Relationship Between Polymorphisms in Glucose Glycolytic Pathway Associated Genes and Risk of Nasopharyngeal Carcinoma Development

Zhi-Gang Liu (Key Laboratory of Translational Radiation Oncology, Hunan Province; Department of Radiotherapy, Hunan Cancer Hospital, The Affiliated Cancer Hospital of Xiangya School of Medicine, Central South University, P.R. China), Yu Zhao(Key Laboratory of Translational Radiation Oncology, Hunan Province; Department of Radiotherapy, Hunan Cancer Hospital, The Affiliated Cancer Hospital of Xiangya School of Medicine, Central South University, P.R. China), Zhen Guo(Department of Clinical Pharmacology, Xiangya Hospital, Central South University and Institute of Clinical Pharmacology, Central South University; Hunan Key Laboratory of Pharmacogenetics, P.R. China), Jiao Tang(Key Laboratory of Translational Radiation Oncology, Hunan Province; Department of Radiotherapy, Hunan Cancer Hospital, The Affiliated Cancer Hospital of Xiangya School of Medicine, Central South University, P.R. China), Wei Zhang(Department of Clinical Pharmacology, Xiangya Hospital, Central South University and Institute of Clinical Pharmacology, Central South University; Hunan Key Laboratory of Pharmacogenetics, P.R. China), Hui Wang(Key Laboratory of Translational Radiation Oncology, Hunan Province; Department of Radiotherapy, Hunan Cancer Hospital, The Affiliated Cancer Hospital of Xiangya School of Medicine, Central South University, P.R. China)

BACKGROUND: Altered glucose-metabolism is the most common metabolic hallmark of malignancies. We aimed to characterize different polymorphisms in glucose glycolytic pathway associated genes and evaluate its association with nasopharyngeal carcinoma (NPC) development.

HYPOTHESIS: Some polymorphisms in glucose glycolytic pathway associated genes could affect the development of nasopharyngeal carcinoma.

METHODS: We have developed a hospital-based case-control study using the haplotype-tagging single-nucleotide polymorphism (SNP) approach. 30 SNPs from 4 glucose-metabolism genes were genotyped in 379 patients with NPC (cases) and 516 healthy individuals (controls) using the Mass ARRAY system.

RESULTS: Hexokinase (HK) rs2229629 GA/AA (HR = 0.679, 95 % CI 0.478–0.964), HK rs656489 GA (HR = 0.733, 95 % CI 0.541–0.993), Hypoxia Inducible Factor-1α (HIF-1α) rs17099567 TT (HR = 0.542, 95 % CI 0.329–0.894) were significantly associated with reduced NPC risk. HIF-1α rs10136168 AA/GA (HR = 1.419, 95 % CI 1.066–1.889) was associated with increased NPC risk. This study firstly discovered the association between glucose glycolytic pathway SNP and NPC risk. Further studies in larger populations are needed to validate these observations.