

中医体质与肠道微生物群互作: 理论框架与未来展望

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中医体质理论是中医的核心组成部分, 通过识别个体的体质特征, 为疾病预防、诊断和治疗提供指导框架. 体质被定义为在先天禀赋与后天环境因素相互作用下形成的相对稳定的生理和心理特征^[1]. 中医将体质分为九种主要类型: 平和质(balanced constitution, BC)、阳虚质(Yang deficiency constitution, YADC)、阴虚质(Yin deficiency constitution, YIDC)、气虚质(Qi deficiency constitution, QDC)、气郁质(Qi stagnation constitution, QSC)、痰湿质(phlegm-dampness constitution, PDC)、湿热质(dampness-heat constitution, DHC)、血瘀质(blood stasis constitution, BSC)和特禀质(inherited special constitution, ISC). 在中医基础理论的指导下, 体质理论具备四个基本原理(禀赋遗传、生命过程、形神构成与环境制约)与三个关键科学问题(体质可分、体病相关与体质可调). 禀赋遗传原理是指先天差异极大影响了体质的不同. 生命过程原理强调体质是在个体一生中受先天和后天因素影响而形成的稳定特征. 形神构成原理指出体质是由躯体与心理素质组合而成. 环境制约原理指出体质发展受到自然和社会环境因素的塑造. 体质可分体现体质具有多样性, 可分为不同类型. 体质可调则表明通过健康管理及针对性干预可调整和改善体质. 体病相关是指体质因素与疾病的发生、发展及转归密切相关, 不同体质类型对疾病的易感性和耐受性各不相同^[2]. 因此, 临床治疗应考虑个体的体质差异. 体质的形成和确定受多种因素影响, 包括年龄、性别、生活方式、环境、个人经历和病史等, 这与现代医学倡导的个性化和精准医疗原则相一致(图1).

近年来, 作为人体微生态系统核心组成部分的肠道微生物群, 因其在营养代谢、免疫调节和疾病发病机制中的关键作用而成为医学研究的焦点. 作为肠道微生态系统的中心, 肠道微生物群由包括细菌、真菌、病毒等在内的多种微生物组成, 其中细菌最为丰富. 这些微生物群履行多种重要的生理功能. 首先, 肠道微生物群通过营养和黏附位点竞争、抗菌物质的产生以及微生物环境的调节等机制抑制病原菌的生长和繁殖, 从而在维持肠道生态平衡中发挥关键作用^[3].



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其次, 肠道微生物群对食物的消化和吸收至关重要. 它降解复杂的大分子营养物质, 如膳食纤维、蛋白质和脂肪, 并合成维生素(如维生素K和B族维生素)及短链脂肪酸等必需营养物质^[4], 为宿主提供重要的能量和营养支持. 再次, 肠道微生物群刺激肠道免疫系统的发育和成熟. 通过调节免疫细胞的活性和功能, 其增强了系统性免疫和抵御病原体入侵的能力^[5]. 最后, 肠道微生物群通过维持肠道微生态系统的平衡, 减少有害物质的产生和吸收, 减轻氧化应激和炎症反应, 并发挥抗衰老和抗肿瘤作用^[6]. 总体而言, 肠道微生物群对于维持人体健康和预防疾病不可或缺, 其多方面的作用凸显了其在塑造和维持人体体质中的重要性.

肠道菌群与体质之间的直接关联性可通过特定“菌种-代谢物-信号通路”三级调控网络实证研究得以阐明. 菌群代谢功能可通过关键信号通路介导体质表型, 如粪产碱菌(*Clostridium scindens*)过度增殖可使DHC患者次级胆汁酸石胆酸水平升高, 激活TGR5受体引发肠道分泌亢进^[7]; 普氏栖粪杆菌(*Faecalibacterium prausnitzii*)产生的丁酸可通过GPR41/43受体促进GLP-1分泌, 改善PDC胰岛素敏感性^[8]. 地理环境亦通过菌群结构差异驱动体质分布, 如高脂饮食地区厚壁菌/拟杆菌比值较南方高, DHC患病率会升高, 与LPS/TLR4通路激活相关^[9]; 岭南地区普雷沃菌(*Prevotella*)显著富集, 促进支链氨基酸分解, 可使DHC人群BMI降低^[10]. 长期高脂/高糖和低纤

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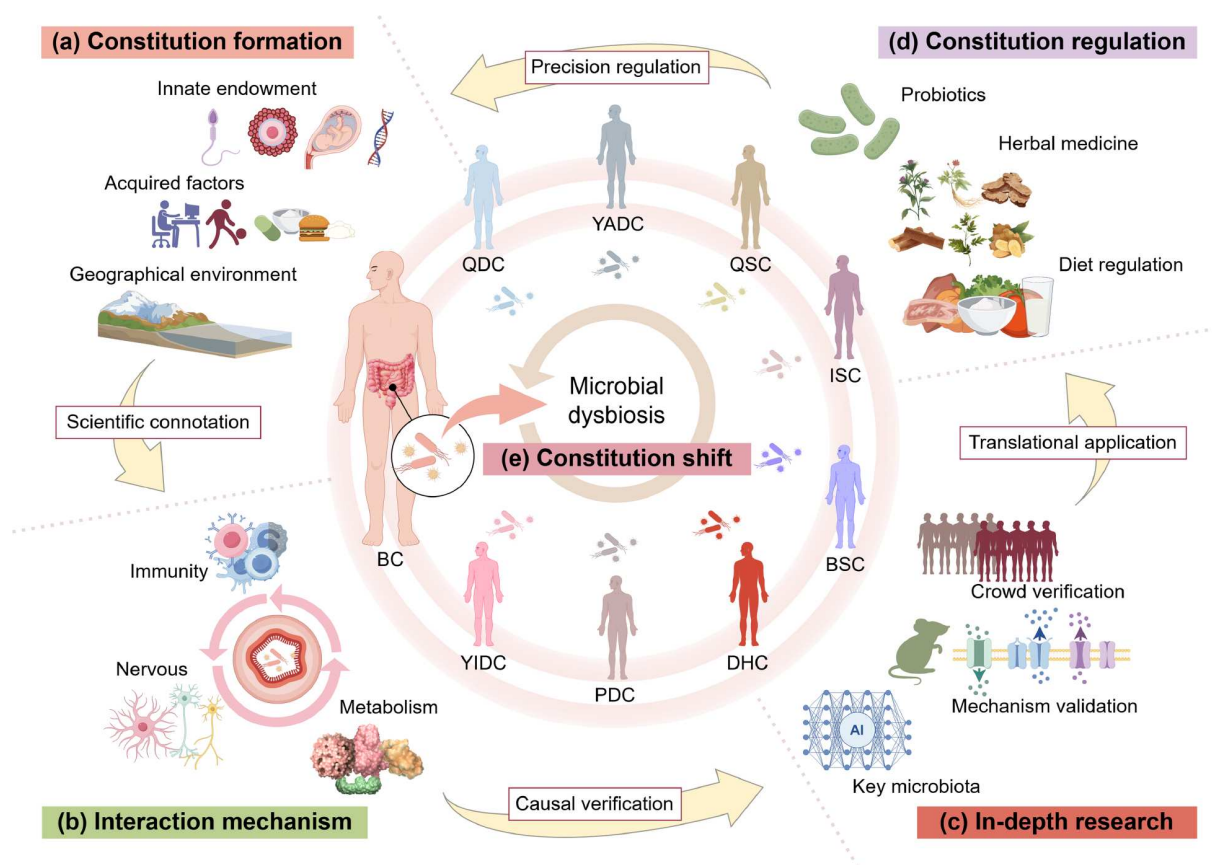


图1 (网络版彩色)基于肠道微生物群精准干预的中医体质科学研究策略。(a) 中医体质由先天禀赋、后天因素及地理环境塑造,与肠道微生物群密切相关。(b) 肠道微生物群与免疫、神经和代谢功能紧密相连,在塑造体质中发挥关键作用。(c) 通过关键细菌筛选、机制探索和人群验证等科学方法,可推动基于肠道微生物群的体质分析和调节的临床转化与应用。(d) 基于(c)部分的技术,开发针对肠道微生物群失调的精准干预策略是可行且客观的。这些策略包括益生菌、中药和饮食干预,可用于科学调节体质。(e) 中医体质分为九种类型,不同体质组的肠道微生物群结构存在显著差异。体质失衡个体表现出明显的肠道微生物群失调,微生物群调节可能是体质迁移和调整的重要研究方向。中医体质的九种基本类型为:平和质(BC)、阳虚质(YADC)、阴虚质(YIDC)、气虚质(QDC)、气郁质(QSC)、痰湿质(PDC)、湿热质(DHC)、血瘀质(BSC)和特禀质(ISC)。该图由Figdraw绘制

Figure 1 (Color online) Scientific research strategy for TCM constitution based on precision intervention of gut microbiota. (a) TCM constitution is shaped by innate endowment, acquired factors, and geographical environment, and is closely associated with gut microbiota. (b) Gut microbiota is closely linked to immune, neurological, and metabolic functions and plays a crucial role in shaping the body's constitution. (c) Scientific approaches such as key bacterial screening, mechanism exploration, and population validation can facilitate the clinical translation and application of constitution analysis and regulation based on gut microbiota. (d) Building on technologies from part c, it is feasible and objective to develop precise intervention strategies for gut microbiota dysbiosis. These include probiotics, TCM, and dietary interventions, which can be used for scientific constitution modulation. (e) TCM constitution is classified into nine types, with significant differences in gut microbiota structure among different constitution groups. Individuals with imbalanced constitutions exhibit marked gut microbiota dysbiosis, and microbiota modulation is likely an important research direction for constitution migration and adjustment. The nine basic types of TCM constitution are: balanced constitution (BC), Yang deficiency constitution (YADC), Yin deficiency constitution (YIDC), Qi deficiency constitution (QDC), Qi stagnation constitution (QSC), phlegm-dampness constitution (PDC), dampness-heat constitution (DHC), blood stasis constitution (BSC), and inherited special constitution (ISC). This figure was created by Figdraw

维饮食会减少有益菌并增加有害菌,破坏肠道微生态系统平衡。相反,高纤维饮食促进有益细菌的生长并稳定肠道微生物群^[11]。缺乏运动、慢性睡眠不足和过度压力会扰乱其节律,降低多样性和稳定性^[12]。此外,抗生素的使用和环境污染可导致菌群失调,影响体质状态^[13]。肠道微生物群失调导致代谢功能障碍,引起肥胖、糖尿病和心血管疾病,这些疾病

与PDC和YADC的病理特征相似。肠道微生物群还通过“微生物群-肠-脑轴”影响宿主的心理和行为,这是一种涉及迷走神经、免疫系统和代谢信号的双向通信途径。通过产生如GABA和5-HT等神经递质,肠道微生物群能够调节大脑功能和情绪,凸显了其在心理和认知健康中的作用^[14]。这与中医的“形神合一”概念相一致,表明肠道微生物群可能影响中医

体质的心理方面。新证据表明, PDC患者中普氏梭杆菌(*Flavonifractor plautii*)丰度降低和植物鞘氨醇(phytosphingosine)耗尽会扰乱代谢途径, 使其易患代谢紊乱^[15]。这些发现表明肠道微生物群与中医体质之间存在紧密关联。

中医体质的九种类型展现出独特的生理和病理特征, 这些特征与肠道微生物群的组成和功能密切相关。研究表明, 不同体质类型个体的肠道微生物群结构存在显著差异。例如, PDC个体常表现出肥胖、腹胀和舌苔油腻等症状。他们的肠道微生物群以厚壁菌门增加和拟杆菌门减少为特征, 可能扰乱能量代谢并促进脂肪堆积和肥胖^[16]。同样, YIDC个体常出现口干、手心发热等症状。其肠道微生物群可能表现出有益菌(如双歧杆菌、乳酸菌)相对减少和有害菌增加, 导致肠道微生态系统失衡, 影响正常代谢和免疫功能^[17]。肥胖个体的后代更易表现出肥胖表型, 这与家族生活方式和饮食习惯密切相关, 导致父母与后代之间肠道微生物群结构相似。适当的益生菌干预和微生物群调节可能为改善肥胖及相关疾病提供新的希望。这些发现表明, 体质迁移可能发生在肠道微生物群演变之后, 为通过调节肠道微生物群来调节人体体质的医学策略提供了坚实基础。总之, 与BC个体相比, 偏颇体质个体展现出了独特的肠道微生物群结构, 且不同体质类型之间能够观察到微妙关联性, 这可能与还未揭示的肠道微生物群规律性迁移模式密切相关。

在整体观和辨证论治的指导下, 中医提供了调节人体体质和预防/治疗疾病的有效方法。中药复方通常是包含多种活性成分(如多糖、生物碱和黄酮类)的复杂混合物, 可通过调节肠道微生物群来影响药物的吸收、代谢和疗效。研究表明, 中药方剂如葛根芩连汤可调节有益肠道微生物群的生长, 增加双歧杆菌和乳酸菌等有益菌的数量, 同时抑制有害菌。这一作用改善了肠道微生态环境, 从而增强代谢功能并改善代谢指标^[18]。合理的中医饮食疗法可提供促进肠道微生物群平衡的营养物质。针灸和按摩可能通过调节肠道神经内分泌功能间接影响肠道微生物群的分布和功能^[19]。重要的是, 现在被广泛认可具有临床治疗潜力的益生菌干预和粪菌移植(fecal microbiota transplantation, FMT)不仅可缓解疾病, 还可微妙地影响体质平衡。FMT在古代中医文献中就有记载, 结合新兴技术, 可为开发合理的基于微生物群的干预策略提供新的可能, 也将推动中医理论和实践的发展。通过肠道微生物群的视角探索中医体质理论, 可为临床疾病的诊断、治疗和预防提供新的见解和方法。分析肠道微生物群的组成和功能有助于确定个体的体质类型, 预测疾病风险, 并为个性化治疗策略提供信息。总之, 针对个体肠道微生物群和体质类型的益生菌、益生元、中医方药和饮食调整等针对性干预措施, 有助于调节肠道微生物群, 纠正体质失衡, 并预防/治疗相关疾病, 从而推进精准医疗和健康管理(图1)。

值得注意的是, 中医体质学说强调个体在先天禀赋与后天环境共同作用下形成的相对稳定的生理和心理特征, 而肠

道菌群作为动态变化的微生态系统, 其物种组成和功能虽易受饮食、药物、环境等因素快速改变, 但两者可通过多层次、多维度的相互作用机制形成“稳态-适应”的动态平衡系统。从先天禀赋角度看, 体质与肠道菌群的初始定植均受遗传因素影响, 如母体遗传背景和分娩方式不仅塑造婴幼儿体质基础, 也决定了菌群的早期结构, 而核心菌种的长期稳定性, 如拟杆菌属、厚壁菌属, 通过短链脂肪酸等代谢产物持续调控宿主的能量代谢和免疫应答, 可成为体质特征的重要支撑。在后天调控层面, 饮食、药物等环境因素既能快速改变菌群组成, 又通过代谢通路影响体质表现。肠道菌群的动态性恰与体质的“可变性”相耦合, 其代谢产物和免疫调节作用成为连接两者的关键桥梁。临床应用上, 基于体质分型的菌群靶向干预和时序性调整策略已证实可通过菌群的动态调节实现体质的长期稳定优化。因此, 体质的“稳定性”源于遗传与核心菌群的深层互作, 菌群的“动态性”则通过代谢-免疫网络快速响应环境变化, 二者共同构成个体健康状态的适应性调控系统。

此外, 证候与体质存在相似之处, 二者均是中医理论中的重要概念, 都涉及个体的生理状态和病理变化, 是中医对人体健康和疾病状态的综合概括。然而, 它们在具体含义和应用上有所不同。证候是疾病发展过程中某一阶段的病理概括, 反映了疾病的病因、病性、病位和病势, 具有一定的动态性和时效性。相比于体质的相对稳定性, 证候与肠道菌群之间可能存在更为直接的“快关联”, 例如口腔肠道微生物传播可促进糖尿病冠心病的进展^[16]。从另一个角度而言, 体质形成与变迁过程中可能伴随着不同时序的多种证候转换及菌群结构改变, 这三者之间必然存在紧密联系, 在实际研究过程中应充分关注。

虽然在肠道微生物群与中医体质理论关联方面已取得显著进展, 但仍有许多问题尚待解决。应进一步深入探讨它们之间的因果关系, 阐明肠道微生物群在体质形成和演变中的作用, 并加强不同体质微生物群特征的研究。与此同时, 建立全面的肠道微生物群和中医体质数据库将可帮助提升实际临床应用转化。开发基于微生物群的干预策略, 创建安全的益生菌和中药制剂, 并提高干预效果将进一步促进中医体质理论与现代医学融合。中医体质评估的标准化仍需探索, 而肠道微生物群客观分析与生物标志物发掘将为此带来希望。人工智能的发展为大规模队列研究和大数据分析提供了强大的工具, 能够更深入地帮助了解肠道微生物群结构和功能特征。此类研究可为理解体质迁移、精准调节和疾病预防奠定科学基础, 使中医体质研究更加可量化、可评估和可重复。值得注意的是, 如果基于肠道微生物群对体质进行分类, 人类体质的数量可能与现有的中医体质分类数量不同, 但这一假设还需要进一步研究。此外, 还需从居民种族和地理差异角度考虑肠道微生物群及相关研究方案适用性的问题。除了肠道微生物群, 还需要继续研究气候、地理、情绪和认知

等其他能够影响体质的关键因素。这些未解决的问题突显了本文的重要性,它将推动基于肠道微生物群的体质研究工作。

总之,中医体质与肠道微生物群之间存在密切关联(图1)。肠道微生物群可影响中医体质的形成和发展,其失调可能导

致体质偏颇和疾病。反之,中医干预可调节肠道微生物群并改善体质状态。通过肠道微生物群研究中医体质,可为这一理论提供现代科学解释,并为疾病预防、治疗和健康管理的提供新的策略,帮助推动中医理论和临床实践的突破。

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Summary for “中医体质与肠道微生物群互作: 理论框架与未来展望”

Interaction between Traditional Chinese Medicine constitution and gut microbiota: theoretical framework and future prospects

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Traditional Chinese medicine (TCM) constitution theory, a foundational framework in TCM, categorizes human constitutions into nine distinct types according to the interplay of congenital endowment and acquired environmental factors: balanced constitution (BC), Yang deficiency constitution (YADC), Yin deficiency constitution (YIDC), Qi deficiency constitution (QDC), Qi stagnation constitution (QSC), phlegm–dampness constitution (PDC), dampness–heat constitution (DHC), blood stasis constitution (BSC), and inherited special constitution (ISC). Rooted in four principles (innate inheritance, life course development, psychosomatic integration, and environmental regulation), the theory addresses three core scientific questions: constitutional typeability, constitution–disease correlation, and constitutional adjustability. This paradigm emphasizes individual variability in physiological and psychological traits, aligning TCM with modern precision medicine by linking constitutional profiles to disease susceptibility, progression, and therapeutic responses. The human gut microbiota, a dynamic ecosystem of trillions of microorganisms, has emerged as a critical mediator of host health that influences nutrient metabolism, immune modulation, and neuroendocrine signaling. Emerging evidence reveals intricate associations between microbiota composition and TCM constitutions, primarily through a “strain–metabolite–signaling pathway” regulatory network. For example, the overproliferation of *Clostridium scindens* in DHC individuals elevates secondary bile acid (lithocholic acid) levels, which then activate the TGR5 receptor to induce intestinal hypersecretion and inflammatory responses. In PDC individuals, the butyrate produced by *Faecalibacterium prausnitzii* enhances insulin sensitivity via GPR41/43-mediated GLP-1 secretion, thus mitigating metabolic dysregulation. Geographical and dietary factors further modulate these relationships. High-fat diets increase the Firmicutes/Bacteroidetes ratio, correlated with DHC prevalence through LPS/TLR4 pathway activation. Meanwhile, *Prevotella*-enriched microbiomes in subtropical regions (e.g., Lingnan) reduce DHC-associated BMI via branched-chain amino acid catabolism. Constitutional imbalances are often mirrored in microbiota dysbiosis. PDC individuals exhibit increased Firmicutes abundance and reduced Bacteroidetes count, both linked to enhanced energy extraction and adipose accumulation. YIDC is characterized by depleted *Bifidobacterium* and *Lactobacillus* populations and elevated pathobionts, compromising gut barrier function and immune homeostasis. The “gut–brain axis” adds another dimension: microbiota-derived neurotransmitters (e.g., GABA and 5-HT) influence emotional regulation, which is consistent with TCM’s “body–mind unity” concept. For instance, the reduced *Flavonifractor plautii* and phytosphingosine levels in PDC correlate with metabolic syndrome and psychological symptoms, highlighting the microbiota’s role in constitutional psychology. TCM interventions offer multifaceted strategies to modulate constitutions and microbiota. Herbal formulas such as Gegen Qinlian Tang promote beneficial bacteria (e.g., *Bifidobacterium*) while inhibiting pathogens, thereby improving gut microecology and metabolic parameters in DHC. Dietary therapies (e.g., high-fiber diets for QSC) and acupuncture indirectly regulate microbiota via neuroendocrine pathways. Modern microbiome therapies, including fecal microbiota transplantation (FMT) and probiotics, align with TCM’s historical use of microbial interventions (e.g., ancient FMT records) to restore constitutional balance. This bidirectional interaction forms a “genetic-stable/microbial-dynamic” system: core microbiota taxa (e.g., *Bacteroides* and *Firmicutes*) maintained across generations support constitutional stability, whereas environmental factors (such as diet, stress, and antibiotics) induce rapid microbiota shifts via short-chain fatty acid and bile acid signaling. Constitutions differ from TCM syndromes in stability: the former reflect long-term physiological patterns, whereas the latter represent dynamic pathological states with immediate microbiota associations. Challenges for future research include clarifying causal mechanisms, standardizing constitutional assessment with microbiota-derived biomarkers, and addressing ethnic/geographical microbiota variations. By leveraging AI and big data analytics, researchers may develop microbiota-based predictive models for constitutional typing to expand or revise the traditional nine-type taxonomy. Integrating TCM’s holistic philosophy with microbiome science could unlock personalized interventions—such as tailored herbal–microbiome cocktails—to optimize constitutional balance, enhance disease prevention, and bridge traditional and modern medicine.

Traditional Chinese Medicine constitution, gut microbiota, intervention strategies, health maintenance

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