

ABSTRACT

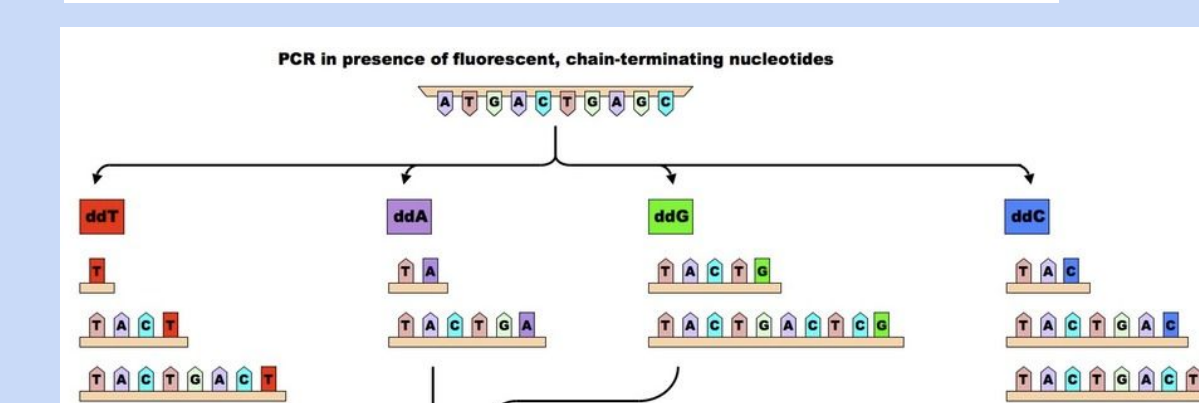
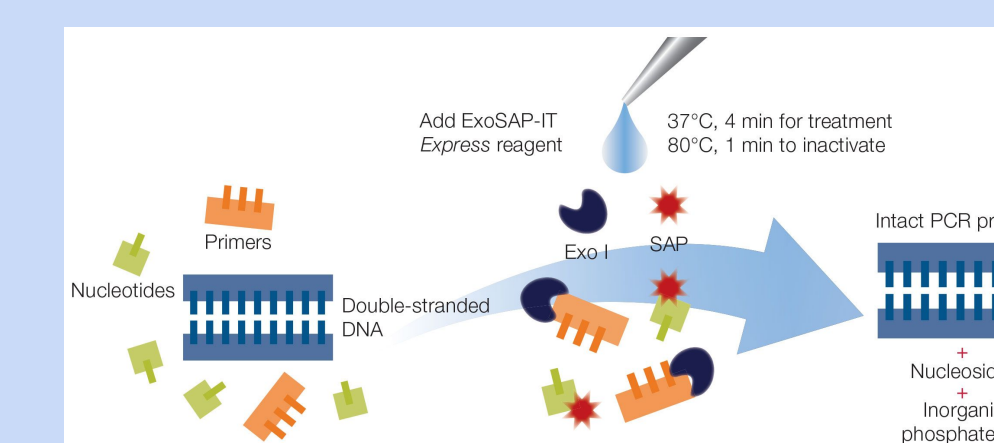
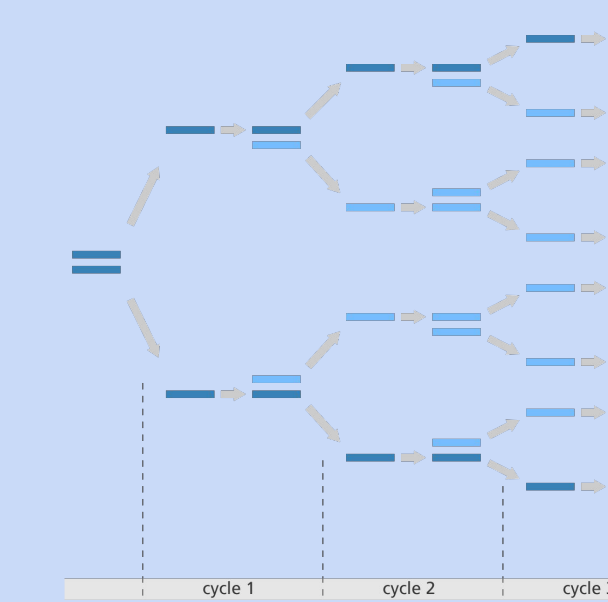
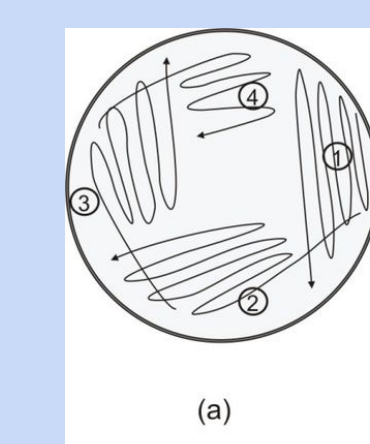
Previous studies have shown that various microorganisms make up diverse ecosystems on the human skin, which come together to make the skin microbiome. Our team identified several bacteria from our foreheads through the use of gene sequencing of the 16s rRNA gene along with various other techniques used for the analysis of bacterial colonies. From our culture, we identified the species *Staphylococcus Hominis* from the forehead of one team member and *Staphylococcus Epidermidis* on the foreheads of the other three, both are gram-positive and common inhabitants of the skin. By finding different bacteria common to the skin on different individuals, our results further fit with the narrative of past microbiome research.

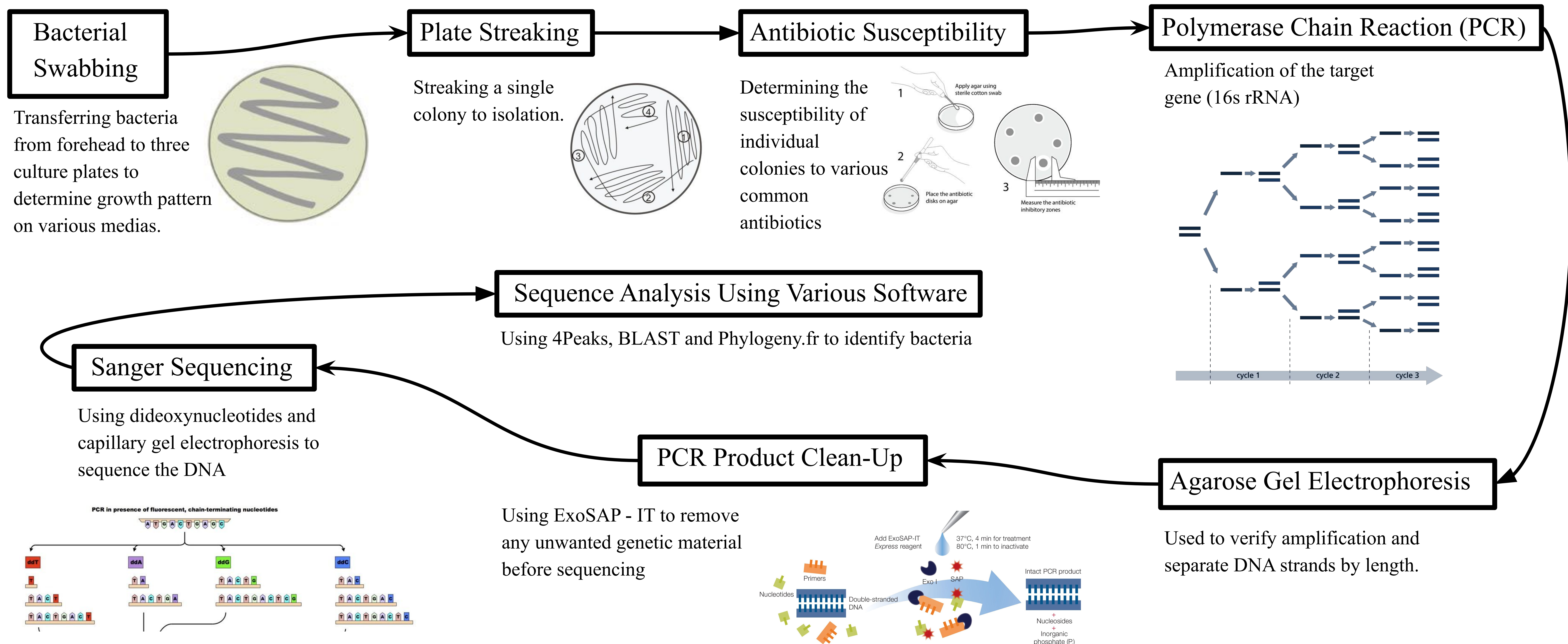
BACKGROUND

Over a six-week period, our group conducted research into the human skin microbiome, which is the collection of all bacterial ecosystems on the skin. This project was conducted to further the understanding of the human microbiome and explore the variability of the bacteria that can inhabit the glabellas of different hosts. Each team member swabbed their glabella (forehead) and, from there, our main objective was to culture, isolate and identify one bacterium from the glabella of each member. Our work consisted of multiple parts, including determining growth patterns, antibiotic susceptibility and using various techniques for the proper identification of each bacterium.

METHODS

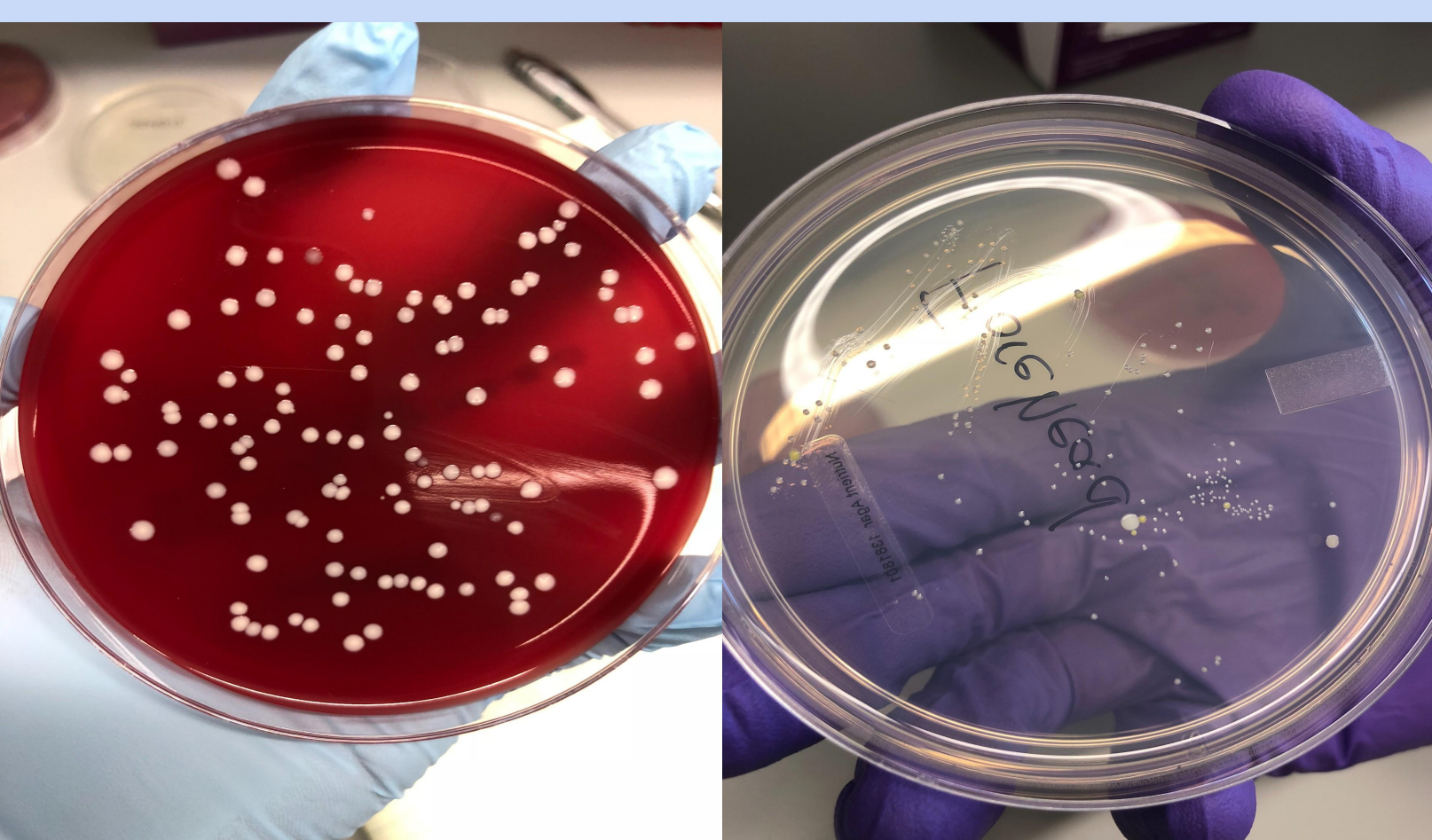
- **Bacterial Swabbing**
 - Transferring bacteria from forehead to three types of culture plates to determine growth pattern on various medias
- **Plate Streaking**
 - Streaking a single colony to isolation
- **Antibiotic Susceptibility**
 - Determining the susceptibility of individual colonies to various common antibiotics
- **Polymerase Chain Reaction (PCR)**
 - Amplifying the target gene (16s rRNA)
- **Agarose Gel Electrophoresis**
 - Verifying amplification and separate DNA strands by length
- **PCR Product Clean-Up**
 - Using ExoSAP - IT to remove any unwanted genetic material before sequencing
- **Sanger Sequencing**
 - Using dideoxynucleotides and capillary gel electrophoresis to sequence the DNA
- **Sequence Analysis Using Various Software**
 - Interpreting the 4-peaks chromatogram, then using BLAST and Phylogeny.fr to identify bacteria



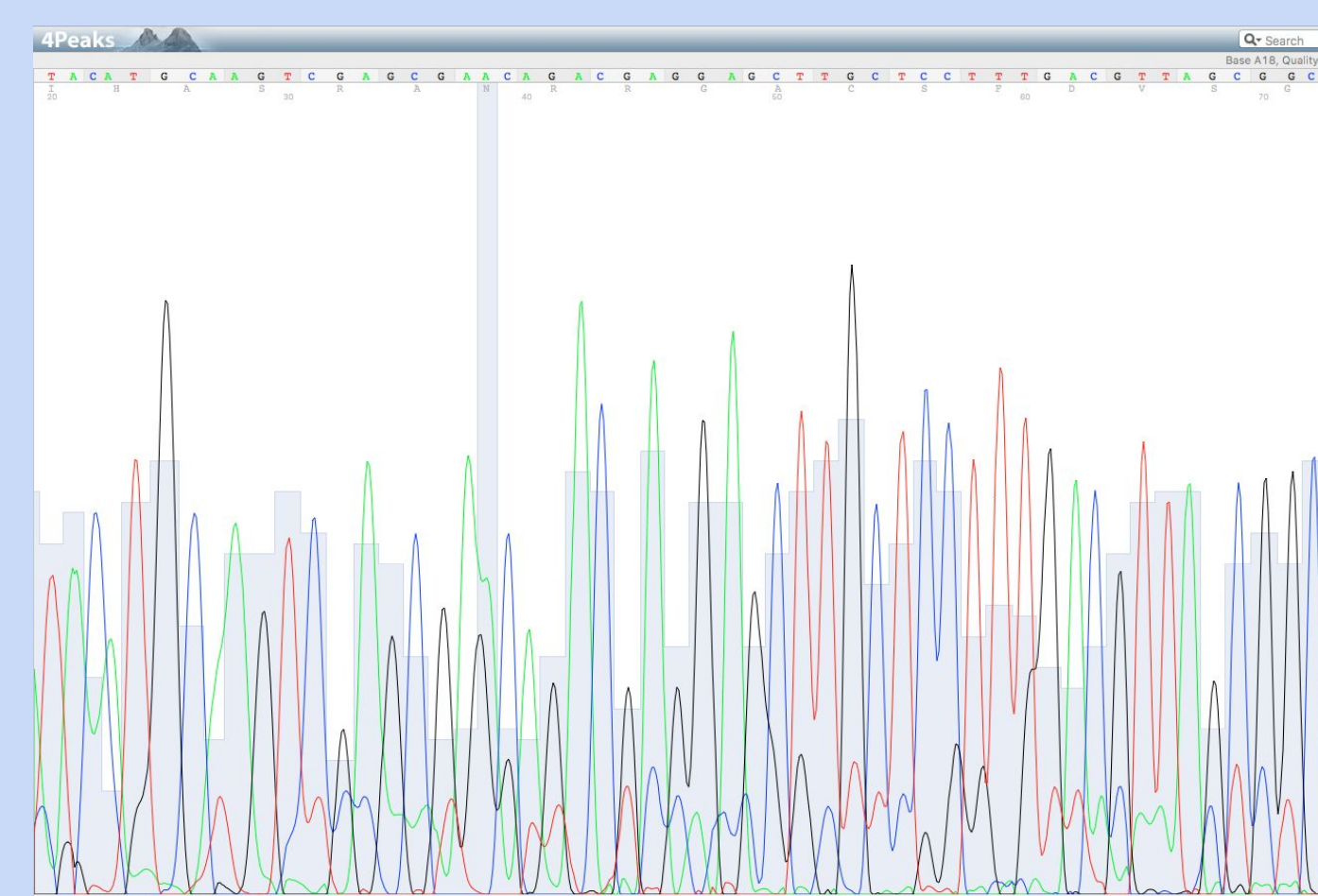


RESULTS

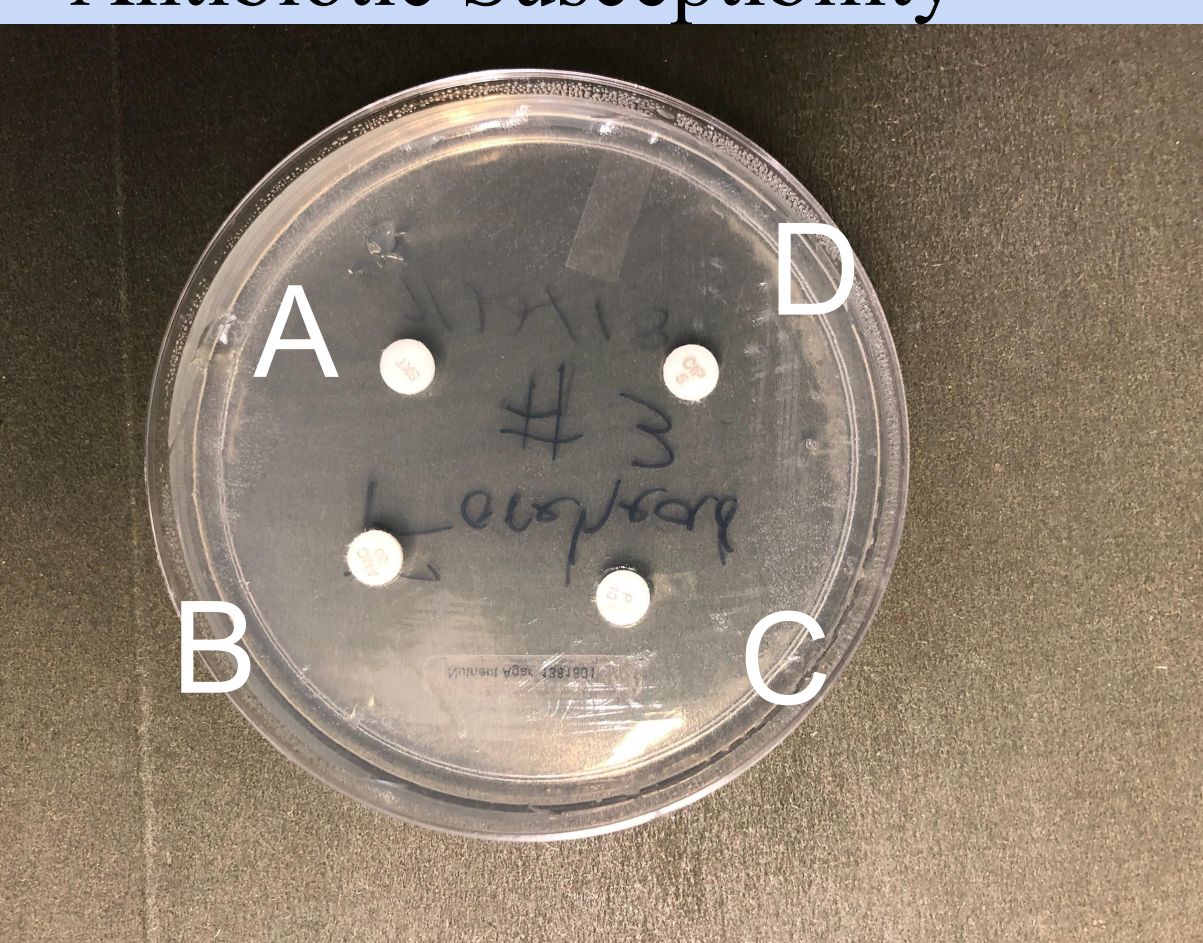
Bacterial Colonies on Sheep Blood Agar and Nutrient Agar Plates



4Peaks of Colony 4



Antibiotic Susceptibility



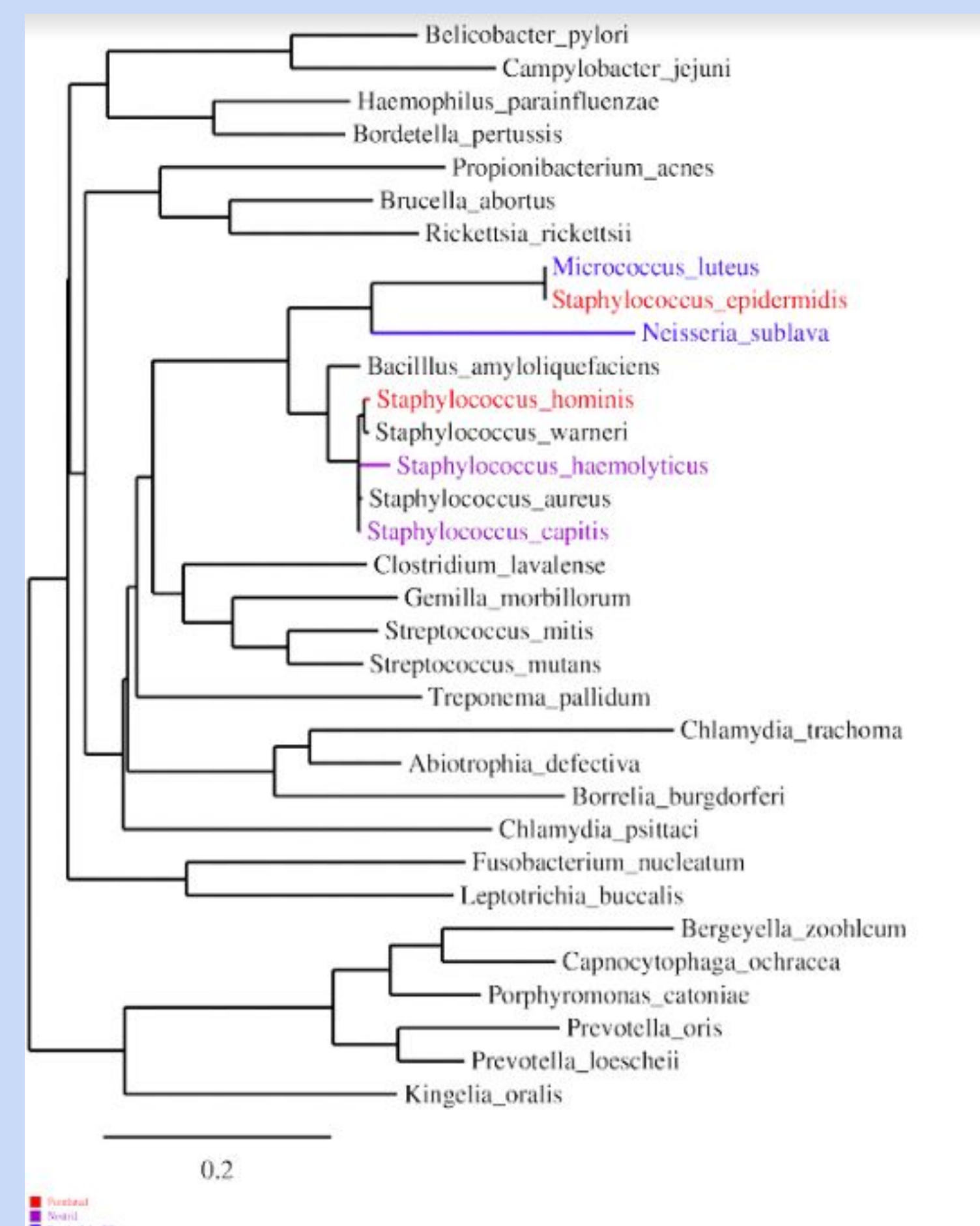
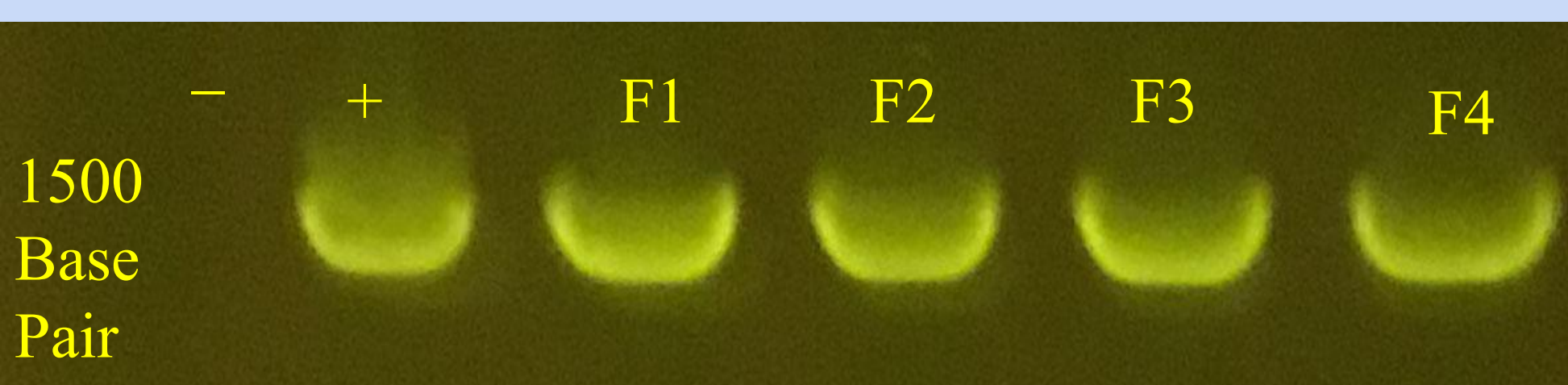
Phylogeny Tree

F1: *Staphylococcus epidermidis*
F2: *Staphylococcus epidermidis*
F3: *Staphylococcus epidermidis*
F4: *Staphylococcus hominis*

Antibiotics:

A - Ciprofloxacin
B - Sulfamethoxazole-trimethoprim
C - Amoxicillin
D - Penicillin

PCR/Gel Electrophoresis



CONCLUSIONS

Staphylococcus epidermidis is a gram-positive, coagulase-negative cocci common bacteria that is found in the human skin microbiome. It is not hemolytic, and it forms a cloudy white, circular, raised and with an entire margin colony. It is not usually pathogenic; however, it can produce nosocomial infections, especially in persons with a compromised immune system. Infections by this bacteria are of concern to people who have catheters or surgical implants because it forms biofilms that grows on these devices. *Staphylococcus hominis* is also a gram-positive, coagulase-negative bacteria that is commonly found on human and animal skin. It also contributes to our body odor since it is known for producing thioalcohol compounds. The colonies have the same shape and color as *Staphylococcus epidermidis*. It can also produce infections in people with a weak immune system. These two bacteria are closely related in our phylogenetic tree. In addition, they are both sensitive to desferrioxamine which treats iron toxicity. Their similarity is a great example on how individuals with different individual factors (age, diet, environment, etc.) can have the same bacteria. Nevertheless, this is not a full representation of the skin microbiome.

ACKNOWLEDGEMENTS

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REFERENCES

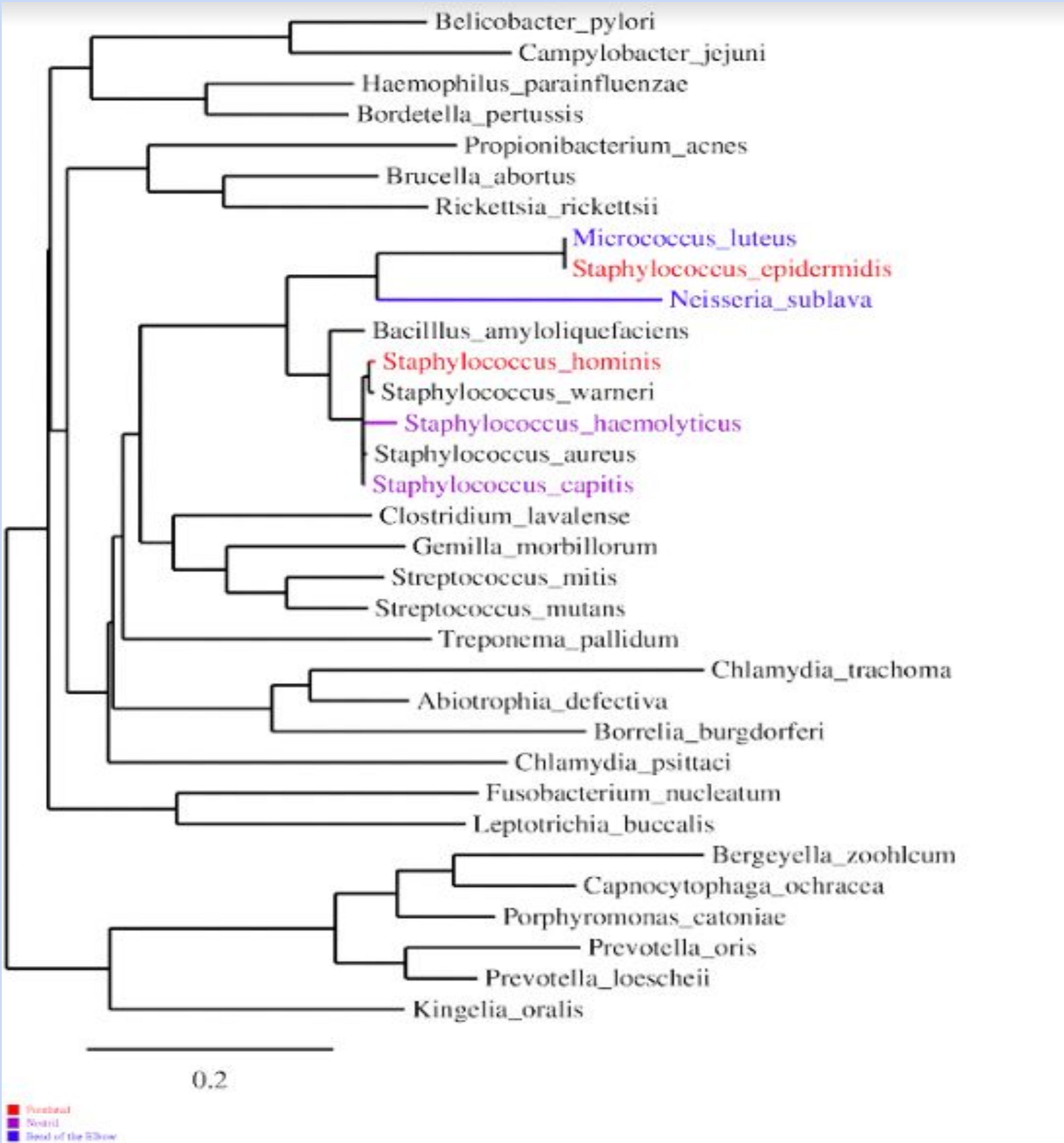
Otto, Michael. "*Staphylococcus Epidermidis* – the ‘accidental’ Pathogen." *Nature reviews. Microbiology* 7.8 (2009): 555–567. *PMC*. Web. 25 July 2018.

Identifying Bacteria Cultured from the Glabella using 16s rRNA gene



The Broad Team

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Red - Forehead
Purple - Nostril
Blue - Bend of Elbow