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2-2021

Defining and Detecting Bacterial Consortia Within Urine Samples of Patients with Symptomatic Urinary Tract Infection

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STRAIN NAME	decreasing oxygenation →			
	AEROBIC	5% CO ₂	MICROAEROPHILIC	ANAEROBIC
	S-BAP	S-BAP	S-BAP	S-BAP
C33	+	+	++	+++
C33 (seyl)	-	-	-	-
DS16	-	-	-	-
OG1RF	-	-	-	-
JH2-2	-	-	-	-

Table Hemolytic Activity of Various *E. faecalis* Strains Under Different Atmospheric and Culture Conditions. (-) denotes no hemolysis, (+) denotes less hemolysis, (++) denotes slight hemolysis, and (+++) denotes hyperhemolysis. *S-BAP= Columbia Blood Agar supplemented with 5% sheep blood.

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Funding: The Welch Foundation

#BS29 | DEFINING AND DETECTING BACTERIAL CONSORTIA WITHIN URINE SAMPLES OF PATIENTS WITH SYMPTOMATIC URINARY TRACT INFECTION

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Introduction: Bacterial consortia are non-random patterns of bacterial communities that work synergistically to provide growth and survival advantages over planktonic, free-floating, microbes. In this study, we aim to characterize bacterial consortia identified by multiplex polymerase chain reaction (M-PCR) in symptomatic patients with polymicrobial urinary tract infections (UTI).

Methods: We performed a retrospective analysis of 2493 UTI-symptomatic patients over the age of 60 from 37 geographically disparate urology clinics from July 2018 to February 2019. M-PCR was performed to detect 24 different bacterial species. A cutoff of 10 detections was used to distinguish a bacterial consortium from a random association of bacteria in a polymicrobial specimen.

Results: Bacteria were detected in 68.8% (1710/2493) of specimens. Of these, 60.1% (1027/1710) were polymicrobial. Of these, bacterial consortia were found in 42.2% (433/1027). Eight bacteria formed 18 different consortia, which ranged in count from 2 to 4 bacterial species, **Table 1**. All consortia contained Gram-positive bacteria. Half of consortia contained gram negative bacteria, and no consortium had more than one Gram-negative bacterium. *A. Schaalii* and *A. urinae*, which are both Gram-positive, were the most commonly detected bacteria within the consortia, 73.0% and 67.7%, respectively, and were found in 14 of the 18 consortia. *A. Schaalii* and *A. urinae* were found together in 55.9% of consortia polymicrobial specimens, but in only 33% of non-consortia polymicrobial specimens. In contrast, some bacteria, such as *P. aeruginosa* and *S. aureus*, were detected in polymicrobial infections but not in any consortia.

Conclusion: The balance of bacteria in consortia is shifted not only toward Gram-positive bacteria but also toward specific Gram-positive bacteria. The high prevalence of *A. schaalii* or *A. urinae* in the consortia suggests that the organisms could be keystone bacteria in formation of pathogenic consortia.

Table 1. Frequencies of the bacterial consortia. Gram-negative organisms are bolded. (VGS = Viridans group streptococci, CoNS = Coagulase negative staphylococci)

Number of Species	Number of patients	Bacteria			
2	101	<i>A. schaalii</i>	<i>A. urinae</i>		
2	27	<i>E. coli</i>	VGS		
2	24	<i>A. schaalii</i>	<i>E. coli</i>		
2	21	<i>A. urinae</i>	<i>E. coli</i>		
2	20	<i>A. urinae</i>	VGS		
2	19	<i>A. schaalii</i>	VGS		
2	15	CoNS	<i>E. coli</i>		
2	14	CoNS	VGS		
2	10	<i>A. schaalii</i>	<i>K. pneumoniae</i>		
2	10	<i>A. urinae</i>	CoNS		
2	10	CoNS	<i>E. faecalis</i>		
3	50	<i>A. schaalii</i>	<i>A. urinae</i>	<i>E. coli</i>	
3	33	<i>A. schaalii</i>	<i>A. urinae</i>	VGS	
3	21	<i>A. schaalii</i>	<i>E. coli</i>	VGS	
3	15	<i>A. schaalii</i>	<i>A. urinae</i>	CoNS	
3	14	<i>A. schaalii</i>	<i>A. urinae</i>	<i>K. pneumoniae</i>	
3	11	<i>A. schaalii</i>	<i>A. urinae</i>	<i>C. rogelli</i>	
4	18	<i>A. schaalii</i>	<i>A. urinae</i>	<i>E. coli</i>	VGS

Funding: Pathnostics