



# EBD spotlight: The impact of vaping on the oral microbiome



**Manas  
Dave<sup>1</sup>**  
discusses  
a topic  
featured

in our sister journal  
*Evidence-Based Dentistry*.

‘Is there a significant difference in the oral microbiome in vapers vs non-vapers?’ was published in *Evidence-Based Dentistry* in 2024.<sup>1</sup>

### Background

Electronic cigarettes (e-cigarettes) come in various sizes; most will have a battery, a heating element and place to hold the liquid. They produce an aerosol by heating a liquid

### Author information

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that usually contains nicotine (the addictive drug in cigarettes) along with flavouring chemicals. The users inhale this aerosol into their lungs. E-cigarettes have different names such as ‘vapes’, ‘vape pens’ and ‘electronic nicotine delivery systems (ENDS)’. The Centers for Disease Control and Prevention<sup>2</sup> and the NHS<sup>3</sup> provide a useful summary of e-cigarettes.

The impact of e-cigarettes on the oral microbiome is not fully understood however emerging research is identifying the association between vaping and increased prevalence of candidiasis or growth/abundance of certain species (eg *Candida albicans*, *proteobacteria* etc). Therefore, the aim of this cross-sectional comparative study was to compare the oral microbiome of vapers vs non-vapers.<sup>4</sup>

microbiome samples taken from various oral sites.

### Results

There was a total of 36 adults included in this study (18 vapers and 18 non-vapers)

Dual users comprised 55.6% of the cohort (e-cigarettes and conventional cigarettes)

After bioinformatic processing, 3,901 operational taxonomic units (OTUs) – this involves grouping organisms based on similarity of genes – were identified with a significant difference in library size between vapers and non-vapers. After processing, 241 OTUs remained for analysis

There were no significant differences in microbiome diversity between vapers and non-vapers controlling for race, sex and smoking. However, a statistical test

### Conclusions

The authors stated:

‘...the findings of this pilot exploration suggest an association between exclusive vaping and variations within the oral microbiome.’

### Commentary

This study investigated the impact of e-cigarette vapour exposure on the oral microbiome and found no significant differences in microbiome diversity between vapers and non-vapers; however, it did observe a significant difference in the microbial community composition, showing vapers had a higher relative abundance of *Veillonella* species. These findings suggest that vaping, in conjunction with smoking, may influence the oral microbiome composition and diversity – however the clinical implications are unclear. In context of this research study, there are several limitations such as the same size, the use of secondary data collection and sequencing limitations which the authors acknowledge. Further research is needed to understand the long-term changes of the oral microbiome with the use of e-cigarettes and its clinical implications.

### References

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### Methods

A cross-sectional comparative design by focusing on the use of saliva and saliva and exhaled breath condensate to detect passive e-cigarette vapour exposure in children. Participants were selected through convenience sampling from the local community, targeting parents who used e-cigarettes daily in the presence of children at home or in cars. The primary outcome was changes in the oral microbiome, influence by e-cigarette use, with participants divided into groups based on their vaping status and further sub-divided by those exclusively vaping or also smoking conventional cigarettes. Data collection involved oral

(PREMANOVA) showed significant differences in community composition based on Bray-Curtis and Jaccard distances, indicating a distinct microbial community structure between vapers and non-vapers

Specifically, vapers had a significantly higher relative abundance of unclassified species of *Veillonella* compared with non-vapers ( $p = 0.04$ )

Dual users had a higher alpha diversity compared with exclusive vapers and several OTUs were more likely to present in dual users than in exclusive users indicating that dual use may influence the presence of specific taxa in the oral microbiome.

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