Genotoxicity and DNA methylation patterns associated with Electronic Cigarettes

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Cigarette consumption is the leading cause of preventable death worldwide. In recent years, it has been claimed that electronic cigarettes (EC) present a safer alternative since they don't use tobacco directly but rather derivatives of it, such as nicotine. Under this premise, indiscriminate consumption was opened and without normative regulation, which has favored a significant increase in the use of EC. Given this background is important to determine the impact of EC use on human health. The aim of this work was to evaluate levels of genotoxicity and LINE-1 methylation levels associated with exposure to EC.

For these purpose, 64 whole blood samples from vaping individuals (n=32) and controls (n=32) were analyzed, in which genotoxicity frequency was determined through cytokinesis blockade micronucleus assay (CBMN). LINE-1 methylation levels were evaluated by quantitative methylation specific assay (qMSP) coupled to quantitative PCR. Additionally, LINE-1 expressions were analyzed by quantitative PCR. Finally, logistic regression analyzes were performed between demographic variables, consumption, serum cotinine biomarker and genotoxicity levels, methylation patterns and transcriptional expressions.

Significant increases in genotoxicity levels associated with use of electronic devices were identified. Additionally, epigenetic alterations related to loss of methylation of LINE-1 elements were detected as a result of exposure to EC aerosol, which in turn was consistent with transcriptional expression increases.

This work highlights the biological impact of vaping and provides a first approach to the scientific evidence that shows that these devices are not completely innocuous and that their use has an impact at the genetic and epigenetic level.