Candidate SNPs in xenobiotic metabolism pathways involved in childhood acute lymphoblastic leukemia susceptibility

Abstract

Childhood acute lymphoblastic leukemia (ALL) is the most common pediatric cancer and the etiology is still largely unknown. Previous studies have demonstrated associations between environmental exposures and childhood ALL risk. When a child is exposed to various carcinogens, enzymes involved in xenobiotic metabolism are responsible for eliminating these compounds. Polymorphisms in genes encoding xenobiotic-metabolizing enzymes may lead to interindividual variation in the ability to eliminate carcinogens which might have influences on the susceptibility to ALL. In order to investigate the role of genetic factors in childhood ALL, we conducted association analyses among a series of 564 cases and 4,015 controls in Japanese. We found that the *UGT1A* family, *EPHX1*, *NAT2*, and *CYP1B1* genes might contribute to the risk of ALL. We also observed evidence of gene-gene interaction between the *UGT1A* family and *NAT2*, *UGT1A* family and *CYP1A2*, within *UGT1A* family, and within *NAT1*. Further analyses are warranted, but identifying an association within these genes might provide insight and inform next steps regarding the effect of environmental carcinogen exposures on risk of childhood ALL. Cumulative evidence from both environmental and genetic epidemiological studies can help us to build the case for implementing appropriate public health interventions.