

Original article

Sociodemographic variation in the oral microbiome

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ABSTRACT

Purpose: Variations in the oral microbiome are potentially implicated in social inequalities in oral disease, cancers, and metabolic disease. We describe sociodemographic variation of oral microbiomes in a diverse sample.

Methods: We performed 16S rRNA sequencing on mouthwash specimens in a subsample ($n = 282$) of the 2013–2014 population-based New York City Health and Nutrition Examination Study. We examined differential abundance of 216 operational taxonomic units, and alpha and beta diversity by age, sex, income, education, nativity, and race/ethnicity. For comparison, we examined differential abundance by diet, smoking status, and oral health behaviors.

Results: Sixty-nine operational taxonomic units were differentially abundant by any sociodemographic variable (false discovery rate < 0.01), including 27 by race/ethnicity, 21 by family income, 19 by education, 3 by sex. We found 49 differentially abundant by smoking status, 23 by diet, 12 by oral health behaviors. Genera differing for multiple sociodemographic characteristics included *Lactobacillus*, *Prevotella*, *Porphyromonas*, *Fusobacterium*.

Conclusions: We identified oral microbiome variation consistent with health inequalities, more taxa differing by race/ethnicity than diet, and more by SES variables than oral health behaviors. Investigation is warranted into possible mediating effects of the oral microbiome in social disparities in oral and metabolic diseases and cancers.

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Introduction

Health disparities by race/ethnicity, socioeconomic status (SES), sex, and other sociodemographic factors have long been observed

but their mechanisms have yet to be fully elucidated. In particular, racial/ethnic and socioeconomic disparities have been consistently observed in oral health outcomes [1], cardiovascular disease (CVD) [2], diabetes [3], preterm birth and low birth weight [4,5], and rheumatoid arthritis [6].

Variations in human oral microbiome structure and function have been associated with oral disease [7,8], as well as a wide range of systemic illnesses including CVD [9–11], diabetes [12,13], cancers [14–17], birth outcomes [18,19], and rheumatoid arthritis [20,21]. Hypothesized pathways for such associations include both direct

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virulence and modulation of systemic immune response [14], although causal evidence is limited. In addition, regardless of their causal role, the microbiota represents potential biomarkers for early disease detection and prognosis.

This combination of findings has led researchers to call for investigation into the role of the microbiome in health disparities [22] but little empirical work has yet been done in this area. A number of mechanisms potentially link social factors to the microbiome [23]. Such mechanisms have been discussed in relation to common pathogens such as CMV and EBV; these may include household crowding, use of public transportation, and differences in susceptibility due to breastfeeding and poor sleep [4,5], mechanisms which may apply to commensal microbes as well. Changes in immune function related to psychosocial stress [24], nutrition [25], smoking [26], or other environmental exposures can alter host interactions with microbes. Differences in microbiome characteristics may also persist via mother-to-child transmission, as infant microbiomes are seeded from the birth canal and via breastfeeding [27,28]. Furthermore, assortative social networks and shared built environments may represent reservoirs of shared microbiota membership [29].

So far, limited research has examined sociodemographic associations with the oral microbiome. The Human Microbiome Project (HMP) collected microbiome samples at nine distinct oral sites on a volunteer sample in the United States with minimal race/ethnic variability (approx. 80% white) [30,31]. Nonetheless, the HMP found differentially abundant taxa comparing non-Hispanic white, non-Hispanic black, Asian, Mexican, and Puerto Rican ethnicities [32]. In another U.S. volunteer sample, distinct subgingival microbiomes were identified by race/ethnicity, with non-Hispanic blacks having lower microbiome diversity than other groups [33]. In a comparison of salivary microbiomes of Cheyenne and Arapaho versus nonnative individuals in the United States, strong bacterial species composition clustering, differences in species richness, and numerous differentially abundant taxa were found by ethnicity [34]. Several low-throughput studies examining specific periodontal pathogens found significant differences in abundance and/or presence by race/ethnicity [35–37]. To our knowledge, only one study has tested associations between SES and the oral microbiome, finding substantial differences (20% of variation) by municipal-level SES in the Danish Health Examination Survey [38].

To explore the relationship between the oral microbiome and health disparities, sociodemographic associations from diverse samples must be assessed. Our aim was to assess sociodemographic variation in the human salivary microbiome. Specifically, we examined whether bacterial taxa were differentially abundant, and whether variation existed in alpha and beta diversity by sociodemographic characteristics using high-throughput sequencing data from a subsample of a population-based sample.

Methods

Data source

Samples came from the 2013–2014 New York City Health and Nutrition Examination Survey (NYC HANES-II) previously described [39]. Briefly, the 2013–2014 NYC HANES was the second population-representative, cross-sectional survey of adult NYC residents, using a three-stage cluster sampling design. Overall response rate was 36% ($n = 1524$). Eligible participants completed a two-part interview and physical examination, and nearly all (95%) provided an oral mouthwash specimen. This study was approved by the institutional review boards of the City University of New York and the New York City Department of Health and Mental Hygiene, and all participants gave informed consent. Participants

providing mouthwash specimens in the current substudy also consented to use these specimens in future studies.

Subsample selection

The present study uses 297 NYC HANES participants selected to examine oral microbiome associations with tobacco use, as described elsewhere [40]. Briefly, we selected 90 self-reported current cigarette smokers with the highest serum cotinine, 45 randomly selected never smokers with cotinine <0.05 ng/mL, 45 randomly selected former smokers with cotinine <0.05 ng/mL, all 38 former and never smokers with serum cotinine between 1 and 14 ng/mL, and 79 participants reporting hookah, cigar, cigarillo, and/or e-cigarette use within 5 days. Table 1 shows descriptive statistics in the subsample and overall NYC HANES sample.

Oral rinse collection and microbiome sample processing

Participants were asked to fast for 9 hours before oral rinse collection. A 20-second oral rinse was divided into two 5-second swish and 5-second gargle sessions using 15 mLs of Scope mouthwash. After each session, participants expectorated into a sterile cup. Timers built into the computer-assisted personal interview program signaled the timing of the swish, gargle, and expectoration. Oral rinse specimens were stored cold before delivery to the New York Public Health Laboratory where they were transferred into 50 mL centrifuge tubes, frozen, and stored at -80°C . The oral rinse samples were then transported on dry ice to Albert Einstein College of Medicine, where they were stored at -80°C until processing.

Specimen processing and sequence analysis methods are described in detail in the appendix. Briefly, we extracted DNA using QIAamp DNA mini kit (QIAGEN), and amplified DNA in the V4 region of the 16S rRNA using primers 16SV4_515F (GTGYCAGC MGCCGCGTA) and 16SV4_806R (GGACTACHVGGGTWTCTAAT) [38,39], followed by amplicon sequencing using a MiSeq (Illumina, San Diego, CA) with 2×300 paired-end fragments. We merged raw Illumina paired-end reads using the QIIME v1.9.1 [41] command `fastq-join` [42] and discarded low-quality reads (PHRED score < 30) when joining split reads (`qiime split_libraries_fastq.py`). We performed open-reference operational taxonomic unit (OTU) picking by clustering using UCLUST at 97% similarity and assigned taxonomy using the SILVA 123 [43] database. We removed samples with <1000 reads ($n = 15$) and collapsed genera with mean relative abundance $<2 \times 10^{-4}$ into a category labeled “other” [41–44].

Statistical analysis

We compared oral microbiomes by seven sociodemographic factors (race/ethnicity, age, group, sex, educational attainment, income tertiles, marital status, nativity) and by several behavioral/oral health measures: diet (sugar sweetened beverages, meat, poultry, fish, vegetables, and fruits, recorded as times consumed in the past week); oral health behaviors (mouthwash use, flossing, time since last dental visit) and smoking status (categories defined previously). We assessed pairwise correlation between sociodemographic variables using Cramer's V, a correlation coefficient for nominal variables.

To assess differential abundance (DA) by sociodemographic variables, we used edgeR [45] to estimate a series of log-linear generalized linear models predicting each OTU abundance. OTUs were considered differentially abundant at false discovery rate (FDR) < 0.01 . Before edgeR, we filtered out OTUs for which less than three samples had a count of at least eight, leaving 216 OTUs for analysis. To examine potential mediators, we fit crude models and models adjusted for oral health behaviors, diet, smoking status, and

Table 1
Demographics

Variable	Oral microbiome subsample	Full NYC HANES sample
Total	282	1527
Age in years—median [range]	42 [20–94]	42 [20–97]
Age group (%)		
20–29	70 (24.8)	360 (23.6)
30–39	60 (21.3)	337 (22.1)
40–49	51 (18.1)	252 (16.5)
50–59	51 (18.1)	264 (17.3)
60 and over	50 (17.7)	314 (20.6)
Sex = female (%)	150 (53.2)	885 (58.0)
Educational achievement (%)		
College graduate or more	87 (30.9)	628 (41.1)
Less than high school diploma	65 (23.0)	316 (20.7)
High school graduate/GED	63 (22.3)	244 (16.0)
Some college or associate's degree	67 (23.8)	337 (22.1)
Missing	0 (0.0)	2 (0.1)
Annual family income (%)		
\$60,000 or more	82 (29.1)	429 (28.1)
Less than \$30,000	105 (37.2)	537 (35.2)
\$30,000–\$60,000	59 (20.9)	348 (22.8)
Missing	36 (12.8)	213 (13.9)
Marital status (%)		
Married	96 (34.0)	590 (38.6)
Widowed	15 (5.3)	76 (5.0)
Divorced	23 (8.2)	156 (10.2)
Separated	12 (4.3)	51 (3.3)
Never married	101 (35.8)	511 (33.5)
Living with partner	35 (12.4)	143 (9.4)
Race/ethnicity (%)		
Non-Hispanic white	97 (34.4)	513 (33.6)
Non-Hispanic black	75 (26.6)	340 (22.3)
Hispanic	71 (25.2)	390 (25.5)
Asian	22 (7.8)	204 (13.4)
Other	17 (6.0)	80 (5.2)
Place of birth (%)		
U.S., PR, and territories	90 (31.9)	668 (43.7)
Other	190 (67.4)	851 (55.7)
Missing	2 (0.7)	8 (0.5)
Gum disease (self-reported) (%)		
Yes	27 (9.6)	175 (11.5)
No	254 (90.1)	1322 (86.6)
Missing	1 (0.4)	30 (2.0)
Mouthwash use (times per week) (%)		
None	115 (40.8)	591 (38.7)
1 to 5	68 (24.1)	370 (24.2)
6 to 7	99 (35.1)	565 (37.0)
Missing	0 (0.0)	1 (0.1)
Sugar-sweetened beverages (per week) (%)		
0–<1	152 (53.9)	985 (64.5)
1–5	67 (23.8)	313 (20.5)
6 or more	62 (22.0)	227 (14.9)
Missing	1 (0.4)	2 (0.1)
Smoking status (%)		
Cigarette	86 (30.5)	215 (14.1)
Never smoker	43 (15.2)	843 (55.2)
Former smoker	43 (15.2)	285 (18.7)
Alternative smoker	72 (25.5)	142 (9.3)
Secondhand	38 (13.5)	42 (2.8)

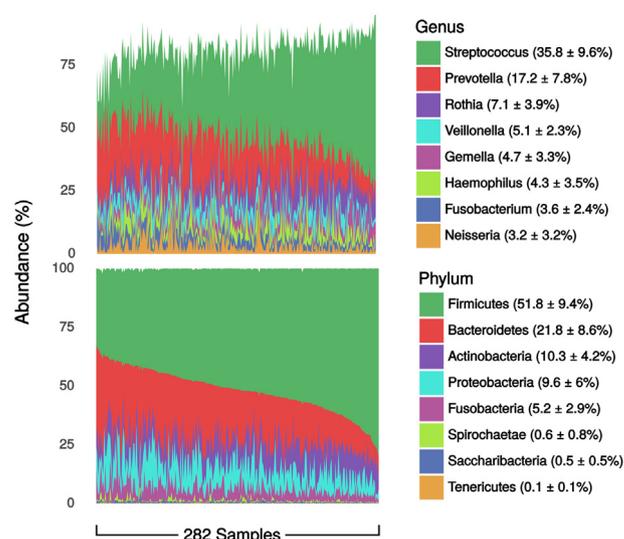


Fig. 1. Genus- and phylum-level relative abundances. Data are percent of overall communities within samples, summarized as mean \pm SD of percent across samples. Data are from the oral microbiome subsample ($n = 282$) of the New York City Health and Nutrition Examination Survey, 2013–2014.

Jenson Shannon, weighted and unweighted UniFrac distances [49]. Prediction strength (PS) was calculated for $k = 2:10$ clusters on each distance measure, using $PS \geq 0.9$ to signify strong support for k clusters [49].

Sensitivity analysis

As described previously, the sample was selected based on smoking status, which is plausibly a mediator and/or effect measure modifier for the effect of sociodemographics on the microbiome. In particular, evidence supports the existence of socioeconomic status disparities in smoking prevalence [50,51], and effects of smoking on the oral microbiome [26,40,52]. To characterize the potential bias due to selecting on smoking, we generated sampling weights defined as the inverse of the predicted probability of selection into the substudy, using logistic regression on self-reported smoking status, logarithm serum cotinine, and their interaction, fitted to the entire NYC HANES sample. We also tested models with second and third order polynomials, and splines for log-transformed cotinine, and conclusions were identical. We applied these weights to edgeR models and compared the logFCs and numbers of OTUs differential at $FDR < 0.01$.

Statistical analyses were conducted with R version 3.4 [53] for Linux.

Results

Descriptive statistics

The initial subsample included 297 participants; after removing samples with <1000 reads, there were 282 participants for analysis. Table 1 shows descriptive statistics for sociodemographic characteristics including age (median [range]: 42 [20–94]), sex (53.2% female), race/ethnicity (34.4% non-Hispanic white, 26.6% non-Hispanic black, 25.2% Hispanic), annual family income (42.7% less than \$30K, 33.3% \$60k, or more), and educational achievement (23.0% less than high school diploma, 30.9% college degree or greater). Cramer's V on pairwise combinations of sociodemographic variables showed only minor collinearity (all $V < .35$) (Fig. A1), indicating associations with the microbiome for each

age and sex (when applicable). edgeR was conducted at the taxonomic level of highest specificity allowed, which was the genus in all cases where FDR was less than 1%; therefore, DA findings are presented at the genus level.

We measured alpha diversity using Chao1 richness [46], which we compared by each sociodemographic variable using Kruskal–Wallis tests. Beta diversity was assessed using principal coordinates analysis and permutation multivariate analysis of variance [47] on weighted UniFrac distances [48].

We performed clustering of samples with respect to OTUs using partitioning around medoids on Bray–Curtis, Jenson–Shannon, root-

sociodemographic variable do not merely reflect correlations between sociodemographic variables.

Relative abundance and alpha diversity

Oral microbiomes were characterized at the phylum level by a gradient between Firmicutes and Bacteroides abundance, with overall dominance by Firmicutes (mean = 52 ± 10%). Streptococcus was the most abundant genus (36 ± 10%) followed by Prevotella (17 ± 8%) (Fig. 1). The mean Chao1 was 462, with no differences by age group (P = .79), sex (P = .13), educational achievement (P = .92), annual family income (P = .62), marital status (P = .54), race/ethnicity (P = .13), or nativity (P = .97) (Fig. A2).

Differential abundance

Numerous taxa were differentially abundant (DA) by race/ethnicity, nativity, marital status, gender, family income, education, and age. Figure 2 displays log-2 fold change (logFC), or coefficient from edgeR log-linear models, for each comparison group and all significant OTUs. The logFC can be interpreted as the log-base-2

ratio of relative abundance compared to the reference group, so that, for example, Lactobacillus is found to be 2^{2.5} = 5.7 times as abundant in family incomes of \$30–\$60,000 per year, compared to \$60,000 or more. In total, 69 OTUs were DA by any sociodemographic variable, including 56 by age group, 27 by race/ethnicity, 21 by family income, 19 by education, 19 by marital status, 7 by nativity, and 3 by sex. We found 12 unique DA OTUs by oral health behaviors, 49 by smoking status, and 23 by diet variables. The most frequent DA were Lactobacillus (all variables), and Prevotella (age, education, family income, marital status, race/ethnicity, nativity, Fig. 2). DA findings for selected taxa are presented in Table 2 (see Table A1 for all DA findings).

Figure 3 displays boxplots of absolute values of logFCs for crude and adjusted models. The OTUs displayed for all models are those meeting FDR <0.01 in crude models. Comparing adjusted versus crude boxplots allows visual assessment of effects of adjustment on the entire set of OTUs: a shift toward zero reflects attenuation while a shift away from zero reflects amplification. Over all sociodemographic variables, a minor attenuating effect was observed after adjusting for smoking (mean change in logFC, -3.9%), oral health behaviors (-4.9%), diet (-6.3%), age and sex (-3.3%). Adjustment

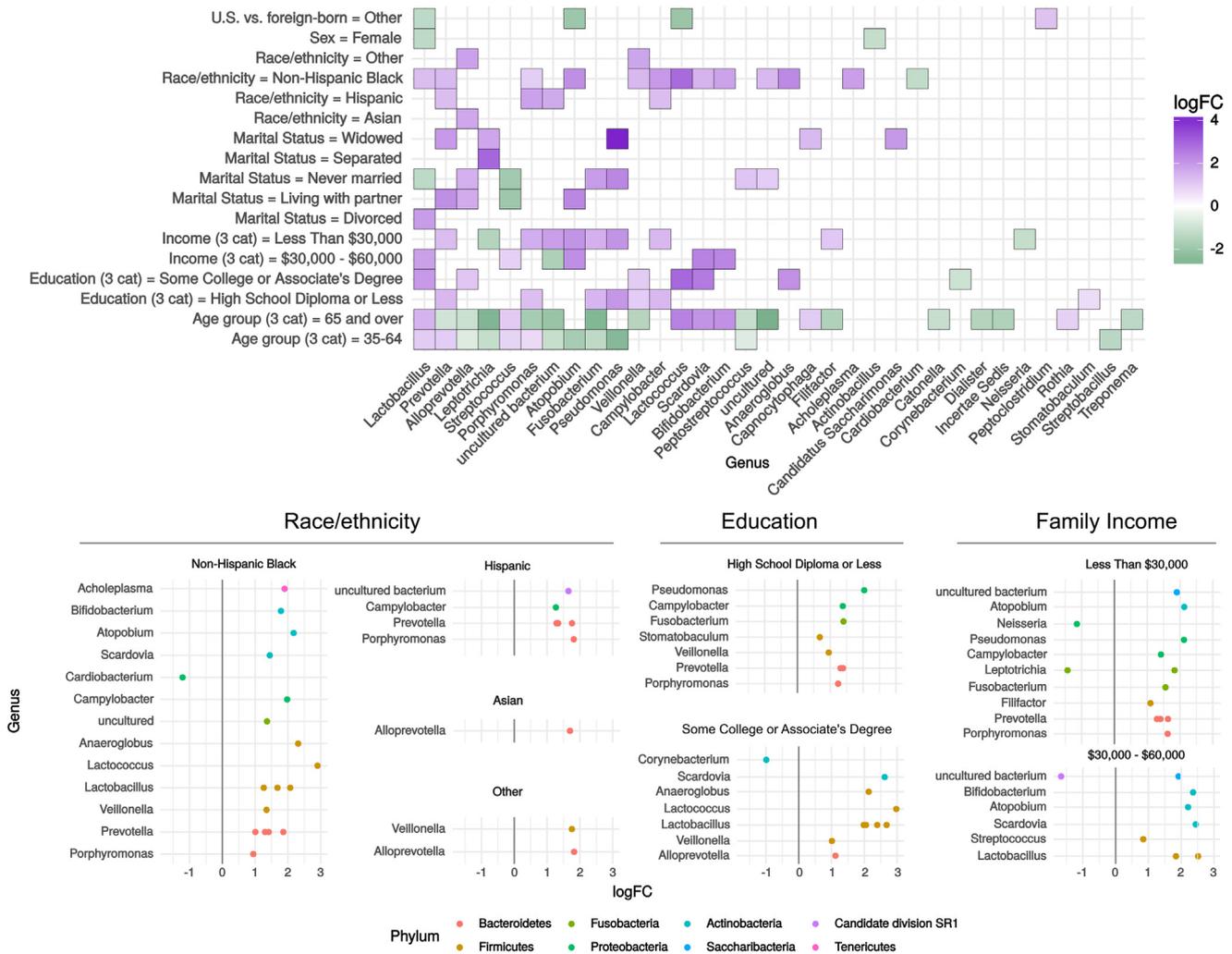


Fig. 2. Differential abundance by sociodemographic characteristics. OTUs meeting unadjusted FDR <0.01 in negative binomial log-linear GLMs using edgeR. Data are from the oral microbiome subsample (n = 282) of the New York City Health and Nutrition Examination Survey, 2013–2014. Filled tiles in (A) indicate the genus had at least one OTU differentially abundant by at least one coefficient contrast within the sociodemographic factor. Where more than one OTU was significant within one genus, the maximum logFC is displayed in (A). Reference groups for sociodemographic variables are as follows: sex: male, age: 20–34, education: college graduate or more, family income: \$60,000 or more, marital status: married, race/ethnicity: non-Hispanic white, U.S.- versus foreign-born: U.S.-born, 50 states, DC, PR, and territories. cat = categories; GLM = generalized linear model; logFC = log fold change; PR = Puerto Rico.

Table 2
Differential abundance findings for OTUs selected based on clinical relevance

Variable	Lactobacillus		Prevotella		Streptococcus		Porphyromonas		Fusobacterium		Lactococcus	
	logFC	FDR	logFC	FDR	logFC	FDR	logFC	FDR	logFC	FDR	logFC	FDR
Race/ethnicity												
Non-Hispanic white	0.	Ref	0.	Ref	0.	Ref	0.	Ref	0.	Ref	0.	Ref
Non-Hispanic black	2.1	<0.0001	1.9	<0.0001	0.6	0.01	0.9	0.002	0.4	0.5	2.9	<0.0001
Hispanic	0.9	0.1	1.8	<0.0001	0.4	0.1	1.8	<0.0001	1.1	0.04	1.8	0.02
Family income												
\$60,000 or more	0.	Ref	0.	Ref	0.	Ref	0.	Ref	0.	Ref	0.	Ref
\$30,000–\$60,000	2.5	<0.0001	1.2	0.03	0.9	0.003	0.6	0.2	1.8	0.03	1.7	0.06
Less than \$30,000	1.1	0.06	1.6	0.003	1.1	0.03	1.6	<0.0001	1.5	0.003	–1.1	0.1
Education												
College graduate or more	0.	Ref	0.	Ref	0.	Ref	0.	Ref	0.	Ref	0.	Ref
Some college or associate's degree	2.7	<0.0001	0.8	0.1	0.5	0.1	0.8	0.03	1.4	0.1	3.0	<0.0001
High school diploma or less	1.0	0.04	1.4	0.006	0.6	0.02	1.2	0.0008	1.4	0.006	1.3	0.07

Data are from the oral microbiome subsample ($n = 282$) of the New York City Health and Nutrition Examination Survey, 2013–2014. logFC = log fold change; Ref = reference group.

for oral health had the largest impact on logFCs for age group (–4.0%), sex (–27.4%), and nativity (–13.5%); diet had the strongest impact on logFCs for education (–13.1%) and marital status (–16.9%), smoking had the strongest impact on logFCs for family income (–11.9%), and age and sex had the strongest impact on logFCs for race/ethnicity (–4.2%). Figure A3 illustrates the effects of the sensitivity analysis with inverse probability of selection weights applied; distributions of logFC estimates were nearly identical and nearly all DA OTUs in unweighted crude analysis were also DA (FDR<0.01) in weighted models. However, weighted models detected a substantially larger number of DA OTUs for every variable, suggesting that selecting on smoking may have biased toward the null for most associations.

Beta diversity and clustering

Figure 4 illustrates between-versus-within-group weighted UniFrac distances by each sociodemographic variable. We observed differences in composition by age group ($P = .017$, $r^2 = 0.026$), with no other variables showing greater between- than within-group

variation, a result that was not changed by adjusting for smoking. Principal coordinates plots showed little patterning by any variable (not shown). Clustering scores were sensitive to the distance metric used, with Bray–Curtis indicating moderate support for two clusters ($PS = 0.86$), and all other measures providing little support for clustering.

Discussion

In a diverse subsample of a population-based study, we found that a large number of bacterial taxa in the oral microbiome were DA by age, race/ethnicity, family income, education, nativity, and sex. Notably, we found a greater number of associations with SES variables (21 by family income, 19 by education) than with sex, marital status, or nativity. There were also more associations with SES than oral health behaviors [12]. Adjustment for smoking, oral health behaviors, or dietary behaviors did not appreciably diminish sociodemographic associations.

Many genera found DA by multiple variables represents taxa that have documented associations with health and disease.

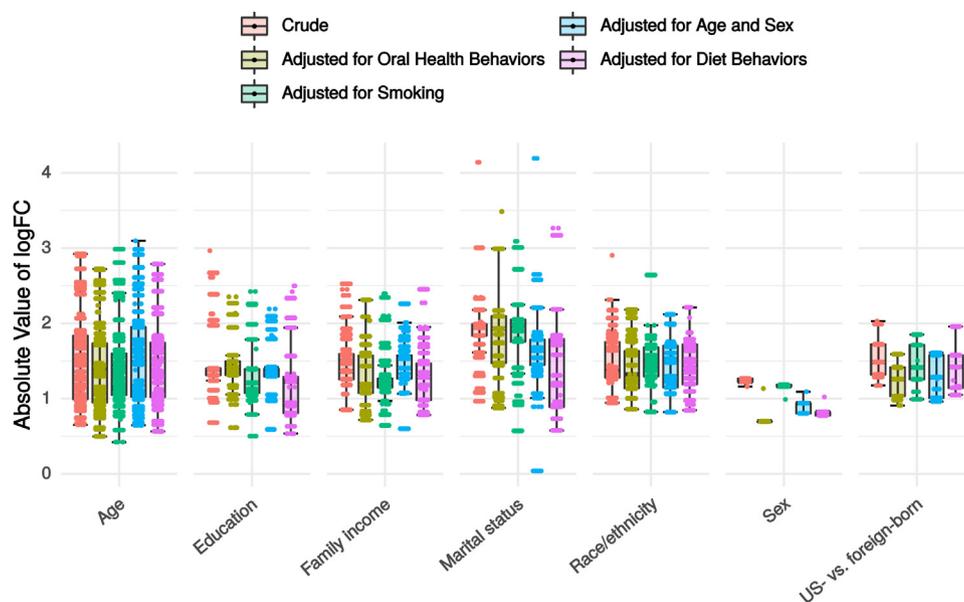


Fig. 3. Distribution of absolute values of log-fold change (logFC) in crude and adjusted negative binomial log-linear GLMs edgeR models for each sociodemographic variable. Data are from the oral microbiome subsample ($n = 282$) of the New York City Health and Nutrition Examination Survey, 2013–2014. GLM = generalized linear model; logFC = log fold change.

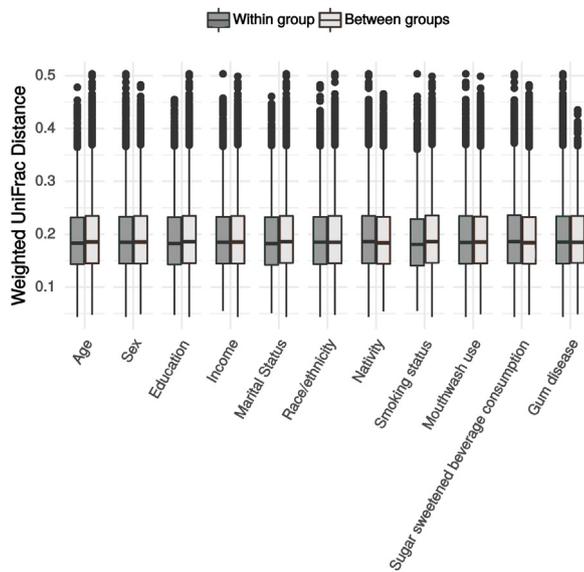


Fig. 4. Within- and between-group beta diversity estimate distributions. Data are from the oral microbiome subsample ($n = 282$) of the New York City Health and Nutrition Examination Survey, 2013–2014.

Streptococcus, *Lactobacillus* [54], *Prevotella* [55], *Fusobacterium* [56], and *Porphyromonas* [57,58] are understood to play a role in oral disease. Furthermore, many of these organisms likely play a role in systemic conditions [14]. Specifically, *Fusobacterium* have been linked to colorectal cancer [59,60], adverse pregnancy outcomes, CVD, and rheumatoid arthritis [61]. *Porphyromonas gingivalis* is a key determinant of oral microbiome structure [62] and is hypothesized to mediate multiple systemic pathogenic processes [14], including stroke [10], CHD [11], a number of cancers [16,17,63], and rheumatoid arthritis [21].

To our knowledge, our study is the first to examine differences in oral microbiota by individual-level sociodemographic factors in a diverse population-based sample. Our finding of DA taxa by race/ethnicity is consistent with previous studies with small convenience samples. The HMP found that, for all body sites, ethnicity was the host phenotypic variable with the most associations [32]. For the oral microbiome, a study examining 40 periodontal disease-related taxa found differences among Asian, Hispanic, and blacks [35]. Two lower-throughput studies found greater *Prevotella* and *Porphyromonas* [37], and lower *Fusobacterium* [36] in blacks versus whites. Our finding of differential OTUs by SES variables is also consistent with findings from the Danish Health Examination Survey (DANHES, $n = 292$), which found nine DA taxa by municipal-level SES [38].

Adjustment for smoking, diet, and oral health behaviors each moderately attenuated DA findings across sociodemographic categories. This stands to reason in light of findings by our group [40] and others [26] that smoking is associated with major shifts in the oral microbiome, along with similar findings for diet [64] and indicates that some portion of observed sociodemographic patterning reflects differences in health habits or access to dental care. However, the finding that differential abundance was not eliminated by adjustments suggests that additional mechanisms underlie sociodemographic variation in the oral microbiome. These may include upstream social factors such as psychosocial stress [24] or features of the built environment [29].

While existing oral microbiome studies are limited, the absence of differences in alpha and beta diversity by race/ethnicity contrasts with two previous studies among non-population-based samples. These found differences in alpha diversity and ethnicity-based

clustering in oral microbiomes in non-Hispanic blacks versus whites [33], and in Cheyenne and Arapaho versus nonnative individuals [34]. Differences in alpha and beta diversity can indicate larger-scale shifts in composition; our finding that specific OTUs were differentially abundant but that overall shifts were less present would tend to indicate that, at a population level, socio-demographic patterns in oral microbiome composition are more subtle. An alternative explanation is that our sampling design attenuated alpha and beta diversity difference estimates.

Limitations

Despite the strength of NYC-HANES as a diverse population-based sample, the selection of the substudy on the basis of smoking means that the microbiome sample was not population representative. Based on our sensitivity analysis with inverse-probability weighting, this sample selection most likely biased toward the null, yielding conservative estimates of our focal associations. In addition, our findings are limited by having primarily genus-level information, and in many cases, salient differences exist at a greater degree of taxonomic specificity—for example, with *P. gingivalis*, *Fusobacterium nucleatum*, and *Prevotella intermedia*. There may also be wide variability in virulence even at the species level, as is the case with *P. gingivalis* [65]. Given the importance of many of the differentially abundant genera in health and disease, our findings suggest that further investigation into the role of the oral microbiome in health disparities is warranted. Future investigations should consider use of whole genome shotgun sequencing or other methods able to provide more specific taxonomic classification and describe functional, as well as taxonomic, composition.

Conclusion

Our results lend support to potential role of the social environment in shaping microbiome composition at the population level [23,66]. The finding of differentially abundant OTUs, many of which are health relevant, for every sociodemographic variable, suggests that these associations may be important in determining population health patterns. In particular for race/ethnicity and SES, but also for nativity and marital status, the finding that multiple health-relevant microbes are differentially abundant supports a growing hypothesis that the microbiota may partially mediate long-observed social disparities in major disease outcomes. At a minimum, these results highlight that social factors may be important potential confounders in studies of the human oral microbiome and health.

Mechanisms for the observed associations are currently unknown, and one important next step will be to examine the multiple levels of exposures underlying these associations, including macrolevel social and health policy, exposure to psychosocial stressors, outdoor and built environment features, and social interactions [23]. Importantly, if the microbiome is a partial mediator of health disparities, then identifying modifiable features of the social environment that are most strongly associated with the microbiome can inform effective interventions to improve population health and reduce health disparities.

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Supplementary data

Supplementary data associated with this article can be found in the online version at <https://doi.org/10.1016/j.annepidem.2019.03.006>.

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Appendix

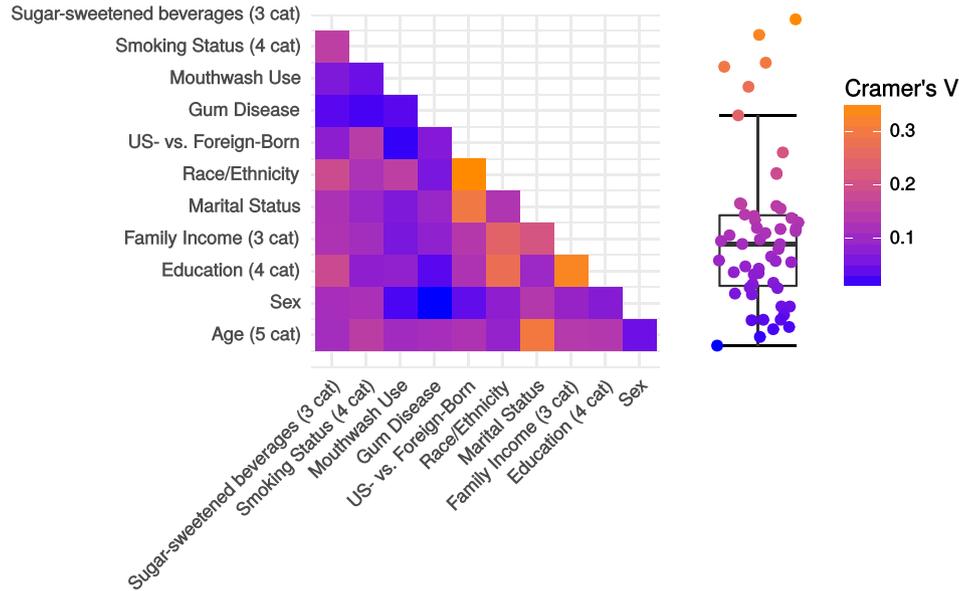


Figure A1. Examining collinearity among sociodemographic variables. Data are absolute value of pairwise Cramer's V correlation coefficient between sociodemographic factor levels. Data are from the full sample (n = 1527) of the New York City Health and Nutrition Examination Survey, 2013–2014. cat = categories.

DNA extraction

All laboratory procedures were performed under a hood (Air-Clean Systems) to minimize environmental contamination and negative controls were used throughout. From each oral rinse sample, a 1.5 mL aliquot was centrifuged at $750 \times g$ for 5 min and all but 150 μL of supernatant was removed. The pellet was

resuspended in the remaining supernatant and incubated in an enzyme mixture consisting of lysozyme (0.84 mg/mL, Sigma Aldrich), mutanolysin (0.25 U/mL, Sigma Aldrich), and lysostaphin (21.10 U/mL, Sigma Aldrich), at 37°C for 30 minutes. This was followed by incubation at 56°C for 10 minutes in 15 μL proteinase K and 150 μL Buffer AL. Samples were then transferred to screw top tubes with 100 g of 0.1-mm-diameter Zirconia/Silica Beads

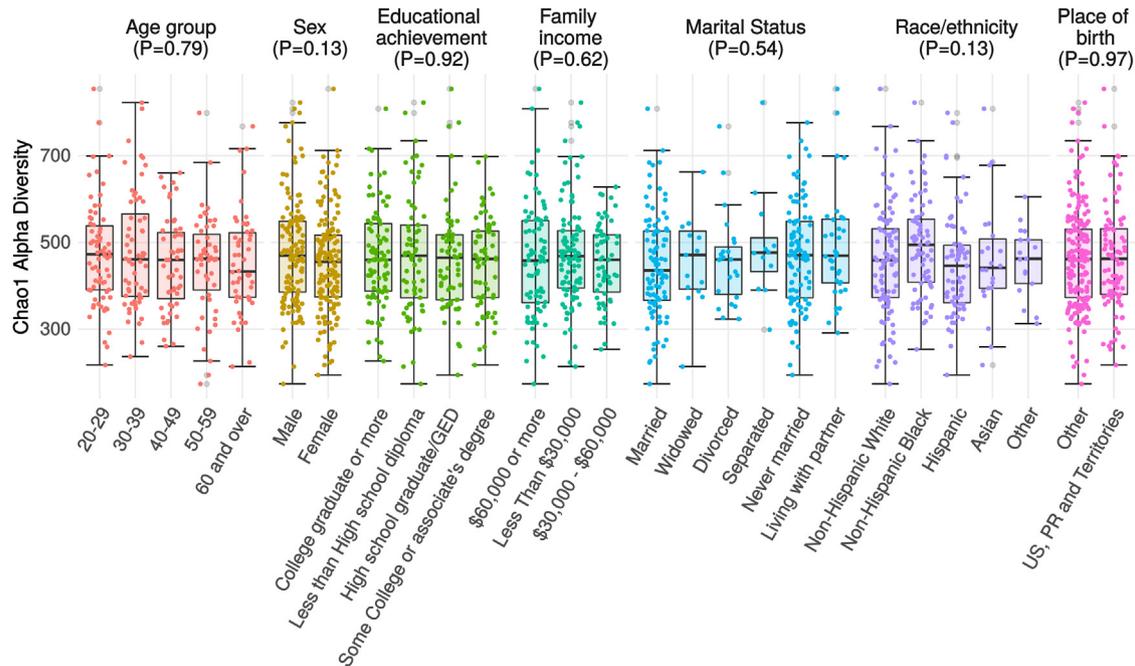


Figure A2. Alpha diversity by sociodemographic characteristics. Chao1 alpha diversity of 16S rRNA oral microbiome samples. Measures were compared using a null hypothesis of no difference between groups (Kruskal–Wallis test, $P > .1$ for all tests). Data are from the oral microbiome subsample (n = 282) of the New York City Health and Nutrition Examination Survey, 2013–2014. GED = general equivalency diploma; PR = Puerto Rico.

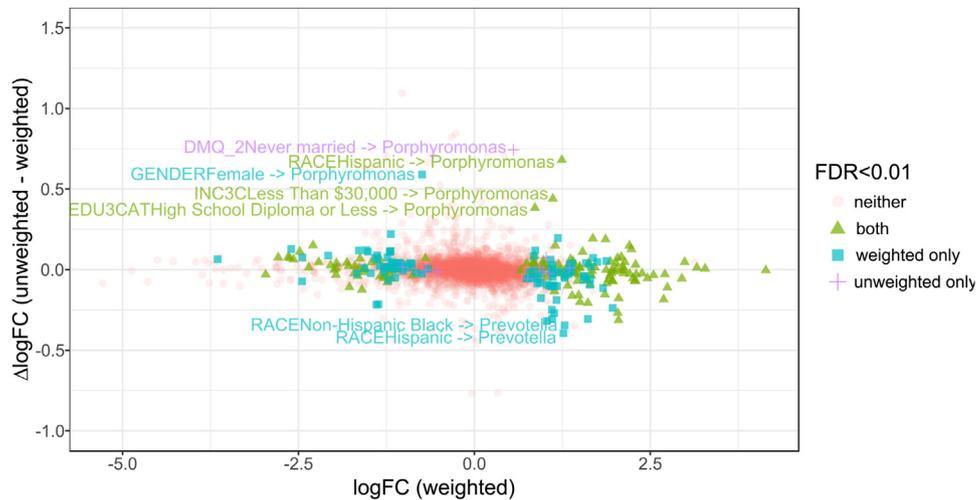


Figure A3. Comparison of log fold change (logFC) estimates between crude unweighted models and models weighted for inverse probability of selection conditional on self-reported smoking status, logarithm cotinine, and their interaction. Differences in logFC estimates between unweighted and weighted models on the y-axis represent an approximation of the bias due to selection on smoking. Estimates are overall fairly concordant, with nearly all (99%) of OTU-variable pairs having an absolute difference in point estimate less than 0.35. Very few ($n = 10$) hypotheses that were significant ($FDR < 0.01$) in unweighted analysis were nonsignificant in weighted analysis. Of these, 9/10 had nearly identical point estimates but larger variance in the weighted models. By contrast, a large number of hypothesis tests that were nonsignificant in unweighted analysis were significant in weighted analysis. Specifically, weighting by selection for smoking identified 10 new significant OTUs for gender, 13 for age, 24 for education, 10 for income, 13 for marital status, 26 for race, and 8 for nativity. Where the two models disagreed on significance tests, the vast majority of disagreements were characterized by significance in the weighted model and nonsignificance in the unweighted model. Furthermore, the point estimates from the weighted models were more often further from the null than unweighted models.

(BioSpec) and bead beaten using a FastPrep-24 homogenizer (MP Biomedicals) at speed 6.0 for 40 seconds. Tubes were centrifuged at $750 \times g$ for 30 sec, and 150 μ L of supernatant was added to a new 1.7 mL tube with 150 μ L of 100% ethanol and mixed by vortexing for 15 seconds. Supernatant was then added to the spin column from the QIAamp DNA mini kit (QIAGEN) and centrifuged at $6000 \times g$ for 1 minute. Column purification was performed according to the QIAamp DNA mini kit directions starting at the AW1 wash step. Final elution was performed in 100 μ L of Buffer AE.

16S rRNA gene amplification

DNA was amplified for the V4 variable region of the 16S rRNA gene using the primers 16SV4_515F (GTGYCAGCMGCCGCGTA) and 16SV4_806R (GGACTACHVGGGTWTCTAAT) [45,46]. Each primer had an 8-bp unique Hamming barcode with forward primers containing a 3-bp (TCG) and 4-bp (ACTG) pad on either side, with reverse primers including a 3-bp (GTA) and 4-bp (TC) pad on each side of the barcode [47]. PCR reactions were performed with 17.75 μ L of nuclease-free PCR-grade water, 2.5 μ L of 10X Buffer w/MgCl₂ (Affymetrix, Santa Clara, CA), 1 μ L of MgCl₂ (25 mM, Affymetrix, Santa Clara, CA), 0.5 μ L of dNTPs (10 mM, Roche, Basel, Switzerland), 0.25 μ L of AmpliTaq Gold DNA Polymerase (5 U/ μ L, Applied Biosystems, Foster City, CA), 0.5 μ L of HotStart-IT FidelityTaq (2.5 U/ μ L, Affymetrix, Santa Clara, CA), 1 μ L of each primer (5 μ M), and 0.5 μ L of DNA extraction template. Thermal cycling conditions consisted of initial denaturation of 95°C for 5 min, followed by 15

cycles of 95°C for 1 min, 55°C for 1 min, and 68°C for 1 min, followed by 15 cycles of 95°C for 1 min, 60°C for 1 min, and 68°C for 1 min, a final extension for 10 min at 68°C on a GeneAmp PCR System 9700 (Applied Biosystems, Foster City, CA).

PCR products were combined before running 100 μ L of the pooled products on a 4% agarose gel at 80 V for 2 hours. The ~450 bp bands were excised from the gel and purified using a QIAquick Gel Extraction Kit (Qiagen, Hilden, Germany) and eluted in 30 μ L of elution buffer. Purified PCR products were quantified using a Qubit 2.0 Fluorometric High Sensitivity dsDNA Assay (Life Technologies, Carlsbad, CA).

Library preparation and sequencing

Library preparation of the purified PCR products was performed using a KAPA LTP Library Preparation Kit (Kapa Biosystems, Wilmington, MA). The size integrity of the amplicon was validated with a 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA). High-throughput amplicon sequencing was conducted on a MiSeq (Illumina, San Diego, CA) using 2×300 paired-end fragments. The fastq sequences from the Illumina MiSeq were demultiplexed using Novobarcode (Novocraft Technologies, Selangor, Malaysia) and the 5'-pads and primers were trimmed from each read.

Bacterial taxa were determined by clustering the 16S rRNA sequences into OTUs using 97% similarity; taxonomy was assigned at the genus level using the SILVA 123 (43) database as reference, excluding samples with less than 1000 reads.