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Extensive richness of the human vaginal microbiome

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Abstract

Alterations in the composition of the microbiome of the human vagina have been implicated in preterm birth and stillbirth, susceptibility to sexually transmitted infections, and other pathological states. However, specific causality of these diseases, and the contribution of the bacterial components of the microbiome to them, have for the most part remained elusive. The Vaginal Microbiome Project at VCU has addressed these relationships by applying metagenomic rRNA gene taxonomic analysis to vaginal and associated samples selected from over 5,000 volunteers recruited from our women's health clinics over the past three years. In parallel, we have performed whole metagenomic shotgun sequence analysis on a panel of particularly interesting samples, and we have bacteriologically cloned, sequenced and analyzed the genomes of dozens of previously uncharacterized procaryotes. Our results illustrate a remarkable diversity in vaginal microbiomes that can be distilled into a dozen or so discrete 'vagitypes', some of which are associated with unanticipated states of health. Moreover, we have been able to culture, clone, microbiologically define, and sequence mjultiple previously uncharacterized bacterial species that can be described as likely 'emerging' pathogens. One of these bacteria, *Sneathiaamnii*, has been associated with spontaneous abortion and bacterial vaginosis. Others also currently under investigation exhibit previously undetected associations with common sexually transmitted diseases. Our objective in this research is to clarify the roles of the vaginal microbiota in the health of the female urogenital tract.

Biography

Gregory A. Buck earned a Ph.D. 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 director of the Center for the Study of Biological Complexity at VCU, which includes the University's Genomics, Bioinformatics and High Performance Computing Cores. His current research focuses on microbial and parasite genomics and metagenomics. He has published over 100 papers and chapters in reputed journals and books.