Salivary Screening for Selenomonas Noxia in the Oral Cavity of Pediatric Patients

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Abstract
Objectives: The oral microbiome may be affected by patient medications, disease conditions and systemic disorders. *Selenomonas noxia* is an anaerobic, motile, non spore-forming, gram-negative rod that has been repeatedly associated with periodontal disease and other disorders, including obesity. Based upon the paucity of evidence regarding oral prevalence, the objective of the study was to evaluate *S. noxia* prevalence by sampling saliva from the oral cavity to screen for this pathogen.

Experimental Methods: Using an existing saliva repository, DNA was isolated and screened using quantitative real-time polymerase chain reaction (qPCR). Demographic analysis of study samples and qPCR results was also performed.

Results: Approximately half of the samples (n=96) were derived from females (51%) and the majority were from Hispanic patients (62.5%). Following DNA isolation and qPCR screening 37.5% (n=35) were found to harbor *S. noxia* DNA, which was more prevalent among the samples derived from adults (n=22 or 22.9%) than pediatric patients (n=13 or 13.5%).

Conclusions: This study provides novel information regarding the oral prevalence of *S. noxia* among both pediatric and adult populations from a dental school population. These data are an important part of the overall epidemiologic analysis of this organism and may provide some initial information regarding the risk for periodontal or other health issues related to the presence among these populations.

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Keywords
*Selenomonas Noxia*; Saliva sampling; qPCR Screening.
**Abbreviations:** Institutional Review Board (IRB), Office for the Protection of Human Research Subjects (OPRS), University of Nevada, Las Vegas (UNLV), deoxyribonucleic acid (DNA), quantitative real-time polymerase chain reaction (qPCR), American Type Culture Collection (ATCC), glyceraldehyde 3-phosphate dehydrogenase (GAPDH), limit of detection (LOD), signal band intensity (SBI), body mass index (BMI), periodontal pocket depth (PPD), decayed, missing, filled teeth (DMFT).

**Introduction**

The oral microbiome may be affected by patient medications, disease conditions and systemic disorders. For example, specific microflora may be associated with diseases of the oral cavity like caries, periodontal disease and oral cancer. In fact, many studies have demonstrated strong correlations between the oral microbiome and periodontal disease across the lifespan.

*Selenomonas noxia* is an anaerobic, motile, non spore-forming, gram-negative rod that has been repeatedly associated with periodontal disease. More specifically, it has been found in cases of generalized aggressive periodontitis and chronic periodontitis, as well as gastric ulcers. Besides the relation between *S. noxia* and periodontal disease, some studies have found an association between *S. noxia* and obesity. These correlations have been a driving force towards the development of screening tools to detect and identify this oral pathogen.

These data suggest that the composition of salivary bacteria changes could function as a biological indicator of developing periodontal disease and/or obesity, although few studies have examined oral prevalence of this organism. Based upon the paucity of evidence regarding oral prevalence, the objective of was to evaluate *S. noxia* prevalence by sampling saliva from the oral cavity to screen for this pathogen.

**Methodology**

**Human Subjects**

This project was reviewed and approved by the Institutional Review Board (IRB) and Office for the Protection of Human Research Subjects (OPRS) at the University of Nevada, Las Vegas (UNLV) under Protocol# 1502-5068M. The original approved collection protocol OPRS#880427-1 was titled “The Prevalence of Oral Microbes in Saliva from the University of Nevada Las Vegas (UNLV) School of Dental Medicine (SDM) pediatric and adult clinical population”.

**Sample Collection**

This was a retrospective study of previously collected saliva samples, stored in an existing biomedical repository. In brief, all samples were taken from

<table>
<thead>
<tr>
<th>Study sample (n=96)</th>
<th>UNLV-SDM clinic</th>
<th>Statistical analysis</th>
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<tbody>
<tr>
<td><strong>Sex</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Female</td>
<td>51.0% (n=49)</td>
<td>50.9%</td>
</tr>
<tr>
<td>Male</td>
<td>49.0% (n=47)</td>
<td>49.1%</td>
</tr>
<tr>
<td><strong>Race / Ethnicity</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>White</td>
<td>23.9% (n=23)</td>
<td>41.4%</td>
</tr>
<tr>
<td>Minority</td>
<td>76.1% (n=73)</td>
<td>58.6%</td>
</tr>
<tr>
<td>Hispanic</td>
<td>62.5% (n=60)</td>
<td>35.9%</td>
</tr>
<tr>
<td>Black</td>
<td>7.3% (n=7)</td>
<td>13.1%</td>
</tr>
<tr>
<td>Asian / Other</td>
<td>6.3% (n=6)</td>
<td>9.6%</td>
</tr>
<tr>
<td><strong>Age</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pediatric (n=54)</td>
<td>Range: 5 – 17 yrs.</td>
<td>Range: 0 – 17 yrs.</td>
</tr>
<tr>
<td></td>
<td>Ave.=12.9 yrs.</td>
<td>Ave.=10.14 yrs.</td>
</tr>
<tr>
<td></td>
<td>Ave.=43.1 yrs.</td>
<td>Ave.=52.3 yrs.</td>
</tr>
</tbody>
</table>
UNLV-SDM clinic patients that previously provided Informed Consent (Adults) or Pediatric Assent (Children). At the time of sample collection, each sample was assigned a non-duplicated, randomly generated number to prevent any linkage with the patient information or other patient-specific information. Basic demographic information was collected for each sample (Sex, Age, Race/Ethnicity) with no other information that could be linked to the original voluntary study participants.

Each study participant was provided with a sterile 50 mL container for unstimulated saliva collection and asked to provide up to 5.0 mL in total. Each sample was transferred on ice to the biomedical laboratory and kept at -80°C.

The original sampling protocol required patients to provide Informed Consent (adult) and Pediatric Assent (pediatric) prior to the collection of saliva. The inclusion criteria were pediatric patients aged seven (7) years or older and their parents or guardians who agreed to participate. Pediatric assent and Parental permission to consent for voluntary participation were obtained at the time of study enrollment. Adult parents or guardians provided Informed Consent. Exclusion criteria included any person that was not a patient of record at UNLV-SDM, any patients who declined to participate, and any parent or guardian that declined to let their child participate.

DNA Isolation
Each sample was then thawed and 1.0 mL was used for DNA isolation. The GenomicPrep DNA isolation kit from Amersham Biosciences (Buckinghamshire, UK) was used, according to the procedure recommended by the manufacturer. DNA isolations were subsequently screening using a NanoDrop spectrophotometer from ThermoFisher (Fair Lawn, NJ). Absorbance readings at A230, A260 and A80 were collected and analyzed for DNA concentration, purity and contamination.

The A260:A280 ratio was used to calculate the initial purity and the A260:A230 ratio was used as a secondary measure of nucleic acid purity and potential contamination.

PCR Screening
All samples with sufficient DNA quantity (> 1.0 ng/μL) and sufficient DNA purity (A260:A280 ratio greater than 1.65) were then processed using quantitative real-time polymerase chain reaction (qPCR). In brief, qPCR used initial incubation of 50°C for 120 seconds, followed by denaturation at 95°C for ten minutes and 40 cycles, consisting of 95°C for 15 seconds and 60°C for 60 seconds. Positive control human glyceraldehyde 3-phosphate dehydrogenase (GAPDH) and standards were derived from American Type Culture Collection (ATCC). S. noxia reference strains ATCC-43541, -51893, and -700225), as previously described.13,15,16

Positive Control
Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)

GAPDH 5′-ATCTTCCAGGAGCGAGATCC-3′ (sense); 20 nt; 55% GC; Tm=66°C

GAPDH 5′-ACCACTGACACGTGGCAGT-3′ (antisense); 20 nt; 55% GC; Tm=70°C

Optimal PCR Tm: 65°C

Forward primer- SNF1, TCTGGGCTACACGCTACTACAATG (25 bp)

Reverse primer- SNR1, GCCTGCAATCGGACTCGAGA (20 bp)

SnP[6 ~ FAM CAGAGGGCAGCGAGAGTGATCTTAAGC [TAMRA]

Table 2: DNA isolation and study sample analysis

<table>
<thead>
<tr>
<th></th>
<th>DNA concentration</th>
<th>DNA purity</th>
<th>Recovery/yield</th>
</tr>
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<tbody>
<tr>
<td>Study sample</td>
<td>521.26 ng/μL +/- 92.9</td>
<td>A260:A280=1.645</td>
<td>100% (n=96)</td>
</tr>
<tr>
<td>Manufacturer range</td>
<td>100 – 1000 ng/μL</td>
<td>1.70-2.00</td>
<td>90-95%</td>
</tr>
</tbody>
</table>
The selected probe (SnP) was labeled with the reporter dye 6-carboxyfluorescein (FAM) at the 5'-end and with the reporter dye tetramethyl-6-carboxyrhodamine (TAMRA) at the 3'-end.

Statistical Analysis
Basic demographic information was compiled and presented using descriptive statistics. Analysis of these demographics was performed using non-parametric statistics (Chi square). Results of the qPCR screening were also analyzed using descriptive statistics and Chi square analysis.15,16

Results
The demographic information for all potential saliva samples was organized and analyzed (Table1). These data demonstrated that slightly more than
half of samples (56.3%, n=54/96) were derived from pediatric patients, with the remainder from adult patients (43.7%, n=42/96), which was similar to the demographics of the overall clinic population. The majority of these patients were Hispanic (minority) 76.1%, which was higher than the overall percentage from the UNLV-SDM clinic population (58.6%). The average age and range of the pediatric samples (5-17 yrs, 12.9 yrs) was slightly higher than the average of the pediatric clinic in general – mainly due to the ability of subjects to provide Pediatric Assent and provide sufficient sample quantity. The average age and range of the adult samples (18-73 yrs, 43.1 yrs) was slightly lower than the overall clinic population – presumably due to random variations in the clinic patients present on the specific days of the initial study sample collection.

Each of the saliva samples were processed to extract DNA for PCR screening and analysis (Table 2). These data demonstrated a yield (recovery rate) of 100%, which was slightly more than the expected range according to the manufacturer protocol (90-95%). The concentration of DNA isolated from the saliva samples was 521.26 ng/μL, which was well within the expected range according to the manufacturer protocol (100 – 1000 ng/μL). The DNA quality or purity as measured by the ratio of absorbance readings at 260 and 280 nm demonstrated an average of 1.645, which is close to the average range according to the manufacturer protocol (1.7 – 2.0).

The DNA isolated from each patient sample was then screened for the presence of the positive control - human glycolytic pathway enzyme glyceraldehyde 3-phosphate dehydrogenase (GAPDH) (Figure 1). These data revealed that all samples screened using PCR were found to harbor GAPDH above the limit of detection (LOD). Each sample was then sorted by age and graphed, which did not reveal any patterns based upon the age of the patient and the signal band intensity (SBI).

Screening of all samples using S. noxia-specific primers revealed slightly more than one third of the total samples (n=35/96 or 37.5%) harbored DNA for this organism (Figure 2). More specifically, 24.1% or the pediatric samples (n=13/54) harbored S. noxia, while 52.4% (n=22/42) tested positive.

Discussion
Based upon the paucity of evidence regarding oral prevalence, the objective of was to evaluate S. noxia prevalence by sampling saliva from the oral cavity to screen for this pathogen. Using an existing saliva repository, this retrospective study was able to analyze samples from a dental school patient population using isolated DNA and qPCR screening for the presence of S. noxia.

These data confirm previous reports from this group regarding the high oral prevalence among adult patients.15 However, the presence of this organism in pediatric populations was not previously observed in other studies from this group.16 This may suggest that studies, such as this current study, with larger sample sizes may be sufficient to adequately assess the oral prevalence of this organism among pediatric populations that may not exhibit similar microbial profiles as adult populations.

Despite these significant findings, this study has limitations that must also be considered. For example, this was a retrospective study involving a one-time (cross sectional) sampling of pediatric and adult patients. Therefore, no temporal information regarding the timing or duration of this organism was available for analysis. In addition, due to the retrospective nature of this study, only basic demographic information that was previously collected was available to the study authors (Sex, Age, Race / Ethnicity) – therefore no other oral or systemic health information, such as body mass index (BMI), periodontal pocket depth (PPD) or decayed, missing, filled teeth (DMFT) were available.

Conclusions
However, this study provides novel information regarding the oral prevalence of S. noxia among both pediatric and adult populations from a dental school population. These data are an important part of the overall epidemiologic analysis of this organism and may provide some initial information regarding the risk for periodontal or other health issues related to the presence among these populations.

Acknowledgements
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Competing Interests
The authors have declared that no competing interests exist.

Author Contributions
KK was responsible for sample collection and experimental protocol. KK and RD were responsible for DNA isolation and PCR screening, as well as project design and funding. RD, KK and KH participated in data analysis and manuscript preparation.

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