Remodeling of human oral flora upon close contact to oral flora of Canis lupus familiaris

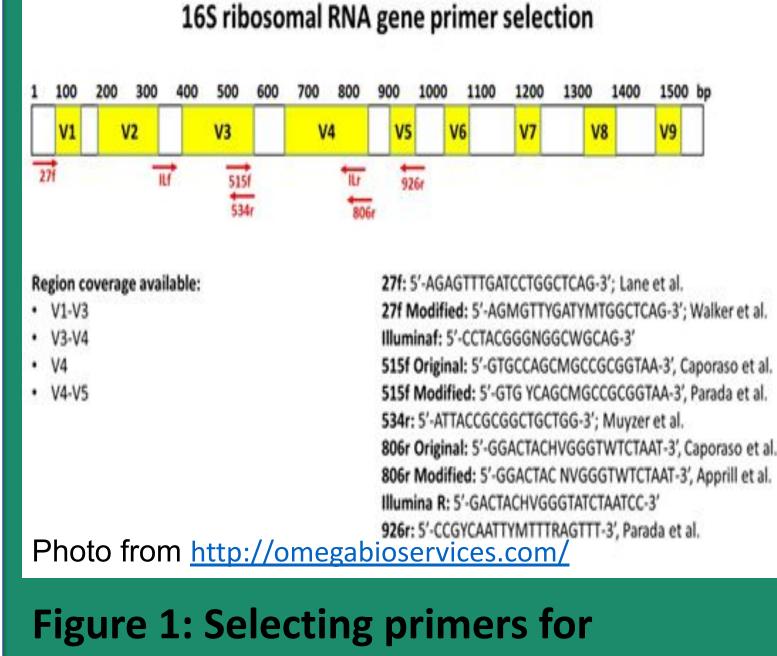


Evandy Murphy Mentored by Dr. Rita Pujari **Great Basin College, Biology Department**



Overview

It is possible that human oral flora is remodeled when exposed to oral flora from Canis lupus familiaris. Using RNA-seq of bacterial 16s rRNA, oral flora of pet owners will be sequenced in a before-and-after method. 27F and 518R primers will target the V1 and V3 sequences during PCR amplification. Data will be analyzed using 454 pyrosequencing.



Experimental design

- Collect oral sample from pet owners who exercise frequent oral contact with pets
- Collect oral sample from pet owners after one, three and five weeks without oral contact with pets
- Isolate samples, apply 27F and 518R primers for V1, V3 regions

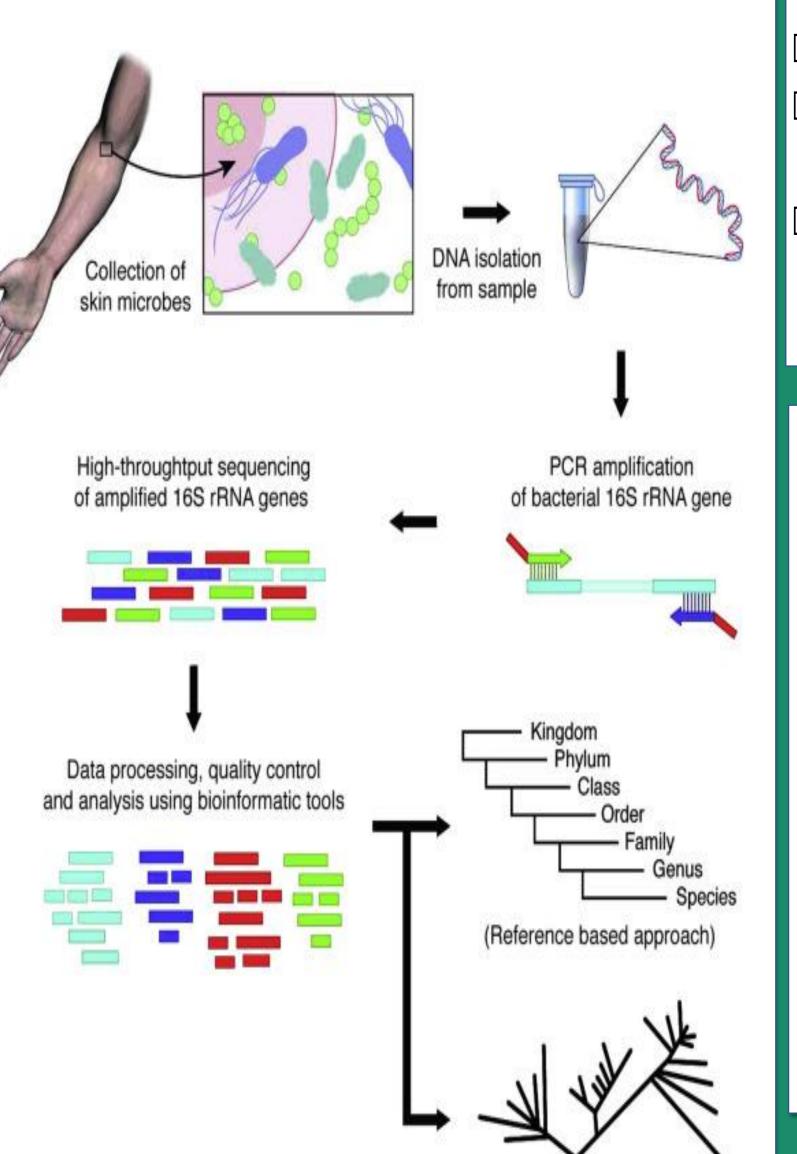
Introduction

Studies¹ show that small amounts of dissemination between pets and their owners may occur in households where oral contact is frequent. This study will compare flora of pet owners during normal oral contact and avoidance thereof. Results will determine if remodelling of human flora occurs.

Hypothesis

Oral flora of pet owners undergoes remodelling upon prolonged oral contact with

RNA-seq of 16s rRNA



- Amplify with PCR
- Sequence with 454
 - pyrosequencing
- Analyze data of OTU's in graph

Conclusion

To our knowledge, there are no current studies that analyze pet owners' flora in before-and-after method... Previous studies conclude symbiosis between the two floras is unlikely, however contact between the two floras may induce remodelling of human oral flora.

Canis lupus familiaris.

This material is based upon work supported by the National Aeronautics and Space Administration under Cooperative Agreement No. 80NSSC20M0043.

Grant No: 80NSSC20M0043

Figure 2: Collection, amplification and classification using RNA-seq.

(Diversity based approach)

Photo from https://www.sciencedirect.com

References 1.Oh, C., Lee, K., Cheong, Y., Lee, S.-W., Park, S.-Y., Song, C.-S., Choi, I.-S., & Lee, J.-B. (2015, July 2). Comparison of the oral microbiomes of canines and their owners using next-generation sequencing. PloS one. Retrieved April 10, 2022, from https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4489859/#pone.013146 8.ref010