

## Characterization of oral microbiota and acetaldehyde production

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## 論 文 内 容 の 要 旨

### 論文要旨

ABSTRACT Background: *Neisseria* has been reported to be a high producer of acetaldehyde (ACH), a carcinogen, from ethanol in vitro, but no information exists regarding whether the ACH production depends on oral microbiota profiles. Objective and Design: To explore the salivary microbiota profiles with respect to ACH production ability in the oral cavity using a cross-sectional design. Results: Using 16S rRNA gene amplicon sequencing, we classified 100 saliva samples into two types of communities (I and II). Salivary ACH production ability from ethanol was measured using gas chromatography and was found to vary over a 30-fold range. ACH production ability was significantly higher in the type I community, where the relative abundance of *Neisseria* species was significantly lower. Multivariate logistic regression analysis showed that the subjects with the type I community exhibited significantly higher probability of high ACH production ability than those with the type II community ( $P = 0.014$ ). Moreover, the relative abundance of *Neisseria* species was inversely correlated with the ACH production ability ( $P = 0.002$ ). Conclusion: The salivary microbiota profile with a lower relative abundance of *Neisseria* species was independently associated with high ACH production ability, despite *Neisseria* species are dominant producers of ACH in vitro.

