

## Major Epigenetic Changes in Polycystic Ovary Syndrome

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### Abstract

**Background and Objective:** Polycystic Ovary Syndrome (PCOS) is one of the most common causes of female infertility. The etiology of this condition is complex. Various genetic and environmental factors have been identified in the pathogenesis of PCOS. In recent years studies have demonstrated that the epigenetic factors may also be involved in this syndrome. For gathering data about the role of epigenetic alterations, a review study was performed.

**Method:** This study was done on 110 papers that were indexed by Pubmed before August 2020. The literature review was based on the following keywords: Epigenetic, Polycystic Ovary Syndrome, epimutation, Hyperandrogenism, Genomic Imprinting, Epidrug, oligomenorrhea, CpG islands and DNA methylation.

**Findings:** Based on recent articles, multiple metabolic genes show aberrant DNA methylation in PCOS, including PPARG, and SVEP1. Patients with PCOS also show epigenetic differences in skeletal muscle and adipose tissue. Furthermore, several studies have confirmed hypomethylation of DNA in the cells of the immune system, including monocytes, B-cells and T-helper cells. Additionally, expression of miR-16 was also significantly down-regulated in serum and ovarian cortex of the patients.

**Conclusion:** In recent years, various epigenetic alterations have been identified among patients with PCOS, however still more studies are needed to find further epimutations. Comprehensive studies should investigate the exact effect of these changes on the pathology of the disorder in order to find epidrugs or environmental factors that can modify these alterations.

**Keywords:** Epigenomics, Infertility, Hyperandrogenism, Oligomenorrhea