93 The role of next generation sequencing of semen samples in the diagnosis and treatment of chronic bacterial prostatitis

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Introduction & Objectives: The diagnosis and treatment of patients with chronic bacterial prostatitis (CBP) remains to be challenging. Patients are often treated empirically based on symptoms and positive results for detected bacteria in expressed prostatic secretions, while studies with urine and/or semen cultures are generally lacking using typical culture methodology. Furthermore, the most studies suggested that only a minority of patients with CBP had a positive culture results. The aim of our study was to evaluate deoxyribonucleic acid next generation sequencing (DNA NGS) as a potential new test in the diagnosis and subsequent management of patients with symptoms of CBP.

Materials & Methods: A retrospective review of the semen DNA NGS results of 17 patients with symptoms of chronis CBP (NIH category II) was performed. All fresh semen specimens were collected from patients and processed through the whole bacterial and fungal semen microbiota spectrum by MicroGen DX, a US based CLIA certified laboratory. Two methods of molecular microbial diagnostic testing were performed: Level 1 Panel is a quantitative real-time PCR test for bacterial and fungal genes with specific assay for presence of antimicrobial drug resistance genes. The Level 2 Panel is a comprehensive NGS of all genomic DNA present in the patient specimen which aims to catalog all microbial and fungal pathogens present based on a database of 25,000 known species. The catalog of the microbial species, including drug resistance targets, provides detailed data that clinicians can utilize to supplement their local antibiograms and/or clinical pathways.

Results: All 17 patients had positive DNA NGS results. The average number of microorganisms present in each specimen was of 4.4 species, range (1-10). Resistance genes to different antibiotics detected were found in 4/17 specimens. 9/17 semen samples had primarily gram-positive bacteria mostly from Enterococcus family, 6/17 had mixed and 2/17 primarily gram-negative pathogens. In two cases a high bacterial load (>10^7microorganisms} was revealed, in 4- a moderate load (10^6-10^7), and in 11/17 - a low load (≤10^5), respectively. Two patients had fungal species in association with bacterial pathogens.

Conclusions: The diagnosis and treatment of CBP represents a difficult task for practicing urologists. This new technology of DNA NGS may provide a new diagnostic tool to analyze complete genomes of microorganisms in a timely manner and implement targeted and individual treatment of CBP. A significant number of patients had gram-positive organisms representing mostly Enterococcus family, which may stimulate us to revisit our approach to the treatment paradigms for CBP in the prospective studies further.