Summary

The present study showed the significant impaired antioxidant profile in the pesticide exposed group as compared to unexposed group, suggested the more risk of oxidative stress related disorder in the population due to an imbalance between the free radicals production and the antioxidant defenses. Although, the age, BMI, and alcohol intake are other independent risk factors apart from pesticide exposure to imbalance the oxidant-antioxidant balance inside the body. The AChE and BChE activities significantly declined in the pesticide exposed group that suggests the organophosphate-induced toxicity in the body.

The organophosphate (chlorpyriphos, dichlorvos, and ethoprophos) and herbicides (atrazine, alachlor, metolachlor, and butachlor) residues have been detected in the blood samples of pesticide exposed individuals. The in vitro cytotoxicity analysis revealed that the dose-dependent decrease in cell viability following chlorpyriphos, dichlorvos, atrazine and butachlor pesticides treatment in A549 and hPBMC cells. Also, the cell viability decreased further with the combined effect of different pesticide. The pesticides treatment showed more reactive oxygen species and cell cycle arrest at G0/G1 phase following treatment of chlorpyriphos, dichlorvos, atrazine and butachlor in a dose-dependent manner; thereby the cells would be interrupted at DNA synthesis phase.

Genetic variation has not been detected in the CYP1A2 and PON1 gene products. The two missense mutations has been identified on chromosome 19 in the coding region (exon 1) of CYP2B6 gene .i.e. g.40991390G>T (SNP ID: rs33926104), g.40991388T>C (unknown) that results in R29S and D28G amino acid change in CYP2B6 protein. Besides one missense variants g.99758180C>T (change of valine to isoleucine amino acid (V489I) at 489) and three 3’ UTR allelic variants i.e. g.99757990A>T, g.99758050A>C and g.99758022A>T had been predicted in CYP3A4 gene. The resultant mutation may have an impact on the xenobiotic metabolism that needs to be explored further via in vivo proteomic functional analysis.