A Study on the Urinary Metabolite by PAHs and Genetic Susceptibility Markers

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Abstract

In this study, the methods were developed to measure polycyclic aromatic hydrocarbons(PAHs) in the air, metabolites of pyrene and benzo(a)pyrene via human urine, genetic polymorphisms in human buccal cell for evaluation of the health effects about environmental pollution. We have also performed a preliminary molecular epidemiology study on residents in the metropolitan area and workers in workplace for these method applications.

Introduction

In urban areas, PAHs are important ambient pollutants because of their detrimental effects on human health and their role in the chemistry of atmosphere precursors of ozone, peroxyacetylnitrate(PAN), and other oxidants. The profile of PAH concentrations differs from one country to another due to several factors such as legislative control for PAHs, composition of vehicle fuel, differences in heating pattern in residential area and meteorological conditions. Therefore, to develop effective strategies on the reduction of ambient levels of PAHs. The study was performed in a workplace where the case-control study is being used. Workers were recruited exclusively from the work place where the highest concentration of PAH was expected. As a control group, dwellers of the Seoul Metropolitan Region were recruited. The study group consisted of 9 workers and 26 controls.

Methods

The analytical method utilized HPLC(High Performance Liquid chromatography) for metabolites measure of pyrene and benzo(a)pyrene in human urine. Modifying the analytical procedure for the determination of 1-hydroxypyrene(1-OHP), 1-OH-pyrene-glucuronide(1-OHPG), 7,8-diol-benzo(a)pyrene(Diol) and 7,8,9,10-tetrol-benzo(a)

pyrene(Tetrol), we developed HPLC method for the simultaneous determination of 1-OHP, 1-OHPG, diol and tetrol. We used QIAgene DNA extraction kit that made quickly and cleanly DNA extraction. We can utilize that buccal cell DNA, for decision genetic susceptibility markers which were GSTM1, GSTT1, GSTP, CYP1A1, CYP2E1 and NQO1, instead of blood DNA.

Results

Metabolites product of pyrene(1-OHP, 1-OHPG) were not significant both in urban and workplace area. The average concentration of 1-OHP and 1-OHPG in participant's urine were 0.037±0.062 and 0.714±1.095 $\mu g/g_{creatinine}$, each.

Diol as metabolite product of benzo(a)pyrene was significant between urban and workplace area. The average concentration of diol and tetrol in participant's urine were 0.249±0.528 and 0.750±0.792 $\mu g/g_{creatinine}$, respectively.

In the case of CYP1A1, 42.86% of them has homozygous wild type(W) and who has heterozygous variant type(H) was 48.57% and 8.57% of homozygous variant type(M) genetic type. In the case of CYP2E1, 69.44% of them has homozygous wild type(D) type, 25.00% of each has heterozygous variant type(DC) and 5.56% of them has homozygous variant type(CC).

Who doesn't have GSTM1 gene was 48.57% and who has GSTM1 gene was 51.43%. Who doesn't have GSTT1 gene was 63.89% in study groups and who has GSTT1 gene was 36.11%.

Who has W genetic type, which is homozygous wild type of GSTP1, was 79.41% and H genetic type, which is heterozygous variant type was 20.59%..

Who has C/C genetic type, which is homozygous wild type of NQO1, was 37.14% and C/T genetic type, which is heterozygous variant type was 48.579%. T/T genetic type which is homozygous variant type was 14.29%.

Conclusions

Concentration differences of metabolites such as 1-OHP, 1-OHPG, diol and tetrol in urine, which is generated by genetic polymorphism of CYP1A1, CYP2E1 gene of Phase I and GSTM1, GSTT1, GSTP1, NQO1 gene of Phase II, was examined. As a result, GSTM1, GSTP1, CYP1A1, CYP2E1, NQO1 and indicate slight differences depend on the amount of metabolites in urine, it was not statistically significant.

Keywords : urinary metabolites, genetic polymorphism