Sequence analysis and phylogentic context of Firmicutes and Gammaprotobacteria

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# Background

I was given 40 sequences of 16S ranging from 5-1,310 bases long in ab1 format derived via Sanger sanquencing. The primary aims of this analysis were to assess sequence usability, quality, and length for the 16S sequences, and then place them in phylogenetic context. First I cleaned the sequences in Geneious Prime to remove incorrect or low quality calls from Sanger sequencing. The sequences were cleaned conservatively, especially for phylogentic inference, to ensure the integrity of the data. After cleaning the data, I sorted them into groups based on their quality for further analysis.

I found BLAST matches for the cleaned, acceptable sequences against NCBI’s GenBank database and developed phylogenetic trees through Maximum Likelihood and Bayesian approaches. The Maximum Likelihood approach finds the most probable tree by maximizing a likelihood function. In contrast, the Bayesian approach creates many trees and uses the previous results to make the new tree. I used two contrarian approaches to provide different insights on the sequences. In this case, both approaches built the same tree with similar confidence levels. This provides strong support for the phylogenetic inferences made from the 16S sequences. BLAST matches were found for 22 of the 40 sequences. All of the sequences I analyzed were likely to come from the domain Bacteria. I inferred a monophyletic clade of *Staphylococcus* sequences and possibly identified taxa of at least six sequences from the dataset with strong confidence. The six strongest inferences were *Firmicutes* and *Gammaprotobacteria*.

# Methods

First, I sorted each of the 40 sequences into two categories: useable and unusable. Unusable sequences had either very short (only 5 base pairs long) or did not have any long stretches of high to medium quality reads. I considered all other sequences to be useable. I investigated the unusable sequences to determine possible reasons for their Sanger sequencing failures. I carefully looked for repeating patterns, messy underlying contamination, or messy peaks. I trimmed and cleaned the useable sequences and further sorted into very good and acceptable. The very good sequences had long stretches of high quality reads, which show up light blue in Geneious Prime. I considered all other sequences to be acceptable. I aligned the 6 very good sequences and created two phylogenies with different methods. Both the very good and acceptable sequences were matched to the BLAST nucleotide database.

All data files are stored in the data folder of this project. The raw data files are contained in raw\_data and were not altered during this analysis. I placed the clean sequence .fasta files in sequence\_data, with three folders for the corresponding acceptable, unusable, and very good sequences. A thermus aquaticus 16S sequence is also in the sequence data folder. I used this sequence during the alignment and as an outgroup for both phylogenies. The multiple sequence alignment and the geneious files for PhyML and MrBayes alignments are contained in the alignments folder. In addition, I saved the sorted topologies and posterior output in the alignments folder. Both trees are saved as png images in the images folder.

## Sequence Cleaning

I used Geneious Prime (v 2019.2.1) (Kearse *et al.*, 2012) to trim, clean, and assess the quality of sequences. I trimmed both ends of the sequences to reduce low quality, common to the ends of Sanger sequences. I conducted the trimming conservatively to have higher confidence in downstream analyses. I trimmed bases if they contained any baseline contamination, low peaks, messy peaks, or if the peaks began to span multiple nucleotide positions with only one clear peak. The end of Sanger sequence data is typically messy, so I carefully analyzed the last 100-200 base pairs of each sequence. After trimming, I assessed the usability of the sequences, separating them into three groups: very good, acceptable, and unusable. Very good sequences had long stretches (more than 100 base pairs) of high quality reads. I inspected the entirety of the very good sequences to catch any internally miscalled bases and add the associated ambiguity codes. Acceptable sequences had mostly high quality reads without long stretches. Poor sequences had some high quality reads, but overall looked messy. I considered sequences unuseable when they were either very short (5 base pairs), or had multiple peaks throughout the sequence.

## Sequence Alignment

I used the MAFFT (Katoh *et al.*, 2002) multiple sequence aligner to align the trimmed, very good 16S sequences. I used the following settings for the MAFFT algorithm: scoring matrix of 200PAM / k=12, gap open penalty of 1.53, and offset value of 0.123. I aligned the six very good sequences with a 16S sequence from *Thermus aquaticus* with accension code NR\_025900.1 (Saul *et al.*, 1993). I trimmed the *Thermus aquaticus* sequence to match the size of the alignments of the other six sequences, or 872 base pairs long. Then, I ran the alignment a second time to tighten the alignment on these specific base pairs.

## Phylogeny

I used two approaches (Maximum Likelihood and Bayesian) to make phylogenetic inferences of the six very good sequences. Both approaches were ran through Geneious Prime after downloading the methods from the web. I compared the results of both phylogenies to each other to see if the contradictory methods gave different results.

### Maximum Likelihood

I created a Maximum Likelihood phylogeny using the PhyML algorithm (Guindon *et al.*, 2009). This analysis was ran with General Time Reversible (GTR) substitution model, 100 bootstraps, Gamma and Invariants model, four substitution rate categories, and optimized for topology/length/rate. I used the 16S sequence from *Thermus aquaticus* as an outgroup. This outgroup was rooted through Geneious Prime. I considered a bootstrap value above, or equal to, 80 to be strong.

### Bayesian

I built a Bayesian phylogeny using the MrBayes 3.6.2 algorithm (Huelsenbeck and Ronquist, 2001). This analysis was ran with General Time Reversible (GTR) model, invgamma rate variation, chain length of 1,100,000, 4 heated chains, heated chain temperature of 0.2, subsampling frequency of 200, burn-in length of 100,000, random seed of 23,107, and unconstrained branch lengths with GammaDir(1, 0.1, 1, 1). I used the 16S sequence from *Thermus aquaticus* as an outgroup. This outgroup was rooted through Geneious Prime. I considered a probability above 95 to be strong.

## BLAST

All sequences rated very good, average, or poor were used to search for BLAST matches in NCBI’s GenBank database (Benson *et al.*, 2000). More specifically, I searched the (nr/nt) database in GenBank. All BLAST searches were done using the highly similar sequences (megablast) algorithm. All matches were selected by choosing which species was most represented at the top of the results list. Results from the initial list, sorted by query cover, graphical representation, and taxonomy were all considered. If I found a couple of good matches for the sequences the more general, higher, taxa was chosen.

# Results

## Sequences and Alignments

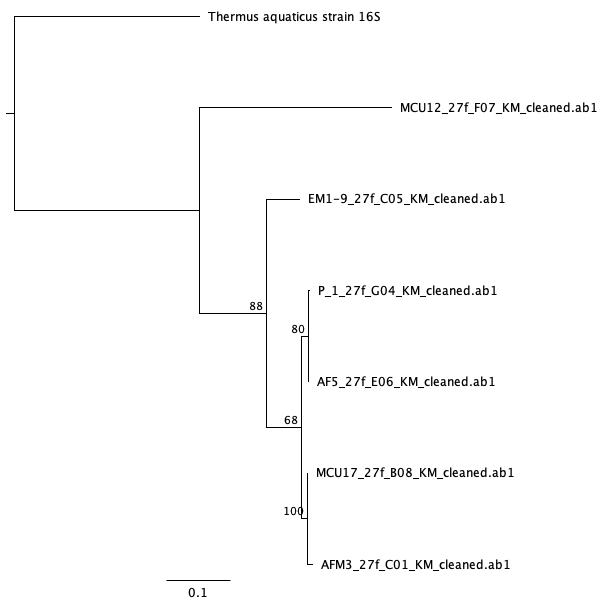
Of the 40 sequences provided 22 were useable with 16 acceptable for BLAST analysis and 6 good enough to place into a phylogeny. The longest sequence was 907 base pairs after trimming while the shortest was 147. The average sequence length was 500 base pairs. Eleven sequence were above 500 base pairs while eleven sequence were below 500 base pairs. Of the 6 sequences used for sequence alignment the longest sequence was 797 while the smallest was 404 base pairs. Seven sequences were total fails producing only 5 N’s after Sanger sequencing. Another 11 had messy sequences throughout with frequent unidentifiable bases scattered throughout the middle of the sequence. All of the 40 sequences were located in 16S. I edited, or added ambiguity codes, to 8 sequences. Of these only two had more than one edit, while the largest number of edits I made to a single sequence was 5. Table 1 below summarizes the sequence files including original filename, corrected filename, usability, length after trimming, and the number of corrected bases after trimming.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Locus | Original Filename | Corrected Filename | Usability | Length after Trimming | Number of Corrected Bases |
| 16S | AFM3\_27f\_C01.ab1 | AFM3\_27f\_C01\_KM\_cleaned.ab1 | useable | 613 | 3 |
| 16S | P\_1\_27f\_G04.ab1 | P\_1\_27f\_G04\_KM\_cleaned.ab1 | useable | 797 | 0 |
| 16S | MCU17\_27f\_B08.ab1 | MCU17\_27f\_B08\_KM\_cleaned.ab1 | useable | 653 | 1 |
| 16S | AF5\_27f\_E06.ab1 | AF5\_27f\_E06\_KM\_cleaned.ab1 | useable | 404 | 1 |
| 16S | EM1-9\_27F\_C05.ab1 | EM1-9\_27f\_C05\_KM\_cleaned.ab1 | useable | 608 | 5 |
| 16S | MCU12\_27f\_F07.ab1 | MCU12\_27f\_F07\_KM\_cleaned.ab1 | useable | 695 | 0 |
| 16S | PC4A\_27f\_C10.ab1 | PC4A\_27f\_C10\_KM\_trimmed.ab1 | useable | 562 | 1 |
| 16S | PC3A\_27f\_A10.ab1 | PC3A\_27f\_A10\_KM\_trimmed.ab1 | useable | 241 | 0 |
| 16S | CVC1B\_27f\_B03.ab1 | CVC1B\_27f\_B03\_KM\_trimmed.ab1 | useable | 461 | 0 |
| 16S | SB3\_27f\_C06.ab1 | SB3\_27f\_C06\_KM\_trimmed.ab1 | useable | 147 | 0 |
| 16S | P3\_27f\_C08.ab1 | P3\_27f\_C08\_KM\_trimmed.ab1 | useable | 467 | 1 |
| 16S | CVC7A\_27f\_E02.ab1 | CVC7A\_27f\_E02\_KM\_trimmed.ab1 | useable | 621 | 1 |
| 16S | CSB3B\_27f\_F10.ab1 | CSB3B\_27f\_F10\_KM\_trimmed.ab1 | useable | 239 | 0 |
| 16S | CLS6\_27f\_F04.ab1 | CLS6\_27f\_F04\_KM\_trimmed.ab1 | useable | 516 | 0 |
| 16S | FL2A\_27f\_A09.ab1 | FL2A\_27f\_A09\_KM\_trimmed.ab1 | useable | 383 | 0 |
| 16S | Cntrl\_2\_27f\_D05.ab1 | Cntrl\_2\_27f\_D05\_KM\_trimmed.ab1 | useable | 410 | 0 |
| 16S | I5\_27f\_D10.ab1 | I5\_27f\_D10\_KM\_trimmed.ab1 | useable | 268 | 0 |
| 16S | 16A\_C\_27f\_F03.ab1 | 16A\_C\_27f\_F03\_KM\_trimmed.ab1 | useable | 672 | 0 |
| 16S | M3\_2\_27f\_B01.ab1 | M3\_2\_27f\_B01\_KM\_trimmed.ab1 | useable | 258 | 0 |
| 16S | 3A-B\_27f\_B04.ab1 | 3A-B\_27f\_B04\_KM\_trimmed.ab1 | useable | 836 | 1 |
| 16S | CLS2\_27f\_B04.ab1 | CLS2\_27f\_B04\_KM\_trimmed.ab1 | useable | 246 | 0 |
| 16S | PC1B\_27f\_A06.ab1 | PC1B\_27f\_A06\_KM\_trimmed.ab1 | useable | 907 | 0 |
| 16S | CLS1\_27f\_E04.ab1 | CLS1\_27f\_E04\_KM\_unusable.ab1 | unusable | 271 | 0 |
| 16S | UE3B\_27f\_G09.ab1 | UE3B\_27f\_G09\_KM\_unusable.ab1 | unusable | 685 | 0 |
| 16S | EN\_27f\_F02.ab1 | EN\_27f\_F02\_KM\_unusable.ab1 | unusable | 492 | 0 |
| 16S | I6\_27f\_C10.ab1 | I6\_27f\_C10\_KM\_unusable.ab1 | unusable | 746 | 0 |
| 16S | CSB3A\_27f\_E10.ab1 | CSB3A\_27f\_E10\_KM\_unusable.ab1 | unusable | 733 | 0 |
| 16S | M2\_2\_27f\_D01.ab1 | M2\_2\_27f\_D01\_KM\_unusable.ab1 | unusable | 269 | 0 |
| 16S | EVM3\_27f\_C08.ab1 | EVM3\_27f\_C08\_KM\_unusable.ab1 | unusable | 455 | 0 |
| 16S | D6\_27f\_B09.ab1 | D6\_27f\_B09\_KM\_unusable.ab1 | unusable | 317 | 0 |
| 16S | D3\_27f\_G08.ab1 | D3\_27f\_G08\_KM\_unusable.ab1 | unusable | 608 | 0 |
| 16S | CVCWA\_27f\_A02.ab1 | CVCWA\_27f\_A02\_KM\_unusable.ab1 | unusable | 386 | 0 |
| 16S | b1b\_27f\_B02.ab1 | b1b\_27f\_B02\_KM\_unusable.ab1 | unusable | 267 | 0 |
| 16S | IF3\_27f\_E07.ab1 | IF3\_27f\_E07\_KM\_unusable.ab1 | unusable | 5 | 0 |
| 16S | EVN\_27f\_A02.ab1 | EVN\_27f\_A02\_KM\_unusable.ab1 | unusable | 5 | 0 |
| 16S | EVM2\_27f\_G01.ab1 | EVM2\_27f\_G01\_KM\_unusable.ab1 | unusable | 5 | 0 |
| 16S | E1\_27f\_B02.ab1 | E1\_27f\_B02\_KM\_unusable.ab1 | unusable | 5 | 0 |
| 16S | D1\_27f\_E08.ab1 | D1\_27f\_E08\_KM\_unusable.ab1 | unusable | 5 | 0 |
| 16S | CLS5\_27f\_A05.ab1 | CLS5\_27f\_A05\_KM\_unusable.ab1 | unusable | 5 | 0 |
| 16S | APP1\_27f\_G09.ab1 | APP1\_27f\_G09\_KM\_unusable.ab1 | unusable | 5 | 0 |

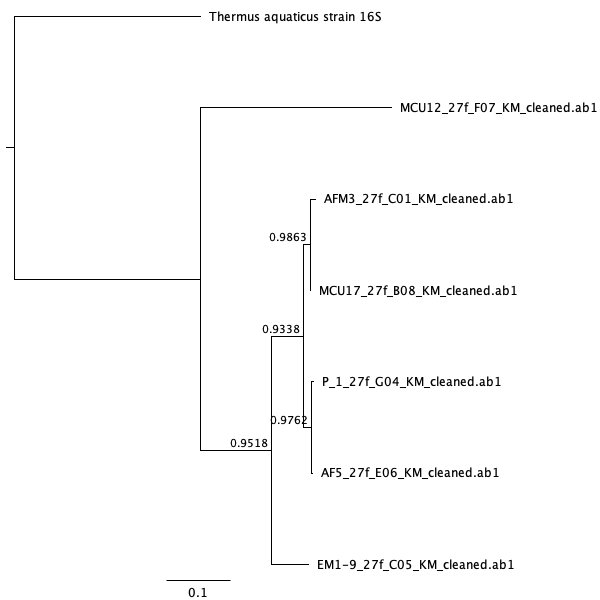
**Table 1.** Short description of each sequence including locus (16S), original filename, filename after edits, usability, sequence length after trimming, and the number of modified bases after cleaning.

## Phylogenies

I found that P\_1\_27f\_G04, AF5\_27f\_E06, AFM3\_27f\_C01, MCU17\_27f\_B08, and EM1-9\_27f\_C05 grouped together in a monophyletic clade (Figure 1; ML bootstrap > 80, Figure 2; Bayesian posterior probability > 95 ). Of this I inferred P\_1\_27f\_G04 and AF5\_27f\_E06 group together (Figure 1; ML bootstrap = 80, Bayesian posterior probaility > 95); and AFM3\_27f\_C01 grouped with MCU17\_27f\_B08 with strong confidence (Figure 1; ML bootstrap > 80, Bayesian posterior probaility > 95). I found a closer relationship between AFM3\_27f\_C01, MCU17\_27f\_G04, P\_1\_27f\_G04 and AF5\_27f\_E06 to EM1-9\_27f\_C05 than MCU12\_27f\_F07 (Figure 1; ML bootstrap > 80, Bayesian posterior probaility > 95). The length of the tips for P\_1\_27f\_G04 and AF5\_27f\_E06 show extremely high similarity between these two sequences. Both maximum likelihood and bayesian phylogenies supported the same groupings for the seven sequences used. Both trees can be seen below in figures 1 and 2.



**Figure 1.** Maximum Likelihood phylogeny of very good sequences using the PhyML algorithm (Guindon *et al.*, 2009). *Thermus aquaticus* was set as an outgroup.



**Figure 2.** Bayesian phylogeny of very good sequences using the MrBayes algorithm (Huelsenbeck and Ronquist, 2001). *Thermus aquaticus* was set as an outgroup.

## BLAST Results

I matched the 22 very good and acceptable sequences to the BLAST database. I found strong matches for 16 of the samples with 5 samples from the genus *Staphylococcus*, three from the genus *Neisseria perflava*, and two *E. coli*. All matches to these samples were bacterial with 7 *Firmicutes* and 6 *Proteobacteria*. Only one sample, 3A-B\_27f\_B04, had a query cover below 90%. Sixteen sequences had a quary cover of 100%. Every percent identity was above 80% with 6 sequences with 100% identify and 11 sequences over 95% identity. This analysis can be seen below in Table 2.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sequence | Description | Percent Identity (%) | Query Cover (%) | Accession | E-value |
| AFM3\_27f\_C01 | *Staphylococcus capitis* partial | 99.51 | 100 | LT978442.1 | 0.0 |
| P\_1\_27f\_G04 | *Staphylococcus hominis strain* WS1-7 | 100.00 | 100 | MN448417.1 | 0.0 |
| MCU17\_27f\_B08 | *Staphylococcus epidermidis* strain 15 | 99.85 | 100 | MK465356.1 | 0.0 |
| AF5\_27f\_E06 | *Staphylococcus hominis* strain WS3-1 | 99.75 | 100 | MN448433.1 | 0.0 |
| EM1-9\_27f\_C05 | *Bacillus licheniformis* strain XIXJ053 | 99.18 | 100 | MH801084.1 | 0.0 |
| MCU12\_27f\_F07 | *Brevundimonas vesicularis* strain A33 | 100.00 | 100 | MN252083.1 | 0.0 |
| PC4A\_27f\_C10 | *Neisseria perflava* strain 17-P17 | 99.82 | 100 | MF374824.1 | 0.0 |
| PC3A\_27f\_A10 | *Neisseria perflava* strain 17-P17 | 99.59 | 100 | MF374824.1 | 1e-119 |
| CVC1B\_27f\_B03 | *Pantoea sp.* strain ST18.17/028 | 100.00 | 100 | MK875130.1 | 0.0 |
| SB3\_27f\_C06 | *Staphylococcus epidermidis* strain IBK-11 | 100.00 | 100 | MN428237.1 | 3e-69 |
| P3\_27f\_C08 | *Bacillus licheniformis* strain Xuyi\_293\_3 | 98.93 | 100 | MN309987.1 | 0.0 |
| CVC7A\_27f\_B03 | *Enterobacteriaceae bacterium* X6/SB50 | 98.87 | 100 | LC007901.1 | 0.0 |
| CSB3B\_27f\_F10 | *Klebsiella granulomatis* strain 2-7-8 | 100.00 | 99 | JF91986.1 | 4e-119 |
| CLS6\_27f\_F04 | Uncultured bacterium partial | 100.00 | 91 | FM162220.1 | 5e-17 |
| FL2A\_27f\_A09 | *Steptococcus salivarius* strain JF | 98.96 | 100 | CP014144.1 | 0.0 |
| Cntrl\_2\_27f\_D05 | *Escherichia coli* stain NCTC9040 | 97.80 | 100 | LR134247.1 | 0.00 |
| I5\_27f\_D10 | *Pseudomonas sp.* strain 273 | 94.12 | 100 | MK681820.1 | 3e-111 |
| 16A\_C\_27f\_F03 | *Escherichia coli* strain SJA92 | 92.12 | 100 | MN147836.1 | 0.0 |
| M3\_2\_27f\_B01 | *Bacillus licheniformis* strain FMB2-2 | 96.86 | 98 | KP992871.1 | 1e-115 |
| 3A-B\_27f\_B04 | *Pseudomonas sp.* m8 | 83.46 | 33 | DQ219815.1 | 6e-58 |
| CLS2\_27f\_B04 | Uncultured *Paenibacillus sp.* clone R7SP1T1H06 | 94.63 | 98 | HQ018234.1 | 2e-103 |
| PC1B\_27f\_A06 | *Neisseria sp.* strain CMUL044 | 85.55 | 96 | MK258031.1 | 4e-168 |
| CLS1\_27f\_E04 | Sequencing Failed |  |  |  |  |
| UE3B\_27f\_G09 | Sequencing Failed |  |  |  |  |
| EN\_27f\_F02 | Sequencing Failed |  |  |  |  |
| I6\_27f\_C10 | Sequencing Failed |  |  |  |  |
| CSB3A\_27f\_E10 | Sequencing Failed |  |  |  |  |
| M2\_2\_27f\_D01 | Sequencing Failed |  |  |  |  |
| EVM3\_27f\_C08 | Sequencing Failed |  |  |  |  |
| D6\_27f\_B09 | Sequencing Failed |  |  |  |  |
| D3\_27f\_G08 | Sequencing Failed |  |  |  |  |
| CVCWA\_27f\_A02 | Sequencing Failed |  |  |  |  |
| b1b\_27f\_B02 | Sequencing Failed |  |  |  |  |
| IF3\_27f\_E07 | Sequencing Failed |  |  |  |  |
| EVN\_27f\_A02 | Sequencing Failed |  |  |  |  |
| EVM2\_27f\_G01 | Sequencing Failed |  |  |  |  |

**Table 2.** BLAST results for each sequence including a description of the match, percent identitiy, query cover, accession number, and e-value.

# Discussion

## Overview of Findings

Of the 40 sequences I was given, 18 were unusable, 16 were acceptable, and 6 were very good high quality reads. The unusable sequences resulted from a variety of reasons including: insufficient template, template contamination, and camera blockage. All 22 of the acceptable and high quality reads had BLAST matches with the GenBank database. All samples were bacterial with 7 *Firmicutes*, 6 *Proteobacteria*, and 5 *Staphylococcus*. Most of the BLAST matches had very high query covers and percent identities. A few of the BLAST matches had very few matches in the Genbank database, suggesting more information needs to be gathered about the sample to infer identity. Both the Maximum Likelihood and Bayesian approach produced the same phylogeny, providing strong evidence the correct relationships were identified for the 6 very strong sequences of at least 400 base pairs long. In addition, the sequences with BLAST matches to *Staphylococcus* species grouped together in a monophyletic clade. Further analysis with additional *Staphylococcus* species are suggested to further support the inferences made in this analysis.

## Unuseable Sequences

There are a few possible reasons for the unuseable sequences in this group of 40 sequences. The 5 sequences in table 1 with only 5 base pairs did not have one element necessary for Sanger sequencing. The most likely cause is insufficient template. The sequences from b1b\_27f\_B02, UE3B\_27f\_G09, D6\_27f\_B09, and D6\_27f\_B09 had multiple peaks throughout suggesting there was template contamination in the sample. CVCWA\_27f\_A02 had messy and low peaks which might be due to poor quality template. D3\_27f\_G08, CLS1\_27f\_E04, UE3B\_27f\_G09, and M2\_2\_27f\_D01 had sharp high-intensity spikes mixed throughout the sequence. One possible cause for this is a blockage of the camera used to sequence the sample, causing light to scatter. EVM3\_27f\_C08 had messy peaks which spanned multiple nucleotides suggesting poor template. I6\_27f\_C10 and EN\_27f\_F02\_KM had a repeated pattern every 20-30 base pairs suggesting the sample was ran through PCR without template. A few of the samples had small stretches with the same base pair called repetitively, indicating potentional dye blobbing. Further sampling of the sequences is necessary to make any inference on their identities and place them in phylogenetic context. Especially for the samples which may have failed due to light scattering because a well maintained machine may achieve cleaner sequences.

## BLAST

AFM3\_27f\_C01 is likely to be in the genus *Staphylococcus*, however the specific species could not be identified with high confidence. The top hit on BLAST was *Staphylococcus capitis*, while *Staphylococcus epidermidis* was also highly prevalent. PC4A\_27f\_C10 is likely to be in the genus *Neisseria*, but the species could not be identified with high confidence. The species *perflava*, *flavescens*, and *subflava* were all highly rated matches on BLAST. CVC1B\_27f\_B03 is likely a gram-negative bacterium and could either be in the genus *Pantoea* or the class Gammaproteobacteria. CSB3B\_27f\_F10 is likely to be in the family Enterobacteriaceae, falling under the *Klebsiella* or *Raoultella* genus. CLS6\_27f\_F04 and CLS2\_27f\_B04 both had relatively few matches (only 8) in the GenBank database. 3A-B\_27f\_B04 was highly likely to be a *Pseudomonas sp.*. All other analyzed sequences were matched with strong confidence. The BLAST matches require additional evidence because the BLAST database is not curated to ensure accuracy. Further sequencing and phylogentic inferences should be used to strengthen the identifications of all of the BLAST matches.

## Phylogenetic Context

Based on phylogenetic and BLAST results I inferred the identity of the top six sequences with strong confidence. AFM3\_27f\_C01, MCU17\_27f\_G04, P\_1\_27f\_G04 and AF5\_27f\_E06 were grouped together in a monophyletic clade in both trees. BLAST analysis matched all of these sequences with different species of *Staphylococcus*. In total, this provides strong evidence to suggest these are closely related species of *Staphylococcus*. In addition, P\_1\_27f\_G04 and AF5\_27f\_E06 were grouped together in both phylogenies and BLAST results matched two different strains of *Staphylococcus hominis*. AFM3\_27f\_C01 and MCU17\_27f\_B08 also grouped together in both phylogenies with BLAST results matching *S. capitis* and *S. epidermidis* respectively. These matching results indicate two species *Staphylococcus* which are more related to each other than *Staphylococcus hominis*. Additional analyses with *Staphylococcus* species would be useful to place these sequences in further phylogenetic context and confirm their identity. A larger phylogeny with more *Staphylococcus* species would provide more comparisons for these sequences, showing how closely related they are. In addition, sequencing other genes in these organisms could help solidify their identities since 16S sequences are highly conserved across different species. If possible observing the samples sequenced under a microscope would be useful. This would allow a comparison of the physical attributes associated to each species, giving an additional comparison point for the species identification.

Since the tips for P\_1\_27f\_G04 and AF5\_27f\_E06 are both very small, there is a chance they are the same sequence. They were both matched with *Staphylococcus hominis* further analysis should be done with these two sequences, including sequence alignment. If possible sequencing on another gene with these two samples would be very helpful.

The other two sequences added to the phylogenies are more distantly related with BLAST matches outside of *Staphylococcus*. It is likely the *Brevundimonas* genus is a more recent common ancestor to *Staphylococcus* than the *Bacillus* genus. In fact, previous work shows *Staphylococcus* and *Bacillus* are both *Firmicutes* while *Brevundimonas* is a *Gammaproteobacteria* (Costa *et al.*, 2012). However, additional phylogenies should be built with more *Bacillus* and *Gammaproteobacteria* to confirm this relationship. In addition, future work should be done to resolve a larger phylogeny with the other bacterial sequences in the larger dataset these 40 sequences were pulled from, especially with other *Firmicutes*. Physical observation of these species should note the presence of a gram-positive cell wall. This is a common attribute of *Firmicutes* and could further substantiate the relationship of these samples. An additional tree with *proteobacteria* would also be very informative for the other samples in this dataset. Overall, I likely identified four *Staphylococcus sp* from this dataset and may have determined the identity of a *Brevundimonas* and *Bacillus* species. In addition, this data supported the claims of previous research on the placement of *Staphylococcus* and *Bacillus* in the *Firmicute* phylum.

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