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# **RISK OF SPECIFIC LYMPHOMA SUBTYPES IS ASSOCIATED TO POLYMORPHISM IN GENES IMPLICATED IN THE METABOLISM OF WORKPLACE CARCINOGENS**

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**Objectives** Exploring lymphoma risk associated with metabolic gene polymorphisms might provide clues on the role of gene-environment interactions in lymphomagenesis.

**Methods** We assessed polymorphisms in genes encoding for the metabolic enzymes CYP1A2, CYP2E1, GSTM1, GSTT1, NAT1, NAT2, NQO1, and PON1 in 255 incident lymphoma cases and 204 population controls. The OR for lymphoma overall, B lymphoma, and the diffuse large B cell lymphoma (DLBCL) and chronic lymphocytic leukaemia (CLL) subtypes, associated to the less frequent allele was calculated along with the respective 95% CI, adjusting by age and gender.

**Results** GSTT1 gene polymorphism significantly increased risk of DLBCL (OR = 5.0, IC 95% 3.0 to 8.3). An excess risk of DLBCL was also related to polymorphisms in the CYP1A2, PON1, NAT1 and NAT2 genes. CLL risk was reduced in relation to CYP1A2 polymorphisms, increased in relation to GSTM1 deletion, and strongly associated with NAT1, and NAT2 mutant haplotypes.

**Conclusions** Caution is recommended in interpreting the high risks in our study, due its small size. However, our results suggest that polymorphisms in genes encoding for the metabolic enzymes might affect risk of specific lymphoma subtypes associated with exposure to workplace carcinogens.