

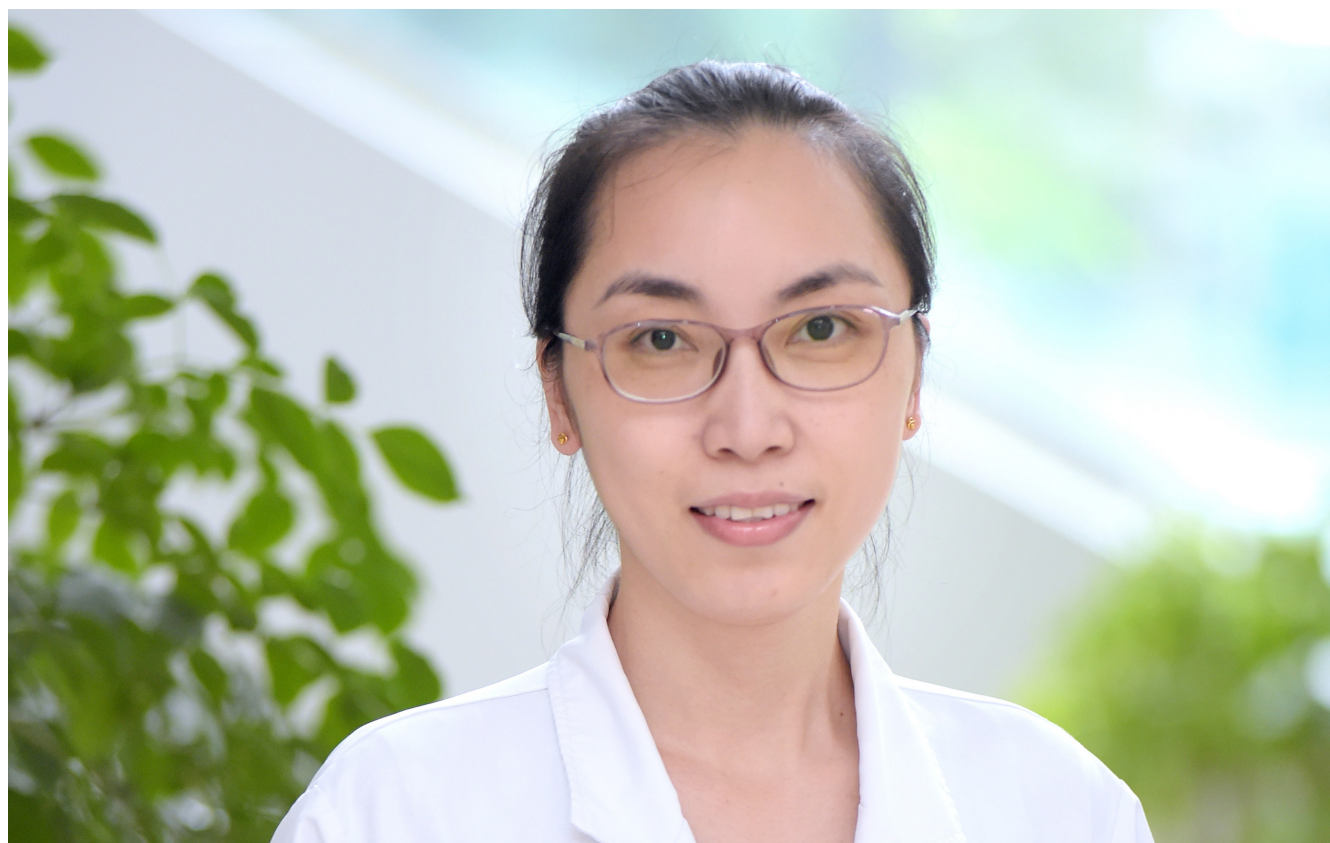
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肠道菌群与胃肠动力关系的研究进展

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Progress in understanding of relationship between gut microbiota and gastrointestinal motility

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Abstract

Gastrointestinal motility disorders are a group of common clinical disorders in which abnormal gastrointestinal motility is the major pathogenesis, including irritable bowel syndrome, functional dyspepsia, and diabetic gastroparesis. With the rapid development of microbial sequencing technology in the past 10 years, the understanding of the gut microbiota has greatly improved, and it is generally found that patients with gastrointestinal motility diseases have gut microbiota disorders. Some progress has been made on the correlation between gut microbiota and gastrointestinal motility. This review aims to elucidate the relationship between gut microbiota and gastrointestinal motility and the mechanism of their interaction.

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Key Words: Gut microbiota; Gastrointestinal motility; Enteric nervous system; Intestinal barrier; Intestinal immunity

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摘要

胃肠动力障碍性疾病是一类以胃肠动力异常为主要发病机制的临床常见病, 包括肠易激综合征、功能性消化不良、糖尿病胃轻瘫等. 近十余年来随着微生物测序技术的迅猛发展, 人们对肠道菌群的了解日益深入, 普遍发现胃肠动力障碍性疾病存在肠道菌群的紊乱. 关于肠道菌群与胃肠动力的相关性研究也取得了

一些进展, 本文就肠道菌群与胃肠动力的关系及二者相互作用的机制作一综述。

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关键词: 肠道菌群; 胃肠动力; 肠神经系统; 肠屏障; 肠道免疫

核心提要: 胃肠动力障碍性疾病患者普遍存在肠道菌群的紊乱, 肠道菌群与胃肠动力之间的关系逐渐引起人们的关注. 研究发现二者在生理及病理上相互关联, 相互影响, 并通过肠神经系统、肠屏障、肠道免疫等途径发生紧密的交互作用。

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0 引言

肠道菌群是指定居在人体胃肠道内所有微生物的总称. 正常人肠道微生物的细胞数高达100万亿, 为人体细胞总量的10倍, 其涵盖了500多万个基因, 是人类基因组的100多倍^[1,2]. 肠道菌群构建了一个极其庞大且复杂的微生态系统, 具有防止病原菌定植、参与物质代谢、合成人体必需的氨基酸和维生素以及调节肠道免疫等功能^[1,3]. 研究发现肠道菌群具有强大的新陈代谢能力, 等同于肝脏的代谢水平, 对维持人体健康意义重大, 因此又被称为“隐藏的器官”^[4]. 胃肠运动是消化系统最核心的生理功能之一, 以前人们很少把肠道菌群与胃肠动力联系在一起, 但越来越多的研究发现这两者之间的关系比我们想象的要复杂的多^[3,5-8].

1 肠道菌群概述

肠道菌群包括细菌、真菌和古生菌, 其中细菌占绝大多数, 其中又以厌氧菌为主, 其数量是需氧和兼性厌氧菌的100-1000倍^[9-11]. 由于解剖结构及生理特性的差异, 胃肠道的不同区域肠道菌群的定植数量(以每克或毫升肠内容物计算)及种类有所区别. 胃内由于胃酸的存在, 微生物的数量偏少($0-10^3$ 个), 近端小肠虽然PH值较胃区升高, 但由于肠蠕动致肠液流动较快, 微生物较难定植($0-10^5$ 个). 胃和近端小肠分布的微生物以需氧且耐酸的链球菌、乳杆菌为主, 厌氧菌较少. 远端小肠(回肠)是一个过渡区, 它比上肠道有着更丰富的细菌数量(10^3-10^7 个)且微生物多样性增多, 逐渐以属于厌氧菌的双歧杆菌、类杆菌属为主, 兼有需氧菌链球菌. 大肠(结肠)由于肠

内容物周转缓慢, 因此是微生物定植的主要部位, 其特点是细菌数量最多($10^{11}-10^{12}$ 个)且丰度最大, 分布的微生物以严格厌氧菌为主, 如双歧杆菌、类杆菌属、消化球菌、优杆菌等^[9,12,13].

肠道菌群的种类及相对丰度受到诸多因素的影响, 如宿主出生情况(顺产/剖腹产)、遗传、饮食、环境、新陈代谢、免疫等^[10,14], 但多数情况下, 上述因素诱发的肠道菌群的改变与机体内外部环境保持相对平衡, 一旦某些因素引发肠道菌群的稳态失衡就会导致疾病的发生. 目前研究发现肠道菌群紊乱与人的消化系统(如功能性胃肠病、非酒精性脂肪肝、消化道肿瘤)、内分泌系统(如糖尿病、肥胖症)、神经系统(如帕金森病、阿尔茨海默病、神经退行性疾病、焦虑、抑郁)及循环系统(心血管疾病)等多个系统疾病相关^[14].

2 肠道菌群与胃肠动力存在相互作用

胃肠运动受神经系统(肠神经系统、中枢神经系统、自主神经系统)、平滑肌、Cajal间质细胞(interstitial cell of Cajal, ICC)和神经递质等因素协同调控^[15,16]. 以上任一因素结构和(或)功能异常, 均可导致胃肠道动力障碍. 研究发现肠道菌群与胃肠动力也存在紧密的交互作用. 缺乏肠道菌群的无菌(germ free, GF)小鼠比正常小鼠的胃排空和肠道运输时间延长^[17,18], 用无特定病原体的微生物群定植后小鼠的小肠移行运动复合体恢复正常^[19], 而不同种属的细菌对肠道动力的调节作用不同, 如嗜酸乳杆菌、双歧杆菌或烟草梭菌定植后能使GF小鼠小肠移行运动复合体和肠道运输时间接近正常, 定植大肠杆菌则抑制肠道肌电活动^[20]. 反之胃肠道运动异常也会加重肠道菌群失调. 小肠在消化期和消化间期的正常运动具有清除细菌的作用^[21], 若小肠动力发生障碍则导致细菌在小肠局部滞留, 从而大量繁殖.

目前将肠道某一区域微生物群与胃肠动力的联系研究的较为深入的领域是小肠细菌过度生长(small intestinal bacterial overgrowth, SIBO), SIBO指小肠生理性分布的菌群被来自大肠的病原菌取代, 随之引发以腹泻、腹胀、腹痛、营养吸收不良为主要临床表现的疾病, 其以空肠或十二指肠液细菌培养 $>10^5$ /mL为诊断金标准^[22]. SIBO的致病菌群通常以口咽和结肠型细菌为主^[23]. SIBO菌群紊乱会导致脂溶性维生素A、D和E的缺乏以及胆汁酸代谢异常, 导致脂肪消化和吸收障碍, 引起腹泻、营养不良^[24-26], 而碳水化合物发酵失调导致二氧化碳、氢气和甲烷的产生, 从而引起腹胀、腹痛等不适^[26], 细菌对维生素B12的过度消耗则会导致恶性贫血的发生^[27]. 机体对SIBO有一系列的自我防御机制, 如分泌胃酸、正常的胃肠运动、完整的回盲瓣功能、分泌免疫球蛋白以及胰

液、胆汁等, 其中最重要的防御因素是分泌胃酸和正常的小肠运动^[28]。目前大多数研究认为胃肠运动障碍特别是小肠运动减慢导致了SIBO的发生^[21,28-30]。但也有研究持相反意见, 如Suri^[31]认为是SIBO产生的甲烷诱发了肠运动障碍。他和他的同事们对78名接受乳果糖呼气试验(lactulose breath test, LBT)和全肠道传输闪烁检查的患者进行了回顾性研究分析。比较LBT阳性患者与正常患者的小肠转运(small bowel transit, SBT)和结肠转运(colonic transit, CT)是否存在差异, 同时对消化道症状进行分析时将SIBO分为2个亚型: 产氢型(H-SIBO)和产甲烷型(M-SIBO)。在亚型之间分析时发现, M-SIBO患者的SBT和CT较H-SIBO患者有明显延迟, 即LBT中甲烷含量高的患者存在肠运动障碍。既往也有其他报道证实甲烷通过影响小肠的收缩运动而延缓小肠的转运时间^[32,33]。

3 肠道菌群与胃肠动力相互作用的途径

虽然已有证据表明肠道菌群与胃肠动力存在紧密的交互作用, 但具体机制尚未明确。目前研究认为肠道菌群可能通过改变肠神经系统(肠神经元和神经胶质细胞)、肠屏障(肠嗜铬细胞)、肠免疫(肠肌层巨噬细胞)功能来影响胃肠动力。

3.1 肠道菌群通过肠神经系统改变胃肠动力 以新生GF小鼠为研究对象发现, 肠道菌群可能直接参与调控胚胎出生后的肠神经系统的发育^[34,35], 而肠道菌群可能是通过改变肠神经系统的神经元数量及不同类型神经元的比例调节胃肠运动^[8]。Hung等^[36]的两项研究虽然都是采用万古霉素干预小鼠, 实验结果却截然相反。他先用万古霉素干预新生GF小鼠, 发现小鼠结肠肌间神经元密度降低, 胆碱能钙结合蛋白神经元增加, 氮能神经元减少, 结肠收缩的频率增快。而后当其采用万古霉素干预6周龄小鼠, 发现干预后小鼠肠道菌群的丰度及组成与正常小鼠有显著差异, 与预期一致。但小鼠肌间胆碱能神经元减少, 结肠移行性复合运动减慢, 肠道动力下降。值得注意的是, 实验还检测了粘膜5-羟色胺(5-HT)的含量, 发现其含量未发生改变^[37]。作者认为可能是由于万古霉素对不同年龄阶段的小鼠诱导的肠道菌群失调有差异, 进而导致小鼠结肠运动的改变不同^[37]。因为处于不同生长阶段的小鼠, 肠道菌群的种类及相对丰度差异较大, 如胚胎时期受到母体的肠道菌群影响居多, 而青少年时期自身肠道菌群已逐渐形成, 但具体机制尚有待进一步研究。

早期研究认为肠神经胶质细胞(enteric glia cells, EGCs)只是对肠神经元起机械支持作用, 但越来越多证据发现其在调节胃肠道运动及屏障功能方面发挥重要作用^[38-40]。粘膜EGCs在发育中会逐渐形成一个复杂网状结构, 而这个结构的形成与肠道菌群的成熟时间是一

致的^[41]。GF小鼠EGCs的数量减少及其形成的网状结构较简单, 但当植入无特定病原体的微生物群4周后, 小鼠EGCs数量增多且网状结构的复杂性增加^[41]。Beraldi等^[42]发现肥胖小鼠的结肠肌间神经元和EGCs数量减少, 从而导致结肠传输延迟, 在饮食中加入菊粉后小鼠肠道菌群里有益菌的比例增加, 结肠运动障碍有所改善, 但是肌间神经元与EGCs的数量并没有增多。

3.2 肠道菌群通过影响肠屏障改变胃肠动力 肠上皮细胞是肠道粘膜屏障的主要组成部分。肠内分泌细胞(enteroendocrine cells, EECs)虽然仅占肠上皮细胞的1%, 但具有分泌激素和神经递质并与肠神经元之间进行信号传递的功能, 这对维持肠道正常功能是不可或缺的^[43,44]。研究认为, 肠道菌群及其代谢产物通过影响EECs分泌胃肠激素, 向肠神经元发出信号^[44], 进而调控胃肠运动。5-HT是具有调节胃肠运动作用的神经递质^[45], 主要是由一种特殊的EECs, 即肠嗜铬细胞(enterochromaffin cells, EECs)分泌。肠道细菌可直接影响5-HT的代谢从而影响胃肠动力。Yano等^[46]发现GF小鼠结肠和血液中5-HT含量减少, 并伴有胃肠运动障碍, 用芽孢形成菌(一种肠内原生菌)定植GF小鼠后其结肠和血液中5-HT含量增加, 小鼠的胃肠动力得以恢复。色氨酸羟化酶-1(tryptophan hydroxylase, TPH1)是5-HT合成的关键限速酶, 益生菌大肠杆菌尼氏1917能通过调节TPH1来增加5-HT的合成^[47]。Wikoff等^[48]发现无特定病原体微生物群定植的小鼠血清5-HT的浓度是GF小鼠的2.8倍, 但作者认为如此显著的差别不仅仅在于肠道细菌介导的直接作用, 还可能有细菌代谢产物的叠加效应。肠道菌群还可通过其代谢产物作用于肠粘膜从而间接影响胃肠动力。短链脂肪酸(short-chain fatty acids, SCFAs)是肠道菌群的主要代谢产物之一, SCFAs可增加小鼠结肠运动, 这与其刺激肠粘膜释放5-HT有关^[49]。SCFAs还可以诱导人EC细胞模型中的TPH1表达并呈浓度依赖性^[50]。Vincent等^[51]通过给TPH1 KO小鼠注射SCFAs混合物(乙酸、丁酸、丙酸)发现结肠的蠕动增加, 进一步实验发现丁酸可通过激活粘膜5-HT信号传递进而促进肠运动, 丙酸则抑制肠蠕动。

3.3 肠道菌群通过影响肠道免疫功能改变胃肠动力 肠道菌群可激活包括巨噬细胞在内的粘膜免疫细胞, 而粘膜免疫细胞又能反作用于肠道菌群^[52]。肌层巨噬细胞(muscularis macrophages, MMs)是指分布在肠道肌层的巨噬细胞, 其与肌间神经元、EGCs、平滑肌细胞、ICC紧密相连^[53-55]。在健康人胃肠道中, MMs是被ICC围绕住的, 提示它们在维持ICC网络的完整性中起一定作用, 也对维持肠道运动发挥重要作用^[56]。MMs主要是通过分泌骨形成蛋白2(bone morphogenetic protein 2, BMP2)激活肠神

神经元上BMP2相关受体,影响神经元活性,从而影响肠动力^[54]。研究认为肠道菌群与MMs能够相互作用,进而影响胃肠动力,其中BMP2可能发挥了关键作用^[52]。在一项术后肠梗阻的研究中发现,来源于树突状细胞的IL-12能激活MMs诱导型一氧化氮合酶(iNOS)的表达,其产物一氧化氮可直接抑制平滑肌细胞^[57]。此外,IL-17A也能诱导MMs表达iNOS从而降低肠动力^[58]。肠神经元分泌的巨噬细胞生长因子CSF1是MMs维持正常功能所必须的^[53]。Muller等^[59]发现抗生素治疗后小鼠出现胃肠运动障碍,进一步实验发现小鼠MMs数量减少以及BMP2、CSF-1表达降低,这提示抗生素治疗后小鼠肠道菌群紊乱对MMs有一定影响,经增加CSF1的含量或直接粪菌移植后,可纠正部分胃肠动力障碍。

4 结论

综上所述,肠道菌群与胃肠动力在生理及病理上相互关联,相互影响。本文从细胞角度入手,分别从肠神经系统、肠屏障及肠道免疫三方面探讨了肠道菌群与胃肠动力之间相互作用的可能机制。但由于胃肠动力的调控本身是一个非常复杂的过程,因此笔者根据文献报道的情况,尝试从三个主要方面阐释其可能机制。因为胃肠动力不同调控因素间存在交互作用,故肠道菌群与胃肠动力之间相互作用的机制也存在交叉作用,如本文提到的5-HT和MMs影响胃肠动力的最后环节都是通过向肠神经元发送信号来实现的。肠道菌群是个巨大的微生态系统,虽然我们对它的了解逐渐增多,但是还有很多未解之谜。例如肠道菌群与胃肠道其他细胞有无关联性或因果关系、菌群紊乱的核心菌株如何确定等等,这都需要进一步研究证实。随着近年来对肠道菌群深入研究,人们对希波克拉底关于“所有疾病都始于肠道”的说法赋予了新的意义。

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• 消息 •

《世界华人消化杂志》性质、刊登内容及目标

本刊讯 《世界华人消化杂志》[国际标准刊号ISSN 1009-3079 (print), ISSN 2219-2859 (online), DOI: 10.11569, *Shijie Huaren Xiaohua Zazhi/World Chinese Journal of Digestology*], 是一本由来自国内31个省、市、自治区、和香港特别行政区和719位胃肠病学和肝病学专家支持的开放存取的同行评议的半月刊杂志, 旨在推广国内各地的胃肠病学和肝病学领域临床实践和基础研究相结合的最具有临床意义的原创性及各类评论性的文章, 使其成为一种公众资源, 同时科学家、医生、患者和学生可以通过这样一个不受限制的平台来免费获取全文, 了解其领域的所有的关键的进展, 更重要的是这些进展会为本领域的医务工作者和研究者服务, 为他们的患者及基础研究提供进一步的帮助。

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