If future studies support a causal role of the cervicovaginal microbiome and [disease progression](#), then it might be possible to manipulate the cervicovaginal [microbiome](#) in a manner to activate a local immune response and prevent disease progression.

The authors add, "The investigators prospectively demonstrate that progression of a persistent high-risk HPV infection to cervical precancer

is in part explained by unique features of the cervicovaginal microbiota."

**More information:** Usyk M, Zolnik CP, Castle PE, Porras C, Herrero R, Gradissimo A, et al. (2020) Cervicovaginal microbiome and natural history of HPV in a longitudinal study. PLoS Pathog 16(3): e1008376. [doi.org/10.1371/journal.ppat.1008376](https://doi.org/10.1371/journal.ppat.1008376)

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