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Assessing the DNA damage potential of cigarette and iQOS emissions in human bronchial epithelial cells.

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It is widely recognized that use of combustible cigarettes (CCs) is associated with an increased risk of developing different types of cancer. Nowadays, heated tobacco products (HTPs) such as iQOS are gaining popularity worldwide, mainly because they are considered less harmful than CCs due to the lower levels of toxicants in their emissions. However, it is unknown whether the impact of iQOS emissions on human health is indeed significantly lower compared to cigarette smoke. Specifically, the potential of iQOS emissions to damage DNA in comparison with cigarette smoke is unexplored.

Therefore, in this study, the bronchial epithelial cell line BEAS-2B was exposed to different (v/v) % of extracts of cigarette or iQOS emissions for 1h and (oxidative) DNA damage was assessed by the alkaline comet assay. In addition, to determine the oxidative potential of both extracts, we quantified the radicals and the reactive oxygen species by means of electron spin resonance (ESR).

Strikingly, HTP extract (HTPE) was found to contain significantly higher levels of (carbon-centred) radicals and reactive oxygen species compared with cigarette smoke extract (CSE), suggesting higher oxidative potential and presumably higher genotoxic impact. Moreover, all the assessed CSE concentrations (1%, 3% and 5%) induced significantly more oxidative DNA damage compared to vehicle-exposed cells. We are currently assessing DNA damage in response to different HTPE concentrations. Furthermore, we are also assessing mRNA abundance of several DNA repair genes in BEAS-2B cells exposed to CSE and HTPE. In addition, we performed RNA sequencing of human primary bronchial epithelial cells (PBECs) exposed to sub-lethal CSE and HTPE concentrations, and we are investigating whether the exposure significantly affected pathways involved in DNA damage and/or DNA repair.

Keywords:

Heated Tobacco Products; DNA damage; oxidative potential; DNA repair genes; RNA sequencing.