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Relationship between glutathione S-transferase P1 polymorphisms and chronic obstructive pulmonary disease in a Tunisian population

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ABSTRACT. Chronic obstructive pulmonary disease (COPD) is a multifactorial disease with possible genetic predisposition and involvement of various environmental factors. Several candidate genes have been reported as potentially associated with this lung disease. The glutathione S-transferase P1 gene (*GSTP1)* was proposed to be involved in susceptibility to develop COPD. It belongs to the GST family, which is a group of phase II enzymes that catalyze the glutathione conjugation of many endogenous and exogenous electrophilic compounds, such as carcinogens, therapeutic drugs, environmental toxins, and oxidative stress products. We conducted a case-control study to investigate genetic polymorphisms of this enzyme [exon 5 (Ile105Val) and exon 6 (Ala114Val)] in 234 unrelated COPD cases and 182 healthy controls from a Tunisian population. Genotyping was carried out using polymerase chain reaction and restriction fragment length polymorphism methods. *GSTP1* Ala114/

Val114 and Val114/Val114 genotypes were not found in either patients or healthy controls. However, there were differences in the distribution of various exon 5 GSTP1 genotypes between COPD patients and healthy controls. GSTP1 Val105/Val105 was significantly more common in patients compared to controls (OR = 2.67; 95%CI = 1.45-4.92; P = 0.0013). Multivariate logistic regression analysis confirmed a significant relationship between the mutant genotype and COPD (OR = 2.58; 95%CI = 1.31-5.09; P = 0.026), after adjustment for classic risk factors. Analysis of variance showed no correlation between age, body-mass index, pack-years, percentage of predicted FEV1 values, and any of the GSTP1 genotypes. We conclude that subjects with GSTP1 Val105 allele are at higher risk of COPD.

Key words: Chronic obstructive pulmonary disease; Genetic polymorphism; Glutathione S-transferase

