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论著

系统性红斑狼疮患者血浆和血细胞DNA中p16基因启动子区甲基化现象和意义

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摘要 摘要：目的 检测系统性红斑狼疮（SLE）患者血浆和血细胞DNA中p16基因的甲基化状态并观察其与临床表现的关系。方法 采用甲基化特异性PCR（MSP）法分别检测活动期（24例）和非活动期SLE（21例）患者以及健康人（20名）血浆与血细胞中p16基因启动子区甲基化状态。结果 SLE患者血浆p16甲基化率（MP%）为64.4%,高于对照组的5%（P＜0.05）;活动期SLE患者的MP%为83.3%,高于非活动期的42.9%（P＜0.05）。SLE患者血细胞p16甲基化率（MC%）为48.9%,低于对照组的80.0%（P＜0.05）;活动期SLE患者的MC%为29.2%,低于非活动期的71.4%（P＜0.05）;非活动期MC%为71.4%,和对照组80.0%差异无显著性（P＞0.05）。SLE患者血浆和血细胞p16甲基化状态呈4种模式。活动期伴血浆p16甲基化+/血细胞p16甲基化-（MP+/CP-）模式与非活动期伴MP-/CP+模式的2组SLE患者部分临床和实验室检查有明显不同表现。SLE患者病情严重性判断评分与MP%呈正相关(r=0.93),与MC%呈负相关 (r=-0.96), MC%与MP%之间则呈负相关 (r=-0.79)。结论 SLE患者血浆和血细胞DNA中p16甲基化状态分析可提供诊断、病情评估以及与发病机制相关的重要信息。

关键词 系统性红斑狼疮 p16基因 甲基化

分类号

Phenomena and Pathological Significances of the Methylated p16 Promotor in DNA Derived from Plasma and Blood Cells of Patients with Systemic Lupus Erythematosus

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Abstract ABSTRACT:Objective To detect the methylation status of p16 gene promotor in DNA derived from plasma and blood cells of patients with systemic lupus erythematosus （SLE）, and it's relationship with clinical symptoms. Methods p16 promotor methylation in plasma and peripheral blood cells (PBCs) DNA were simultaneously detected with the methylation specific PCR （MSP） method in 24 active SLE patients, 21 inactive SLE patients, as well as 20 healthy controls. Results In the plasma DNA, p16 gene methylation ratio (MP%) was higher in SLE patients than in the healthy controls (64.4% vs. 5.0%, P＜0.05). MP% in the active SLE patients was significantly higher than that in the inactive SLE patients (83.3% vs. 42.9%, P＜0.05). In the PBCs, p16 gene methylation ratio(MC%) in the healthy controls was significantly higher than that in SLE (80.0% vs. 48.9%, P＜0.05). MC% in the active SLE patients (29.2%) was the lowest among three groups. There was no significant difference between the inactive SLE patients and healthy controls (71.4% vs. 80.0%, P>0.05). Each patient could be judged as one of the four methylation patterns: MP/MC, UP/MC(UP: unmethylated plasma p16), MP/UC (UC: unmethylated PBCs p16) , and UP/UC. The ratios of MP/MC and UP/UC were similar between the active and inactive SLE patients. However, different distributions of other two patterns were found in the active and inactive SLE patients as UP/MC 4.2% vs. 42.9% (P＜0.05) and MP/UC 58.3% vs. 14.3% (P＜0.05), respectively. The active SLE patients with MP/UC and the inactive SLE patients with UP/MC showed different clinical symptoms and laboratory examinations. Significant correlation was found between the disease activity index for lupus patients (SLEDAI) scores and MP%(r=0.93), between the SLEDAI scores and MC%(r= -0.96) also between MC% and MP% (r=-0.79). Conclusion The p16 methylation assay provides available information for the diagnosis, judgment of disease activity, as well as novel insights into the pathogenesis underlying this disease.

Key words systemic lupus erythematosus p16 gene methylation

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