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**Title:** Role of the Vaginal Microbiome on Human Papilloma Virus Carcinogenicity – Implications for Racial Disparities

Forbes magazine called the eradication of cervical cancer (CCa) a “low hanging fruit”: We have cost-effective screening, we know its cause: human papillomavirus (HPV), and we have an effective vaccine. Though effective, CCa screening leads to thousands of biopsies on indolent cervical lesions. Why? Because most HPV infections clear and some lesions regress on their own. So, which ones will not? Vaginal microbes (VMB) are implicated in sustaining HPV infection and cervical lesions. Non-Latina (nL)-Black women are less likely to have what is considered an “optimal” VMB compared to nL-whites. We explored whether this explained their higher risk of cervical lesions compared to nL-whites and found that among women with “optimal” VMB, nL-Black women had eight times the risk of cervical lesions than nL-whites.

However, risk did not differ by race among women with “suboptimal” VMBs. Since HPV is necessary for CCa, perhaps the VMB influences the path through which HPV leads to CCa differently for nL-Blacks than nL-whites. HPV has hundreds of types, some more carcinogenic and more common in nL-Blacks than nL-whites. We will test whether genetic changes in HPV types correlate to VMB differences, and if this explains excess risk of cervical lesions among nL-Blacks versus nL-whites. If the VMB plays a role, then it could be used during CCa screening to guide clinicians in their decision to treat or not to treat. Also, if some HPV genetic changes are more common in different VMB, they could be exploited as potential targets to treat the virus.