The Observable Amino Acid Divergence in Late Visit Clones (and the impact of those changes).

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Outline

- Scope of the project
- Subject 10 gives the most amount of data points with the most drastic drop in CD4-T cell count.
- Multiple sequence alignment of amino acid and nucleotide sequences reveals disproportionate values for S, theta, min, and max.
- Clones of later visits showed an increased amount of divergence as compared to the original sequence.

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Research Direction

Question: Will there be a visible protein sequence change that correlates with a decline in CD4-T cell count?

Hypothesis: Given that the amino acids of the clones of subject 10 are changing simultaneously there will be an observable drop in CD4-T cell count in response to the ongoing changes in the clones' proteins.

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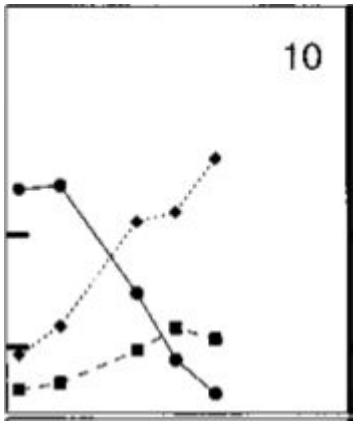
Subject 10 shows a drastic drop in CD4-T cell count with a large increase in diversity

- Subject 10 recorded 6 visits with a total of 49 clones.
- The change in condition in the subject suggests an amino acid composition change.



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A Change in DNA Sequence Doesn't Ensure Amino Acid Sequence Change

	Subject	# Clones	S	θ	Min	Max
Amino Acid	10	50	13	8.55	1	15
Nucleic Acid	10	50	74	48.65	1	21

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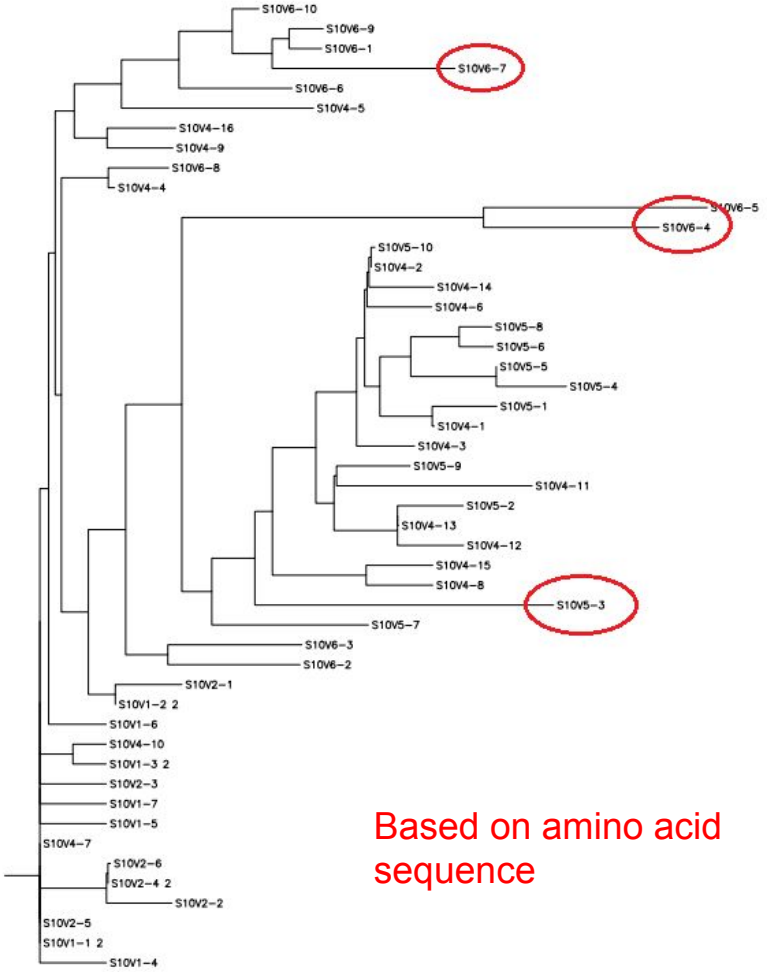
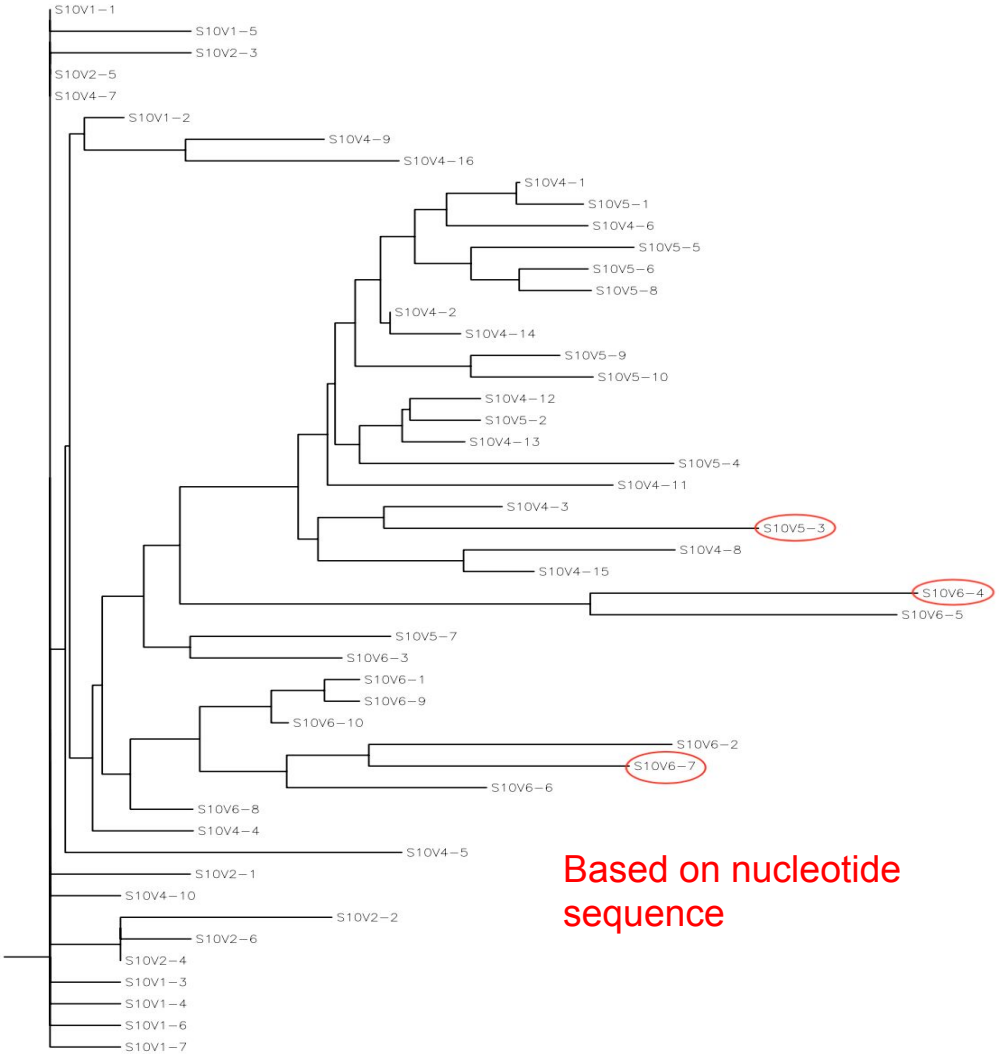
S10V5-3, S10V6-4, and S10V6-7 showed the highest divergence.

- When compared to the original strain these select samples showed the highest changes in their amino acid sequences.
- This was discovered through the CLUSTALDIST program highlighting where the intersections of individuals showed the most divergence.



Based on amino acid sequence



Based on nucleotide sequence

Continued work

- We hope to further investigate the clones of interest and to discern which amino acid changes were made and predict how those significant amino acid changes would affect the greater protein.
- Potentially compare the regions of change to the 3D model of the V3 region given by the Huang et al. (2005) data.
- Are these divergent samples the reason that subject 10 became a constituent of the “rapid progressor” data set of the Markham et al. (1998) paper.

Acknowledgments

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- LMU Department of Biology
- Classes of 2017 and 2018

References

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