Correlation analysis between CD4 T Cell counts and genetic diversity indicate no relationship

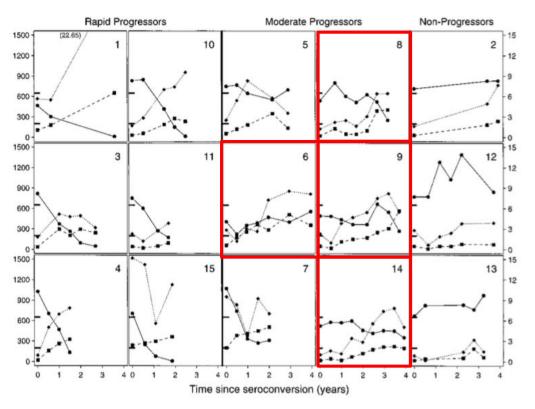
Mia Huddleston and Anindita Varshneya

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- Markham et al. indicated a relationship between increased genetic diversity and divergence, and a decrease in CD4 T cell counts.
- Markham et al. analyzed their data according to three progressor groups instead of a correlation across all data points.
- A trend exists between genetic diversity and CD4 T cell counts, but it could not be confirmed through correlation analysis.
- Other studies indicate a correlation between genetic diversity and progression of HIV-1.

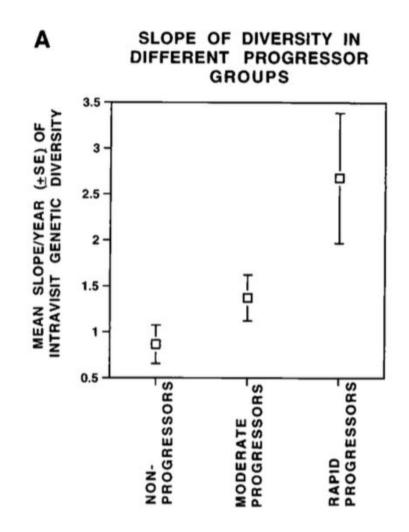
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Variable declines in CD4 T Cell Counts were observed across all 15 participants.



A significant difference in rate of genetic diversity existed between rapid progressors and moderate progressors.

 No such relationship between non-progressors and moderate progressors.

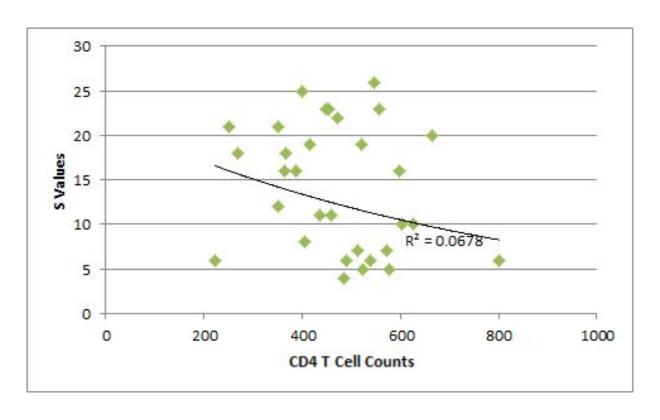


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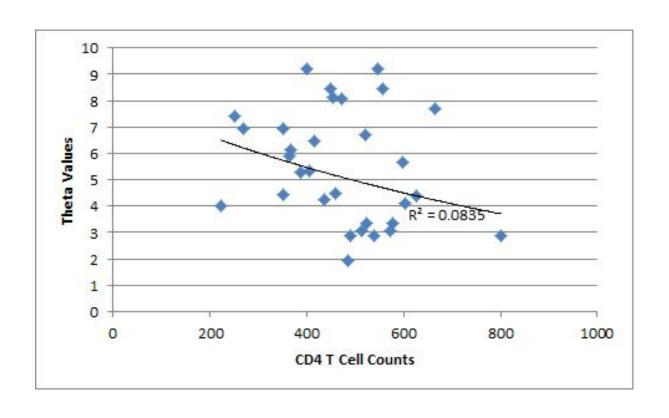
Correlation analysis between genetic diversity and CD4 T Cell count should result in an inverse relationship.

- Subjects 6, 8, 9, and 14 were analyzed
 - Had the most number of clones across the most visits
- CD4 T cell counts were plotted against both S and theta values
- Direct correlation and trends over time were analyzed
- Rooted trees were created of each subject
 - Signify relationship between different clones

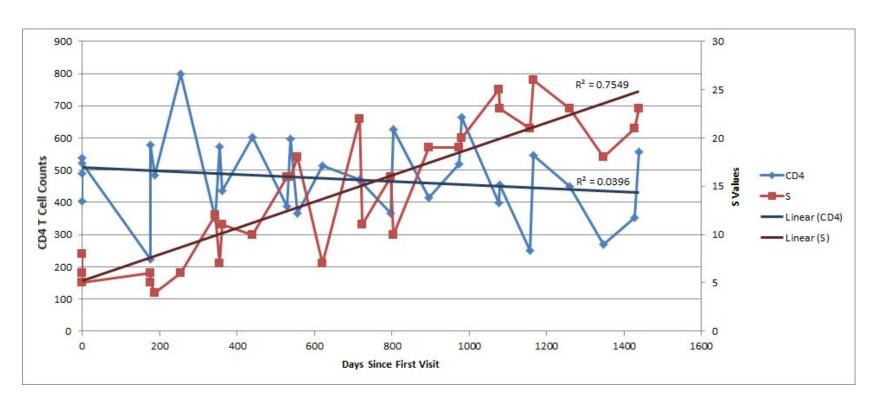
No correlation exists between S values and CD4.



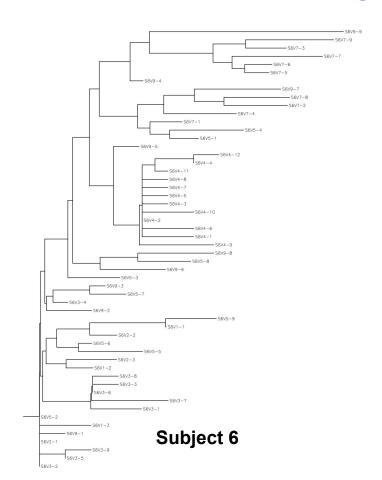
No correlation exists between theta values and CD4.

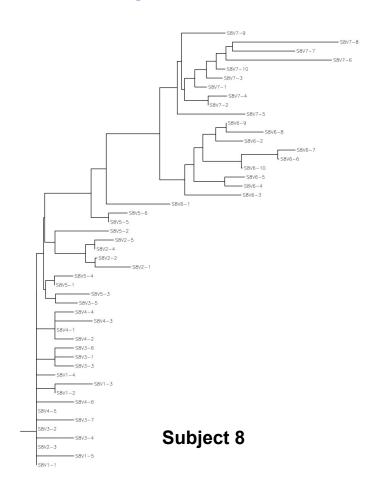


Inconclusive trend exists between genetic diversity and CD4 counts over time.

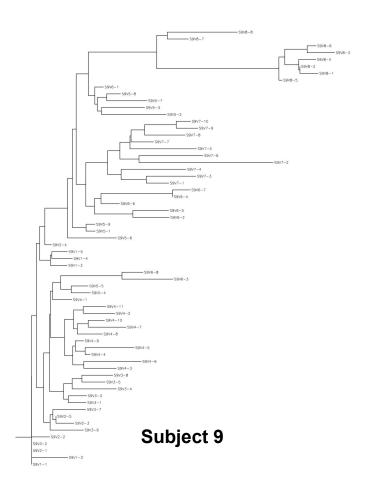


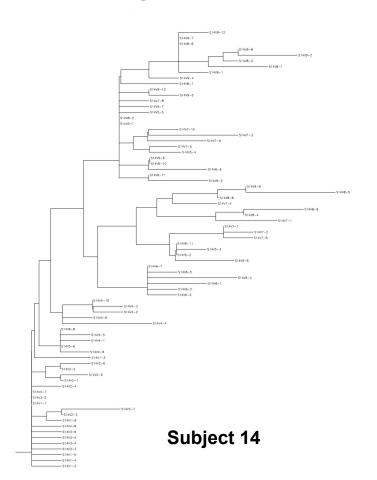
Rooted Trees indicate genetic diversity between visits.





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No correlation was found between CD4 T cell count and genetic diversity.

- However, inconclusive trend appears over time.
- With more data points across more subjects, a more conclusive result could have been found.
- Rooted trees and current sequence data are only representative of genetic diversity with greater numbers of clones per visit.
- Rachinger et al. found that CD4 counts are representative of viral diversity and immune activation.
 - Theta values were used to determine genetic diversity, and patients were sorted into three groups based on genetic diversity.
- Araujo et al. explained that genetic diversity of the Env gene has been studied extensively, but the functional diversity of these proteins has not.

More data is required to complete a correlation analysis between CD4 T cell counts and genetic diversity.

- More participants across more visits and more clones per visit
- Increased sophistication in calculating genetic diversity
 - HRM scores are a comprehensive analysis method of studying genetic diversity
 - Encompass differences in synonymous and nonsynonymous mutations affecting DNA melting point and insertions and deletions
 - James et al.

Summary

- Markham et al. indicated a relationship between increased genetic diversity, and a decrease in CD4 T cell counts.
- Data was analyzed using a correlation analysis across all participants' CD4 T cell counts and genetic diversity.
- A trend exists between genetic diversity and CD4 T cell counts, but it could not be confirmed through correlation analysis.
- Other studies indicate a correlation between genetic diversity and progression of HIV-1.
- More data points are required in order to confirm the results of our correlation analysis.

References

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