Genetic Susceptibility and Lung Cancer Risk in Korean

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Lung cancer has been considered as a disease determined solely by exposure to environmental carcinogens. However, there is a growing realization that genetic constitution is of importance in determining individuals susceptibility to lung cancer. Interindividual variation in cancer susceptibility to similar carcinogen exposure may be due to functional polymorphism in genes controlling carcinogen metabolism and DNA repair. Biomarker research to identify smokers with the highest risks of developing cancer is exceeding important in lung cancer, for which only minimal progress has been made in early detection and treatment. Several studies have suggested that the genotypes of GSTM1, CYP1A1, and XRCC1 genes, etc are independent risk factors for lung cancer in Japanese and/or Caucasian. Since it is unlikely that one genotype has strong effect on risk, in order to represent the true dimensions of gene-environment interactions, multiple susceptibility factors must be identified and accounted for. Moreover, since the frequency of the genetic traits can differ by race and ethnicity, the identification and characterization of Korean-specific single nucleotide polymorphism (SNP) related to lung cancer are necessary. In the future, microarray technology will enable the performance of large scale and low cost genotyping using automated workstations that will capable of extracting DNA from blood samples and performing DNA amplification, hybridization and detection.