

**[P-47]****THE MICROSOMAL EPOXIDE HYDROLASE(MEPHX)  
POLYMORPHISMS AND THE ASSOCIATION OF  
MICRONUCLEI(MN) IN THE BENZENE-EXPOSED WORKERS**

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In order to investigate whether genetic polymorphisms in the mEH exon3 (Tyr139His), exon4 (His113Arg) interact with the formation of MN in benzene exposed workers, the PCR-RFLP based genotyping of 76 exposed and 115 controls were performed and cytokinesis-block micronucleus (CBMN) analysis of 56 exposed and 53 controls was employed. There was no difference in the frequencies in mEH3 and mEH4 genotypes (n=191) in the exposed and control groups except mEH4 homozygous (Arg/Arg genotype) variant genotype (p<0.05). The frequencies of mEHs [very low, low, intermediate, and high] enzyme activities were 18.9%, 45.3%, 28.3%, 7.5% and 20.7%, 45.3%, 28.3%, 5.7% in the exposed and control groups, respectively. There was no significant difference in the distribution of mEHs enzyme activities between the study groups. The mean frequency of MN (n=109) was 0.037 per 100 cells (SE, 0.019) in the exposed workers and 0.021 per 100 cells (SE, 0.013) in the controls, which was statistically significant (p=0.00). Logistic regression analysis showed that the frequency of MN was significantly associated with the benzene exposure and mEH3 polymorphisms. The mEH3 variant alleles (Tyr/His or His/His genotypes), which confer the low and very low enzyme activities, were associated with an increase in the frequency of MN (p<0.05) compared with the wild type allele (Tyr/Tyr genotype). These results suggest that mEH genetic polymorphisms have a role in individual susceptibility to genotoxicity of benzene.

keyword : mEPHXs, polymorphism, MN, Benzene