



Reply to “ARID5B rs7089424 and rs10994982 and association with B-lineage ALL susceptibility”

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DEAR EDITOR,

We first thank Dr. Joob and Prof. Wiwanitkit for their interests¹ and constructive queries on our study entitled “Genetic polymorphisms of ARID5B rs7089424 and rs10994982 are associated with B-lineage ALL susceptibility in Chinese pediatric population.”² The association of specific alleles of ARID5B rs7089424 and rs10994982 with B-lineage acute lymphoblastic leukemia (B-ALL) susceptibility in our study was based on the statistical differences of allele frequencies between B-ALL patients and healthy controls. As the data shown in Table 3 of our article,² frequencies of ARID5B rs7089424 G allele and rs10994982 A allele in B-ALL patients were significantly higher comparing with those in controls (rs7089424 G allele: 49.1% vs 37.8%, $p = 0.001$; rs10994982 A allele: 61.4% vs 48.9%, $p = 0.000$). Therefore, we concluded rs7089424 G allele and rs10994982 A allele as the risk alleles of B-ALL susceptibility in Chinese pediatric population. As for the affection of nonstudied genetic polymorphisms on our results, there was too much uncertainty to define the presence and extent of this influence. The genetic polymorphisms in *CYP2E1*, *GSTM1*, *NQO1*, *NAT2*, *MDR1*,

and *XRCC1* modulated ALL risk through different mechanisms such as xenobiotic system, DNA repair, and gene–environment interaction.³ To our knowledge, there was no evidence that the genetic linkages really existed between ARID5B and the above-mentioned genes or the genetic polymorphisms of these genes affected the possible mechanisms of ARID5B in B-ALL development. In a word, the results and conclusions in our article were logical and credible on the basis of statistical analysis of large sample population data and lacked of direct evidence of being influenced by the genetic polymorphisms of other genes.

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