

NAT2 POLYMORPHISMS IN A GROUP OF INDIVIDUALS FROM RIO DE JANEIRO

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Arylamine *N*-acetyltransferases (NATs) play an important role in detoxification and metabolic activation of several xenobiotics including therapeutic drugs, occupational chemicals and carcinogenic substances. They are phase II enzymes and act on many primary arylamines, hydrazines and their *N*-hydroxylated metabolites by transferring an acetyl group from the acetyl coenzyme A to the nitrogen or oxygen atom of these compounds. There are two human *N*-acetyltransferases - *NAT1* and *NAT2*, both encoded by genes located on chromosome 8. Variant alleles showing combinations of single nucleotide exchanges are known in both genes and produce different acetylation phenotypes. In this study the genotypic frequency of the *NAT2* gene in a group of 92 individuals from Rio de Janeiro state was determined. Genomic DNA was extracted from peripheral blood of the volunteers and used as template to amplify the *NAT2* gene by PCR. Genotyping of the *NAT2* polymorphisms was performed using the RFLP technique. The amplicons were separately digested with *KpnI* (M1 allele, C481T), *TaqI* (M2 allele, G590A), *BamHI* (M3 allele, G857A) and *MspI/AIuI* (M4 allele, G191A). The population was in agreement with Hardy Weinberg Equilibrium regarding to alleles M1 and M3. The four nucleotide substitutions were analyzed in 18 individuals. In this group approximately 45% of the subjects showed slow *NAT2* phenotype, an intermediate value considering the data described in the literature. Financial support: UERJ, FAPERJ.