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Diversity of the human vaginal microbiome

In the NIH Common Fund-sponsored Vaginal Human Microbiome Project at VCU, extensive health histories and vaginal samples (from the cervix, mid vaginal wall, and introitus) from over 6,000 visitors to our women's clinics, generally without regard to their state of urogenital health were collected. Of these, it has been performed deep, targeted 16S rRNA gene sequence analysis to generate microbiome profiles on samples from nearly 4,000 women. These participants were 62% self-identified African Americans, 21% Caucasian, 9% Latina, and 8% other. The health histories of these participants reveal a rich background of urogenital health issues, including approximately 27% with a history of Chlamydia infection, 17% with gonorrhea, 41% with UTI, 29% with bacterial vaginosis, 18% with trichomoniasis, 44% with yeast infection, etc. 724 of the participants were pregnant. Our analyses revealed a reproducible discrete panel of microbiome clusters, or vagitypes, that generally follow the pattern of a having single dominant taxon. Clear differences were observed between the vaginal microbiome profiles of healthy women, pregnant women, and women with histories of urogenital disease. Not unexpectedly, women of various racial and ethnic backgrounds exhibited predictable differences among their microbiomes. This work has led to a follow-up longitudinal study of the role of the vaginal and related microbiomes on the development of adverse outcomes including preterm birth and stillbirth during pregnancy.

Biography

Gregory A Buck earned a PhD in the Department of Microbiology and Immunology at the University of Washington in Seattle, and completed his postdoctoral training in molecular parasitology at the Institut Pasteur in Paris. He is currently Professor of Microbiology and Immunology and Director of the Center for the Study of Biological Complexity at VCU. The latter administrative unit which includes the University's Genomics, Bioinformatics and High Performance Computing Cores, and administers VCU's bioinformatics programs. His current research focuses on microbial and parasite genomics and metagenomics. He has published over 100 papers and chapters in reputed journals and books.

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