

Identification of Microbes Associated with the Urethra during Health and Inflammation

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The number of cases of urethritis, or inflammation of the male urethra, in the US has been estimated to be 2.8 million each year in the United States.¹ It is the most common reason young men seek primary care and this syndrome is associated with acute proctitis, epididymitis, and orchitis.² Approximately half of the cases are idiopathic, meaning that a causative agent cannot be identified. The goal of my project is to identify and characterize novel microorganisms that may be associated with male idiopathic urethritis. We used a variety of approaches to cultivate microorganisms from archived urethral swabs collected from men with idiopathic urethritis and healthy controls. We defined the phylogeny of the isolates using 16S rRNA sequencing to identify organisms that are not presently represented in microbial databases. Currently, we are scaling up a number of novel taxa we identified for genome sequencing. By adding these new genome sequencing to the existing databases we will be able to assign a higher proportion of reads from corresponding metagenomic sequence data and achieve a more complete survey of the male urethral microbiota in health and urethritis. This will provide crucial information which may permit us to identify urethritis associated organisms, develop new molecular diagnostics for these organisms, and discern if how these organisms are sexually transmitted

References

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