

Doctoral Thesis

Microbiota in Human Diseases

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Department of Biomedical Engineering

Ulsan National Institute of Science and Technology

2024

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CHURCH OF THE FLYING SPAGHETTI MONSTER

February 09, 2021

Letter of Good Standing

Dear Sir or Madam:

I am pleased to verify that _____

JAEWOONG LEE

is an ordained minister of the Church of the Flying Spaghetti Monster and recognized
within our organization as a member in good standing.

We hereby consent to this minister performing ceremonies and request that they are
granted all privileges and respect appropriate to a spiritual leader.

Any questions can be directed to the undersigned.

Representative,
Church of the Flying Spaghetti Monster
Bobby Henderson



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Abstract

The microbiome refers to the complex community of microorganisms, including bacteria, viruses, fungi, and other microbes, that inhabit various environments within living organisms (Ursell, Metcalf, Parfrey, & Knight, 2012; Gilbert et al., 2018). In humans, the microbiome plays a crucial role in maintaining health (Lloyd-Price, Abu-Ali, & Huttenhower, 2016), influencing processes such as digestion (Lim, Park, Tong, & Yu, 2020), immune response (Thaiss, Zmora, Levy, & Elinav, 2016; Kogut, Lee, & Santin, 2020; Kim, 2018), and even mental health (Mayer, Tillisch, Gupta, et al., 2015; Zhu et al., 2017; X. Chen, D'Souza, & Hong, 2013). These microbial communities are not static nor constant but rather dynamic ecosystem that interact with their host and respond to environmental changes. Recent studies have revealed that imbalances in the microbiome, known as dysbiosis, can contribute to a wide range of diseases, including obesity (John & Mullin, 2016; Tilg, Kaser, et al., 2011; Castaner et al., 2018), diabetes (Barlow, Yu, & Mathur, 2015; Hartstra, Bouter, Bäckhed, & Nieuwdorp, 2015; Sharma & Tripathi, 2019), infections (Whiteside, Razvi, Dave, Reid, & Burton, 2015; Alverdy, Hyoju, Weigerinck, & Gilbert, 2017), inflammatory conditions (Francescone, Hou, & Grivennikov, 2014; Peirce & Alviña, 2019; Honda & Littman, 2012), and cancers (Helminck, Khan, Hermann, Gopalakrishnan, & Wargo, 2019; Cullin, Antunes, Straussman, Stein-Thoeringer, & Elinav, 2021; Sepich-Poore et al., 2021; Schwabe & Jobin, 2013). Thus, understanding the composition of the human microbiome is essential for developing new therapeutic approaches that target these microbial populations to promote health and prevent diseases.

(PTB)

(Periodontitis)

(Lung)

(Conclusion)

This doctoral dissertation is an addition based on the following papers that the author has already published:

- Hong, Y. M., Lee, J., Cho, D. H., Jeon, J. H., Kang, J., Kim, M. G., ... & Kim, J. K. (2023). Predicting preterm birth using machine learning techniques in oral microbiome. *Scientific Reports*, 13(1), 21105.

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List of Abbreviations

ACC Accuracy

ASV Amplicon sequence variant

AUC Area-under-curve

BA Balanced accuracy

C-section Cesarean section

DAT Differentially abundant taxa

F1 F1 score

Faith PD Faith's phylogenetic diversity

FTB Full-term birth

GA Gestational age

MWU test Mann-Whitney U-test

PRE Precision

PROM Prelabor rupture of membrane

PTB Preterm birth

ROC curve Receiver-operating characteristics curve

rRNA Ribosomal RNA

SEN Sensitivity

SPE Specificity

t-SNE t-distributed stochastic neighbor embedding

1 Predicting preterm birth using machine learning techniques in oral microbiome

This section includes the published contents:

Hong, Y. M., Lee, J., Cho, D. H., Jeon, J. H., Kang, J., Kim, M. G., ... & Kim, J. K. (2023). Predicting preterm birth using machine learning techniques in oral microbiome. *Scientific Reports*, 13(1), 21105.

1.1 Introduction

Preterm birth (PTB), characterized by the delivery of neonates prior to 37 weeks of gestation, is one of the major cause to neonatal mortality and morbidity (Blencowe et al., 2012). Multiple pregnancies including twins, short cervical length, and infection on genitourinary tract are known risk factor for PTB (Goldenberg, Culhane, Iams, & Romero, 2008). Nevertheless, the extent to which these aspects affect birth outcomes is still up for debate. Henceforth, strategies to boost gestation and enhance delivery outcomes can be more conveniently implemented when pregnant women at high risk of PTB are identified early (Iams & Berghella, 2010).

Prediction models that can be utilized as a foundation for intervention methods still have an unacceptable amount of classification evaluations, including accuracy, sensitivity, and specificity, despite a great awareness of the risk factors that trigger PTB (Sotiriadis, Papatheodorou, Kavvadias, & Makrydima, 2010). Several attempts have been made to predict PTB through integrating data such as human microbiome composition, inflammatory markers, and prior clinical data with predictive machine learning methods (Berghella, 2012). Because it is affordable and straightforward to use, fetal fibronectin is commonly used in medical applications. However, with a sensitivity of only 56% that merely similar to random prediction, it has a low classification evaluation (Honest et al., 2009). Due to the difficulty and imprecision of the method in general, as well as the requirement for a qualified specialist cervical length measuring is also restricted (Leitich & Kaider, 2003).

Preterm labor and/or preterm pre-labor rupture of membranes (PROM) brought on by gestational inflammation and infection contribute to about 70% of PTB cases (Romero, Dey, & Fisher, 2014). However, the mechanism of PTB cannot be fully explained by inflammatory and infectious pathways as anti-inflammatory and antibiotic treatments could not reduce PTB incidence rates (Romero, Hassan, et al., 2014). With advancements in molecular genetic technology, studies on maternal microbiomes using 16S ribosomal RNA (rRNA) sequencing have emerged to explore unknown pathways of PTB (Fettweis et al., 2019).

However, as anti-inflammatory and antibiotic therapies were insufficient to lower PTB occurrence rates, the mechanism of PTB cannot be completely explained by inflammatory and infectious pathways. It has been hypothesized that the microbiota linked to PTB originate from either a hematogenous pathway or the female genitourinary tract increasing through the vagina and/or cervix. (Han & Wang, 2013). Vaginal microbiome compositions have been found in women who eventually acquire PTB, and recent studies have tried to predict PTB risk using cervicovaginal fluid (Kindinger et al., 2017). Even though previous

investigation have confirmed the potential relationships between the vaginal microbiome compositions and PTB, these studies are only able to clarify an upward trajectory.

Multiple unfavorable birth outcomes, including PROM and PTB, have been linked to periodontitis as an independence risk factor, according to numerous epidemiological researches (Offenbacher et al., 1996). It is expected that the oral microbiome will be able to explain additional hematogenous pathways in light of these precedents; however, the oral microbiome composition of fetuses is limited understood.

Hence, in order to identify the salivary microbiome linked to PTB and to establish a machine learning prediction model of PTB determined by oral microbiome compositions, this study examined the salivary microbiome compositions of PTB study participants with a full-term birth (FTB) study participants.

1.2 Materials and methods

1.2.1 Study design and participants

Between 2019 and 2021, singleton pregnant women who received treatment to Jeonbuk National University Hospital for childbirth were the participants of this study. The Ethical Research Committee authorized this study (IRB file No. 2019-01-024). Written informed authorization was acquired with preterm labor or PROM, as well as those admitted for induction birth or elective cesarean sections (C-sections), were eligible participants.

1.2.2 Data collection and grouping

Questionnaires and electronic medical records were implemented to gather information on both previous and current pregnancy outcomes. These data included maternal risk factors, including maternal age at delivery, C-section, PROM, prior history of PTB, gestational or overt diabetes mellitus, pregnancy-induced or chronic hypertension, pre-pregnancy overweight and/or gestational weight gain, along with demographic factors, namely gestational age, birth weight, and sex.

1.2.3 Oral microbiome sample collection

Using mouthwash, salivary microbiota samples were obtained 24 hours before to delivery. Standard sterilization techniques were used. All sample collection processes were overseen by medical professionals. Thirty minutes prior to sampling, participants were cautioned not to eat, drink, or brush their teeth. By rinsing the mouth for 30 seconds with 12 mL of a gargle solution (E-zen Gargle, JN Pharm, Pyeongtaek, Korea), saliva samples were gathered. Before going through further processing, the samples were stored at 4 °C and labeled with the subject's anonymous ID. A microcentrifuge tube was filled with the reconstituted sample. Following the instruction from the manufacturer, genomic DNA was extracted using an ExgeneTM Clinic SV kit (GeneAll Biotechnology, Seoul, Korea) and kept at -20 °C.

1.2.4 16s rRNA gene sequencing and taxonomy assignment

For taxonomic assignment, specimens were transported to Department of Biomedical Engineering of Ulsan National Institute of Science and Technology . Afterward, using an Illumina MiSeq Reagent Kit v3 (Illumina, San Diego, CA, USA) commissioned, 16S rRNA sequencing was performed. The V3 and V4 regions were amplified using library methods. After diluting the samples to a final concentration of 6 pM with 20% PhiX control, the pooled library was sequenced using a v3 600 cycle chemistry to generate 300 base-pair paired end reads.

1.2.5 Bioinformatics and statistical analysis

To analyze differences between the PTB participants and the FTB participants, independent *t*-test and χ^2 -square test were implemented. SPSS (version 20.0) was used for clinical measurement comparisons (Spss et al., 2011). Statistical significance was considered at $p < 0.05$.

16S rRNA sequences from the salivary samples of study participants were imported with QIIME2 (version 2022.2) for further bioinformatics processing (Bolyen et al., 2019). DADA2 was implemented to check qualities of sequences and to filter low-quality sequences (Callahan et al., 2016). Amplicon sequence variants (ASV) were assigned taxonomy with HOMD (version 15.22) (T. Chen et al., 2010). Alpha diversity, a measure of species within a single microbiome community, was calculated using the Faith's phylogenetic diversity (Faith PD) index (Faith, 1992). Communities numerically dominated by a few species will exhibit a low Faith PD index, whereas communities in which abundance is distributed equally among species will exhibit a high evenness. Mann–Whitney–Wilcoxon *U*-test was used to estimate statistically significant differences in Faith PD index. Beta diversity measures dissimilarity between pairs of communities. It was calculated using the Hamming diversity index (Hamming, 1950). PERMANOVA multivariate test was performed to calculate statistically significant differences in the Hamming diversity index (Anderson, 2014; Kelly et al., 2015).

To identify differentially abundant taxa (DAT) that have statistically significant differences between the PTB participants and the FTB participants, DESeq2 was implemented using `DESeqDataSetFromMatrix` method as described in the package tutorial (Love, Huber, & Anders, 2014). Taxa with $|\log_2 \text{FoldChange}| > 1$ and adjusted $p < 0.05$ are considered as DAT.

1.2.6 Machine learning prediction model development

Following qualitative and quantitative analyses of associations between the PTB group and each bacterium, a random forest classifier was used to find the criteria to predict PTB with oral microbiome data. Random forest classification is an ensemble machine learning algorithm that summarizes many decision trees to improve classification evaluations and robustness (Breiman, 2001). Random forest classifier was implemented to predict PTB based on oral microbiome compositions. To assure consistence and reliable classification results (Wong & Yeh, 2019), we performed stratified *k*-fold cross-validation ($k = 5$). Moreover, to decide the best features that could maximize classification evaluations, we performed random forest classification evaluations only with some DAT selected by their importances. Evaluations for classification included accuracy (ACC), balanced accuracy (BA), precision (PRE), sensitivity (SEN), and specificity (SPE).

1.2.7 Ethics approval and consent to participate

The study was approved by the Institutional Review Board of Jeonbuk National University Hospital (IRB No. 2019-01-024) and was performed according to the Declaration of Helsinki (Goodyear, Krleza-Jeric, & Lemmens, 2007).

1.3 Results

1.3.1 Study participant demographics

In this study, a total of 69 volunteer mothers were initially recruited. However, one participant with incomplete data and nine individuals with twin pregnancies were excluded from the study cohort. As a result, 59 women (30 in the PTB group and 29 in the FTB group) were included in the final analysis. Demographic and clinical characteristics of subjects in the PTB group and the FTB group are summarized in Table 1. Because PROM is a major cause of preterm birth, it was significantly higher in PTB group. There was no significant difference in other maternal clinical characteristics between the PTB group and the FTB group. There were no cases with a history of smoking or concurrent periodontal disease in both groups.

1.3.2 Comparison of oral microbiomes

The oral microbiome comprised 13953804 sequences from 59 salivary samples, with 102305.95 ± 19095.60 and 64823.41 ± 15841.65 reads per sample before and after filtering low-quality reads and trimming extra-long tails, respectively. After filtering low-quality reads and trimming extra-long tails, remaining representative reads were clustered in ASVs with their exact sequence match. There were no significant differences in measures of alpha diversity (Faith PD) and beta diversity (Hamming distance) indices for samples between the PTB group and the FTB group (Figure 4).

Of 465 genera and species analyzed, 32 DAT between the PTB group and the FTB group were selected by DESeq2 (Love et al., 2014), including 26 FTB-enriched DAT and six PTB-enriched DAT. In order to mitigate the confounding effect of PROM, we excluded 7 PROM-related DATs from these 32 DAT (Figure 5). There were a total of 25 DATs between the PTB group and the FTB group, with 22 DATs enriched in the FTB group and three in the PTB group, as depicted in Figure 1.

Figure 2 displays DAT volcano plot in the oral microbiome sorted by differences between FTB-enriched DAT and PTB-enriched DAT proportions, indicating a decrease in gestational age for FTB-enriched DAT proportions. Pearson correlation analysis revealed a strong negative correlation ($r = -0.542$ and $p = 7.8e - 6$) between gestational age and difference between PTB-enriched DAT and FTB-enriched DAT proportions.

1.3.3 Random forest classification

Random forest classifiers were established to classify PTB based on DAT. The best BA(0.765 ± 0.071) was achieved using the nine most important taxa (Figure 3a). The Random forest model calculated the importance of each DAT (Figure 3b). Overall ACC, PRE, SEN, and SPE were 0.714 ± 0.061 , 0.700 ± 0.194 , 0.728 ± 0.058 , and 0.743 ± 0.138 , respectively. To validate the performance of our machine learning prediction model, we conducted a validation test on nine twin pregnancies that were excluded from the paper (Figure 6). On PTB subjects of these twin samples, the machine learning classifications have 87.5% accuracy, comparable to the machine learning classification on the singleton study subjects.

Table 1: **Baseline clinical characteristics of study subjects.** Continuous variable: Mean \pm standard deviation. Categorical variable: count (proportion). Continuous variable for independent *t*-test. Categorical variable for Pearson's χ^2 -square test.

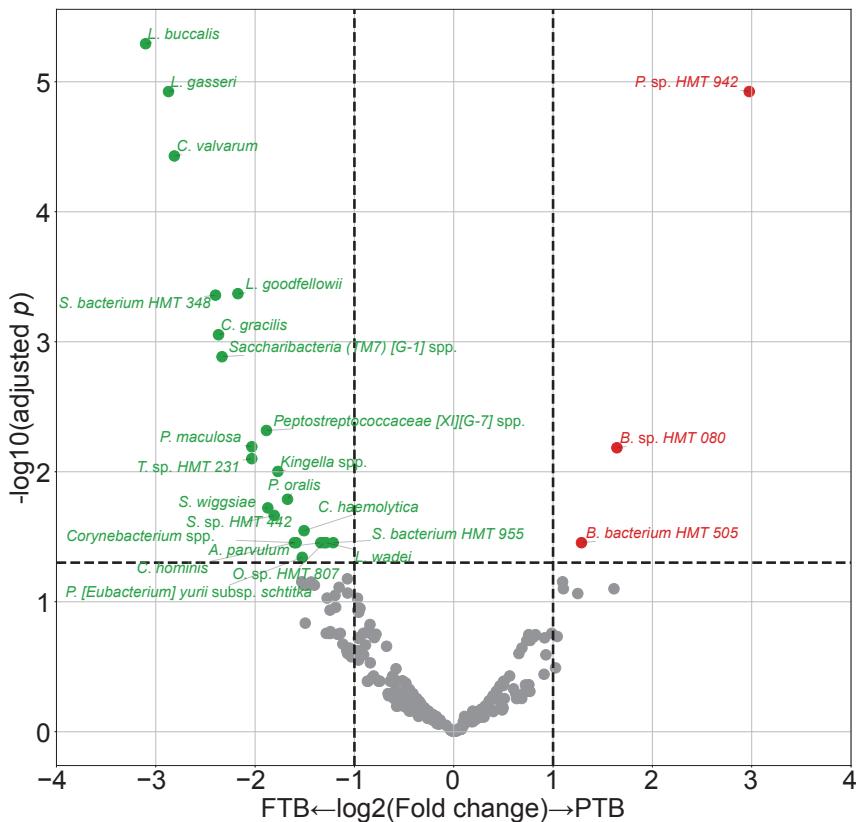


Figure 1: **DAT volcano plot.** DAT volcano plot shows DAT, with PTB-enriched DAT shown as red dots and FTB-enriched DAT shown as green dots. Taxa with $|\log_2 \text{FoldChange}| > 1$ and adjusted $p < 0.05$ are considered as significant different.

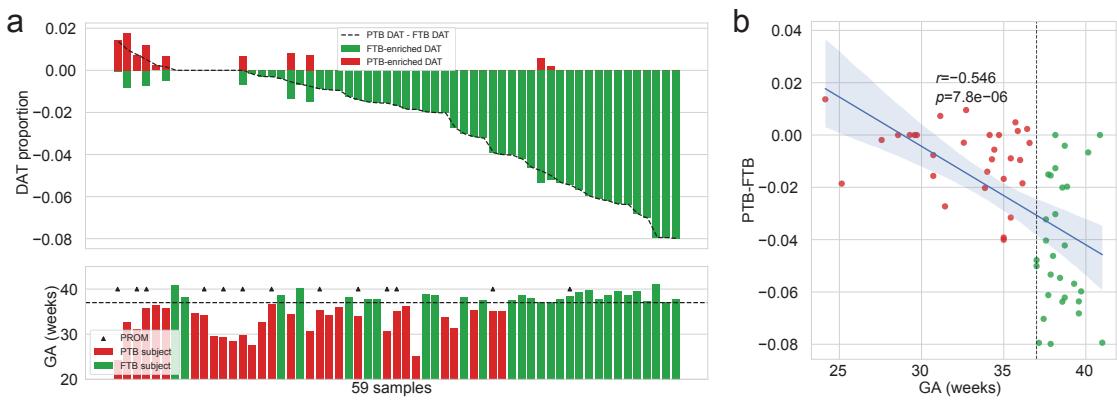


Figure 2: Oral microbiome compositions over DAT. **(a)** Proportions of DAT of study subjects. Samples are sorted by difference between PTB-enriched DAT proportion and FTB-enriched DAT proportion. GA of samples are shown, matched with order of upper panel. PTB: red bar, FTB: green bar. PROM: arrow head. **(b)** Correlation plot with GA and difference between PTB-enriched DAT proportion and FTB-enriched DAT proportion. Pearson correlation shows strong negative coefficient ($r = -0.542$ and $p = 7.8e - 06$) between GA and difference between PTB-enriched DAT proportion and FTB-enriched DAT proportion.

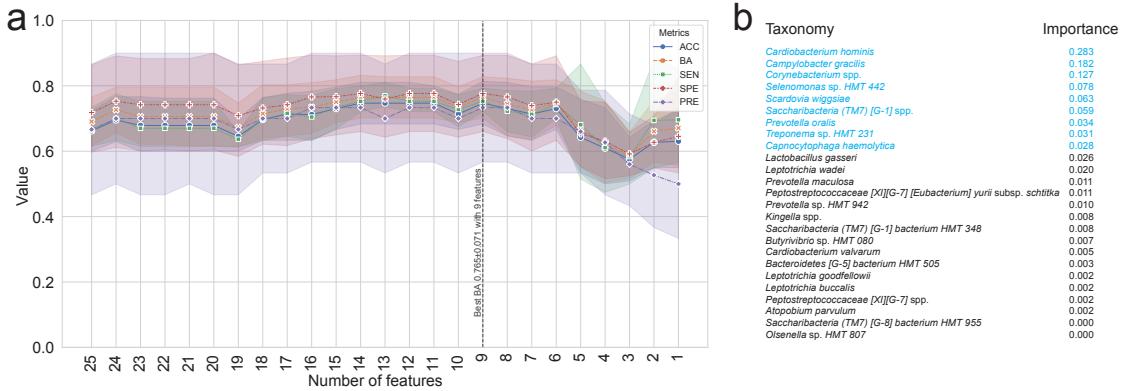


Figure 3: Machine learning evaluations over DAT. **(a)** Machine learning evaluation upon number of features (DAT). Random Forest classifier has the best balanced accuracy (mean \pm standard deviation.; 0.765 ± 0.071) with the nine most important DAT. **(b)** Importance of DAT is shown. Note that $0 \leq$ importance ≤ 1 , and \sum importance = 1. The 20 most important DAT that give the best balanced accuracy is marked with blue.

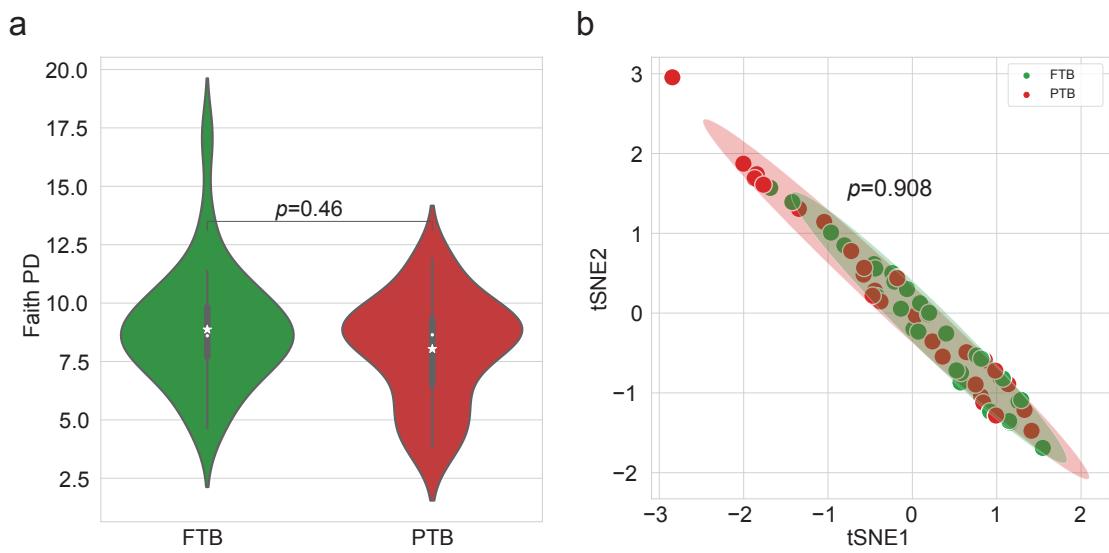


Figure 4: Diversity indices. **(a)** Alpha diversity index (Faith PD). Mann-Whitney-Wilcoxon test did not find statistically significant difference between the PTB group and the FTB group. Mean values are marked with star-point. **(b)** t-SNE plot with beta diversity index (Hamming distance). PERMANOVA multivariate test did not find statistically significant difference between the PTB group and the FTB group.

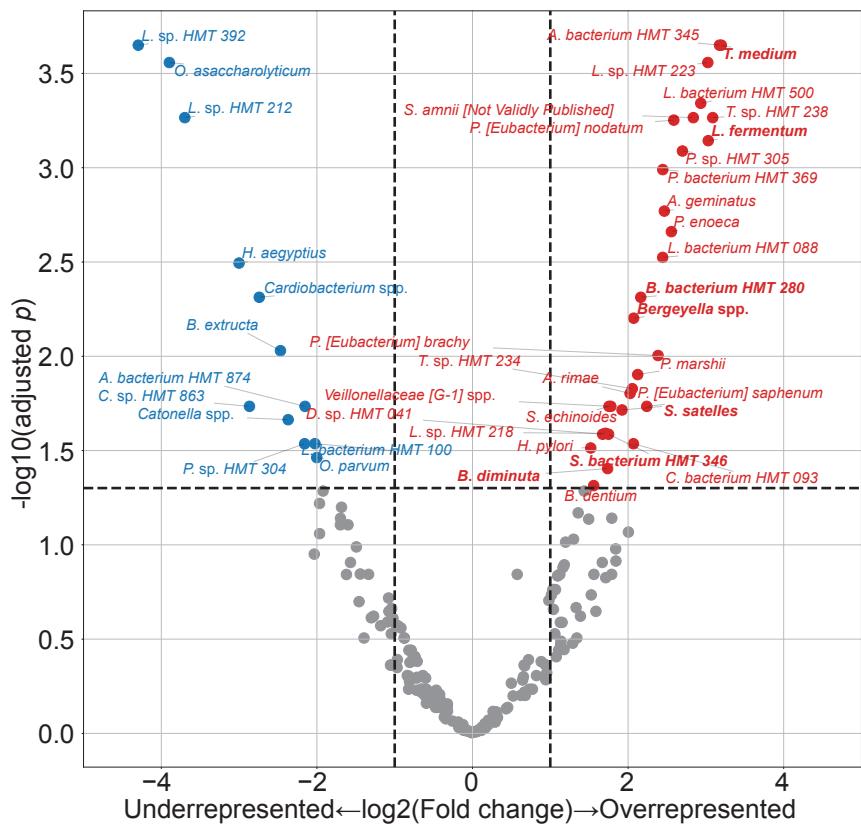


Figure 5: **PROM-related DAT volcano plot.** This is a subgroup analysis between 12 participants in PTB group with PROM and 18 participants in PTB group without PROM, 42 PROM-related DAT were selected between these two groups. Out of these 42 PROM-related DAT, only 7 DAT overlapped with PTB-related DAT, as it indicated by the bold marking. Volcano plot shows PROM-related DAT, with 12 PROM-underrepresented DAT shown as blue dots and 30 PROM-overrepresented DAT shown as red dots. Taxa with $|\log_2 \text{FoldChange}| > 1$ and adjusted $p < 0.05$ are considered as significant different.

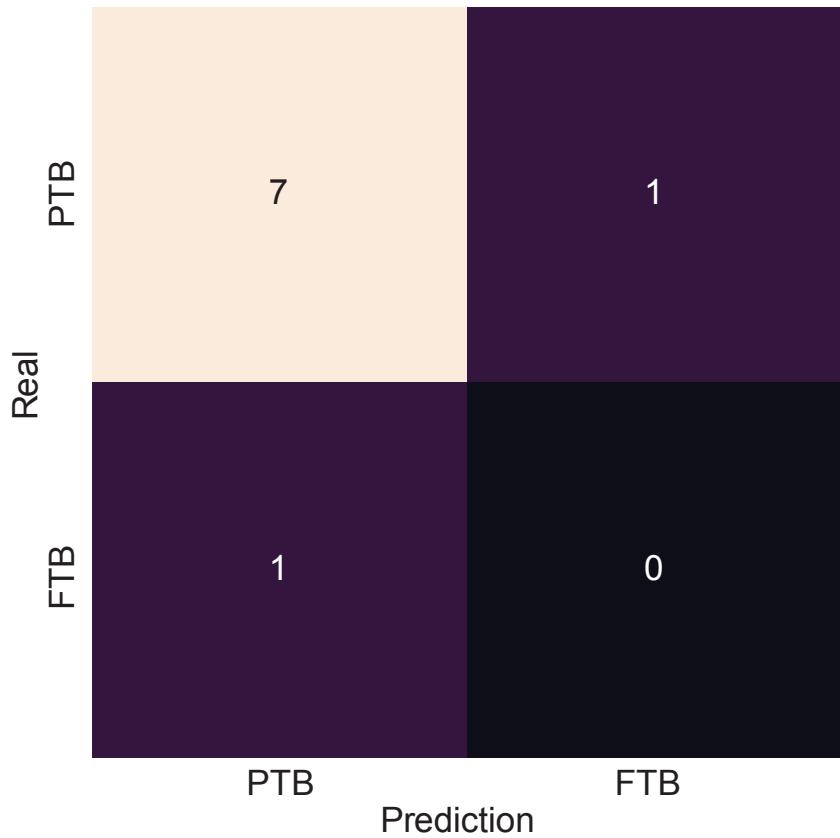


Figure 6: **Heatmap plot of PTB classification with validation data.** A validation test on 9 twin pregnancies that had excluded from the paper was conducted. They consist of 8 PTB subjects and 1 FTB subject. As twin pregnancies have a 7-10 times higher PTB rate than singleton pregnancies, resulting in a majority of the test data falling into the PTB group. The machine learning classifications have 87.5% accuracy, comparable to the machine learning classification on the singleton study subjects (Mean \pm standard deviation. 0.714 ± 0.061)

1.4 Discussion

In this study, we developed a method for predicting PTB based on random forest classifier using salivary microbiome compositions. Recently, several sporadic reports have suggested a bidirectional relationship between oral microbiome and pregnancy (Han & Wang, 2013). However, prenatal oral microbiome is not well understood yet. Some research has shown that oral microbial dysbiosis combined with gingival inflammation can lead to adverse pregnancy outcomes, including low birth weight, PTB, pre-eclampsia, and miscarriages (Ide & Papapanou, 2013). Nevertheless, these results have been inconsistent due to methodologies employed in studies that only target known pathogens.

Fusobacterium nucleatum is the most prevalent oral microbiome studied (Han, 2015; Brennan & Garrett, 2019; Bolstad, Jensen, & Bakken, 1996). *Fusobacterium nucleatum* is a Gramnegative, anaerobic, filamentous oral microbiome. It is considered one of the most abundant species in the oral microbiome. It can also be isolated from vaginal microbiome (Vander Haar, So, Gyamfi-Bannerman, & Han, 2018; Witkin, 2019). Intra-amniotic *Fusobacterium nucleatum* infection leading to PTB has been reported in human and animal studies (Doyle et al., 2014). Other studies have shown that other oral pathogens including *Porphyromonas gingivalis* and intrauterine *Bergeyella* spp. can be isolated from the placenta of women who deliver prematurely (León et al., 2007; Katz, Chegini, Shiverick, & Lamont, 2009). In the present study, although *Bergeyella* spp. was overrepresented in the PTB group with PROM, it was excluded in the finally selected 25 DAT. Furthermore, *Campylobacter gracilis* was one of the FTB-enriched DAT that can aid colonization by periodontal pathogens including *Porphyromonas gingivalis* in subgingival microbiome (Yang et al., 2022). *Lactobacillus gasseri* was also one of the FTB-enriched DAT. It is known that *Lactobacillus gasseri* in vaginal microbiome can decrease early PTB risk (Basavaprabhu, Sonu, & Prabha, 2020; Payne et al., 2021).

We found that decisive species differentiating between two groups were mainly abundant in the FTB group, with DAT consisting of 22 FTB-enriched DAT and three PTB-enriched DAT. We hypothesize that deficiency of species having a protective impact might have triggered the pathophysiology of PTB. Two different mechanisms have been proposed to explain the relationship between unhealthy microbiota composition and adverse pregnancy outcomes. The first mechanism proposed that periodontal bacteria originating in the gingival biofilm could translocate from the unhealthy oral cavity and cross the placenta, reach the intra-amniotic fluid and fetal circulation and directly affect the fetoplacental unit, resulting in bacteremia (Hajishengallis, 2015). The second mechanisms proposed that systemic dissemination of endotoxins and/or inflammatory mediators derived from periodontal plaque and secreted by the subgingival inflammatory site could be carried to the fetoplacental unit (Stout et al., 2013; Aagaard et al., 2014). Although certain microbiota has the same species, their subgroups can have both positive and negative influences on pregnancy outcomes. Following this line of thought, we believe that composition or dysbiosis of the oral microbiome is more important than the presence of specific microbiota.

It is worth noting that microbial changes occurring during pregnancy might be nature consequences of a healthy pregnancy. Three reasons can explain the susceptibility to oral diseases such as periodontitis during pregnancy. These diseases are common in pregnant women due to hormonally driven hyper-

reactivity of the gingiva to bacteria in the subgingival biofilm. Other factors that increase the risk of poor oral health during pregnancy include changes in dietary habits (frequent snacking or increased consumption of carbohydrate-rich foods), stomach acids from nausea and vomiting that contribute to the breakdown of tooth enamel, and a decreased likelihood of seeking dental care during pregnancy. We plan to implement pathway analyses to investigate direct link between the microbiome and PTB.

Even though there was limited power resulting from a small number of participants and restricted validation sample size, our study verified that oral microbiota might provide potential biomarkers for predicting pregnancy complications using machine learning methods including random forest classification. Additionally, the fact that the entire microbiome was not analyzed was a limitation of this study because our analysis only used relative values measured by 16S rRNA sequencing, not 16S metagenome sequencing. We did not investigate other factors could impact the oral microbiome, such as participant's diet and socioeconomic status.

Despite these limitations, this prospective study demonstrated the potential of a PTB prediction model using oral microbiome in mouthwash. Further multi-center and larger-scale studies are needed to confirm our results before applying techniques developed in this study in the clinical field.

2 Prediction model for periodontitis severity based on the salivary microbiomes

This section includes the published contents:

2.1 Introduction

2.2 Materials and methods

2.2.1 Study subjects and clinical procedure

2.2.2 Bioinformatics analysis

2.3 Results

- 2.3.1 Summary of study subjects and sequencing data**
- 2.3.2 Diversity indices reveal differences in diversity among the periodontal statuses**
- 2.3.3 Differentially abundant taxa among healthy and different periodontitis stages and their correlation**
- 2.3.4 Classification of periodontitis stages by random forest models**

Table 2: **Clinical characteristics of the study subjects.** Significant differences were assessed using the Kruskal-Wallis test. NA: Not applicable.

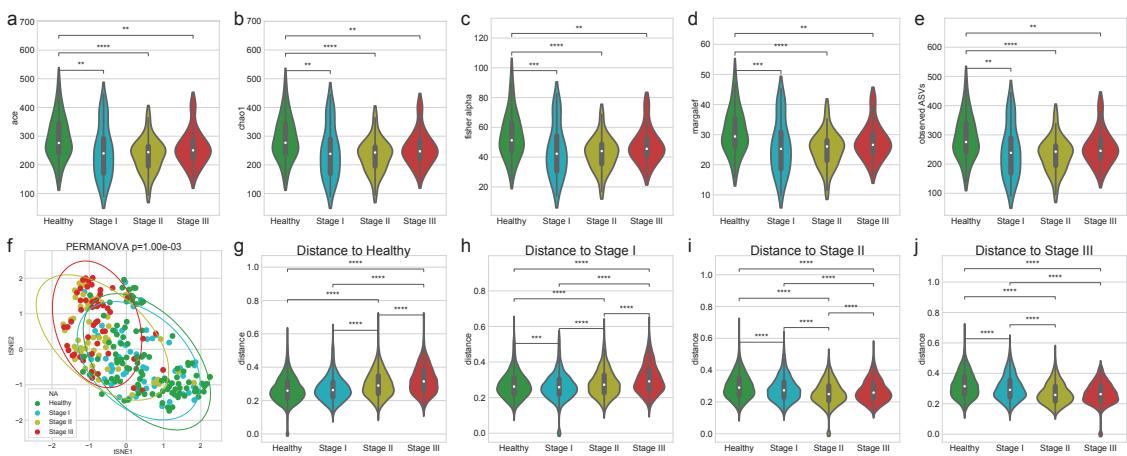


Figure 7: Diversity indices. Comparisons of salivary microbiomes among healthy controls and patients with various periodontitis stages. Alpha-diversity indices (**a-e**) indicate that healthy controls have increased heterogeneity than periodontitis stages as measured by: **(a)** ace **(b)** chao1 **(c)** Fisher alpha **(d)** Margalef, and **(e)** observed ASVs. **(f)** The beta-diversity index (weighted UniFrac) was visualized using a tSNE-transformed plot. The confidence ellipses are shown to display the distribution of each periodontitis stage. The distance to each stage demonstrated that each periodontitis stage was distinguished from the other periodontitis stages: **(g)** distance to Healthy **(h)** distance to Stage I **(i)** distance to Stage II, and **(j)** distance to Stage III. Statistical significance determined by the Mann-Whitney U-test (MWU) test: $p \leq 0.01$ (***) and $p \leq 0.0001$ (****).

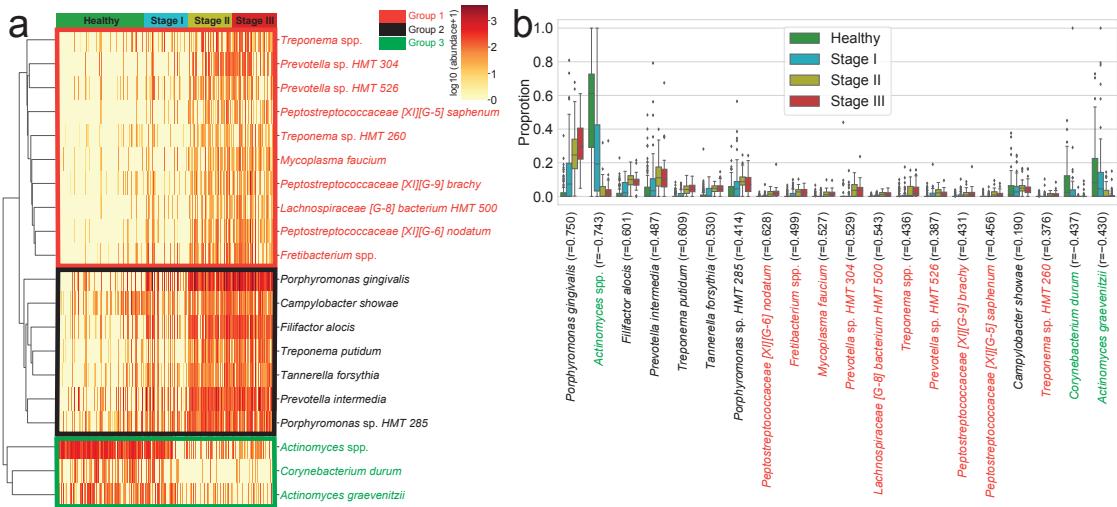


Figure 8: Differentially abundant taxa. Differentially abundant taxa (DAT) that were identified by ANCOM. **(a)** Heatmap of clustered DAT with similar distribution among subjects. Group 1, Group 2, and Group 3 are marked in red, black, and green, respectively. **(b)** Box plots showing the proportions of DAT. Taxa were sorted by their importance according to ANCOM.

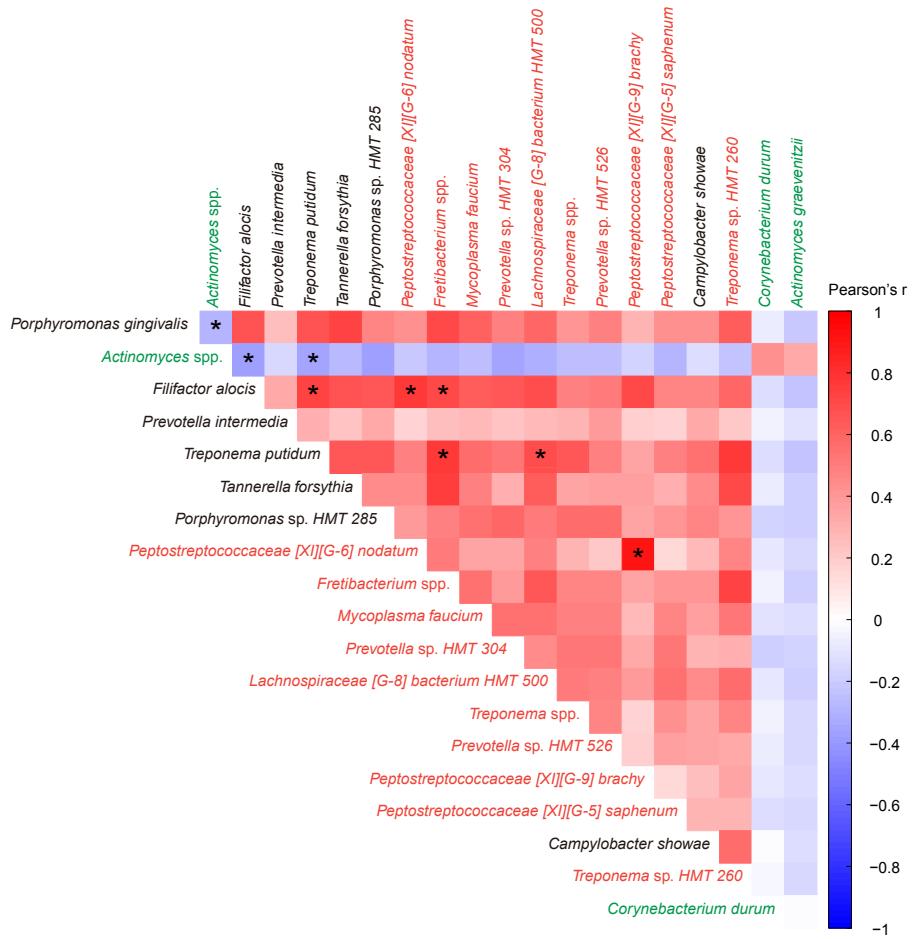


Figure 9: **Correlation heatmap.** Pearson's correlations between differentially abundant taxa in healthy status and periodontitis stages. Statistical significance was determined by strong correlation, i.e., $|\text{coefficient}| \geq 0.5$ (*).

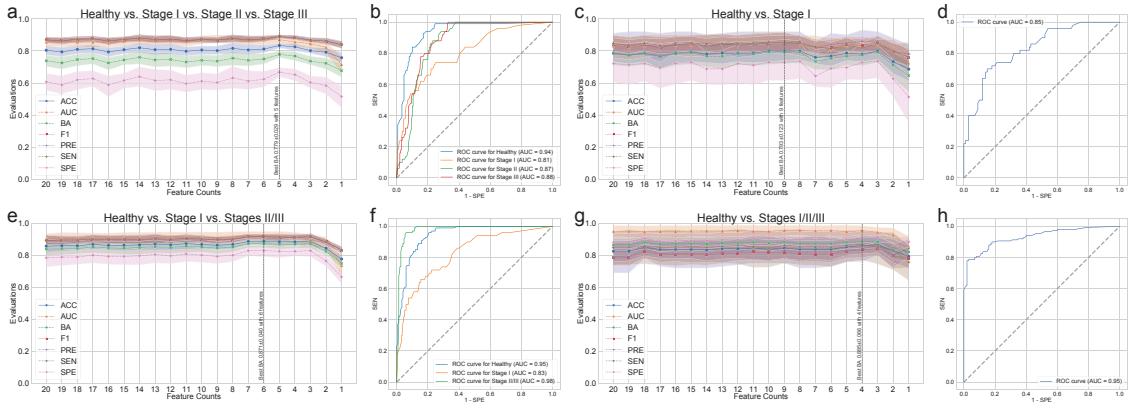


Figure 10: Random forest classification metrics. The classification metrics in the random forest classifications were as follows: accuracy (ACC), area-under-curve (AUC), balanced accuracy (BA), F1 score (F1), precision (PRE), sensitivity (SEN), and specificity (SPE). Every classification metric ranges from [0, 1], with higher values indicating better performance. **(a)** Classification performance for healthy vs. stage I vs. stage II vs. stage III. **(b)** Receiver-operating characteristics (ROC) curve for the highest BA of (a). **(c)** Classification performance for healthy vs. stage I. **(d)** ROC curve on the highest BA of (c). **(e)** Classification performance for healthy vs. stage I vs. stages II/III. **(f)** ROC curve for the highest BA of (e). **(g)** Classification performance for healthy vs. stages I/II/III. **(h)** ROC curve for the highest BA of (h).

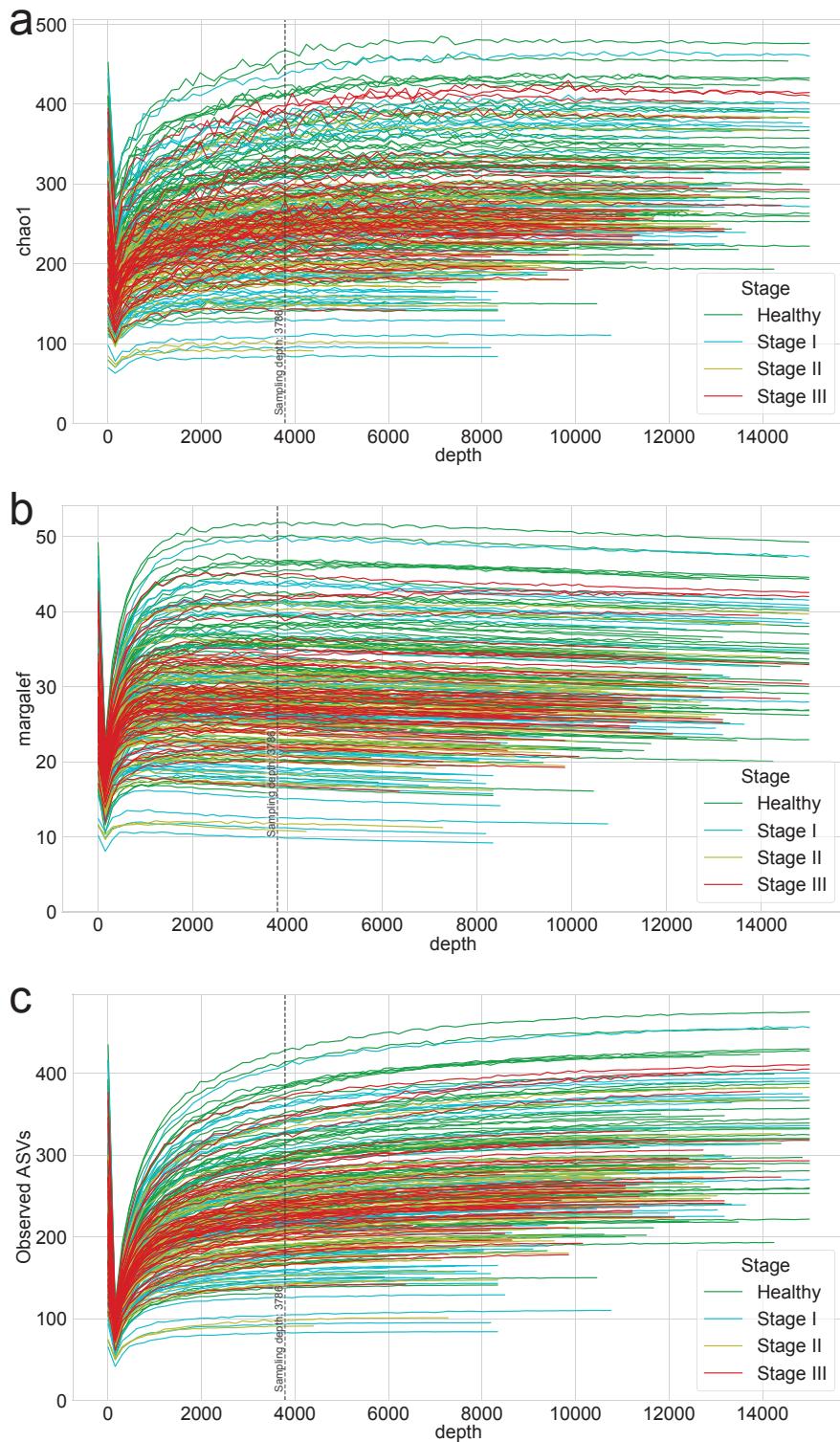


Figure 11: Rarefaction curves for alpha diversity indices. Rarefaction of (a) chao1 (b) margalef, and (c) observed ASVs were generated to measure species richness and determine the sampling depth of each sample.

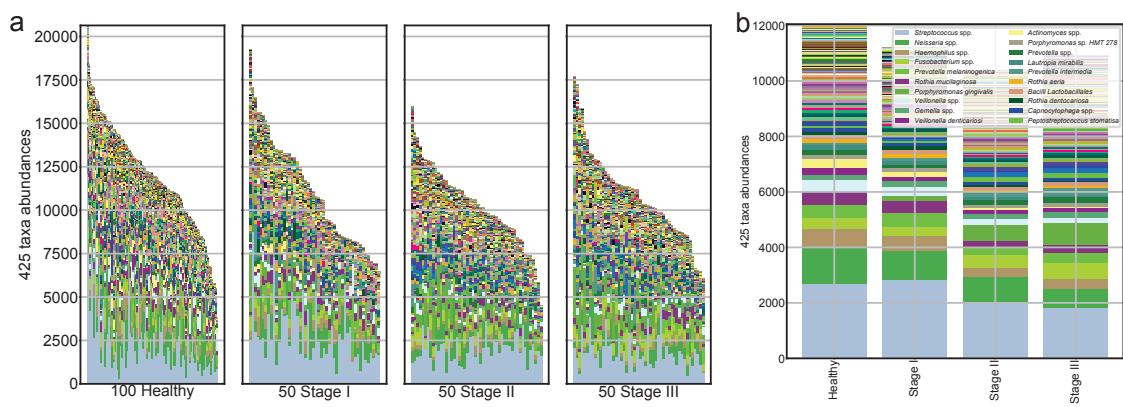


Figure 12: Absolute abundance of salivary bacterial taxa in the different periodontal statuses at the species level. Stacked bar plot of the absolute abundance of bacterial species for all samples (**a**) and the mean absolute abundance of bacterial species in the healthy, stage I, stage II, and stage III groups (**b**).

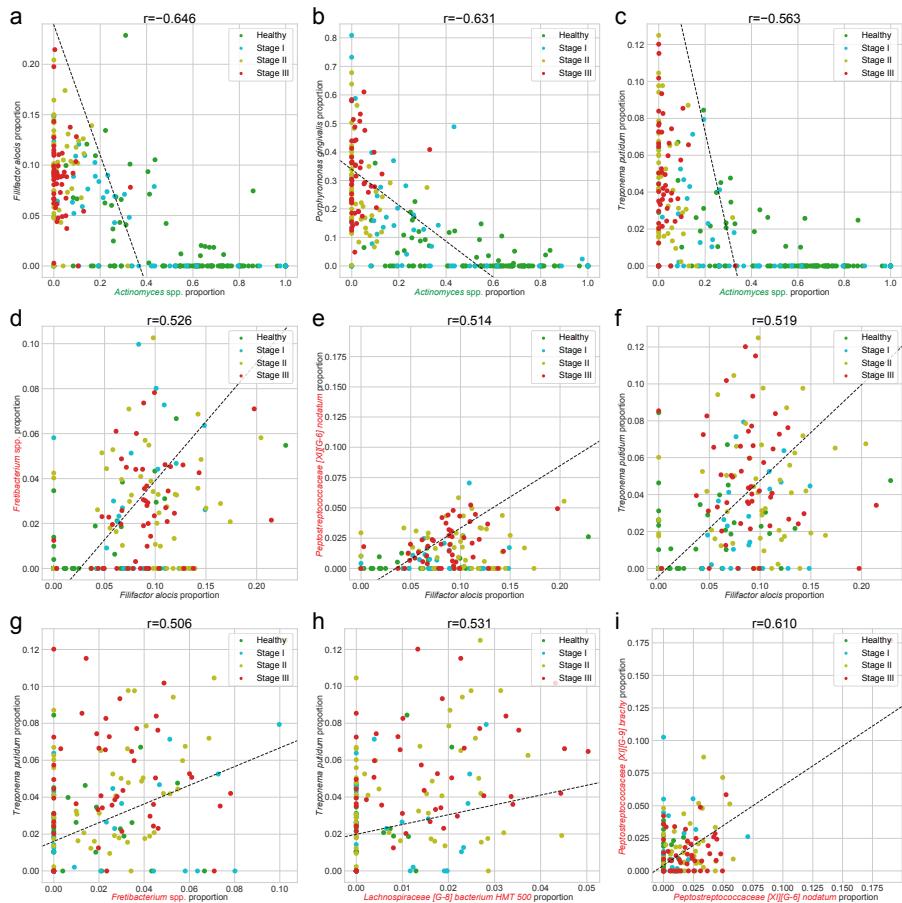


Figure 13: Correlation plots for differentially abundant taxa. We selected the combinations of DAT with absolute Spearman correlation coefficients greater than 0.5. The color represents periodontal healthy periodontal statuses (green: healthy, cyan: stage I, yellow: stage II, and red: stage III).

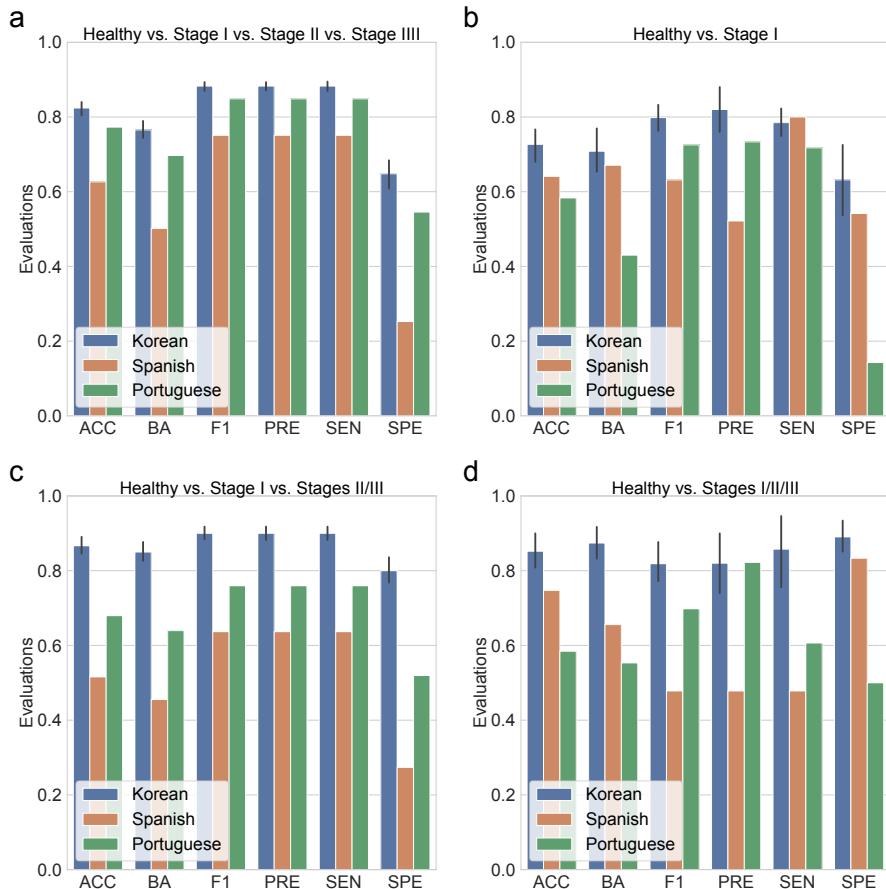


Figure 14: Random forest classification metrics from external datasets. The classification metrics in the random forest classification included accuracy (ACC), balanced accuracy (BA), F1 score (F1), precision (PRE), sensitivity (SEN), and specificity (SPE). Every classification metric ranges from [0, 1], with higher values indicating better performance. **(a)** Classification performance for healthy vs. stage I vs. stage II vs. stage III. **(b)** Classification performance for healthy vs. stage I. **(c)** Classification performance for healthy vs. stage I vs. stages II/III. **(d)** Classification performance for healthy vs. stages I/II/III.

2.4 Discussion

3 Lung microbiome

3.1 Introduction

3.2 Materials and methods

3.3 Results

3.3.1 Discussion

4 General conclusion and future perspective

4.1 General conclusions

In conclusion, the research described in this doctoral dissertation was conducted to identify significant ...

In the Section 1, I show that

4.2 Plan for future

4.3 Future perspective

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Acknowledgments

I would like to disclose my earnest appreciation for my advisor, Professor Semin Lee, who provided solicitous supervision and cherished opportunities throughout the course of my research. His advice and consultation encouraged me to become as a researcher and to receive all humility and gentleness. I am also grateful to all of my committee members, Professor AAA, Professor BBB, Professor CCC, and Professor DDD, for their critical and meaningful mentions and suggestions.

I extend my deepest gratitude to my Lord, *the Flying Spaghetti Monster*, His Noodly Appendage has guided me through the twist and turns of this academic journey. His presence, ever comforting and mysterious, has been a source of strength and humor during both highs and lows. In moments of doubt, I found solace in the belief that you were there, gently reminding me to keep faith in the process. His Holy Noodle has nourished my mind, and for that, I am truly overwhelmed. May His Holy Noodle continue to guide me in all my future endeavors. R’Amen.

(Professors)

I would like to extend my heartfelt gratitude to my colleagues of the Computational Biology Lab @ UNIST, whose collaboration, friendship, brotherhood, and support have been an invaluable part of my journey. Your willingness to share insights, engage in thoughtful discussions, and offer encouragement during the challenging moments of research has significantly shaped my academic experience. The camaraderie in the Computational Biology Lab made even the most demanding days more enjoyable, and I am deeply grateful for the collaborative environment we created together. I appreciate you for standing by my side throughout this Ph.D. journey.

I would like to express my heartfelt gratitude to my family, whose unwavering support has been the foundation of everything I have achieved. Your love, encouragement, and belief in me have sustained me through every challenge, and I could not have come this far without you. From your words of wisdom to your patience and understanding, each of you has played a vital role in helping me navigate this journey. The strength and comfort I have drawn from our family bond have been my greatest source of resilience. Your presence, both near and far, has filled my life with warmth and motivation. I am deeply grateful for your unconditional love and for always being there when I needed you the most. Thank you for being my constant source of strength and inspiration.

I am incredibly pleased to my friends, especially my GSHS alumni (○망특), for their unwavering support and encouragement throughout this journey. The bonds we formed back in our school days have only grown stronger over the years, and I am fortunate to have had such loyal and understanding friends by my side. Your constant words of motivation, and even moments of levity during stressful times have helped keep me grounded. Whether it was a late-night conversations, a shared laugh, or a simple message of reassurance, you all have played a vital role in keeping me focused and motivated. I am relieved for the ways you celebrated each small achievement with me and how you patiently listened to my worries. The memories of our shared past provided me with comfort and a sense of stability when the road ahead felt uncertain. I could not have reached this point without the love and friendship that you all have generously given. Each of your, in your unique way, has contributed to this dissertation, even if indirectly, and for

that, I am forever beholden. I look forward to continuing our friendship as we all grow in our individual paths, knowing that the support we share is something truly special.

I would like to express my sincere gratitude to the amazing members of my animal protection groups, DRDR (두루두루) and UNIMALS (유니멀스), whose dedication and compassion have been a constant source of motivation. Your unwavering commitment to improving the lives of animals has inspired me throughout this journey. I am also thankful for the beautiful cats we have cared for, whose presence brought both joy and purpose to our allegiance. Their playful spirits and gentle companionship served as daily reminders of why we continue to fight for animal rights. The bond we share, both with each other and with the animals we protect, has enriched my life in countless ways. I appreciate you all again for your support, dedication, and for being part of this meaningful cause.

I would like to express my deepest gratitude to everyone I have had the honor of meeting throughout this journey. Your kindness, encouragement, and support have carried me through both the challenging and rewarding moments of my life. Whether through a kind word, thoughtful advice, or simply being there when I needed it most, your presence has made all the difference. I am incredibly fortunate to have received such generosity and warmth from those around me, and I do not take it for granted. Every act of kindness, no matter how big or small, has been a source of strength and motivation for me. To all my friends, colleagues, mentors, and beloved ones, thank you for your unwavering support. I am truly grateful for each of you, and your kindness has left an indelible mark on my journey.

My Lord, *the Flying Spaghetti Monster*,
give us grace to accept with serenity the things that cannot be changed,
courage to change the things that should be changed,
and the wisdom to distinguish the one from the other.

Glory be to *the Meatball*, to *the Sauce*, and to *the Holy Noodle*.

As it was in the beginning, is now, and ever shall be.

R'Amen.

