

呼吸道合胞病毒感染继发哮喘的研究进展

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摘要

系统综述呼吸道合胞病毒(RSV)感染与儿童哮喘发生发展的关联, 阐述RSV感染通过气道上皮功能障碍、免疫应答异常、脂质代谢双向调控及易感基因调控等机制诱发哮喘的分子路径, 分析病毒基因型、宿主因素及环境因素的协同调控作用, 并总结当前防御策略, 为RSV感染相关哮喘的早期识别及临床干预提供理论支撑。

关键词

呼吸道合胞病毒, 哮喘, 发病机制, 儿童, 脂质代谢, 防治策略

Research Progress on Asthma Secondary to Respiratory Syncytial Virus

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Abstract

This review systematically summarizes the association between respiratory syncytial virus (RSV) infection and the development and progression of childhood asthma. It elaborates on the molecular pathways through which RSV infection induces asthma, including airway epithelial dysfunction, immune response abnormalities, bidirectional regulation of lipid metabolism, and susceptibility gene regulation. It also analyzes the synergistic regulatory roles of viral genotypes, host factors, and environmental exposures, and summarizes current prevention and treatment strategies, thereby providing

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theoretical support for the early recognition and clinical intervention of RSV-associated asthma.

Keywords

Respiratory Syncytial Virus, Asthma, Pathogenesis, Children, Lipid Metabolism, Prevention Strategies

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1. 引言

哮喘作为儿童期最常见的慢性气道炎症, 以高发病率、严重临床症状给儿童造成了严重威胁。呼吸道合胞病毒(respiratory syncytial virus, RSV)是婴幼儿毛细支气管炎最常见病原体, 其儿童期的相关感染与哮喘发生密切相关。早期 RSV 感染可使 5 岁哮喘风险升高 26%, 是儿童哮喘重要的可改变危险因素, 避免早期 RSV 感染理论可预防约 15%的儿童期哮喘[1]。本文从流行病学、发病机制及防治策略等方面进行综述, 旨在为阐明其发病机制、为优化防治策略提供理论参考。

2. RSV 感染与儿童哮喘的流行病学关联

2.1. 病毒基因型

RSV 基因型是影响哮喘的核心因素。Rosas-Salazar 等[2]发现, 婴儿期感染携带 G 基因重复序列(G)的 RSV-A 型或 RSV-B 型毒株, 5 岁时哮喘风险显著升高(aOR 分别为 2.00 和 1.78)。此外, RSV 与其他呼吸道病毒的混合感染, 可显著放大哮喘发病及急性加重风险, 对 6 岁以下儿童影响更为明显[3]。

2.2. 宿主年龄特征

幼儿期(<3 岁)是 RSV 感染继发哮喘的高风险窗口期。该阶段不仅 RSV 感染重症率(需住院、呼吸支持)最高, 且远期哮喘发病风险显著高于年长儿。46%的 RSV 相关死亡发生于<6 个月婴儿, 其重症率及远期哮喘风险均达到峰值[4]。6~23 个月首次感染 RSV 的儿童, 其喘息及哮喘症状更具持久性[5]。

3. RSV 感染继发儿童哮喘的核心发病机制

3.1. 气道上皮功能障碍

RSV 感染可显著抑制紧密连接蛋白(ZO-1、Occludin、E-钙粘蛋白)的表达, 破坏上皮屏障使外界过敏原更易侵入气道[6]。同时, RSV 感染扰乱气道上皮细胞脂质代谢, 释放大量游离脂肪酸, 通过激活 GPR40 介导的信号轴诱发氧化应激, 驱动 Th2/Th17 免疫极化并抑制调节性 T 细胞(Treg)功能, 导致气道高反应[7]。

脂质代谢的双重调控作用

RSV 的生存繁殖全程依赖脂质, 感染后会扰乱宿主脂质代谢, 诱导其合成所需的脂类, 并通过脂质代谢产物触发肺部炎症反应[8][9]。RSV 感染小鼠模型中, 脂质代谢物(如 ApoA-1、Apoc-1)的失衡与胆固醇转运、气道屏障完整性破坏相关[10]。宿主脂质也能反制 RSV, 既可以直接阻挡病毒入侵, 还能给免疫细胞供能、激活抗病毒信号[9]。基于此, 靶向脂质代谢的干预有前景。

3.2. 免疫应答异常

RSV 感染导致 Th2 型免疫应答过度激活、Treg 功能损伤及多种免疫细胞异常活化, 形成持续性免疫失衡。

3.2.1. Th2 型免疫应答过度激活

RSV 感染可显著驱动以 Th2 型反应为主的异常免疫应答, 其核心特征为 IL-4、IL-5、IL-13 等 Th2 型细胞因子大量释放, 进而诱导嗜酸性粒细胞炎症、气道黏液高分泌及气道高反应性[11]。

3.2.2. 调节性 T 细胞(Treg)功能损伤

早期 RSV 感染损害肺组织内 Treg 细胞的抑制功能, 使其无法有效控制异常免疫应答, 甚至自身分泌 Th2 型细胞因子, 削弱机体对过敏原的免疫耐受[12]。RSV NS1 可通过激活 TSLP-OX40/OX40L-mTOR 信号轴, 使 Foxp3⁺Treg 细胞数量显著减少、抑制功能下降, 同时促进 CD4⁺T 细胞向 Th2 方向极化, 导致 IL-4 水平显著升高, 诱发嗜酸性粒细胞浸润与黏液高分泌, 形成典型哮喘样病理改变[13]。

3.2.3. 免疫细胞异常活化与极化失衡

肺泡巨噬细胞是肺部固有免疫的核心效应细胞, 在维持气道免疫稳态中发挥关键作用。RSV 感染可从多方面破坏肺泡巨噬细胞 M1/M2 极化平衡, 导致 M1/M2 比值升高。极化紊乱的肺泡巨噬细胞可进一步促进肺组织 Th17 与 Th2 细胞异常活化与增殖, 同时抑制 Treg 细胞功能。异常极化的肺泡巨噬细胞还可诱导 Th2 细胞形成免疫记忆, 使其对后续过敏原刺激呈高反应性[14]。2 型固有淋巴细胞(ILC2)的异常激活是 RSV 感染诱导 2 型炎症的重要补充。RSV 感染通过诱导肺组织 ILC2 高表达 MHC II 分子, 使其发挥抗原呈递作用, 直接激活 CD4⁺T 细胞并向 Th2 方向极化, 加剧 Th1/Th2 免疫失衡, 最终介导气道过敏性炎症与哮喘的发生发展[15]。组织驻留记忆 T 细胞(tissue-resident memory T cells, TRM)的富集在哮喘转化过程中也起着重要作用, RSV 感染后, 可通过上调转录因子 PLZF 分子使肺组织内 CD4⁺TRM 大量富集, 持续释放 Th2 型炎性介质, 长期维持气道高反应[16]。

3.3. 非编码 RNA 与易感基因的调控作用

3.3.1. 非编码 RNA

RSV 感染通过下调气道上皮细胞中 miR-34b/c-5p 的表达, 解除其对靶基因 CXCL10 的抑制, 促使 CXCL10 大量分泌并招募巨噬细胞浸润, 进而诱发气道炎症与气道高反应[17]。此外, RSV 感染可通过下调 lncRNA n337374, 激活 ERK 信号通路上调 CD86, 促进树突状细胞异常成熟, 进而启动气道过敏性炎症, 最终诱发或加重哮喘[18]。

3.3.2. 易感基因的调控作用

Gasdermin B (GSDMB)是定位于 17q21 位点的经典哮喘易感基因, 在 RSV 感染后, GSDMB 通过直接识别病毒 RNA 并结合线粒体抗病毒信号蛋白(MAVS), 启动炎症反应, 气道上皮细胞产生大量气道炎症的核心驱动因子如干扰素刺激基因(ISGs)等, 导致气道敏感、黏液增多, 最终增加哮喘风险。临床数据显示, 携带 GSDMB 风险等位基因的儿童哮喘发生率为 38.2%, 是野生型儿童(16.6%)的 2.3 倍[19]。ORMDL3 是同样位于染色体 17q21 区域的基因, 在 RSV 感染模型中, ORMDL3 通过组蛋白乙酰化上调 NLRP3 炎症小体表达, 加剧气道炎症和喘息[20]。ORMDL3 也可通过 SPHK1/ERK 通路下调紧密连接蛋白, 增加上皮通透性[21]。PGAP3 这一哮喘易感基因可通过调控支气管上皮抗病毒免疫与炎症反应, 在 RSV 感染后促进气道慢性炎症与气道高反应性[22]。

3.4. 肺 - 肠轴的功能紊乱

研究表明, 婴儿期 RSV 感染仅轻微影响肺部菌群, 却会长期破坏肠道菌群平衡, 通过“肠 - 肺轴”持续影响肺部免疫功能。婴儿期 RSV 感染及氨苄西林暴露均可引发特征性肠道菌群结构改变, 主要表现为变形菌门持续减少、拟杆菌门丰度下降甚至缺失、疣微菌门(阿克曼菌属)早期显著降低, 同时伴随毛螺菌科与瘤胃球菌科等产短链脂肪酸菌群持续性耗竭, 而卟啉单胞菌科等潜在促炎菌群相对富集。在机制层面, 上述菌群失调通过肠 - 肺轴从多方面破坏肺部免疫稳态与修复过程, 短链脂肪酸、吲哚-3-丙酸、亚精胺等微生物源性保护性代谢物合成不足, 无法有效维持肠道与肺上皮紧密连接、抑制慢性炎症并保障细胞外基质弹性, 此外, 菌群代谢通路异常导致能量代谢、辅因子合成及聚糖代谢相关通路整体下调, 削弱组织修复与免疫调控能力。肠道屏障完整性受损也会引发“肠漏”, 促使促炎信号与免疫细胞向肺部异常归巢与活化, 最终造成肺泡化受阻、气道重塑、肺顺应性下降等长期肺功能损伤。这些解释了临床中“部分 RSV 感染患儿急性期症状不重, 却远期发展为哮喘”的现象, 根源在于肠道菌群失衡导致的肺部长发育与修复异常, 而非急性期肺部炎症本身[23]。

4. RSV 感染继发哮喘的危险因素

RSV 感染继发儿童哮喘的发生, 是宿主、遗传与环境等协同作用的结果。早产是明确的风险因素, 丹麦队列研究显示, RSV 住院的早产儿未来因喘息或哮喘住院的调整风险比(aHR)为 1.48 (0~<1 岁), 且风险随年龄降低[24]。西澳大利亚出生队列表明, 极早产儿(<28 周)RSV 感染后呼吸道并发症发生率高达 50.8/1000 人年, 显著高于足月儿[25]。特应性体质同样关键。研究表明, 特应性儿童感染 RSV 后发生支气管高反应性的比例高达 77.8%, 而非特应性儿童, 仅为 17.4% [26]。此外, 父母过敏史、婴幼儿期嗜酸性粒细胞升高等均可增加发病风险[27] [28]。特异性遗传变异如 IL33 基因变异、GSDMB 风险等位基因可显著增强 RSV 感染后哮喘易感性。环境暴露是 RSV 感染继发哮喘的重要外部诱因, 孕期及产后二手烟暴露、剖宫产、室内空气污染等可与 RSV 感染协同作用, 进一步提升哮喘发病风险[4]。

5. RSV 感染继发哮喘的防治策略

5.1. 免疫预防

尼塞维单抗(Nirsevimab)是针对 RSV F 蛋白的长效单克隆抗体, 单次注射覆盖整个 RSV 流行季[29]-[32]。可降低 70%以上婴儿 RSV 相关住院率[33] [34]。帕利珠单抗可降低高危婴儿未来发生哮喘的风险, 且降低已发展为哮喘患儿的哮喘活动持续时间[35]。但更高依从性($\geq 70\%$ 推荐剂量)的 RSV 免疫预防与儿童期哮喘风险的关联性需要更大规模的前瞻性研究明确[36]。研究表明, 基于呼吸道合胞病毒(RSV)融合前 F 蛋白的重组疫苗诱导 RSVpreF 孕妇疫苗通过胎盘转移抗体保护婴儿[37], 理论上推测可降低远期哮喘的发病率, 但缺乏直接的临床实验数据。

5.2. 抗感染管理及肠道微生态调节

婴儿期 RSV 感染可长期破坏肠道菌群, 通过“肠 - 肺轴”持续影响肺部免疫功能, 不当使用抗生素会进一步加重肠道菌群失调。因此临床治疗 RSV 相关呼吸道感染时应严格把握抗生素使用指征, 以间接降低远期哮喘的发病风险[23]。

5.3. 靶向脂质代谢的干预策略

基于 RSV 与宿主脂质代谢的双重调节关系, 传统中药复方(如金欣口服液、固本防哮汤)可通过调节脂代谢发挥治疗作用。在 RSV 感染小鼠模型中, 金欣口服液(JOL)可逆转 11 种血浆和 16 种肺组织脂质

代谢标志物的异常, 恢复甘油磷脂和鞘脂代谢至近正常水平, 从而减轻炎症[38]。固本防哮汤(GBFXD)可通过上调 ApoA-1 和 ApoC-1 表达, 改善胆固醇运输和脂质代谢平衡, 同时抑制补体因子(如 Cfd)的过度激活, 减少气道炎症和上皮损伤[10]。

6. 总结与展望

RSV 感染与儿童哮喘存在显著因果关联, 机制涉及气道上皮破坏、免疫失衡、脂质代谢、易感基因调控及肺肠轴等多重通路。早产、特应性体质、遗传变异及环境暴露是主要危险因素。目前尚缺乏预测 RSV 继发哮喘的特异性生物标志物, 新型免疫预防措施的长期效果需要随访。未来研究仍需聚焦于开展大规模长期随访队列研究, 明确相关预防策略对哮喘的远期效果。此外, 需基于 RSV 感染后特征性肠道菌群结构与代谢物改变, 联合遗传易感位点构建多组学整合预测模型, 实现高风险儿童早期识别以及精准预防。

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