Evaluation of Subgingival Microbiome After Switching from Cigarettes to Nicotine Pouches

ABSTRACT

Completely switching from cigarette smoking to oral tobacco-derived nicotine products, like nicotine pouches, presents a potential harm reduction opportunity for adult smokers who are unable or unwilling to quit using tobacco. The objective of this study was to compare subgingival microbiome profiles in adult smokers who switched from cigarette smoking (CS) to using on![®] nicotine pouches (NPs) in a single-center, randomized, openlabel, parallel-group study. Adult smokers with moderate gingivitis were randomly assigned into NP (n=88) and CS (n=61) groups at baseline. Subgingival plaque was collected by curettes from two separate sites with the highest gingival inflammation determined by the modified gingival index and bleeding at baseline. Sampling was repeated at 12- and 24 weeks from the same sites. The V1-V3 regions of 16S rDNA were sequenced using an Illumina platform. Alpha (Shannon and Simpson indices) and beta diversities, differential abundance with bias control, and LefSe analyses were determined. In NP users, no statistically significant changes were observed in alpha and beta diversities at both 12- and 24 weeks compared to baseline. However, using LefSe analysis, healthassociated species, e.g., Rothia aeria, Streptococcus cristatus, Kingella oralis, species of Neisseria and Haemophilus, became more predominant while relative abundances of putative pathogens, e.g., Fusobacterium, Saccharibacteria TM7 and Prevotella spp. declined at both time points. In the continued smoking group, no statistically significant changes were observed in alpha or beta diversities at 12- or 24 weeks compared to baseline. In these smokers, using differential abundance analysis, one *Capnocytophaga* species was statistically higher (p<0.05) at 24 weeks compared to baseline while some, albeit low abundance, differences using LefSe were observed over time.

BACKGROUND

Oral disease from the use of tobacco products is a significant public health concern. A consistent association between cigarette smoking and elevated oral disease (e.g. oral cancer) risks has been demonstrated relative to non-tobacco use.¹ Subgingival microflora of smokers with gingivitis is preceded by an increase in the abundance of periodontal pathogens.² Combustible tobacco products confer significant risk due to harmful constituents such as carcinogens, respiratory toxicants, cardiovascular toxicants, and reproductive or developmental toxicants.³ Next-generation oral tobacco products, such as nicotine pouches, do not contain tobacco leaf and thus many of the tobacco-related toxicants are substantially reduced (>95%) or eliminated, which may offer harm reduction opportunities for adult smokers.

STUDY PRODUCT

The test products used in this study were pouch products containing tobacco-derived nicotine and flavors. These nicotine pouch products are currently marketed under the brand name on![®]. The on![®] nicotine pouches are innovative oral tobacco products that do not contain cut, ground, powdered, or leaf tobacco – a point of differentiation compared to smokeless tobacco (ST) products currently commercially marketed in the US. The on![®] nicotine pouches are intended for adult smokers and ST users (including dual users of cigarettes and ST products).



Table 1. Study Products

Study Group	Description	Mode of Use
Test	on! [®] Nicotine Pouches (2, 4, & 8 mg nicotine, mint flavor, manufactured for Helix Innovations, LLC)	Ad libitum
Control	Combustible Cigarette (subject's usual brand cigarette, self-supplied)	Ad libitum

OBJECTIVES

The objective of this study was to compare subgingival microbiome profiles in adult smokers who switched from CS to using on![®] NPs in a single-center, randomized, open-label, parallel-group study.

DISCLOSURES

Altria Client Services LLC (ALCS) funded this study. Authors associated with ALCS are employed by ALCS; the authors associated with Forsyth and Salus received funding from ALCS for the researches.

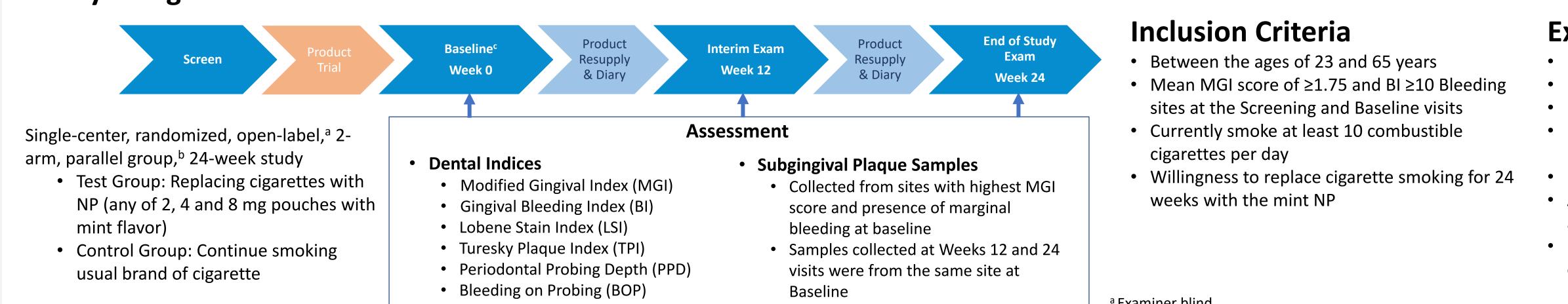




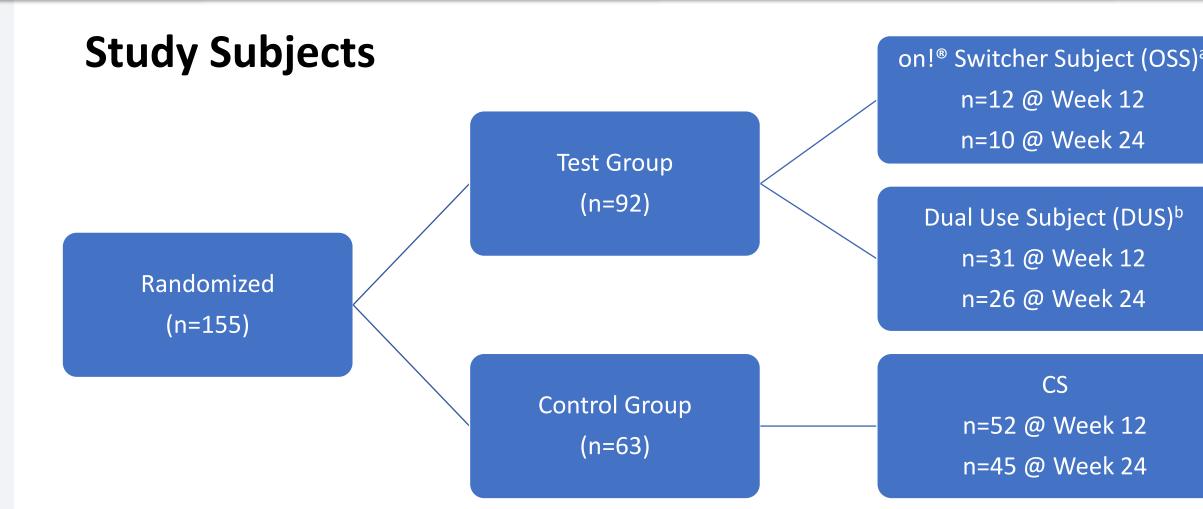
NICOTINE, MINT FLAVOR

METHODS

Study Design



RESULTS



^a OSS: Used NP, Smoked ≤10% and NNAL ≤25% of the baseline ^b DUS: Used NP, Smoked >10% or NNAL >25% of the baseline

Differential Abundance with Bias Control W12 vs Baseline (Test Subgroup OSS)

	Adjusted p-value
Solobacterium moorei (SP106)	<0.001
Streptococcus oralis_subspdentisani_clade 058 (SP14)	<0.001
Neisseria flavescens (SP209)	<0.001
Actinomyces israelii (SP256)	<0.001
Rothia aeria (SP269)	<0.001
Fretibacterium fastidiosum (SP345)	<0.001
Peptidiphaga spHMT 183 (SP428)	<0.001
Prevotella oulorum (SP57)	<0.001
Alloprevotella tannerae (SP63)	<0.001
Capnocytophaga spHMT_380 (SP75)	<0.001
Kingella oralis (SP253)	NS
Streptococcus cristatus (SP214)	NS
Haemophilus parainfluenzae (SP83)	NS
Neisseria sicca (SP215)	NS
Fusobacterium nucleatum (SP17)	NS
Capnocytophaga endodontalis (SP159)	NS
Campylobacter concisus (SP88)	NS
Capnocytophaga gingivalis (SP6)	NS
Capnocytophaga sputigena (SP24)	NS

More Abundant

Health-associated species, e.g., Rothia, Neisseria, and spp. of Streptococcus more abundant (green arrow) at Week 12 as compared to baseline (p<0.001) Kingella oralis, was also more abundant (p=0.08)

Less Abundant

Fusobacterium nucleatum, **a** putative pathogen, and Solobacterium moorei, often associated with **halitosis**, were reduced (red arrow) at Week 12 (p<0.001)



CONCLUSIONS

- Completely switching from cigarettes to on![®] nicotine pouches may improve the oral microbiome by increasing health-associated species.
- The clinical significance of this change has not been established.
- This beneficial change in the oral microbiome was only observed upon complete switching. • Adults who continue to smoke cigarettes or use on![®] nicotine pouches and smoke cigarettes exhibited higher putative pathogens and halitosis-associated species.

76th Tobacco Science Research Conference, September 24-27, 2023, Norfolk, Virginia USA

- Urine NNAL & Nicotine Equivalents

Exclusion Criteria

- Exhibit \geq 30% of teeth with stage II IV periodontitis at Screening or Baseline visits

Observed

W24

^a Examiner blind

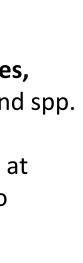
^b Test:Control = 3:2; Stratified by Age, Gender and Bleeding Index ^c Complete dental scaling and polishing at Baseline

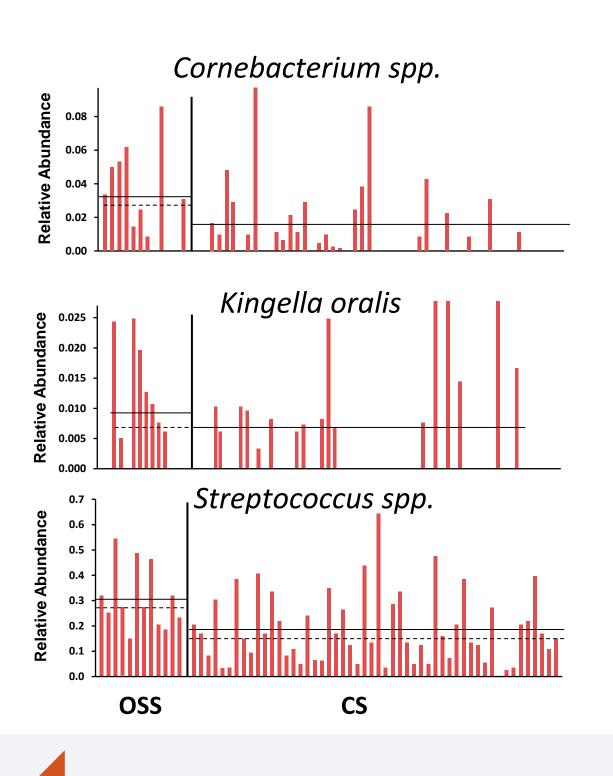
Shannon Simpson Observed 0.9 -**50** · 0.7 -25 W12 W12

W12

LefSe Health Associated Species (Week 12)

Health-associated species (HAS) were more abundant in on![®] switchers (OSS) compared to continued smokers (CS) at Weeks 12 and 24 (data not shown).



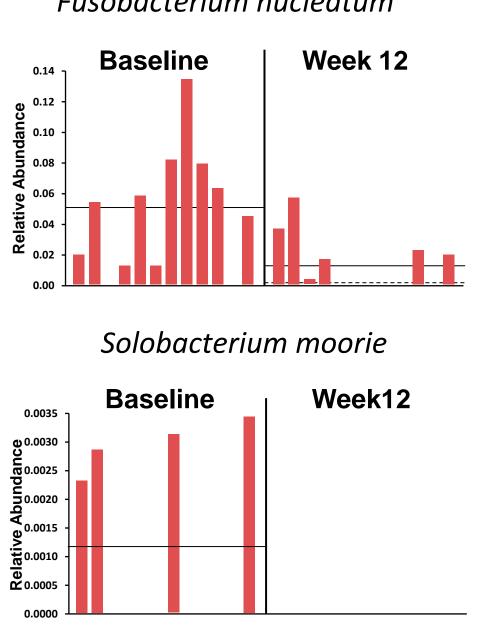


LefSe at Species Level

(Week 12)

Disease-associated species (DAS) *Fusobacterium, Solobacterium* in OSS were prevalent at baseline and reduced at Weeks 12 and 24 (data not shown).

Fusobacterium nucleatum



LIMITATIONS

Due to drop-out and small sample size at the end of study,

- permutation tests (PERMONAVA)—non-parametric permutational analysis and the repeated measure design could not be evaluated
- benefits were seen from switching, but the results cannot be generalized

Alpha Diversities (Test Subgroup OSS)

Jianmin LIU¹, Jingzhu Wang¹, Jeffery S. Edmiston¹, Mohamadi A. Sarkar¹, Maria Gogova¹, Bruce Paster², Tsute Chen², Hatice Hasturk², Kimberly R. Milleman³, Jeff L. Milleman³ and Abbie L. Yoder ¹Altria Client Services, Richmond, VA, USA, ²The Forsyth Institute, Cambridge, MA, USA ³Salus Research, Fort Wayne, IN, USA



 History of any type of malignant tumors • BMI >40 kg/m² or less than 18 kg/m² at screening Uncontrolled Diabetes defined as HbA1c >8.0%

- More than 3 teeth with PPD >5mm
- Any health condition requiring prophylactic antibiotics prior to dental exams

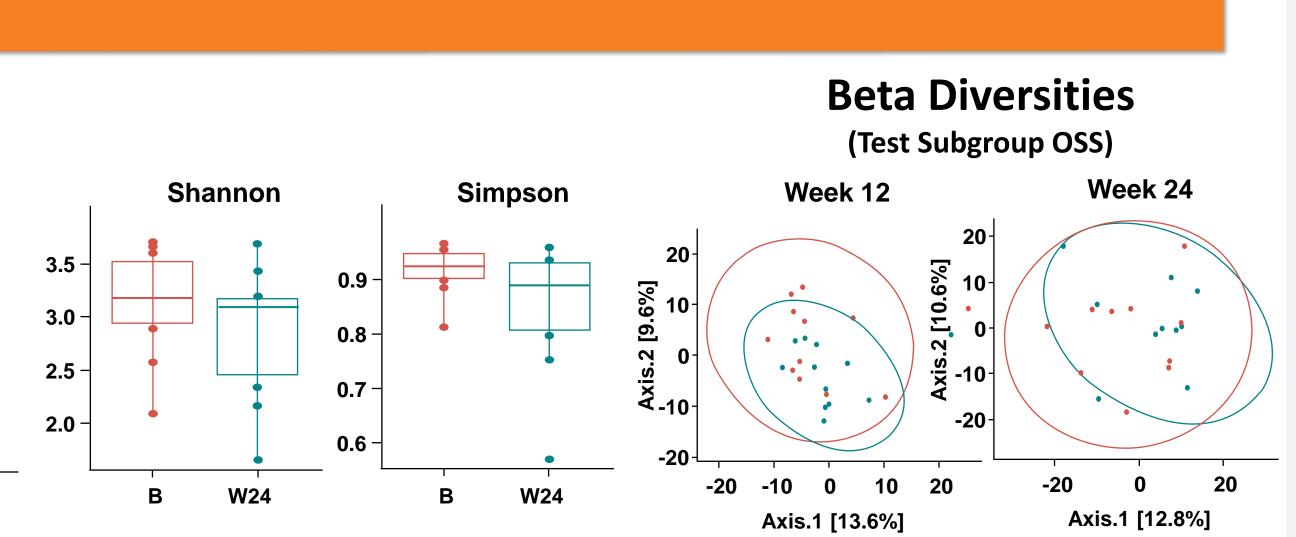
• History of periodontal treatment within 6 months or surgery within 3 years

Subgingival Plaque Microbiome

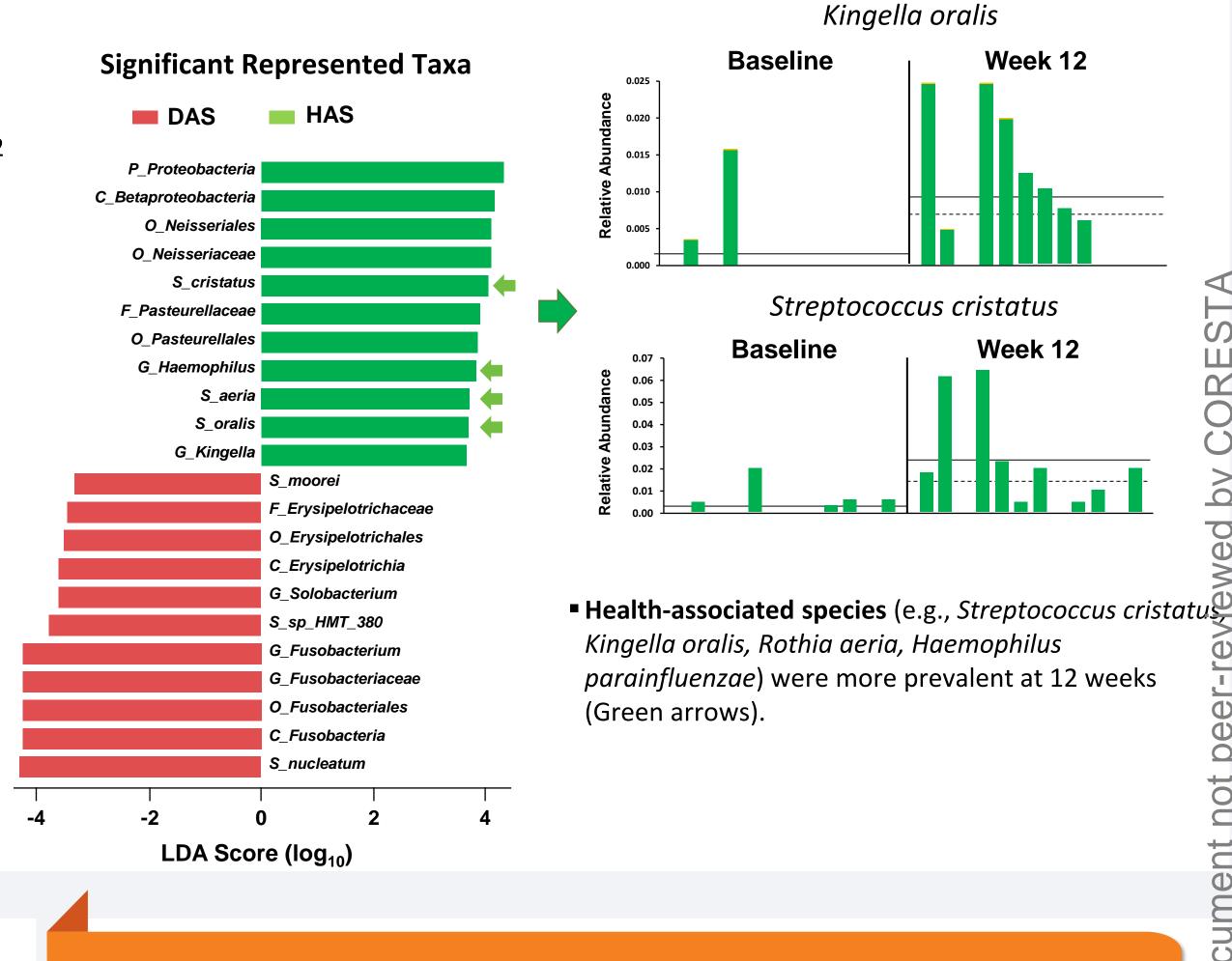
Analysis

DNA isolation + sequencing of V1-V3 regions (16S rRNA NGS using an Illumina platform)

- Alpha (Shannon and Simpson Indices) diversity⁴
- Beta diversity⁵
- Differential abundance with bias control⁵
- LefSe analyses⁷



No significant differences between Baseline (B) and Week 12 (W12), Baseline and Week 24 (W24) for Test, OSS, DUS groups and between Test and Control groups



REFERENCES

- Asthana, S., Labani, S., Kailash, U., Sinha, D. N., & Mehrotra, R. (2019). Association of Smokeless Tobacco Use and Oral Cancer: A Systematic Global Review and Meta
- Analysis. Nicotine & Tobacco Research, 21(9), 1162-1171. doi:10.1093/ntr/nty074
- Jiang Y, Zhou X, Cheng L, Li M. The Impact of Smoking on Subgingival Microflora: From Periodontal Health to Disease. Front Microbiol. 2020 Jan 29;11:66. doi:
- 10.3389/fmicb.2020.00066. PMID: 32063898; PMCID: PMC7000377 Hatsukami DK, Joseph AM, Lesage M, et al. Developing the Science Base for Reducing Tobacco Harm. Nicotine Tob Res (2007); Suppl 4:S537-53. Willis AD. Rarefaction, Alpha Diversity, and Statistics. Front Microbiol. (2019) Oct 23;10:2407. doi: 10.3389/fmicb.2019.02407. PMID: 31708888; PMCID: PMC6819366.
- 5. Bolyen E, Rideout JR, et al. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology 37: 852–857. https://doi.org/10.1038/s41587-019-0209-9
- Mandal S, Van Treuren W, et al. Analysis of composition of microbiomes: a novel method for studying microbial composition. Microb Ecol Health Dis. (2015) Ma 29;26:27663. doi: 10.3402/mehd.v26.27663. PMID: 26028277; PMCID: PMC4450248. Segata N, Izard J, et al. Metagenomic biomarker discovery and explanation. Genome Biol. (2011) Jun 24;12(6):R60. doi: 10.1186/gb-2011-12-6-r60. PMID: 21702898; PMCID: PMC3218848.