Abstract

Objective: The epigenetic hypothesis is one of the research pathways used to explain the complex aetiology of neurodevelopmental disorders. This review highlights the findings of recent studies in the field of epigenetics in ADHD.

Methods: An electronic literature search using Medline.

Results: In the Gene × Environment interaction model, several clinical, genetic and molecular arguments support the epigenetic hypothesis in ADHD aetiology. Environmental ADHD risk factors including toxic, nutritional factors and stressful life events lead to changes in DNA methylation and in histone modification levels. One critical CpG site located in the promoter of the DRD4 gene exhibited a specific pattern in ADHD children. A methylome-wide exploration of DNA showed decreased methylation in vasoactive intestinal peptide receptor 2 gene, which was not replicated by further research.

Conclusion: Current data require consolidation and could lead to the identification of biomarkers and the introduction of new modalities of treatment.