Journal of Urology and Renal Diseases
Rifat UN. J Urol Ren Dis 09: 1384.
www.doi.org/10.29011/2575-7903.001384
www.gavinpublishers.com

Editorial

The Microbiome and Genitourinary Cancer

Usama Nihad Rifat*

Emeritus Professor of Urology, Iraqi Board for Medical Specializations

***Corresponding author:** Usama Nihad Rifat, Emeritus Professor of Urology, Iraqi Board for Medical Specializations

Citation: Rifat UN (2024) The Microbiome and Genitourinary Cancer. J Urol Ren Dis 09: 1384. DOI: 10.29011/2575-7903.001384.

Received Date: 08 May 2024; **Accepted Date:** 08 May 2024; **Published Date:** 10 May 2024

A microbiome (from Ancient Greekμικρός (mikrós) 'small', and βίος(bíos) 'life') is a group of microorganisms that can usually be found living together in any given habitat. The gut microbiome, as defined by molecular biologist Joshua Lederberg, is the whole of microorganisms, bacteria, viruses, protozoa, and fungi, and their collective genetic material present in the Gastrointestinal Tract (GIT). Studies showed the differences in food and nutrient consumption to characterize the relationship between diet and microbes. Data serves as an initial point and documents that overweight and obese men with prostate cancer may manifest a unique microbiome profile. Further investigation is warranted to determine if the touch of prostate cancer exists, whether it is causative, and if it can be manipulated with diet and exercise to serve in efforts aimed toward cancer prevention and control [1]. Given the physiological function and anatomical position of the prostate gland, studies on the genitourinary tract microbiota are of major significance in the research of Prostate Carcinoma (PCa) [2]. Despite the overall present speculations on the possible association between genitourinary tract microbiome and PCa, very few trials have been conducted to date on this topic. One anatomical place is the genitourinary tract. It has been proven that the human genitourinary tract contains a variety of resident microbial communities, hence disapproving of the traditional view of urine being sterile. The presence of shared species in the urinary tract and those found in microbial populations of the gastrointestinal tract, vagina, or even skin was well defined. Nevertheless, some recent studies have suggested that the urinary tract contains microbial populations that are different from those at other sites of the human body that are populated by microbiomes.

There is evidence that the microbiome is involved in the development and treatment of many human diseases, including prostate cancer. There are several potential pathways for microbiome-based mechanisms for the development of prostate cancer: direct impacts of microbes or microbial products in the prostate or the urine, and indirect impacts from microbes or microbial products in the gastrointestinal tract. Unique microbial signs have been identified within the stool, oral cavity, tissue, urine, and blood of prostate cancer patients. Recent studies describe potential diagnostic and therapeutic applications of the microbiome, but further clinical investigation is needed [3]. Other findings suggested that the pathogenesis of prostatic neoplasia progresses from inflammation to post-inflammatory proliferative atrophy to Neoplasia [4]. Systematic characterization of the cancer microbiome provides a unique opportunity to develop cancer diagnostics that abuse non-human, microbial-derived molecules in a major human disease [5]. In an independent sample of 42 bladder cancer tissues, 11 had Fusobacterium nucleatum sequences detected by PCR [6].Further studies showed that the composition of our microbiota should be considered in future clinical studies aimed at assessing the therapeutic efficacy of new anticancer agents [7]. Although several studies suggested an involvement of microbiota dysbiosis in the pathogenesis, progression, and therapeutic response to bladder cancer, an established direct causal relationship remains to be clarified due to the lack of standardized methodologies associated with such studies [8].The range of data was validated by Polymerase Chain Reaction (PCR) and targeted Next-Generation Sequencing (NGS). Specific NGS data suggested that certain viral genomic sequences were inserted into the host somatic chromosomes of the prostate cancer samples. A randomly selected group of these was validated by direct PCR and sequencing. In addition, PCR validation of Helicobacter showed that Helicobacter cagA sequences integrated within specific chromosomes of prostate tumor cells. The viral and Helicobacter integrations are predicted to affect the expression of several cellular genes associated with oncogenic processes [9]. The role of the microbiome in genitourinary cancer is an emerging field that merits further studies. Translating microbiome research into clinical action will require the incorporation of microbiome surveillance into ongoing and future clinical trials as well as expansion of studies to include metagenomic sequencing and metabolomics [10]. There are measurable differences in the GI microbiota of men receiving oral Axis Targeted Therapy (ATT). Oral hormonal therapies for prostate cancer may alter the GI microbiota, influence clinical responses to ATT, and/or potentially modulate the antitumor effects of future therapies [11]. The prostate contains reduced bacteria, suggesting a possible pathophysiological correlation between the composition of the microbiome and PCa. The microbiome may be beneficial in maintaining the stability of the microenvironment of

the prostate and provides interesting perspectives for identifying novel biomarkers in high-PSA patients [12].

References

1. Frugé AD (2018) Dietary changes impact the gut microbe composition in overweight and obese men with prostate cancer undergoing radical prostatectomy. J Acad Nutr Diet 118: 714-723.e1.
2. Kustrimovic N, Bombelli R, Baci D, Mortara L (2023) Microbiome and Prostate Cancer: A Novel Target for Prevention and Treatment. Int. J. Mol. Sci 24: 1511.
3. Borowsky AD, Dingleyy KH, Ubicky E, Turteltauby KW (2006) Inflammation and Atrophy Precede Prostatic Neoplasia in a PhIP-Induced Rat Model, Neoplasia 8: 708-715.
4. Poore GD, Kopylova E, Zhu Q, Carpenter C (2020) Microbiome analyses of blood and tissues suggest cancer diagnostic approach, Nature 579: 567-574.
5. Ma J, Gnanasekar A, Lee A, Li WT (2020) Influence of Intratumor Microbiome on Clinical Outcome and Immune Processes in Prostate Cancer. Cancers 12: 2524.
6. Rescigno M (2015) A 'fit' microbiota to potentiate cancer immunotherapy, Rescigno Genome Medicine 7: 131.
7. Kustrimovic N, Bilato G, Mortara L, Baci D (2024) The Urinary Microbiome in Health and Disease: Relevance for Bladder Cancer, Int. J. Mol. Sci 25: 1732.
8. Banerjee S, Alwine JC, Wei Z, Tian T (2019) Microbiome signatures in prostate cancer, Carcinogenesis 40: 749-764.
9. Markowskia MC, Boorjianb SA, Burtonc JP, Hahn NM (2019) The Microbiome and Genitourinary Cancer: A Collaborative Review, Eur Urol75: 637-646.
10. Sfanos KS, Markowski MC, Peiffer LB, Ernst SB (2018) Compositional differences in gastrointestinal microbiota in prostate cancer patients treated with androgen axis-targeted therapies, Prostate Cancer and Prostatic Diseases 21: 539-548.
11. Ma X, Chi C, Fan L, Dong B (2019) The Microbiome of Prostate Fluid Is Associated with Prostate Cancer, Frontiers in Microbiology 10.