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

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Outline

- 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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Other studies indicate a correlation between genetic diversity and progression of HIV-1.
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.
Rooted Trees indicate genetic diversity between visits.

Subject 9

Subject 14
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- 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.
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