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Polymorphisms of GSTM1, GSTT1, GSTP1 and CYP1A1 genes and susceptibility to lung cancer

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Biotransformation enzymes are related with lung cancer that arises as a consequence of exposure to mutagenic agents. *CYP1A1* gene codifies the phase I enzyme, aryl hydrocarbon hydroxilase, belonging to the Cytochrome P450 system, that plays a major role in the bioactivation of tobacco procarcinogenes, while glutathione-S-transferases genes, *GSTM1*, *GSTT1* and *GSTP1*, codify conjugation enzymes associated with detoxification processes of free radicals, xenobiotics and cytotoxic drugs [1]. Our main goal was to verify possible associations between polymorphisms of these genes and susceptibility to lung cancer.

CYP1A1 polymorphisms, m1 (T6235C) and m2 (A4889G) were studied by RFLP assay, *GSTM1* and *GSTT1* (*GSTM1*0* and *GSTT1*0*) by PCR multiplex and *GSTP1* (rs1695) by real time PCR, in 197 patients and 237 controls. For *CYP1A1* alleles and genotype distributions, no statistically significant differences were found between both populations. *GSTT1 *0/*0* genotype was associated with a higher susceptibility to lung cancer (OR: 1.6; 95%CI: 1.02-2.44; $p < 0.05$). In the patient population, smoking burden of 21-100 pack-years were more frequently associated with *GSTT1 *0/*0* genotype than in controls ($p < 0.02$). This difference was even more significant for ex-smokers ($p < 0.001$). Gene copy number assay exposed an association between *GSTM1*1/*0* and lung cancer ($p < 0.001$).

The results reveal a possible association between *GSTT1 *0/*0* and susceptibility to lung cancer related with smoking habbits.

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