Molecular Definition Of Vaginal Microbiota In East African Commercial Sex Workers

Abstract:

Resistance to HIV infection in a cohort of commercial sex workers living in Nairobi, Kenya, is linked to mucosal and antiinflammatory factors that may be influenced by the vaginal microbiota. Since bacterial vaginosis (BV), a polymicrobial dysbiosis characterized by low levels of protective Lactobacillus organisms, is an established risk factor for HIV infection, we investigated whether vaginal microbiology was associated with HIV-exposed seronegative (HESN) or HIV-seropositive (HIV(+)) status in this cohort. A subset of 44 individuals was selected for deep-sequencing analysis based on the chaperonin 60 (cpn60) universal target (UT), including HESN individuals (n = 16), other HIV-seronegative controls (HIV-N, n = 16), and HIV(+) individuals (n = 12). Our findings indicate exceptionally high phylogenetic resolution of the cpn60 UT using reads as short as 200 bp, with 54 species in 29 genera detected in this group. Contrary to our initial hypothesis, few differences between HESN and HIV-N women were observed. Several HIV(+) women had distinct profiles dominated by Escherichia coli. The deep-sequencing phylogenetic profile of the vaginal microbiota corresponds closely to BV(+) and BV(-) diagnoses by microscopy, elucidating BV at the molecular level. A cluster of samples with intermediate abundance of Lactobacillus and dominant Gardnerella was identified, defining a distinct BV phenotype that may represent a transitional stage between BV(+) and BV(-). Several alpha- and betaproteobacteria, including the recently described species Variovorax paradoxus, were found to correlate positively with increased Lactobacillus levels that define the BV(-) ("normal") phenotype. We conclude that cpn60 UT is ideally suited to next-generation sequencing technologies for further investigation of microbial community dynamics and mucosal immunity underlying HIV resistance in this cohort