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EDITORIAL

Genetic Impact of Second Hand Cigarette Smoke

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Second hand smoke is a complex mixture of more than 4000 chemical compounds that are generated during the burning of tobacco products and affects all those who are exposed to smokers in a closed environment either at home or work place. This mixture contains numerous irritants and toxicants which leave severe as well as carcinogenic health effects in humans[1].

Short as well as long-term effects of tobacco exposure can lead to multiple health implications. It has been estimated that secondhand smoke is responsible each year for 22,000 hospitalizations, between 150,000 and 300,000 cases of bronchitis and pneumonia, and between 8000 and 26,000 cases of asthma. The SHS exhibits hazardous particles and gases. The par¬ticulate phase contains more than 4000 sub¬stances, most of them toxic or otherwise noxious while the gaseous phase contains about 500 substances. Non¬smokers exposed to second hand smoke absorb significant amounts of these harmful substances. The blood levels of carbon monoxide, nicotine and other toxic substances rise in passive smokers. In the long run, non-smok¬ers exposed to ETS could find their respiratory function decreased to the same level as that of a moderate smoker.[2]

Second hand smoke plays a pivotal role in etiology of lung cancer. A large number of models of carcinogenesis provide an outline for considering the associations of lung cancer incidence with smoking intensity, duration, and smoking cessation. These models suggest that carcinogens derived from chemical components in tobacco smoke react with the DNA of respiratory epithelial cells. Some of the carcinogens instigate mutagenic changes while others support the growth of these mutated cells or disable genes that restrain tumor growth. Mutagenesis, growth promotion, and inhibition of tumor suppression may all be compulsory for clinically evident cases of lung cancer. Procarcinogens in tobacco smoke must be metabolically altered in order to exhibit their carcinogenic outcome. Various enzymes are involved in detoxification of these chemicals into inactive compounds. Genetic polymorphisms generate slightly different forms of the enzyme, resulting in variations in enzyme kinetics. These inherited differences in the transformation rate are source of variability in risk of cancers. In this regard, the enzyme CYP2D6 can transform polycyclic aromatic hydrocarbons and acrylamines into reactive chemical species that can bind covalently to DNA and induce mutations. The people who have CYP2D6 enzymes are extensive or intermediate metabolizers, as measured by the speed with which they metabolize the compounds present in second hand tobacco smoke. Extensive and intermediate metabolizers would be expected to have higher concentrations of these carcinogens in the lung than would slow metabolizers. The extensive metabolizing phenotype is associated with more than double the risk of lung cancer.[3]

Second hand smoke has an obvious role in the development of oxidative stress. Free radicals production due to oxidative stress modifies cardiac autonomic control resulting in heart rate variability (HRV). A positive association is found between polymorphisms in oxidant-scavenging glutathione S-transferase (GST) genes and their interactions with second hand smoke. The modifying effect of GSTM1 for the association of second hand smoke with heart rate variability suggests that these exposures cause systemic oxidative stress. This oxidative stress is scavenged by GSTM1 in the liver. The GSTM1 is responsible for the association between second hand smoke, GST polymorphisms, and lung cancer in passive smokers.[4]

Compared to adults, children may be more susceptible to secondhand smoke. This susceptibility may be exacerbated by alterations in inherited genetic variants of innate immunity genes. A genetic polymorphism in the mannose binding lectin-2 (MBL2) gene is found in the children with lung cancer exposed to second hand smoke. Functional MBL2 haplotype associated with high circulating levels of MBL and increased MBL2 activity was associated with increased lung cancer risk among those exposed to childhood.[5] It has long been suspected that cytogenetic deletions and/or loss of heterozygosity on the short arm of chromosome

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3 may be involved. The chromosomally fragile site, FRA3B, has been linked to lung cancers and more recently has been explored in cervical carcinomas. A large number of smokers and passive smokers showed fragility at FRA3B. FRA3B maps within the fragile histadine triad gene (FHIT), which is a tumor suppressor gene involved in tumorogenesis, including cervical neoplasia.[6]

Health professionals are also target of passive exposure to cigarette smoke which makes them also a focal group essential for creating awareness regarding hazards of passive smoking.[7] In our environment, bidi and huqqa smokers is another addiction that needs to be studied from genetic aspect to find out the multi-factorial polymorphism. With new technology enabling scientists to analyze the interactions between genomic structure and environmental stimuli, researchers should be able to make efforts in clarifying the role that SHS exposure plays in different types of cancers. There should be valid methods for describing the interactions between environmental exposures, pathogens, and genetic composition in the trail to understand the mechanism of all cancers.

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ORIGINAL ARTICLE

Zinc and Copper Levels Fluctuate with Altered Glucose Homeostasis

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ABSTRACT

Background: Type 2 diabetes mellitus is becoming one of the major health problems worldwide. Especially in South East Asia, type 2 diabetes has gained critical significance. As pre-diabetes prevalence is increasing worldwide, it has become an important concern to prevent diabetes at an early stage. Trace elements have been gaining attention in improving the glucometabolic conditions like pre-diabetes and diabetes. Zinc and copper are the major trace elements present in the human body and they play a significant role in the pathogenesis of diabetes mellitus and pre-diabetes.

Objectives: The purpose of this study was to compare serum zinc and copper levels in type 2 diabetes and pre-diabetes.

Methods: This study was conducted in department of Biochemistry BMSI, JPMC Karachi. Total 90 subjects were taken out of which 30 were type 2 diabetics, 30 were pre-diabetics and 30 were normal healthy individuals. Serum fasting glucose was measured by glucose oxidase method. Serum zinc and copper were measured by colorimetric method. Statistical analysis was done using SPSS version 16.

Results: Serum zinc levels were significantly lower in type 2 diabetics as compared to pre-diabetics and normal individuals (mean differences were 45.17±15.63μg/dl, 59.97±13μg/dl and 86.57±14.34 μg/dl respectively). Serum copper was significantly increased in type 2 diabetics compared to pre-diabetes and control samples (mean differences were 325.55±88.34 μg/dl, 175.53±47.45μg/dl and 126.87±21.57μg/dl respectively).

Conclusion: It was concluded that serum zinc was significantly lower in type 2 diabetics and pre-diabetics and is inversely related to serum fasting glucose while serum copper is significantly higher and positively related with fasting blood glucose.

KEY WORDS: *Type 2 Diabetes, Pre-Diabetes, Zinc, Copper.*

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