GENETIC FACTORS IN THE PATHOGENESIS OF POLYCYSTIC OVARY SYNDROME IN WOMEN WITH OVERWEIGHT AND OBESITY

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Polycystic ovary syndrome (PCOS) is a multifactorial disorder with high prevalence and marked clinical and metabolic heterogeneity. Genetic variations play a key role in shaping PCOS phenotypes, influencing susceptibility to endocrine and metabolic disturbances. Understanding these genetic factors is essential for personalized diagnosis and therapy.

Keywords: *polycystic ovary syndrome, genetic factors, SNPs, metabolism, hormonal regulation, body mass index, personalized medicine*

This study investigates the influence of single nucleotide polymorphisms (SNPs) in genes related to metabolism and hormonal regulation (DENND1A, FTO, INSR, and others) on the development and course of PCOS in women with different body mass indices, aiming to identify genetic predictors of disease risk and severity.

A case–control design was applied. The main group includes 150 women with PCOS, subdivided into: 50 with normal body weight, 50 overweight, and 50 with obesity. Patients were further stratified by disease severity (mild vs. severe). The control group comprises 50 women without PCOS and with normal body weight. This design allows evaluation of associations between genotypes and phenotypic manifestations.

Clinical and laboratory assessments were conducted to confirm PCOS diagnosis and evaluate endocrine-metabolic parameters. Molecular genetic analysis identified SNPs in candidate genes. Frequencies of polymorphisms were compared among subgroups and controls. Associations between genetic variants and clinical features, including anovulation, hyperandrogenism, and insulin resistance, were analyzed using standard statistical methods.

Expected outcomes include identification of genotype-phenotype correlations and associations with the severity of metabolic and clinical disturbances, providing a foundation for integrating molecular-genetic markers into clinical practice.