

HIF-1 α , VEGF and Tumor Invasion and Metastasis

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Abstract

Tumor invasion and metastasis is an extremely complex process; the mechanism is not clear, involving multiple genes and signal pathways. At present, hypoxia-inducible factor-1 α (HIF-1 α) and vascular endothelial growth factor (VEGF) are important transcription factors. They are deeply involved in the process of tumor invasion and metastasis through various mechanisms, including angiogenesis under hypoxia and various signal pathways regulating tumor invasion and metastasis, which are closely related to the poor prognosis of patients. The purpose of this study is to clarify the interaction and regulatory mechanism between HIF-1 α and VEGF, as well as the possible clinical effects on tumor invasion and metastasis.

Keywords

HIF-1 α , VEGF, Tumor

HIF-1 α 、VEGF与肿瘤的侵袭和转移

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摘要

肿瘤的侵袭和转移是极其复杂的过程, 目前机制尚不明确, 涉及了众多基因和信号通路。缺氧诱导因子

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-1 α (HIF-1 α)和血管内皮生长因子(VEGF)是该通路中重要的转录因子,它们通过各种机制深度参与肿瘤的侵袭和转移过程,包括参与缺氧条件下的血管生成及多种调控肿瘤侵袭和转移的信号通路,与患者的不良预后密切相关。本文旨在阐明HIF-1 α 和VEGF之间的相互作用和调节机制,以及在肿瘤侵袭和转移中可能的临床影响。

关键词

缺氧诱导因子-1 α , 血管内皮生长因子, 肿瘤

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1. 引言

肿瘤严重威胁着公众健康。据报道2020年,中国的癌症病例将达到451万例左右,癌症死亡人数可能达到304万人[1]。可以预见今后很长一段时间,肿瘤都将是危害中国人健康的极其重要的问题之一。目前该病难治和复发的重要原因是肿瘤细胞的侵袭和转移。且肿瘤侵袭和转移的机制仍有待于进一步阐明,特别是当下靶向治疗所依赖的分子机制。不过有研究证实局部微环境缺氧在肿瘤进展过程中起着关键作用,主要通过缺氧/HIF-1 α 的驱动和VEGF的过表达及其受体的激活等机制促进肿瘤持续增殖、持续血管生成和局部侵袭、远处转移等[2]。本文现就HIF-1 α /VEGF在肿瘤的侵袭和转移过程中的研究进展作一综述。

2. HIF-1 α 概述

HIF-1 α 是一个120 kDa的氧依赖转录激活因子,在众多组织中普遍表达(包括肿瘤组织)。其与果蝇(Per and Sim, PAS)具有高度同源性的两个亚单位的碱基-螺旋-环-螺旋(bHLH)基序证明它们都属于bHLH-PAS蛋白家族。除bHLH和PAS结构域外,还有两个反式激活结构域:N-末端的转录激活区(NTAD)和C-末端的转录激活区(CTAD),及一个氧敏感的氧依赖性降解域(ODDD) [3] [4] [5]。有多种机制参与HIF-1 α 分子的活性调节,但目前证实[6]对HIF-1 α 活性影响最大的分子机制是由双加氧酶依赖的泛素-蛋白酶体途径介导的系统。位于HIF-1 α 的P402和P564的两个脯氨酸残基被称为PHD的双加氧酶(包括PHD1-3)脯氨酰羟化通过含有pVHL的E3泛素连接酶触发泛素化反应,通过半衰期为6~8分钟的泛素-蛋白酶体系统导致HIF-1 α 在常氧条件下的蛋白水解。而在缺氧微环境中,PHD活性下降,HIF-1 α 蓄积并移位到细胞核,与 β 亚单位二聚化,并与HIF-1 α 结合位点(HBS)结合,从而促进多种靶基因的转录,并调控靶基因表达。HIF-1 α 进而促进了一些缺氧诱导的细胞事件,如细胞增殖、迁移、侵袭、血管生成和细胞代谢[7] [8]。

3. VEGF 概述

VEGF是1989年由Gospodarowicz [9]分离出的糖基化多肽性分泌因子,其编码基因位于第六号染色体短臂上,由8个外显子和7个内含子交替构成,总长约14 kb。VEGF家族在哺乳动物中表达包含VEGF-A, VEGF-B, VEGF-C, VEGF-D和胎盘生长因子(PLGF)5个成员。不同成员之间功能具有差异性。VEGF-A即通常说的VEGF,是目前发现的调节血管生成的关键因子[10],VEGF-B暂未发现其诱导血管生成和血

管通透性的功能[11], VEGF-C 和 VEGF-D 与淋巴管生成密切相关[12]。VEGF 的生物学效应是通过其亚型与不同的血管内皮细胞表面受体(VEGFR1、2、3)结合后进行信号转导而发挥。VEGF-A 可选择性地结合 VEGFR-1 及 VEGFR-2, 通过血管生成途径, 在肿瘤生长、区域浸润和淋巴转移中起重要作用[10]。VEGF-C 和 VEGF-D 通过与淋巴管内皮细胞表面 VEGFR-3 结合, 调控淋巴管生成, 在胃癌肿瘤细胞淋巴管侵袭和淋巴结的转移中有重要作用[12]。VEGF 还可诱导分泌多种血浆酶原激活物和金属蛋白酶, 促进血管生成, 为肿瘤浸润及转移提供条件[13]。

4. HIF-1 α 和 VEGF 促进肿瘤血管生成

积累表明在肿瘤生长和转移过程中, 由于肿瘤细胞的疯狂增殖, 无法及时建立血管网, 造成肿瘤细胞生长处于缺氧且酸性物质积聚的微环境中。而肿瘤实质微环境的特点, 以及无氧状态诱导一系列参与血管生成和无氧代谢的基因表达, 可以帮助肿瘤细胞更好地适应无氧环境, 并更容易形成侵袭和转移能力[14] [15] [16]。这一过程与新生血管形成密切相关, 新生血管可为肿瘤细胞快速生长提供条件, 进而加速实体肿瘤的发生、侵袭和转移[17] [18]。有报道表明, 通过微血管密度这一肿瘤血管生成最主要的量化指标, 可预测肿瘤浸润和转移程度[19]。而且研究已证实缺氧条件下, HIF-1 α 被激活并调控 VEGF 等转录因子参与肿瘤新血管生成[20] [21] [22]。其机制可能是在缺氧驱动的血管生成中, 缺氧激活 PI3K/AKT 通路, 阻止 HIF-1 α 翻译后羟基化和随后的 HIF-1 α 的降解, 使其积聚, 然后转移到细胞核, 并形成转录起始复合物, 启动靶基因转录, 导致相应的蛋白产物增加, 包括 VEGF 的表达增强, 从而促进肿瘤血管生成[23] [39]。Yokoe [24]等研究也表明在缺氧时, HIF-1 α 可以逃避 pVHL 的识别, 从而稳定存在于缺氧环境中。并通过 PI3K 途径和缺氧激活的 PI3K/Akt/mTOR 途径调节 VEGF 蛋白的合成[25]。Palazon 等[26]还证实, HIF-1 α 磷酸化后也可诱导 VEGF 靶基因的转录。而 VEGF 的过表达, 主要通过受体 VEGFR-1 和 VEGFR-2 发挥作用, 当 VEGF 与其受体结合后激活信号转导, 导致内皮细胞增殖、迁移和新生血管形成。新生血管可以为肿瘤提供营养、氧气, 排出代谢废物, 并刺激肿瘤生长, 加速肿瘤转移[10]。因此, 联合应用抗血管生成药物和 HIF-1 α 抑制剂可能是有效的, 因为抗血管生成药物会切断肿瘤的血液供应, 而 HIF-1 α 抑制剂可以增强抗血管生成药物的作用, 降低耐药的可能性[42]。

5. HIF-1 α 、VEGF 参与肿瘤的侵袭和转移

肿瘤的侵袭和转移是影响患者预后的主要危险因素, 它是一个不受控制的细胞增殖、血管生成、分离、运动、侵入血流、沉积在微血管中, 最后从血管外渗并在次级部位增殖的连续事件。这一过程复杂, 机制不明确, 涉及到了多个基因和信号通路, 而且目前关于这方面的靶向治疗仍未取得突破性进展[27] [28]。如用于治疗转移性肾细胞癌(mRCC)的 5 种抗 VEGF/VEGFR 药物, 尽管患者的无进展生存率和有效率有所提高, 但均未能显著提高患者的生存率[29]。因此研究肿瘤的侵袭和转移机制, 对于探索新的治疗靶点和治疗机制, 提高肿瘤患者的治疗效果和预后具有重要意义。HIF-1 α 与 VEGF 由于其在调节肿瘤血管生成从而促进肿瘤生长、侵袭和转移中的巨大作用早已被人们所熟知并关注。并期待以此开发出在肿瘤的治疗中有更好效果的药物。

多项研究表明高表达的 HIF-1 α 预示着更高的 TNM 分期, 远处转移和血管侵犯, 以及阳性淋巴结[30]。这些现象是可以理解的, 因为增加的 HIF-1 α 可激活磷脂酰肌醇-3 激酶/蛋白激酶 B (PI3K/AKT)和人鞘氨醇激酶-1/1-磷酸鞘氨醇(SphK1/S1P)信号通路, 介导瘤体内新生血管的形成, 增强肿瘤细胞的活动能力, 从而促进肿瘤的进展[31] [32]。而且 HIF-1 α 还可通过激活 Wnt、TGF- β /Smad3 或 Wnt、Notch、TGF- β 等多条信号转导通路调控其关键转录因子表达, 诱导上皮间质转化效应, 进而促进肿瘤浸润转移[33] [34]。甚至 HIF-1 α 通过刺激肿瘤细胞或肿瘤浸润免疫相关细胞中的 PD-L1 表达促进肿瘤细胞免疫逃逸[35]。不

过，更多 HIF-1 α 调节肿瘤转移的机制仍有待进一步阐明。同样 Zhao 等[36]发现 VEGF 的表达与肿瘤侵袭能力呈明显正相关，VEGF 表达越高，促血管生成的作用也越显著，肿瘤的浸润和转移也越早。通过干预 VEGF 的生成或阻断 VEGF 与其受体的结合则可抑制肿瘤的血管生成，从而抑制肿瘤的生长、浸润和转移。Liu 等[37] [38] [39]发现用 siRNA 敲除人结直肠癌(CRC)细胞系中的 VEGF 后，肿瘤细胞的生长被极大地抑制，从而显著的抑制了结直肠癌的迁移和侵袭。并阐述了该现象产生的机制：这一现象不是通过已有的旁分泌或自分泌 VEGF 信号的抑制。而是通过调节结直肠癌细胞中多受体酪氨酸激酶(RTK；例如 EGFR 和 cMET)和下游 AKT 信号的活性介导的。

然而，HIF-1 α /VEGF 的调控机制不单单止于此。近来研究还发现缺氧/HIF-1 α 可直接或间接(后者通过腺苷、乳酸或酸中毒)促进 VEGF 的表达及激活其受体，从而促进肿瘤逃避免疫监视[40]。同时 HIF-1 α 可通过 VEGF 和血小板衍生生长因子参与血管生成的调节，增强 Notch 信号的转录活性，介导肿瘤代谢途径(葡萄糖、脂质和氨基酸代谢)，并通过免疫抑制发挥肿瘤促进作用[41]。这些研究为通过 HIF-1 α /VEGF 通路治疗肿瘤获得更好的效果提供了可能。在研究光动力疗法(PDT)时[42]发现，PDT 的治疗效果通常被肿瘤血管生成所掩盖。其机制是：PDT 后 PAK1 表达上调并防止 HIF-1 α 蛋白在泛素介导下降解，因此造成 HIF-1 α 蛋白积累并转运到细胞核与 VEGF 启动子结合，从而上调 VEGF 的表达，促进肿瘤血管生成。不过当敲除 PAK1 基因后，这些现象被逆转，促进 HIF-1 α 降解，最终抑制肿瘤血管生成。因此，通过敲除 PAK1 以抑制 HIF-1 α /VEGF 的抗血管生成疗法，将可能为 PDT 联合治疗提供一个新思路。

综上所述：HIF-1 α 和 VEGF 可以成为人们研究肿瘤侵袭和转移机制的一个突破口，并可能由此开发出更有效的肿瘤治疗药物，从而提高肿瘤的治疗水平。

6. 展望

肿瘤的侵袭和转移过程涉及众多生长因子、细胞因子、信号级联反应和细胞过程，使得开发出更加有效的靶向药成为一项挑战。不过 HIF-1 α /VEGF 通路是非常值得探索的一个环节。而且我们相信随着研究的越来越深入，在不久的将来以 HIF-1 α 和 VEGF 为治疗靶点的靶向治疗在肿瘤治疗中会越来越成功，并带给肿瘤患者新的希望。

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