

综述

DNA甲基化与系统性红斑狼疮

袁敏¹, 沈南^{1△}, 唐元家², 罗晓兵²

1上海交通大学医学院附属仁济医院风湿病科, 上海市风湿病学研究所, 上海 200001;

2中国科学院上海生命科学研究院-上海交通大学医学院健康科学研究所分子风湿病学研究组, 上海 200025

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摘要

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Role of DNA methylation in the pathogenesis of systemic lupus erythematosus

YUAN Min¹, SHEN Nan¹, TANG Yuan-jia², LUO Xiao-bing²

1Department of Rheumatism, Renji Hospital, Shanghai Jiaotong University School of Medicine,

Joint Molecular Rheumatology Laboratory of Shanghai Renji Hospital, Shanghai 200001, China;

2Institute of Health Sciences, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences and

Shanghai Jiaotong University School of Medicine, Shanghai 200025, China. E-mail: shennand@online.sh.cn

Abstract

Systemic lupus erythematosus (SLE) is an archetypical systemic, autoimmune inflammatory disease, of which the mechanism still not unveiled. Studies on epigenetics in SLE have long been the subject of investigation and as part of epigenetics. DNA methylation has been confirmed to play a role in the pathogenesis of SLE. The high autoreactivity of CD4+T cell from SLE patients is associated with DNA hypomethylation. DNA hypomethylation is crucial to induce SLE-like autoimmune disease in SLE-non-susceptible mice. The reactivation of inactive X chromosome by hypomethylation may lead to high incidence of SLE in women. Drug-induced SLE is also connected with DNA hypomethylation. To understand the role of DNA methylation in the onset of SLE comprehensively, we review the findings reported in the literatures about DNA methylation and SLE.

Key words [Lupus erythematosus](#) [systemic](#) [DNA methylation](#) [CpG island](#) [X chromosome](#)

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通讯作者 沈南 shennand@online.sh.cn

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