中国病理生理杂志 2005 21 (2): 224-229 ISSN: 1000-4718 CN: 44-1187/R

论著

趋化因子受体CXCR4及其配体SDF-1与强直性脊柱炎发病的相关性研究

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收稿日期 2003-7-8 修回日期 2004-4-23 网络版发布日期 2009-9-13 接受日期 2004-4-23

摘要 目的：探讨趋化因子及其受体在强直性脊柱炎（AS）时的变化及其在关节炎发病机制中的作用。方法：用含588个基因的cDNA微阵列方法比较13例AS患者和7例健康志愿者外周血单个核细胞（PBMC）基因的表达水平；用流式细胞术对PBMC表面C-X-C趋化因子受体4(CXCR4)蛋白表达水平进行检测，并以免疫组化方法和ELISA方法检测其配体SDF-1（基质来源因子）在滑膜成纤维细胞和滑膜组织的表达情况。结果： AS的588 个基因谱和健康志愿者有明显区别，其中趋化因子受体(CXCR4)在AS外周血的单核细胞和CD8+的T淋巴细胞表达显著高于健康志愿者组(P＜0.05）。 SDF-1在AS病人的PBMC、滑液单个核细胞（SFMC）、关节液成纤维细胞和关节滑膜衬里层细胞的表达也增高。 结论： 趋化因子受体CXCR4及其产物在AS患者的PBMC表达明显增多，SDF-1在AS关节炎患者滑膜成纤维细胞和滑膜组织表达增多，提示CXCR4及其配体SDF-1这一信息通道在AS炎症病变的发展与持续中可能起重要作用。

关键词 脊柱炎,强直性； 受体,趋化因子； 配体,SDF-1； 寡核苷酸序列分析

分类号 R363

Chemokine receptor CXCR4 and its ligand SDF-1 in the pathogenesis of ankylosing spondylitis

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Abstract

<FONT face=Verdana>AIM: To determine the role of chemokine and its receptors in the pathogenesis of ankylosing spondylitis (AS). METHODS: Gene expression profiles of peripheral blood mononuclear cells (PBMC) in 13 AS patients and 7 healthy volunteers were determined by cDNA microarray with 588 targeting gene filter. Differentiated expressed CXCR4 and its only ligand SDF-1 were confirmed by semi-quantitative RT-PCR, ELISA, immunohistochemistry and FACS analysis using PBMC, synovial fluid mononuclear cells (SFMC) and synoviocytes. RESULTS: The gene expression profile of AS patients was significantly different from those of healthy volunteers. Higher expression of CXCR4 in monocytes and CD8+ T lymphocytes from PBMC in AS patients were found with statistical significance (P< 0.05) compared to those of healthy volunteers. The expression of SDF-1 was increased in PBMC, SFMC, synovial fibroblasts and lining layer cells of synovial membrane. CONCLUSIONS: The expression of CXCR4 was significantly increased in PBMC in AS patients. Its ligand SDF-1 was also found highly expressed in synovial fibroblast cell line and synovial membrane cells of AS patients, indicating that CXCR4 and SDF-1 may play a potential key role in the development and perpetuation of joint inflammation in AS patients.</FONT>

Key words Spondylitis ankylosing Receptors chemokine Ligands SDF-1 Oligonucleotide array sequence analysis

DOI: 1000-4718

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