

**THE DIFFERENTIATION OF SLOW AND FAST TYPES OF  
ACETYLATION IN PARKINSON'S DISEASE – A STUDY USING  
MOLECULAR MARKERS**

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Parkinson's disease (PD) is caused by selective dopaminergic cell loss in the nigro stratal system. The etiology of PD is a combination of genetic and environmental factors. The polymorphism of the detoxification enzyme NAT2 is responsible for the individual differences in the acetylating rate of aromatic amine and hydrazine-drugs, chemical and environmental pollutants (potential carcinogens and mutagenes) and endogenic substances. The rate of acetylation has significance in PD, especially in the case of early onset.

Molecular markers useful for analyses of slow and fast acetylator status are point mutations of the substitution type that may occur in the coding region of the NAT2 gene.

Fast acetylators (FA) have at least one wild-type allele, resulting in a normal rate of acetylation, while slow acetylators (SA) have two mutant alleles, lowering the acetylation rate. Among these, there are mutations occurring in the Caucasian population: G590A (Arg 197 Gln), A803G (Lys 268 Arg), quiet C481T, G857A (Gly 286 Glu) and T341C (Ile 114 Thr). The main alleles of slow acetylation NAT2\*5, NAT2\*6 account for the slow acetylators found among the Caucasian population.

This study aims to identify which polymorphic types of NAT2 are found in patients with early onset of Parkinson's disease and to reveal whether NAT2 could be a risk factor in the development of PD, or whether it could be a molecular marker in the diagnosis of PD.

The material used was genomic DNA, isolated using a Genomic DNA Prep Plus kit (A&A Biotech Company) from venous blood samples acquired from patients with idiopathic, clinically proved Parkinson's disease with early onset (before the age of 50). After amplification via PCR, the DNA fragments were separated on a 5% polyacrilamid gel, and out-stained with silver nitrate (AgNO<sub>3</sub>). The polymorphism of the obtained amplimers was examined employing the RLFP and SSCP technique and DNA sequencing using ABI PRISM 310 equipment.

The preliminary results obtained permitted the estimation of the polymorphism frequency of the NAT2 gene in patients suffering from PD with early onset.