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Species level bacterial classification of the human bladder microbiota.

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Abstract

It has been recently established that the human bladder contains a bacterial community not associated with acute infection. This discovery of the bladder microbiota naturally leads to the question of its influence on the health of the host. Recent results have shown that changes in the composition of the bladder microbiota are associated with bladder disorders. For example, studies have identified characteristics in the urinary microbiota that are associated with symptom severity of urgency urinary incontinence (UUI) and response to the common UUI drug treatment solifenacin. These studies collectively provide evidence that the bladder microbiota is clinically relevant and warrants further investigation.

Understanding the changes of the bladder microbiota and their relationship to human health requires the identification of the bacterial species. Common identification methods avoid culturing bacteria, and instead rely on the comparison of variable regions of the bacterial 16S ribosomal gene sequence obtained directly from biological samples. However, these methods are limited to resolving bacterial identity to the genus level, and obscures the true relation of the bladder microbiota to the host.

Recently, several new approaches to bacterial identification have become available which may improve resolution to the species level. Thus, our primary aim was to determine if species-level identification of bladder microbiota is currently possible using subsequences of the 16S ribosomal gene sequence. We evaluated the ability of taxonomic classifiers to correctly classify 16S ribosomal sequences from bladder microbiota when used with different publicly available databases and taxonomic classifiers. We further evaluated several 16S rRNA gene variable regions for their ability to accurately distinguish between urinary bacterial species. We show that species-level bacterial identification is possible with currently available resources. Our findings allow future studies of the bladder microbiome to understand the effect of changes in species diversity on the health of the human host.