

肠道菌群在前列腺癌中的研究进展

余秋蕊*, 刘 瑞#

重庆医科大学附属第二医院肿瘤科, 重庆

收稿日期: 2026年2月6日; 录用日期: 2026年2月28日; 发布日期: 2026年3月11日

摘 要

近年来, 肠道菌群在癌症发生、发展及治疗中的作用逐渐成为研究的前沿领域。本文系统地探讨了肠道菌群与前列腺癌之间的复杂关系, 重点分析其在免疫调控、代谢途径及雄激素代谢中的多重机制。肠道菌群失调与慢性炎症的加剧及肿瘤微环境的恶化密切相关, 这种失衡可能削弱抗雄激素治疗及免疫检查点抑制剂的疗效。此外, 肠道菌群代谢产物(如短链脂肪酸和胆汁酸)通过多条信号通路影响癌细胞的增殖和存活。益生菌、益生元及膳食干预等策略在癌症治疗中的潜在价值逐步显现, 为精准医学的发展提供了新的方向。最后, 本文呼吁未来研究整合多组学数据, 以进一步推动肠道菌群在前列腺癌防治中的应用。

关键词

肠道菌群, 前列腺癌, 肿瘤微环境

Research Progress on Gut Microbiota in Prostate Cancer

Qiurui She*, Rui Liu#

Department of Oncology, The Second Affiliated Hospital of Chongqing Medical University, Chongqing

Received: February 6, 2026; accepted: February 28, 2026; published: March 11, 2026

Abstract

In recent years, the role of gut microbiota in the occurrence, development, and treatment of cancer has gradually become a cutting-edge research area. This article systematically explores the complex relationship between gut microbiota and prostate cancer, focusing on its multiple mechanisms in

*第一作者。

#通讯作者。

immune regulation, metabolic pathways, and androgen metabolism. Gut microbiota dysbiosis is closely related to the exacerbation of chronic inflammation and the deterioration of the tumor microenvironment; this imbalance may weaken the efficacy of anti-androgen therapy and immune checkpoint inhibitors. Furthermore, gut microbiota metabolites (such as short-chain fatty acids and bile acids) affect the proliferation and survival of cancer cells through multiple signaling pathways. The potential value of strategies such as probiotics, prebiotics, and dietary interventions in cancer treatment is gradually emerging, providing new directions for the development of precision medicine. Finally, this article calls for future research to integrate multi-omics data to further promote the application of gut microbiota in the prevention and treatment of prostate cancer.

Keywords

Gut Microbiota, Prostate Cancer, Tumor Microenvironment

Copyright © 2026 by author(s) and Hans Publishers Inc.

This work is licensed under the Creative Commons Attribution International License (CC BY 4.0).

<http://creativecommons.org/licenses/by/4.0/>



Open Access

1. 引言

前列腺癌是男性中最常见的癌症之一,也是导致癌症相关死亡的主要原因之一[1]。根据全球癌症统计数据,前列腺癌是男性中第二大常见癌症,仅次于肺癌,同时也是癌症相关死亡的第五大原因[2]。随着全球老龄化和预期寿命的延长,前列腺癌的发病率持续上升,其疾病负担不仅体现在高发病率上,还涉及长期治疗所需的医疗资源消耗及患者生活质量的显著下降[2]。

前列腺癌的发生受到多种因素的影响,包括遗传易感性、激素水平波动以及环境和生活方式因素(如饮食、肥胖和缺乏运动)。此外,代谢失衡和慢性炎症在前列腺癌的病理过程中也发挥了重要作用[3]。

近年来,肠道菌群作为人体健康调控关键因素,在癌症研究中备受关注。研究表明,肠道菌群不仅参与宿主的代谢与免疫调节,还与远端器官(包括前列腺)的健康密切相关[4]。通过“肠道-免疫系统-靶器官轴”这一概念,科学家们揭示了肠道菌群在维持全身健康与疾病进展中的重要作用[5]。

本综述旨在系统性回顾肠道菌群与前列腺癌之间的关系,重点探讨肠道菌群如何通过代谢和免疫途径影响前列腺癌的发病风险。此外,本文还分析了肠道菌群在前列腺癌治疗中的潜在应用,特别是益生菌、抗生素等干预手段的最新研究进展。通过梳理和总结这些发现,本文为未来的基础研究和临床实践提供参考,为开发新的个性化治疗策略奠定基础。

2. 肠道菌群的基本概念及其生理功能

肠道菌群是由数以万亿计的微生物组成的复杂生态系统,涵盖细菌、病毒、真菌和古细菌。这些微生物主要定植于结肠,并与宿主建立了共生关系,参与多种重要生理过程,如免疫调节和代谢平衡[6]。肠道菌群的组成和多样性因个体的饮食习惯、遗传背景、生活环境及抗生素使用而异[7]。保持肠道菌群的正常多样性是维持人体健康的重要基础。

肠道菌群通过与先天性免疫系统和适应性免疫系统的相互作用,维持宿主免疫稳态[8]。其中,肠道内的共生菌通过产生短链脂肪酸(SCFAs),如乙酸、丙酸和丁酸,促进肠上皮细胞的生长,并调节免疫反应。研究提示,这些代谢产物可通过影响T细胞的分化,抑制慢性炎症的发生[9]。此外,肠道菌群还通过调控胆汁酸和色氨酸的代谢对多种远端器官的健康产生影响[10]。

近年来,“肠道-肝脏-前列腺轴”这一假设逐渐受到关注[11]。该模型提出,肠道菌群代谢产物(如

SCFAs 和胆汁酸)可经由门静脉进入肝脏, 参与激素代谢, 从而间接影响前列腺健康[12]。此外, 研究发现, 肠道菌群失衡可能导致慢性低度炎症, 从而通过免疫信号通路增加前列腺癌的风险[13]。

肠道菌群的组成和功能失调(即菌群失调)与多种疾病密切相关, 包括肥胖、糖尿病及癌症[14]。具体而言, 肠道菌群失衡会导致致病菌的增殖, 这些致病菌通过产生促炎性因子加剧全身性炎症, 最终促进肿瘤的发生与发展。

3. 肠道菌群参与前列腺癌发生与进展的生物学机制

近年来, 大量研究[4] [6] [12] [13] [15]揭示了肠道菌群不仅与前列腺癌风险相关, 更通过一系列明确的生物学过程参与肿瘤发生与进展。这些作用主要体现在三个核心层面: 免疫调节与慢性炎症、代谢产物介导的信号传导以及细菌源性雄激素代谢调控。三者相互作用, 共同构成“肠道-免疫-前列腺轴”。

3.1. 免疫调节与慢性炎症

肠道菌群是宿主免疫系统的重要调节因子, 对先天性和适应性免疫反应均具有显著影响[8]。在稳态条件下, 共生菌通过促进调节性 T 细胞(Treg)分化以及诱导抗炎性细胞因子(如 IL-10)分泌, 维持免疫平衡并抑制慢性炎症[8] [16] [17]。

当肠道菌群失调时, 肠道屏障功能受损, 通透性增加(“肠漏”现象), 细菌产物如脂多糖(LPS)进入血液循环, 激活系统性炎症反应[18] [19]。持续炎症可通过核因子 κ B (nuclear factor kappa-B, NF- κ B)、信号传导及转录激活蛋白 3 (STAT3)及 JAK/STAT 信号通路在前列腺组织中扩展, 促进癌细胞增殖并增强侵袭能力[20] [21]。

在前列腺癌微环境中, 促炎性细胞因子(如 IL-6、IL-17 和 TNF- α)水平显著升高, 而抗炎性细胞因子(如 IL-10)表达下降[22]-[25]。IL-6 通过激活 STAT3 信号增强癌细胞存活能力, 并与治疗耐药密切相关[21] [22]; IL-17 则参与免疫抑制性微环境的形成, 削弱抗肿瘤免疫反应[24]。临床研究显示, 晚期前列腺癌患者肠道菌群多样性降低, 与炎症水平升高及肿瘤负担增加显著相关[26] [27]。

此外, 肠道菌群状态还可能影响免疫检查点抑制剂(ICI)的疗效, 提示其在肿瘤免疫治疗中的重要作用[28]。

3.2. 代谢产物介导的信号传导

除免疫调节外, 肠道菌群还通过其代谢产物直接参与前列腺癌相关信号通路的调控。主要代谢物包括短链脂肪酸(SCFAs)、胆汁酸及色氨酸代谢产物[29]-[31]。

短链脂肪酸(SCFAs), 如乙酸、丙酸和丁酸, 由肠道菌群发酵膳食纤维产生[29]。丁酸具有抗炎和抗增殖特性, 可通过抑制组蛋白去乙酰化酶(HDAC)调节基因表达, 从而抑制癌细胞增殖并诱导凋亡[32] [33]。此外, SCFAs 还能增强 Treg 功能并促进 IL-10 分泌, 从而缓解慢性炎症[32]。当高脂饮食导致菌群失调时, SCFAs 生成减少, 前列腺组织暴露于更高水平的促炎环境[34] [35]。

肠道菌群还参与初级胆汁酸向次级胆汁酸的转化。某些次级胆汁酸, 如脱氧胆酸(DCA), 可诱导 DNA 损伤, 并激活磷脂酰肌醇 3-激酶/蛋白激酶 B/哺乳动物雷帕霉素靶蛋白(PI3K/AKT/mTOR)信号通路, 促进癌细胞增殖与存活[30] [36] [37]。此外, 胆汁酸代谢改变还可能影响雄激素代谢, 从而间接调节前列腺癌进展[36]。

色氨酸在肠道菌群作用下可转化为吲哚及其衍生物, 这些代谢物通过芳香烃受体(AhR)信号通路调控免疫反应和肿瘤微环境, 其代谢失衡与肿瘤侵袭性增加相关[31]。

饮食结构在上述代谢过程中发挥重要调控作用。高脂及红肉饮食可增加促癌代谢物生成, 而富含膳

膳食纤维的饮食有助于促进 SCFAs 生成并改善菌群结构, 从而降低癌症风险[38]-[40]。

3.3. 细菌源性雄激素代谢与治疗耐药

前列腺癌的发生和进展高度依赖雄激素信号通路[41] [42]。近年来研究发现, 部分肠道细菌具备类固醇代谢能力, 可参与睾酮及二氢睾酮(DHT)的转化, 从而影响体内雄激素水平[43]。

在菌群稳态下, 肠道微生物有助于维持类固醇代谢平衡。然而, 当菌群失调时, 雄激素代谢通路可能受到干扰, 促进癌细胞在低雄激素环境下持续生长[43]。

抗雄激素治疗(ADT)是晚期前列腺癌的标准疗法, 但研究表明, ADT 可显著改变肠道菌群组成, 增加某些致病菌丰度, 并降低抗炎菌比例[44]。此外, 部分细菌可能在去势环境下合成类固醇前体物质, 从而促进 ADT 耐药的发生[45] [46]。

因此, 通过益生元或益生菌调节肠道菌群结构, 可能成为增强 ADT 疗效并延缓耐药的新策略[47]。

4. 肠道菌群对前列腺癌治疗的潜在作用

肠道菌群不仅与前列腺癌的发生密切相关, 还在治疗过程中发挥重要作用。调节肠道菌群可能影响癌症疗效、副作用以及患者的生活质量[48]。越来越多研究者正逐步探索益生菌、益生元、抗雄激素治疗和抗生素等干预手段如何与肠道菌群相互作用, 以改善前列腺癌的治疗效果。

益生菌和益生元有望通过调节肠道菌群和改善免疫功能, 在前列腺癌治疗中起到辅助作用[49]。某些益生菌(如双歧杆菌和乳酸菌)能够通过促进抗炎性细胞因子(如 IL-10)的产生, 抑制促炎性细胞因子(如 IL-6、TNF- α)的释放, 从而减缓肿瘤进展[50]。此外, 益生菌在增强肠道屏障功能方面的作用有助于减少患者在化疗或放疗期间的肠道副作用, 并提高治疗耐受性[51]。

抗雄激素治疗(ADT)和去势治疗是晚期前列腺癌的标准治疗方法。然而, 这些治疗会导致患者体内激素水平的剧烈波动, 从而影响肠道菌群的结构和功能。研究发现, ADT 治疗后肠道中某些有害菌(如拟杆菌属)的丰度增加, 而益生菌的丰度降低, 这可能加剧肠道炎症并降低治疗效果[52]。因此, 通过益生元和益生菌调节肠道环境, 或可提高 ADT 的疗效, 并减轻其副作用[47]。

抗生素的使用对肠道菌群具有显著影响, 这种效应可能干扰癌症免疫疗法的效果。近年来, 免疫检查点抑制剂(如 PD-1 和 CTLA-4 抑制剂)在癌症治疗中取得巨大进展, 但其疗效依赖于肠道菌群的状态[53]。研究表明, 抗生素使用会导致肠道菌群多样性下降, 削弱免疫检查点抑制剂的抗肿瘤活性[54]。

未来的研究可进一步探索肠道菌群在药物治疗中的作用, 特别是在个性化医疗和精准医学领域。通过分析患者的肠道菌群组成, 制定个性化治疗方案, 将有助于优化前列腺癌的治疗效果。此外, 益生菌、益生元及其他微生物干预手段的联合使用或可成为增强癌症治疗的新策略。

5. 未来研究方向

当前, 肠道菌群与前列腺癌之间的关联已受到广泛关注, 但其具体的因果关系仍需进一步探究。纵向研究和大规模队列研究有助于明确肠道菌群变化与前列腺癌进展之间的时间顺序。此外, 基于随机对照试验的研究设计可以在验证干预措施效果的同时, 揭示肠道菌群在癌症治疗中的调控潜力。精准医学的发展依赖于多组学数据的整合分析。宏基因组学、转录组学和代谢组学等技术已广泛应用于癌症研究, 未来可将这些组学数据与肠道菌群分析相结合, 以构建更全面的疾病图谱。

随着研究的深入, 肠道菌群调节已被视为一种潜在的前列腺癌治疗策略[55]。益生菌、益生元和粪菌移植(FMT)等干预手段的探索, 为未来治疗带来了新的希望。研究显示, 粪菌移植有助于恢复因抗生素或化疗破坏的肠道菌群, 并可能提高免疫治疗的效果[56]。未来的研究应进一步优化这些干预措施, 以减少

副作用并提升治疗效果。

大数据分析和机器学习技术为解码肠道菌群与癌症之间复杂关系提供了有力工具。通过深度学习模型, 研究者能从大规模的多组学数据中识别关键生物标志物。这些标志物可用于预测前列腺癌的风险和进展, 并为个性化治疗提供支持。此外, 基于人工智能的分析还可帮助识别特定的菌群特征, 以优化癌症治疗方案。

尽管肠道菌群在前列腺癌治疗中的应用前景广阔, 但如何将这些研究成果转化为临床实践仍面临诸多挑战。例如, 不同个体的菌群组成差异较大, 这为制定通用的干预策略带来了困难。未来的研究需开发更精确的诊断工具和个体化干预手段, 以应对这些挑战。通过整合多组学数据和肠道菌群分析, 精准医学有望实现更高效的癌症防治。

6. 结论

肠道菌群在前列腺癌的发生与治疗中扮演着关键角色。肠道菌群通过免疫调控、雄激素代谢及代谢产物的生成, 影响癌细胞的增殖和对治疗的反应。肠道菌群失调不仅会增加慢性炎症水平, 还可能削弱抗雄激素治疗及免疫疗法的疗效。

然而, 需要指出的是, 目前相关研究仍以横断面分析和动物模型实验为主, 缺乏大规模、长期随访的纵向数据支持, 因果关系尚未完全明确。小鼠模型与人类免疫系统及肠道菌群组成之间存在显著差异, 使部分机制性发现的临床外推受到限制。此外, 不同研究在样本选择、测序方法及数据分析策略方面存在差异, 增加了结果异质性。粪菌移植等干预措施虽显示出潜在应用前景, 但其长期安全性、标准化操作流程及伦理问题仍需进一步验证。

因此, 未来研究应基于多中心前瞻性队列设计, 结合宏基因组学、代谢组学及免疫组学等多组学整合分析, 以更精准地揭示肠道菌群在前列腺癌发生与治疗中的因果作用。同时, 需在严格安全评估基础上探索益生菌、益生元及膳食干预等调节策略的临床价值。通过更加严谨的研究设计与跨学科整合, 肠道菌群有望成为前列腺癌精准诊疗体系中的重要组成部分。

总体而言, 肠道菌群的调控为前列腺癌的防治提供了新的研究方向与潜在干预靶点, 但其临床转化仍需在机制明确性与安全性评估方面取得进一步突破。随着研究不断深入, 基于微生物组的个体化治疗策略或将在未来发挥更加重要的作用。

参考文献

- [1] Rawla, P. (2019) Epidemiology of Prostate Cancer. *World Journal of Oncology*, **10**, 63-89. <https://doi.org/10.14740/wjon1191>
- [2] Sung, H., Ferlay, J., Siegel, R.L., Laversanne, M., Soerjomataram, I., Jemal, A., *et al.* (2021) Global Cancer Statistics 2020: GLOBOCAN Estimates of Incidence and Mortality Worldwide for 36 Cancers in 185 Countries. *CA: A Cancer Journal for Clinicians*, **71**, 209-249. <https://doi.org/10.3322/caac.21660>
- [3] Zitvogel, L., Pietrocola, F. and Kroemer, G. (2017) Nutrition, Inflammation and Cancer. *Nature Immunology*, **18**, 843-850. <https://doi.org/10.1038/ni.3754>
- [4] Routy, B., Gopalakrishnan, V., Daillère, R., Zitvogel, L., Wargo, J.A. and Kroemer, G. (2018) The Gut Microbiota Influences Anticancer Immunosurveillance and General Health. *Nature Reviews Clinical Oncology*, **15**, 382-396. <https://doi.org/10.1038/s41571-018-0006-2>
- [5] Zhu, Q., Gao, R., Wu, W. and Qin, H. (2013) The Role of Gut Microbiota in the Pathogenesis of Colorectal Cancer. *Tumor Biology*, **34**, 1285-1300. <https://doi.org/10.1007/s13277-013-0684-4>
- [6] Kho, Z.Y. and Lal, S.K. (2018) The Human Gut Microbiome—A Potential Controller of Wellness and Disease. *Frontiers in Microbiology*, **9**, Article 1835. <https://doi.org/10.3389/fmicb.2018.01835>
- [7] Zmora, N., Suez, J. and Elinav, E. (2018) You Are What You Eat: Diet, Health and the Gut Microbiota. *Nature Reviews Gastroenterology & Hepatology*, **16**, 35-56. <https://doi.org/10.1038/s41575-018-0061-2>

- [8] Belkaid, Y. and Hand, T.W. (2014) Role of the Microbiota in Immunity and Inflammation. *Cell*, **157**, 121-141. <https://doi.org/10.1016/j.cell.2014.03.011>
- [9] Koh, A., De Vadder, F., Kovatcheva-Datchary, P. and Bäckhed, F. (2016) From Dietary Fiber to Host Physiology: Short-Chain Fatty Acids as Key Bacterial Metabolites. *Cell*, **165**, 1332-1345. <https://doi.org/10.1016/j.cell.2016.05.041>
- [10] Ridlon, J.M., Kang, D. and Hylemon, P.B. (2006) Bile Salt Biotransformations by Human Intestinal Bacteria. *Journal of Lipid Research*, **47**, 241-259. <https://doi.org/10.1194/jlr.r500013-jlr200>
- [11] De Lazzari, G., Opattova, A. and Arena, S. (2024) Novel Frontiers in Urogenital Cancers: From Molecular Bases to Preclinical Models to Tailor Personalized Treatments in Ovarian and Prostate Cancer Patients. *Journal of Experimental & Clinical Cancer Research*, **43**, Article No. 146. <https://doi.org/10.1186/s13046-024-03065-0>
- [12] Fujita, K., Matsushita, M., Banno, E., De Velasco, M.A., Hatano, K., Nonomura, N., et al. (2022) Gut Microbiome and Prostate Cancer. *International Journal of Urology*, **29**, 793-798. <https://doi.org/10.1111/iju.14894>
- [13] Porter, C.M., Shrestha, E., Peiffer, L.B. and Sfanos, K.S. (2018) The Microbiome in Prostate Inflammation and Prostate Cancer. *Prostate Cancer and Prostatic Diseases*, **21**, 345-354. <https://doi.org/10.1038/s41391-018-0041-1>
- [14] Tilg, H. and Moschen, A.R. (2014) Microbiota and Diabetes: An Evolving Relationship. *Gut*, **63**, 1513-1521. <https://doi.org/10.1136/gutjnl-2014-306928>
- [15] Garrett, W.S. (2015) Cancer and the Microbiota. *Science*, **348**, 80-86. <https://doi.org/10.1126/science.aaa4972>
- [16] Tanabe, S. (2013) The Effect of Probiotics and Gut Microbiota on Th17 Cells. *International Reviews of Immunology*, **32**, 511-525. <https://doi.org/10.3109/08830185.2013.839665>
- [17] Atarashi, K., Tanoue, T., Oshima, K., Suda, W., Nagano, Y., Nishikawa, H., et al. (2013) Treg Induction by a Rationally Selected Mixture of Clostridia Strains from the Human Microbiota. *Nature*, **500**, 232-236. <https://doi.org/10.1038/nature12331>
- [18] Fasano, A. (2020) All Disease Begins in the (Leaky) Gut: Role of Zonulin-Mediated Gut Permeability in the Pathogenesis of Some Chronic Inflammatory Diseases. *F1000Research*, **9**, Article 69. <https://doi.org/10.12688/f1000research.20510.1>
- [19] Starling, S. (2018) Lipid Surveillance by Skin ILCs. *Nature Reviews Immunology*, **18**, 78-78. <https://doi.org/10.1038/nri.2018.1>
- [20] Suh, J. and Rabson, A.B. (2003) NF- κ B Activation in Human Prostate Cancer: Important Mediator or Epiphenomenon? *Journal of Cellular Biochemistry*, **91**, 100-117. <https://doi.org/10.1002/jcb.10729>
- [21] Ghandadi, M. and Sahebkar, A. (2016) Interleukin-6: A Critical Cytokine in Cancer Multidrug Resistance. *Current Pharmaceutical Design*, **22**, 518-526. <https://doi.org/10.2174/1381612822666151124234417>
- [22] Culig, Z. and Puhr, M. (2012) Interleukin-6: A Multifunctional Targetable Cytokine in Human Prostate Cancer. *Molecular and Cellular Endocrinology*, **360**, 52-58. <https://doi.org/10.1016/j.mce.2011.05.033>
- [23] Sfanos, K.S., Hempel, H.A. and De Marzo, A.M. (2014) The Role of Inflammation in Prostate Cancer. *Advances in Experimental Medicine and Biology*, **816**, 153-181. https://doi.org/10.1007/978-3-0348-0837-8_7
- [24] Martin-Orozco, N. and Dong, C. (2009) The IL-17/IL-23 Axis of Inflammation in Cancer: Friend or Foe? *Current Opinion in Investigational Drugs*, **10**, 543-549.
- [25] Wang, X., Wong, K., Ouyang, W. and Rutz, S. (2017) Targeting IL-10 Family Cytokines for the Treatment of Human Diseases. *Cold Spring Harbor Perspectives in Biology*, **11**, a028548. <https://doi.org/10.1101/cshperspect.a028548>
- [26] Shyanti, R.K., Greggs, J., Malik, S. and Mishra, M. (2024) Gut Dysbiosis Impacts the Immune System and Promotes Prostate Cancer. *Immunology Letters*, **268**, Article ID: 106883. <https://doi.org/10.1016/j.imlet.2024.106883>
- [27] Candela, M. (2014) Inflammation and Colorectal Cancer, When Microbiota-Host Mutualism Breaks. *World Journal of Gastroenterology*, **20**, 908-922. <https://doi.org/10.3748/wjg.v20.i4.908>
- [28] Yin, Q., Ni, J. and Ying, J. (2024) Potential Mechanisms and Targeting Strategies of the Gut Microbiota in Antitumor Immunity and Immunotherapy. *Immunity, Inflammation and Disease*, **12**, e1263. <https://doi.org/10.1002/iid3.1263>
- [29] Tan, J., McKenzie, C., Potamitis, M., Thorburn, A.N., Mackay, C.R. and Macia, L. (2014) The Role of Short-Chain Fatty Acids in Health and Disease. *Advances in Immunology*, **121**, 91-119. <https://doi.org/10.1016/b978-0-12-800100-4.00003-9>
- [30] Di Ciaula, A., Wang, D.Q.-H., Molina-Molina, E., Lunardi Baccetto, R., Calamita, G., Palmieri, V.O., et al. (2017) Bile Acids and Cancer: Direct and Environmental-Dependent Effects. *Annals of Hepatology*, **16**, S87-S105. <https://doi.org/10.5604/01.3001.0010.5501>
- [31] Sun, M., Ma, N., He, T., Johnston, L.J. and Ma, X. (2019) Tryptophan (TRP) Modulates Gut Homeostasis via Aryl Hydrocarbon Receptor (AHR). *Critical Reviews in Food Science and Nutrition*, **60**, 1760-1768. <https://doi.org/10.1080/10408398.2019.1598334>
- [32] Ozkan, A.D., Eskiler, G.G., Kazan, N. and Turna, O. (2022) Histone Deacetylase Inhibitor Sodium Butyrate Regulates

- the Activation of Toll-Like Receptor 4/Interferon Regulatory Factor-3 Signaling Pathways in Prostate Cancer Cells. *Journal of Cancer Research and Therapeutics*, **19**, 1812-1817. https://doi.org/10.4103/jcrt.jcrt_2032_21
- [33] Lipska, K., Gumieniczek, A. and Filip, A.A. (2020) Anticonvulsant Valproic Acid and Other Short-Chain Fatty Acids as Novel Anticancer Therapeutics: Possibilities and Challenges. *Acta Pharmaceutica*, **70**, 291-301. <https://doi.org/10.2478/acph-2020-0021>
- [34] Feitelson, M.A., Arzumanyan, A., Medhat, A. and Spector, I. (2023) Short-Chain Fatty Acids in Cancer Pathogenesis. *Cancer and Metastasis Reviews*, **42**, 677-698. <https://doi.org/10.1007/s10555-023-10117-y>
- [35] Zhong, W., Wu, K., Long, Z., Zhou, X., Zhong, C., Wang, S., *et al.* (2022) Gut Dysbiosis Promotes Prostate Cancer Progression and Docetaxel Resistance via Activating NF- κ B-IL6-STAT3 Axis. *Microbiome*, **10**, Article No. 94. <https://doi.org/10.1186/s40168-022-01289-w>
- [36] Liu, Y., Zhang, S., Zhou, W., Hu, D., Xu, H. and Ji, G. (2022) Secondary Bile Acids and Tumorigenesis in Colorectal Cancer. *Frontiers in Oncology*, **12**, Article 813745. <https://doi.org/10.3389/fonc.2022.813745>
- [37] Xi, Y., Yani, Z., Jing, M., Yinhang, W., Xiaohui, H., Jing, Z., *et al.* (2021) Mechanisms of Induction of Tumors by Cholesterol and Potential Therapeutic Prospects. *Biomedicine & Pharmacotherapy*, **144**, Article ID: 112277. <https://doi.org/10.1016/j.biopha.2021.112277>
- [38] Abu-Ghazaleh, N., Chua, W.J. and Gopalan, V. (2020) Intestinal Microbiota and Its Association with Colon Cancer and Red/Processed Meat Consumption. *Journal of Gastroenterology and Hepatology*, **36**, 75-88. <https://doi.org/10.1111/jgh.15042>
- [39] Fusco, W., Lorenzo, M.B., Cintoni, M., Porcari, S., Rinninella, E., Kaitsas, F., *et al.* (2023) Short-Chain Fatty-Acid-Producing Bacteria: Key Components of the Human Gut Microbiota. *Nutrients*, **15**, Article 2211. <https://doi.org/10.3390/nu15092211>
- [40] Sidahmed, E., Freedland, S.J., Wang, M., *et al.* (2024) Dietary Fiber Intake and Risk of Advanced and Aggressive Forms of Prostate Cancer: A Pooled Analysis of 15 Prospective Cohort Studies. *Journal of the Academy of Nutrition and Dietetics*, **125**, 11-23.e22.
- [41] Pernigoni, N., Zagato, E., Calcinotto, A., Troiani, M., Mestre, R.P., Cali, B., *et al.* (2021) Commensal Bacteria Promote Endocrine Resistance in Prostate Cancer through Androgen Biosynthesis. *Science*, **374**, 216-224. <https://doi.org/10.1126/science.abf8403>
- [42] Kunc, M., Gabrych, A. and Witkowski, J.M. (2015) Microbiome Impact on Metabolism and Function of Sex, Thyroid, Growth and Parathyroid Hormones. *Acta Biochimica Polonica*, **63**, 189-201. https://doi.org/10.18388/abp.2015_1093
- [43] Lin, G., Zhang, F., Weng, X., Hong, Z., Ye, D. and Wang, G. (2024) Role of Gut Microbiota in the Pathogenesis of Castration-Resistant Prostate Cancer: A Comprehensive Study Using Sequencing and Animal Models. *Oncogene*, **43**, 2373-2388. <https://doi.org/10.1038/s41388-024-03073-6>
- [44] Senchukova, M.A. (2023) Microbiota of the Gastrointestinal Tract: Friend or Foe? *World Journal of Gastroenterology*, **29**, 19-42. <https://doi.org/10.3748/wjg.v29.i1.19>
- [45] Wang, L. (2023) Changes in the Gut Microbial Profile during Long-Term Androgen Deprivation Therapy for Prostate Cancer. *Prostate Cancer and Prostatic Diseases*, **27**, 667-673. <https://doi.org/10.1038/s41391-023-00723-w>
- [46] Terrisse, S., Zitvogel, L. and Kroemer, G. (2022) Effects of the Intestinal Microbiota on Prostate Cancer Treatment by Androgen Deprivation Therapy. *Microbial Cell*, **9**, 190-194. <https://doi.org/10.15698/mic2022.12.787>
- [47] Cao, H., Zhang, D., Wang, P., Wang, Y., Shi, C., Wu, H., *et al.* (2024) Gut Microbiome: A Novel Preventive and Therapeutic Target for Prostatic Disease. *Frontiers in Cellular and Infection Microbiology*, **14**, Article 1431088. <https://doi.org/10.3389/fcimb.2024.1431088>
- [48] Zitvogel, L., Ayyoub, M., Routy, B. and Kroemer, G. (2016) Microbiome and Anticancer Immunosurveillance. *Cell*, **165**, 276-287. <https://doi.org/10.1016/j.cell.2016.03.001>
- [49] Pernigoni, N., Guo, C., Gallagher, L., Yuan, W., Colucci, M., Troiani, M., *et al.* (2023) The Potential Role of the Microbiota in Prostate Cancer Pathogenesis and Treatment. *Nature Reviews Urology*, **20**, 706-718. <https://doi.org/10.1038/s41585-023-00795-2>
- [50] Li, S., Hsu, W., Chang, J. and Shih, C. (2019) Combination of Lactobacillus Acidophilus and Bifidobacterium Animalis Subsp. Lactis Shows a Stronger Anti-Inflammatory Effect than Individual Strains in HT-29 Cells. *Nutrients*, **11**, Article 969. <https://doi.org/10.3390/nu11050969>
- [51] Toucheffeu, Y., Montassier, E., Nieman, K., Gastinne, T., Potel, G., Bruley des Varannes, S., *et al.* (2014) Systematic Review: The Role of the Gut Microbiota in Chemotherapy- or Radiation-Induced Gastrointestinal Mucositis—Current Evidence and Potential Clinical Applications. *Alimentary Pharmacology & Therapeutics*, **40**, 409-421. <https://doi.org/10.1111/apt.12878>
- [52] Kure, A., Tsukimi, T., Ishii, C., Aw, W., Obana, N., Nakato, G., *et al.* (2022) Gut Environment Changes Due to Androgen

-
- Deprivation Therapy in Patients with Prostate Cancer. *Prostate Cancer and Prostatic Diseases*, **26**, 323-330. <https://doi.org/10.1038/s41391-022-00536-3>
- [53] Gao, Y., Xu, P., Sun, D., Jiang, Y., Lin, X., Han, T., *et al.* (2023) *Faecalibacterium prausnitzii* Abrogates Intestinal Toxicity and Promotes Tumor Immunity to Increase the Efficacy of Dual CTLA4 and PD-1 Checkpoint Blockade. *Cancer Research*, **83**, 3710-3725. <https://doi.org/10.1158/0008-5472.can-23-0605>
- [54] Perets, R., Meshner, S., Tirosh, O., Eshar, S., Metz-Breiner, A., Kruger Ben-Shabat, S., *et al.* (2024) Preliminary Results from a FIH, Open-Label Phase 1 Study with BMC128, a Rationally Designed Live Bacterial Consortium, in Combination with Nivolumab. *Journal of Clinical Oncology*, **42**, 8631-8631. https://doi.org/10.1200/jco.2024.42.16_suppl.8631
- [55] Han, Z. and Ai, J. (2024) Editorial: Biomarkers and Immunotherapy for Genitourinary Tumors. *Frontiers in Immunology*, **15**, Article 1394170. <https://doi.org/10.3389/fimmu.2024.1394170>
- [56] Baruch, E.N., Youngster, I., Ben-Betzalel, G., Ortenberg, R., Lahat, A., Katz, L., *et al.* (2021) Fecal Microbiota Transplant Promotes Response in Immunotherapy-Refractory Melanoma Patients. *Science*, **371**, 602-609. <https://doi.org/10.1126/science.abb5920>