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综述

Diabetes—Role of epigenetics, genetics, and physiological factors

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摘要

关键词

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Diabetes—Role of epigenetics, genetics, and physiological factors

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Abstract
Cells of organ systems are endowed with a relatively similar genome while epigenome niches keep varying chronologically and defined explicitly in the respective tissues. The genome of an individual is always influenced by parental, embryonic, tissue-specific, and environmental epigenomes and the same must have been the possible reason for invariable inquiries relating to familial, environmental and life style patterns in the preliminary investigations of diabetic complications. Unprecedented methylation of lysine residues of histones and cytosines of CpG islands of promoter DNA impede the transcription of genes and homocysteine is the metabolic key player of methyl groups. Gck and COX7A1 are the 2 examples in the present review to elucidate the epigenetic influence on the onset of diabetes. miRNAs are additional promising cellular components influencing both at transcriptional and translational levels and promoting either in favour or against (i.e., feed back) TFs, signaling factors and proteins through their pliotropic effects and thus are reported to regulate cellular physiology. miR-124a and miR-9 are primarily endemic to nervous tissue and they are now being exploited in islets for their function in executing exocytosis of insulin, which of course is one of the fundamental canons of diabetes. miR-375 persuades beta cells for glucose-induced insulin gene expression. The current approach to evaluate the constellation of genes and their products involved in diabetes in huge number of samples through GWA studies may unravel intricacies involved in the management of diabetes and its associated consequences.

Key words epigenetics miRNAs genetics genome wide association

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