Lead Apron Contamination Study

Barrier Technologies

Investigators: Dr. Bruce Paster & Dr. Hatice Hasturk;
The Forsyth Institute
Cambridge, MA 02142

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Executive Summary

X-ray protective aprons can be a source of bacterial contamination. The objective of this proposal was to determine bacterial contamination of X-ray protective aprons that are routinely used in dental clinics. Bacterial strains were isolated from the neck collar areas of 5 different X-ray protective aprons. Bacterial species were identified using molecular means.

Conclusions

Viable aerobic and anaerobic bacteria contaminate the inside and outside areas of the neck collars of X-ray protective aprons. Species identified are typical isolates from the skin, the oral cavity and the environment. Patients or clinicians may be at risk for transmission of potentially harmful bacterial contaminants.

Objective

This study was designed to determine bacterial contamination of X-ray protective aprons that are used in dental clinics.

Methods

Study Design: The neck collars of 5 aprons were sampled for the presence of viable bacteria. Sampling was done at the end of a regular clinic day at the Forsyth Institute dental clinics prior to daily decontamination procedures.

Sampling and Bacterial Identification

Sterile cotton swabs were dipped in sterile 0.01M TRIS buffer. Excess buffer was removed. Wet swabs were used to sample the neck collars. Two areas of the collars were sampled: 1) The entire inside surface (surface that comes in contact with patient's neck or skin) of the collar (termed "Inside") and 2) the area outside of the neck collar (termed "Outside").

Immediately after sampling each site, swabs were streaked onto 2 Blood Agar media plates. One plate was incubated aerobically for 3 days and the other plate anaerobically for 7 days at 37^{o}C. Representative bacterial colonies that developed were identified using 16S rRNA gene sequence analysis using a commercially-available service (GENEWIZ, Boston, MA). Resultant sequences were analyzed using BLAST vs the HOMD database (www.homd.org) or NCBI database. Such analyses are standard in our laboratories.

Results

Many isolates were obtained from all apron surfaces tested. The protocol was not set up for enumeration, but the number of resultant colonies per swab ranged from 10 to hundreds per plate as shown in Figure 1.

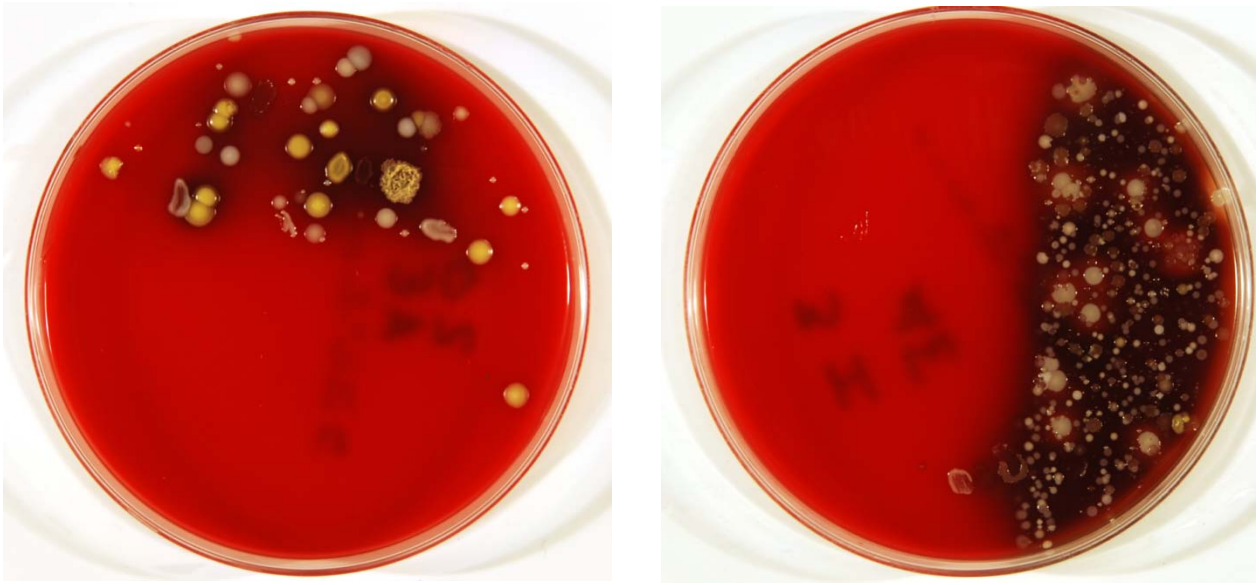

Figure 1. Bacterial isolates from swabs of thoracic collars of X-ray aprons.

Representative colonies, based on apparent differences in colony morphology, were selected for bacterial identification. Overall, 5 to 10 isolates were selected from each plate with a final total of 83 isolates that were ultimately identified at the species level. Results are shown in

Table 1. In all, 26 different bacterial species were identified. Many were typical skin isolates (such as species of *Staphylococcus*), oral isolates (including species of *Streptococcus*, *Rothia* and *Neisseria)*, and others considered as environmental isolates (such as *Micrococcus luteus* and species of *Pseudomonas)*. Likely, these latter species were transient contaminants on the skin.

Table 1. Bacterial species contaminating neck collars of X-ray protective aprons

Isolate ID *	ID-BLAST search in HOMD or GenBank	Comments
1I-AE-1	*Staphylococcus epidermidis*	skin
1I-AE-2	*Staphylococcus hominis*	skin
1I-AE-4	*Staphylococcus caprae*	skin
1I-AE-5	*Staphylococcus caprae*	skin
1I-AN-1	*Staphylococcus epidermidis*	Skin
1I-AN-2	*Staphylococcus caprae*	Skin
1I-AN-3	*Streptococcus sanguinis*	oral
1I-AN-4	*Staphylococcus epidermidis*	Skin
1O-AE-1	*Bacillus cereus*	environmental
1O-AE-2	*Staphylococcus caprae*	skin
1O-AE-3	*Micrococcus luteus*	environmental
1O-AE-4	*Staphylococcus caprae*	skin
1O-AN-1	*Staphylococcus caprae*	skin
2I-AE-1	*Staphylococcus epidermidis*	skin
2I-AE-2	*Micrococcus luteus*	Environmental
2I-AE-3	*Staphylococcus epidermidis*	skin
2I-AE-4	*Staphylococcus caprae*	skin
2I-AE-5	*Staphylococcus caprae*	skin
2I-AN-1	*Staphylococcus epidermidis*	skin
2I-AN-2	*Staphylococcus caprae*	skin
2I-AN-3	*Desulfotomaculum guttoideum*	Environmental, maybe intestinal
2I-AN-4	*Staphylococcus epidermidis*	skin
2I-AN-5	*Staphylococcus caprae*	skin
2O-AE-1	*Streptococcus parasanguinis* II HOT411	oral
2O-AE-2	*Moraxella osloensis*	oral
2O-AE-3	*Micrococcus luteus*	environmental
2O-AE-4	*Micrococcus luteus*	environmental
2O-AE-5	*Staphylococcus epidermidis*	skin
2O-AE-6	*Rothia mucilaginosa*	oral
2O-AE-7	*Streptococcus salivarius*	oral
2O-AN-1	*Staphylococcus epidermidis*	skin
2O-AN-2	*Streptococcus salivarius*	oral
2O-AN-3	*Streptococcus sp. HOT064*	oral
2O-AN-5	*Staphylococcus epidermidis*	skin
3I-AE-1	*Micrococcus luteus*	environmental
3I-AE-3	*Staphylococcus hominis*	skin
3I-AE-4	*Streptococcus mitis*	oral
3I-AE-5	*Neisseria flavescens*	oral
3I-AN-1	*Streptococcus infantis*	oral
3I-AN-2	*Streptococcus infantis*	oral
3I-AN-3	*Staphylococcus epidermidis*	skin

3I-AN-4	*Staphylococcus hominis*	skin
3I-AN-6	*Staphylococcus epidermidis*	skin
3I-AN-7	*Staphylococcus warneri*	skin
3I-AN-8	*Staphylococcus warneri*	skin
3O-AE-1	*Neisseria mucosa* or *N. flava*, or *N. sicca*	oral
3O-AE-2	*Rothia aeria*	oral
3O-AE-3	*Neisseria mucosa or N. flava, or N. sicca*	oral
3O-AE-4	*Staphylococcus warneri*	skin
3O-AE-5	*Staphylococcus epidermidis*	skin
3O-AN-1	*Capnocytophaga gingivalis*	oral
3O-AN-2	*Streptococcus salivarius*	oral
3O-AN-3	*Streptococcus sanguinis*	oral
4I-AE-1	*Staphylococcus warneri*	skin
4I-AE-2	*Staphylococcus epidermidis*	skin
4I-AE-3	*Staphylococcus caprae*	skin
4I-AE-4	*Staphylococcus epidermidis*	skin
4I-AE-5	*Streptococcus parasanguinis* II HOT721	oral
4I-AN-2	*Staphylococcus epidermidis*	skin
4I-AN-4	*Streptococcus salivarius*	oral
4I-AN-5	*Streptococcus gordonii*	oral
4O-AE-1	*Bacillus megaterium*	environmental
4O-AE-2	*Bacillus megaterium*	environmental
4O-AE-3	*Rothia dentocariosa*	oral
4O-AE-4	*Streptococcus infantis*	oral
4O-AE-5	*Micrococcus luteus*	environmental
4O-AE-7	*Staphylococcus epidermidis*	skin
4O-AN-1	*Streptococcus salivarius*	oral
4O-AN-2	*Staphylococcus caprae*	skin
4O-AN-3	*Staphylococcus epidermidis*	skin
4O-AN-4	*Staphylococcus caprae*	skin
5I-AE-2	*Pseudomonas luteola*	environmental Opportunistic pathogen. Can be involved in endocarditis, peritonitis, meningitis
5I-AE-3	*Streptococcus mitis*	oral
5I-AE-4	*Micrococcus luteus*	environmental
5I-AE-5	*Staphylococcus warneri*	skin
5O-AE-1	*Pseudomonas luteola*	environmental
5O-AE-2	*Micrococcus luteus*	environmental
5O-AE-3	*Microbacterium oxydans*	environmental
5O-AE-4	*Micrococcus luteus*	environmental
5O-AE-5	*Micrococcus luteus*	environmental
5O-AE-6	*Moraxella osloensis*	Environmental/oral
5O-AN-2	*Streptococcus mitis*	oral
5O-AN-4	*Streptococcus mutans*	oral

*1 through 5 is apron number, I=inside neck collar, O=outside neck collar, AE-grown aerobically, AN=grown anaerobically, -# =isolate number. Thus, 1I-AE-1 is apron #1, inside collar, aerobically grown isolate #1.

Identification of clinics associated with tested apron is shown in Table 2. Typically, oral bacteria were isolated more frequently from aprons association with the pediatric clinic (apron #3). No oral surgeries were performed using any of the aprons for the day sampling.

Table 2. Clinic associated with apron.

Apron number	Clinic or types of patients
1	Mainly used during endodontics and periodontics
2	Mainly used during implant surgeries and periodontics
3	Mainly used for routine pediatric patients
4	Mainly used for routine X-ray examination or prosthodontic procedures
5	Mainly used for CT-Scan

Conclusions

The inside and outside surfaces of neck collars of X-ray-protective aprons were contaminated with viable bacteria. Abundant bacterial growth on agar media, especially from the inner surfaces, was observed from all aprons.

The sources of the bacterial contamination were from the oral cavity, likely from saliva spilled from intraoral film holders, clinician's gloved hands or patient's mouth and from the skin of the patient. Typical oral bacterial species were identified, including species of *Streptococcus* and *Rothia*, and species commonly found on the skin, such as species of *Micrococcus* and *Staphylococcus*.

These contaminating bacteria are a possible source of cross-contamination. There is risk, albeit low, of transmission of potentially harmful bacteria to patients or clinicians. For example, if a patient had antibiotic resistant bacteria such as MRSA (Methicillin-resistant *Staphylococcus aureus*), there is the possibility of transmission. Although, MRSA was not detected in this study, *Pseudomonas luteola,* a known opportunistic pathogen, was detected on one of the tested aprons. Taken together, contaminated protective aprons routinely used in the dental clinics could pose a risk for microbial transmission to a susceptible host.