MAO-A, COMT, NET GENE POLYMORPHISMS AND THE LEVELS OF CATECHOLAMINES AND THEIR METABOLITES IN PATIENTS WITH PARKINSON’S DISEASE

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Polymorphisms of MAO-A, COMT, NET genes play a crucial role in pathogenesis of many neurological diseases ex. Parkinson’s disease (PD) and may be involved in catecholamine (NE, E) catabolism to their metabolites: Nmeta, Meta respectively. Catecholamines in mammalian are important neurotransmitters in brain and peripheral sympathoadrenal medullary. Measurement of catecholamines concentration provides significant information regarding sympathoadrenal activity. NE and E participate in regulation of blood pressure in autonomic system. Many patients with PD showed symptoms autonomic dysfunction.

The aim of these study was to estimate frequency of MAO-A (c.1460C>T), COMT (c.649G>A), NET (c.1287G>A) genes polymorphisms in DNA isolated from whole blood and analysis of concentration of catecholamines (NE, E) in plasma and their metabolites (NMeta, Meta) in urine of PD and controls.

Studies were conducted on 30 patients with PD (35-81 years) and 30 controls (25-75 years). The polymorphisms of MAO-A, COMT, NET were determined using PCR-RFLP method and the levels of NE, E, NMeta and Meta were estimated using HPLC/EC technique. Statistical analysis of obtained results in PD and control group revealed no significant differences in prevalence of gene polymorphisms only in case of NET. Differences in catecholamine levels between PD and controls were related only to COMT and NET polymorphisms. Simultaneously changes in concentration of NMeta and Meta concerned not only COMT and NET but also MAO-A.

It seems likely that MAO-A, COMT and NET gene polymorphisms may affect the level of catecholamines or their metabolites in patients with PD.