



THE IMPORTANCE OF GENETIC MARKERS IN THE DIAGNOSIS OF HYPERANDROGENY SYNDROME IN WOMEN OF REPRODUCTIVE AGE

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Summary: In our study, according to the sequencing analysis of the CYP21A2 gene, only single nucleotide polymorphism mutations were detected in patients with hyperandrogenism, and 3.97% (n=5) of them had a homozygous wild-type genotype, 46.8% (n=59) had a heterozygous genotype (there is one minor allele) was confirmed. Among all identified polymorphism type mutations, only rs9378252 polymorphism proved to have a statistically reliable positive association between minor allele and heterozygous genotypes and the development of hyperandrogenism.

Relevance of the topic. Hyperandrogen syndrome in women of reproductive age remains one of the most pressing problems of endocrine gynecology. The syndrome of hyperandrogenism in women leads from their appearance to the violation of reproductive functions [1,2]. In 2010, polycystic ovary syndrome (PCOS) occurred in 5-10%, but now this indicator is 15-20%. For this reason, this syndrome causes women to lose their quality of life [3,4]. Determining the percentage of women of reproductive age with non-classical congenital adrenal hyperplasia and hyperandrogenism will help determine the next stage of treatment. It is known from the literature that in the development of non-classical congenital adrenal hyperplasia, 21-hydroxylase enzyme deficiency is the cause in 90% of cases [5,6]. Various changes in the structure of the CYP21A2 gene, which encodes this enzyme, reduce the activity of the enzyme. To confirm the diagnosis of non-classic congenital adrenal hyperplasia, molecular-genetic examination is important.

The aim of the study. Improving differential diagnosis by identifying CYP21A2 gene polymorphisms in women with hyperandrogenism syndrome.

Object of research. 126 women of reproductive age with hyperandrogenism and 32 healthy women without reproductive disorders were admitted to the Bukhara Regional Center for Reproductive Health.

Research method. Amplification of the SYP21A2 gene sequence was performed during a molecular genetic study. Peripheral blood was obtained from selected women. The product obtained for the study was processed using the GeneAmp® PCR System 9700 device. Polymerase chain reaction products

were analyzed on a Complex-3500 automated genetic analyzer (Applied Bio-systems, USA). Amplified genomic DNA sequence was determined using a set of special reagents from Applied Bio-systems (USA) and Data Collection Software 3.0 special computer program. Using the MEGA special computer program, the image of the spectrum reflecting the DNA sequence of all the studied objects was obtained. Molecular genetic research was conducted in the laboratory of the Scientific and Practical Center of Sports Medicine of the Republic.

Results and their discussion: Based on the results of CYP21A2 gene sequencing performed in our study, single nucleotide polymorphism (SNP) type mutations, such as deletion, translocation, micro- and macro-conversion, strongly affecting the conformation of the expressed enzyme, were identified. not found in the main group. Specific minor allele of polymorphism 683 G>A (K102L) in 14.3% of patients (n=18) and 20% (n=6) of the control group, polymorphism rs6468 (L39V) in 13.5% (n=17) of patients and 9, 3% in controls (n=3), rs9378252 (H62L) polymorphism in 19.8% (n=25) of patients and 3.12% (n=1) in controls (p<0.05), rs6477 (Leu249=) 10.3% (n=13) patients and 9.3% (n=3) controls, 1389 T>A (M239K) in 7.1% (n=9) patients and 3.3% (n=1) in the control group, non-wild or minor allele (p>0.05), 2578 C>T (P453S), 655 A/C>G, 999 A>T (I172N) (p>0.05), 2108 C>T The minor allele characteristic of such polymorphisms as (R356W) was detected only in patients and amounted to 3.2% (n=4), 8% (n=10), 5% (n=6) and 0, 8% (n=1), respectively.

Conclusion: In conclusion, according to the results of CYP21A2 gene sequencing, among all identified mutations of the polymorphism type, only the rs9378252 polymorphism with a minor allele and heterozygous genotypes has a statistically significant positive association with the development of hyperandrogenism. On the other hand, it was confirmed that polymorphisms 653 G>A, rs6477 and 1389 T>A do not have such an association. Similarly, mutant alleles of polymorphisms 2578 C>T, 655 A/C>G, 999 A>T and 2108 C>T were found only in patients of the main group. In addition, double minor alleles were found in 18.3% and triple minor alleles in 2.4% of patients.

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