

Patterns of HIV-1: Correlation of Viral Load Number and Genetic Diversity

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Outline

- The correlation between viral load numbers and genetic diversity are investigated.
- Diversity will be determined based on statistical evidence using S , Θ
- Results of diversity will also be demonstrated using phylogenetic trees

Background

- “HIV-1 viral load (VL) levels are used for monitoring disease progression and antiretroviral therapy outcomes in HIV-infected patients.” (Nguyen et al., 2015)
 - How will classification as non-progressors, moderate progressors, and rapid progressors change if subjects are grouped based on viral load number?
 - “High genetic variation observed at the first visit in subjects” (Markham et al., 1998)
 - Subjects chosen based on diversity
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Table 1. Summary data on 15 seroconverters

Subject	No. of observations	Baseline		Annual rate of CD4 T cell decline	Slope of change in intravital nucleotide differences per clone per year	Slope of divergence (% nucleotides mutated from baseline consensus sequence per year)	Median dS/dN
		CD4	Median intravital nucleotide differences among clones				
Rapid Progressor							
Subject 4	4	1,028	0.90	−593	4.64	2.09	0.0
Subject 10	5	833	1.71	−363	3.16	1.00	0.2
Subject 11	4	753	2.27	−363	1.11	0.32	0.0
Subject 15	4	707	15.16	−362	−2.94	0.68	0.7
Subject 3	5	819	1.82	−294	0.53	0.74	1.0
Subject 1	3	464	5.64	−117	5.10	1.55	0.3
Moderate Progressor							
Subject 7	5	1,072	2.27	−392	−0.79	1.35	1.3
Subject 8	7	538	1.24	−92	1.68	1.16	0.5
Subject 14	9	523	1.00	−51	1.69	0.60	0.0
Subject 5	5	749	2.50	−41	0.06	0.50	1.4
Subject 9	8	489	9.49	−11	1.58	1.21	0.0
Subject 6	7	405	2.82	52	1.92	0.82	0.4
Nonprogressor							
Subject 2	5	715	1.64	30	1.32	0.49	1.8
Subject 12	6	772	2.80	44	0.62	0.13	0.9
Subject 13	5	671	0.87	53	0.53	0.28	3.5

(Markham et al., 1998)

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Question?

- Is virus copy number directly correlated with genetic diversity?

Hypothesis

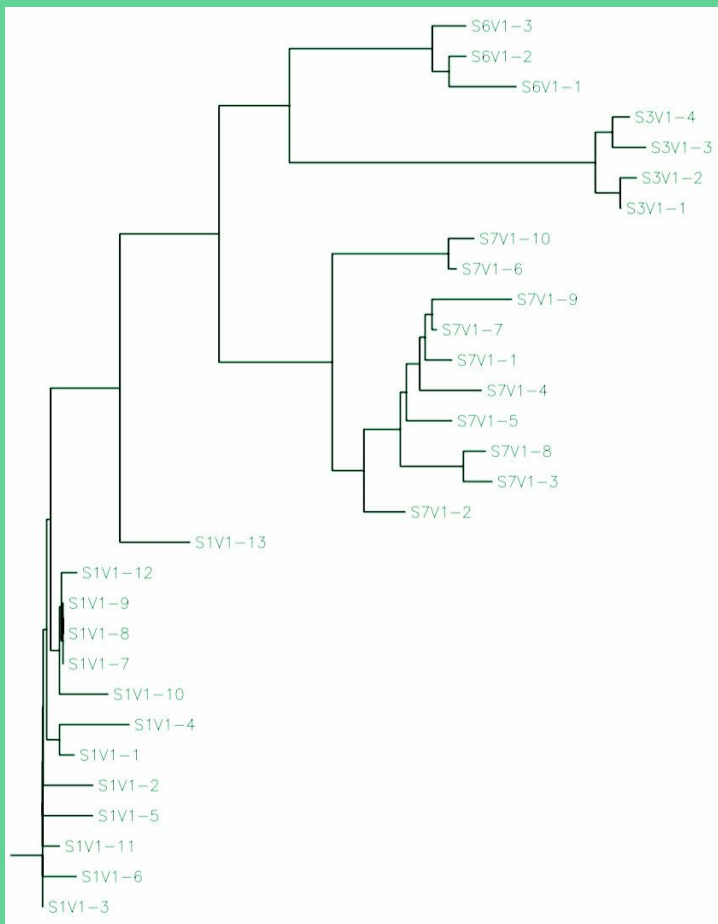
We suspect that the subjects with similar viral load numbers will have less genetic diversity and low theta and S-values.

Methods

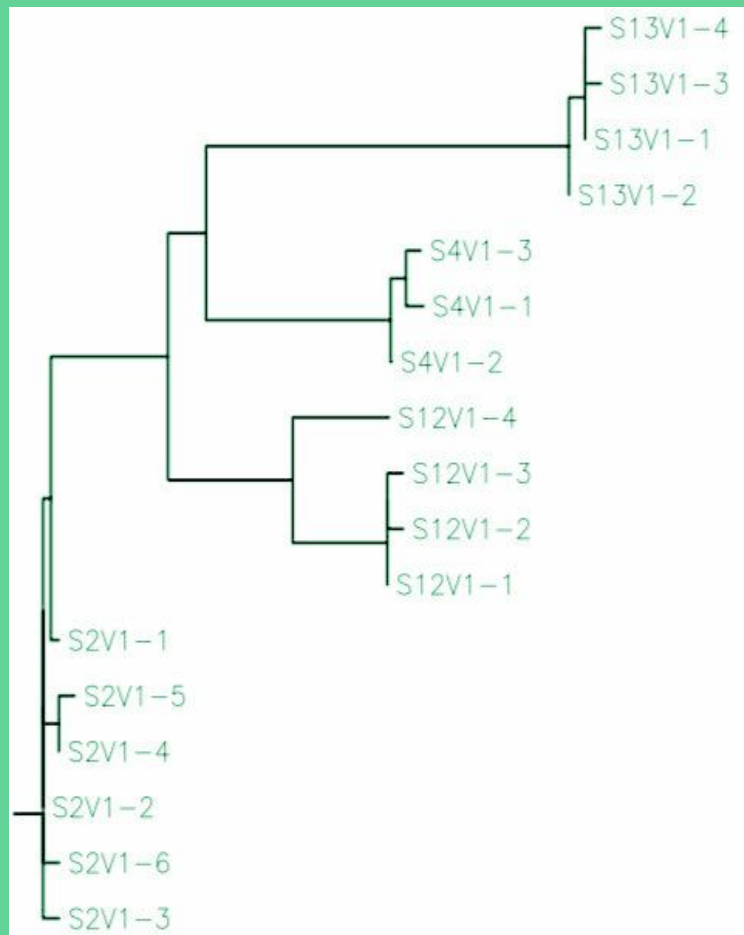
How we answered the question

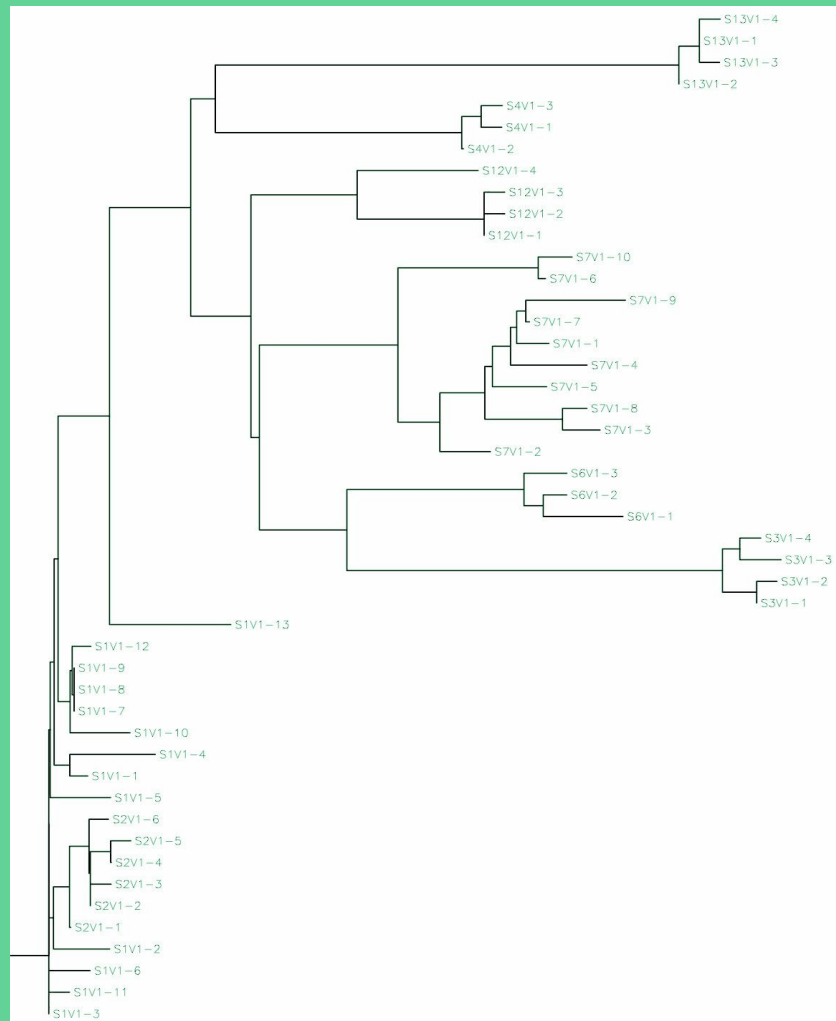
- Subjects regrouped into progressors and nonprogressors
 - Categorized subjects based on virus copy number
 - Data used from Markham et al.
- Subjects used:
 - Non-progressors:
 - 2, 4, 12, and 13
 - Progressors:
 - 1, 3, 6 and 7
- Statistics calculated:
 - S
 - Θ
- Phylogenetic Trees generated

Progressors



Nonprogressors





Statistical Analysis

Group	Subject	Number of Clones	S	Theta
Nonprogressors	Subject 13	4	73	21.59
Nonprogressors	Subject 12	4		
Nonprogressors	Subject 4	3		
Nonprogressors	Subject 2	6		
Progressors	Subject 3	4	91	22.97
Progressors	Subject 1	13		
Progressors	Subject 7	10		
Progressors	Subject 6	3		

Hypothesis Interpretation

- **Similar Θ values**
- **High S and Θ values**
 - **No significant difference in diversity**
- **Subjects grouped by virus on tree**
 - **Mutations of each virus grouped together**
- **No correlation between closely related subject strains on rooted tree and grouping based on viral load number**

Discussion

What our results found

- Almost identical theta values
 - No significant difference
 - Viral load number would not be a sufficient way to categorize subjects.
 - Relationships between subjects on phylogenetic tree does not correlate with the categories they were placed in
 - There is no correlation between diversity and viral load number between the subjects.
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Thank You!

References

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