



Genomic Evolutionary Comparison of Biofilm Forming *Streptomyces* species Living in Different Geological Habitats



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Research Goals

- To determine the evolutionary similarity of *Streptomyces* that live in different geological habitats around the world.
- To compare the conservation of specific genes that are responsible for biofilm formation to the whole genome of that species.

Background Information

- Streptomyces* are Gram-positive, aerobic, filamentous, spore and biofilm forming bacteria within the class of Actinobacteria.¹
- In bacteria, chemical communication involves producing, releasing, detecting, and responding to small signal molecules which are termed autoinducers.²
- The information supplied by these molecules is critical for synchronizing and organizing the activity of a large group of cells.³
- Examples of bacterial communication include bioluminescence and biofilm formation.
- Acetate Na⁺-dependent symporter proteins are necessary for biofilm formation.⁴
- Volatiles are small air-transmittable chemicals with diverse biological functions.
- A specific volatile, acetic acid, plays a central role in the formation of biofilms.⁵



Figure 1. 3D-Structure of the targeted Acetate Na⁺-dependent symporter protein.⁶

Methodology

- Conduct literature research on different *Streptomyces* species and determine their environmental habitats.
- Determine specific genes and proteins that are integral in the formation of bacterial biofilms.
- Isolate one specific gene and protein in each *Streptomyces* species that is responsible for biofilm formation.
- Compare the nucleotide sequence of the *Streptomyces* species whole genome to each other.
- Compare the nucleotide sequence for the biofilm formation gene with each other and the amino acid sequence for the biofilm formation protein to each other.
- Use bioinformatic tools and software such as NCBI Blast, DIVERGE 3.0, and MEGA11 for analysis.

Results

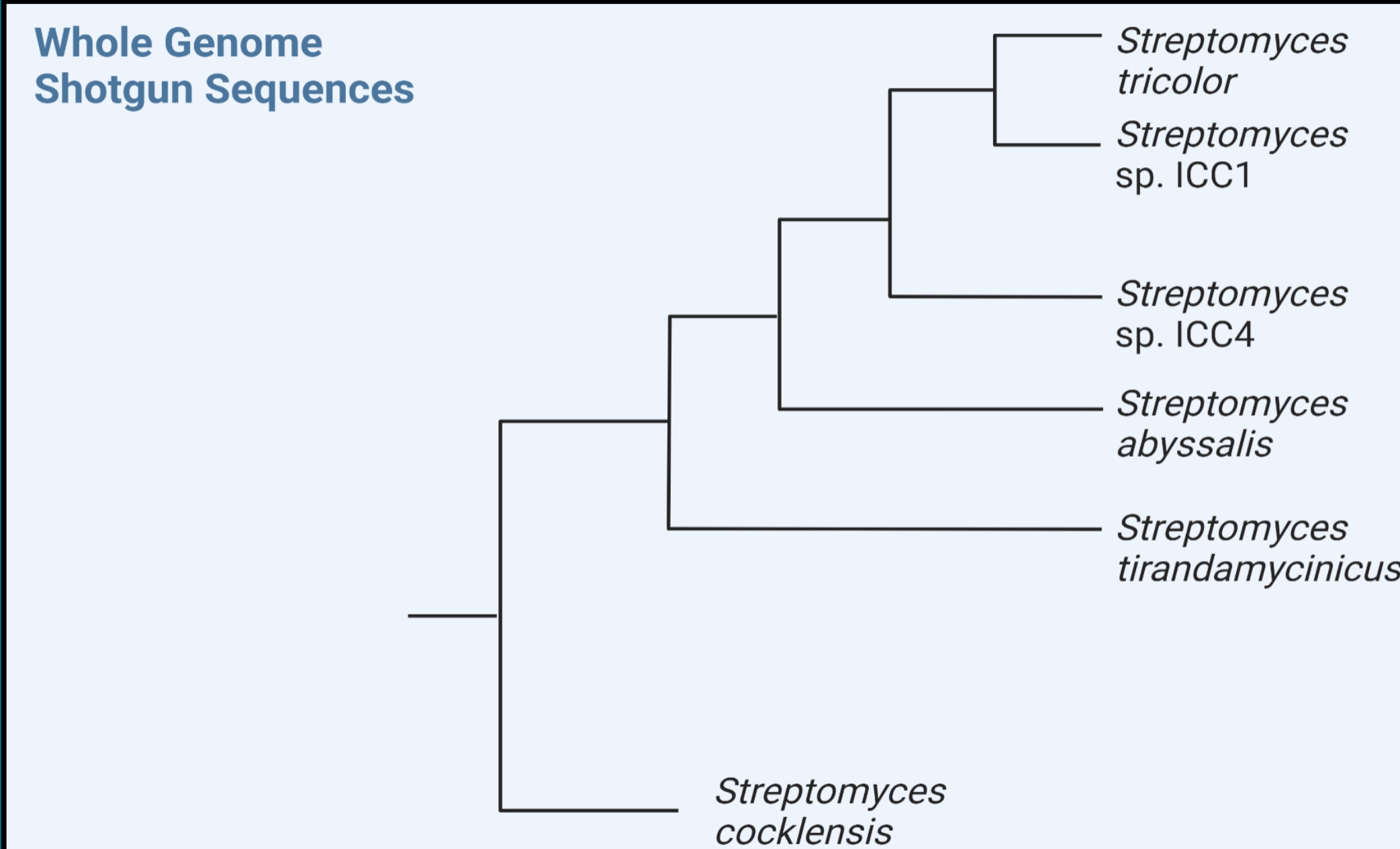


Figure 2. Phylogenetic tree showing full genome similarity of *Streptomyces* species.

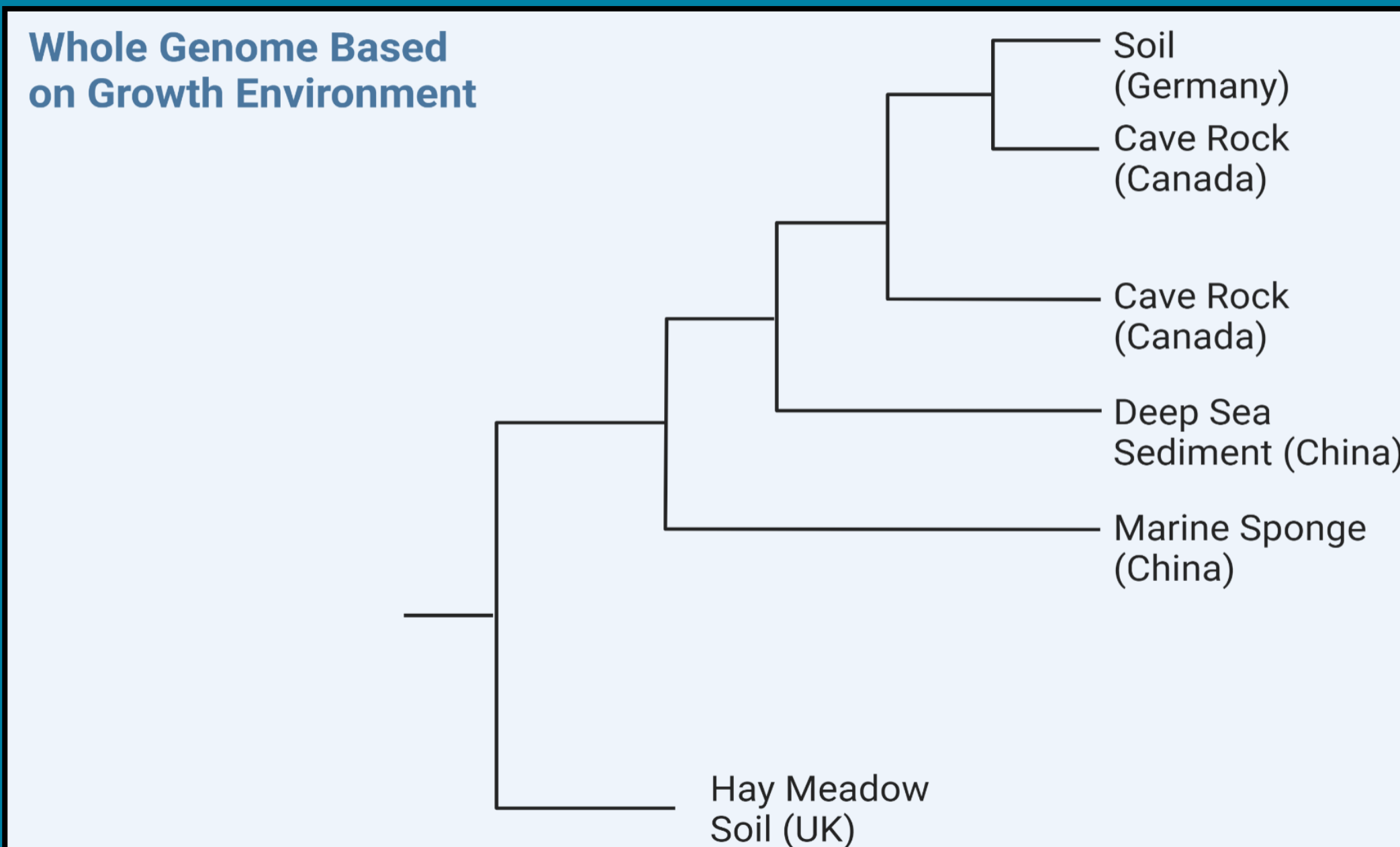


Figure 3. Phylogenetic tree of the species of Figure 2 showing geological habitats of each species

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
acetate Na ⁺ -dependent symporter subunit involved in volatile signal for biofilm formation [Streptomyces cocklensis]	<i>Streptomyces cocklensis</i>	1073	1073	100%	0.0	100.00%	554	CAG6392864.1
cation acetate symporter [Streptomyces cocklensis]	<i>Streptomyces cocklensis</i>	1062	1062	99%	0.0	100.00%	549	WP_251488157.1
cation acetate symporter [Streptomyces tricolor]	<i>Streptomyces tricolor</i>	760	760	96%	0.0	78.81%	530	WP_086700524.1
cation acetate symporter [Streptomyces abyssalis]	<i>Streptomyces abyssalis</i>	660	660	97%	0.0	74.77%	528	WP_070010570.1
cation acetate symporter [Streptomyces sp. ICC4]	<i>Streptomyces sp. ICC4</i>	629	629	96%	0.0	64.37%	546	AWZ10414.1
cation acetate symporter [Streptomyces tirandamycinicus]	<i>Streptomyces tirandamycinicus</i>	321	321	93%	3e-103	40.08%	539	WP_108907898.1
cation acetate symporter [Streptomyces sp. ICC1]	<i>Streptomyces sp. ICC1</i>	147	147	86%	9e-38	30.98%	603	WP_112450370.1

Figure 4. Sample blast search result comparing the variable region of the targeted protein in *Streptomyces cocklensis* to other *Streptomyces* species.

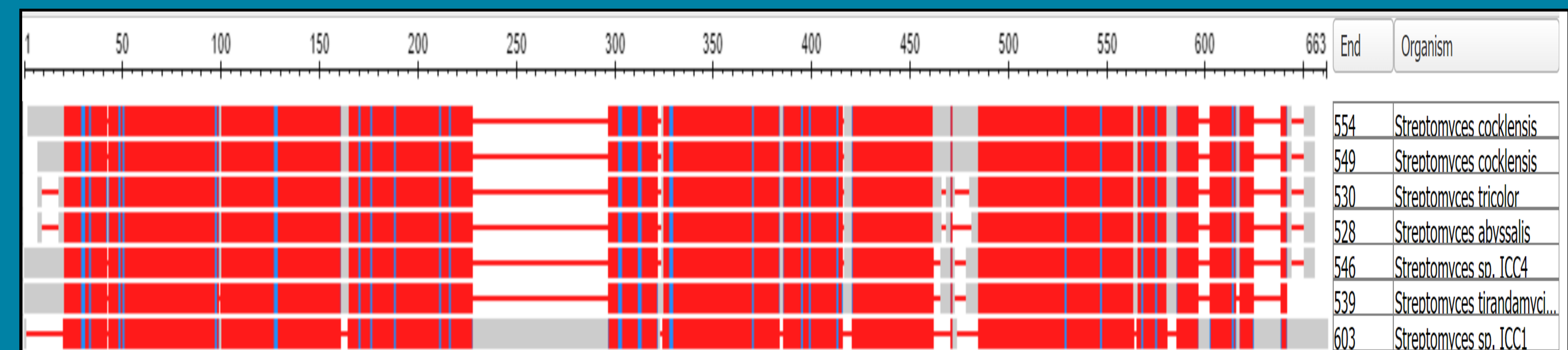


Figure 5. The genes coding for the targeted protein from different *Streptomyces* species in alignment view to show similarities and differences.

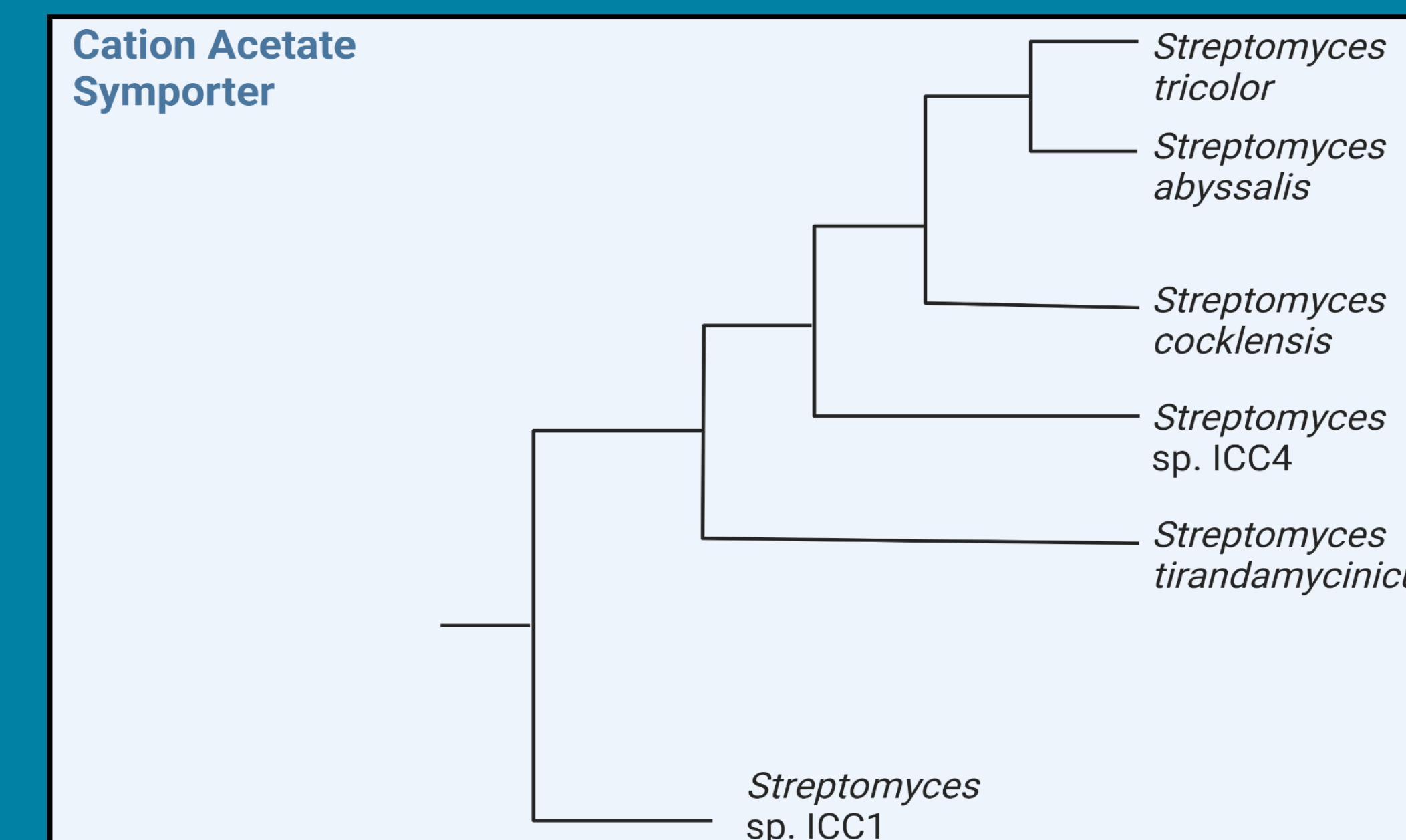


Figure 6. Phylogenetic tree of the targeted cation symporter of each *Streptomyces* species.

Conclusion

- Research suggests that acetate Na⁺-dependent symporter proteins are necessary for biofilm formation.
- The gene coding for this protein has conserved and variable regions.
- The similarity variable region of this gene does not appear to be correlated with the geological habitat and shows large variation between species.
- The similarity of the full genome of different *Streptomyces* species also does not appear to be correlated to the geological habitat or location the sample was taken from.

Future Work

- This is an introduction bacterial cognition, and the concept cell communication is a critical factor in the diverse behaviors found in different bacteria.
- In further research, identifying and labeling the genes that are responsible for different bacterial behaviors would allow us to learn more about the ecological function, adaptation, and evolution of bacteria.

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- I would also like acknowledge that the bioinformatic software NCBI Blast, DIVERGE 3.0, and MEGA11 were used in the analysis of this project

References →

