



Research Week 2022

You Are What They Eat?: Computational Evaluation of Host Glycans Utilization by Bladder Microbiota in Overactive Bladder Syndrome

Jean-Philippe Gourdine¹, Erin Dahl¹, Itallia Pacentine¹, Alec Barstad¹, Lisa Karstens^{1, 2}
gourdine@ohsu.edu

¹ Department of Medical Informatics and Clinical Epidemiology, Oregon Health & Science University, Portland, OR. ²Division of Urogynecology, Oregon Health & Science University, Portland, OR, United States

Keywords

Microbiome, Urobiome, Bladder Disorder, Overactive Bladder Syndrome, Glycobiology, Glycans, Bioinformatics, CAZy, Carbohydrate Active Enzyme database

Abstract

Overactive bladder syndrome (OAB) is a common disorder that negatively impacts quality of life and includes bothersome symptoms such as urinary frequency and urgency. Several factors can contribute to OAB symptoms, including recently discovered bacteria in the bladder (the urobiome). However, compared to other body sites, our knowledge of bacteria in bladder is in its infancy, and there are many questions that need to be addressed to identify the urobiome's clinical utility. The urothelium-lumen interface in the bladder is characterized by the glycocalyx, network of glycans (sugars) represented by cell membrane glycolipids, glycoproteins (e.g., uroplakins) and glycosaminoglycans (GAGs). As urine is not a nutrient rich environment, we hypothesized that the bladder bacteria nourish on the glycans in the glycocalyx, as is the case for some gut bacteria. We further hypothesized that the ability of bacteria in the bladder to forage host glycans is altered in women with OAB symptoms. Using a bioinformatics approach with dbCAN, the Carbohydrate Active Enzyme database (CAZy) and publicly available data, we searched for glycan-utilizing genes in 112 bladder bacterial genomes originating from women with and without OAB. We evaluated the presence of genes involved microbial utilization of host glycans in these bacteria. We identified significant differences ($p < 0.05$) for 10 bacterial glycoside hydrolase (GH) and polysaccharide lyase (PL) genes. Among these, PL8 and PL12, enzymes involved in GAGs degradation, were increased in bacteria from women without OAB. These genes were found in three bacteria - *Lactocaseibacillus rhamnosus* and *Streptococcus agalactiae*, and *Bacillus* species UMB0893 - that are generally more frequently found in women without OAB than women with OAB. These data suggest bacteria in women without OAB may consume more GAGs than bacteria in women with OAB, and that GAGs and associated byproducts may contribute to a healthy bladder.