Does diversity increase within the amino acid sequences over time more within the rapid progressors compared to non-progressors?

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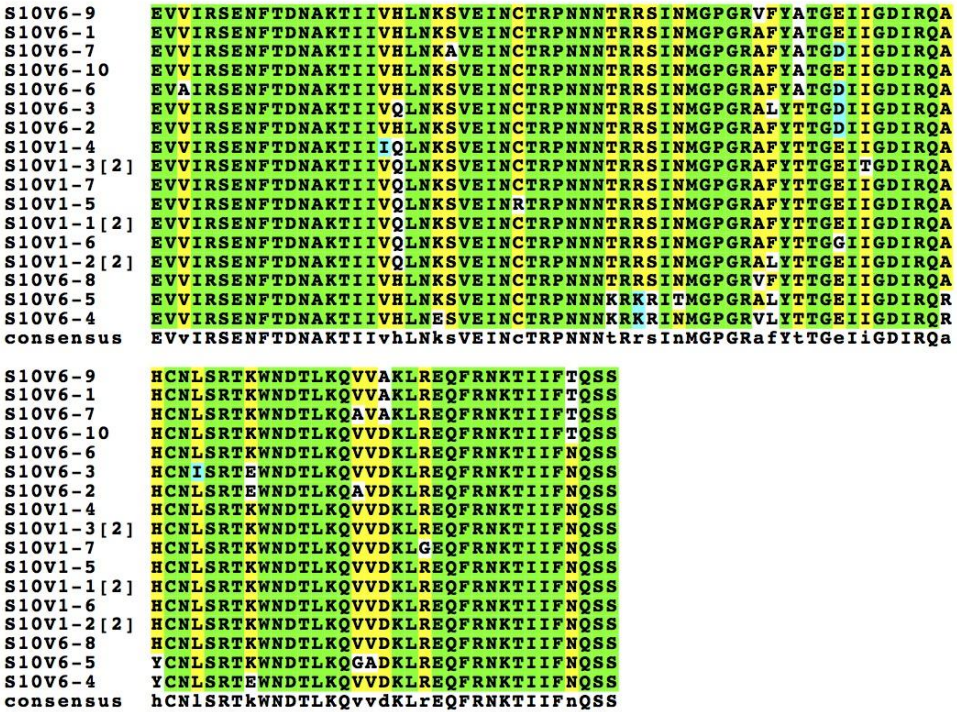
Two subjects from the nonprogressor and rapid progressor groups were chosen comparing each of their first and last visit clones.

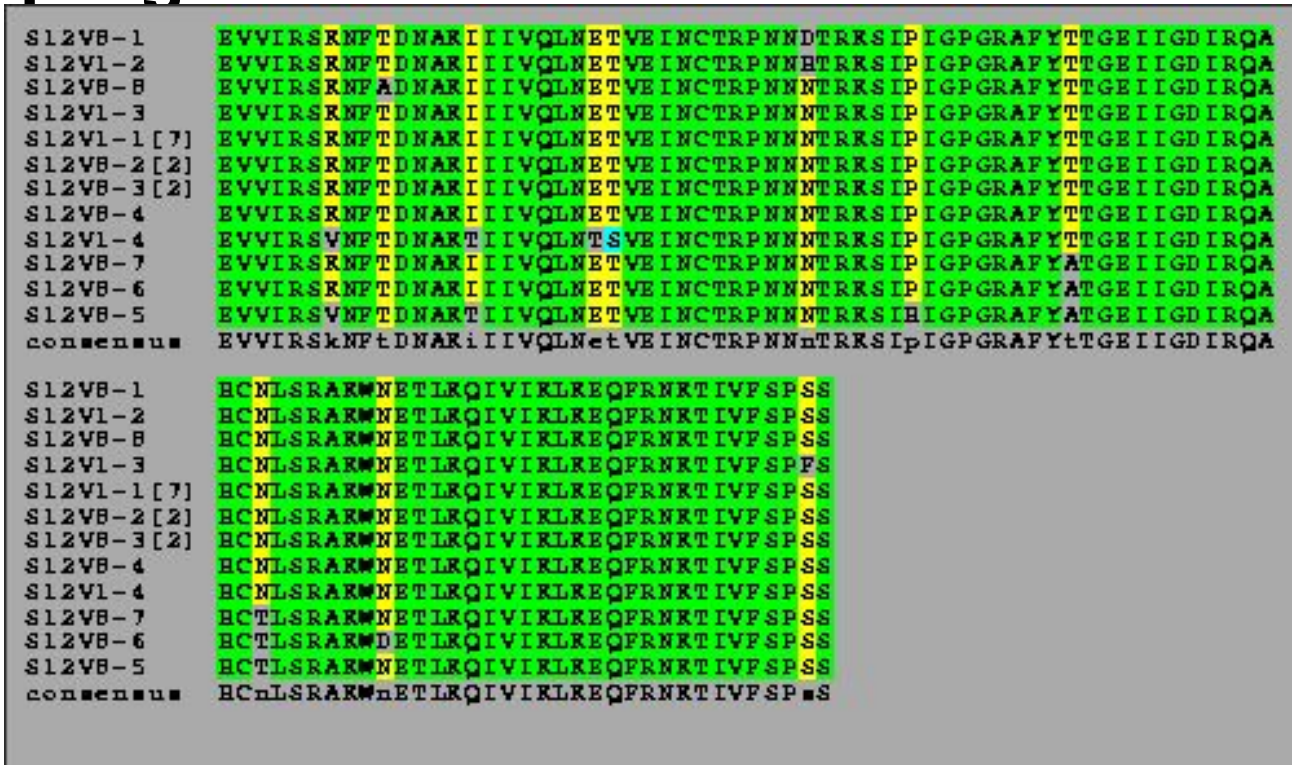
Group	Subject	Number of Clones	Number of Mutations
Nonprogressors	Subject 13	10	5
Nonprogressors	Subject 12	12	11
Rapid Progressors	Subject 3	10	9
Rapid Progressors	Subject 10	17	24

Sequence alignment of rapid progressors shows large number of mutations from first to last

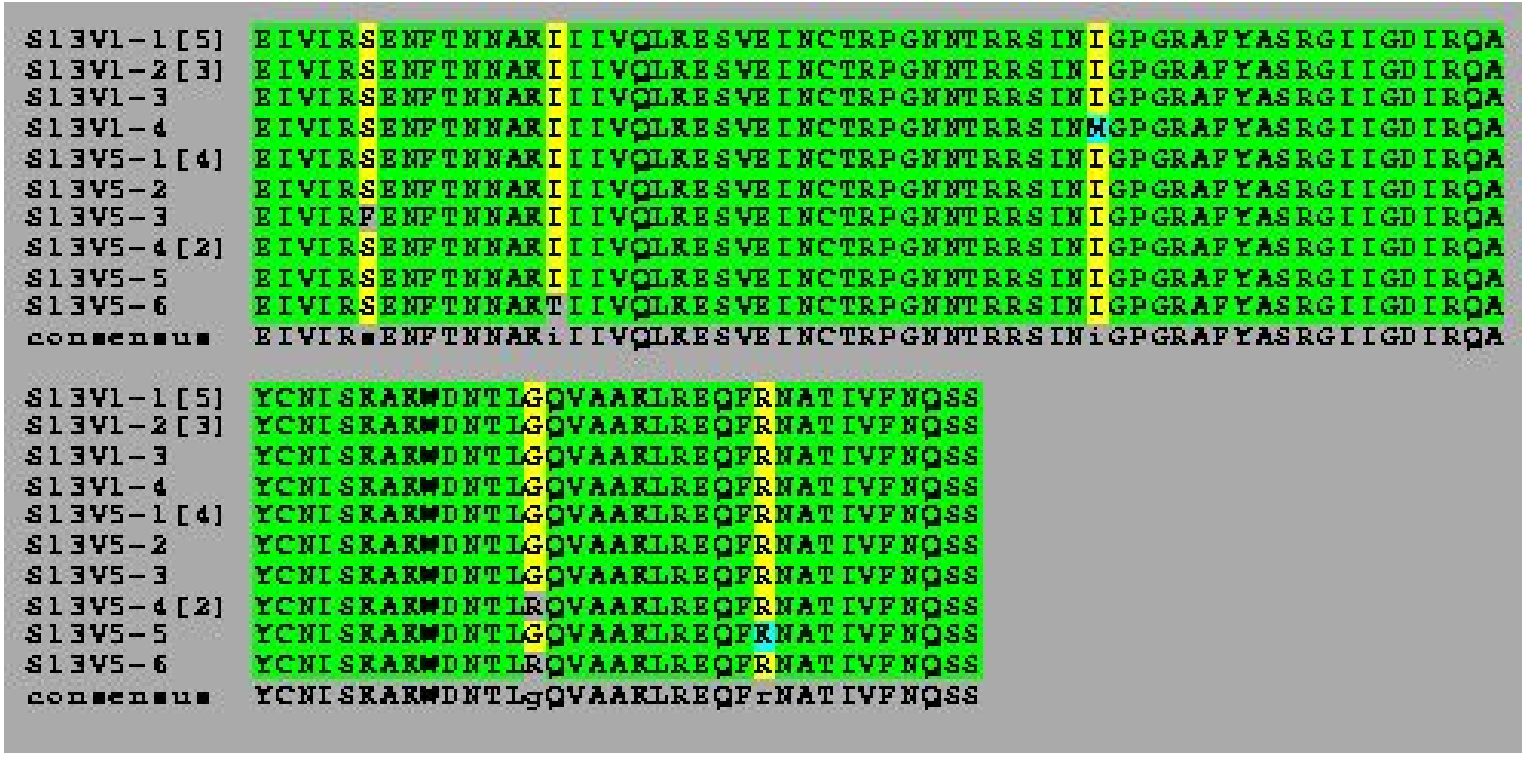


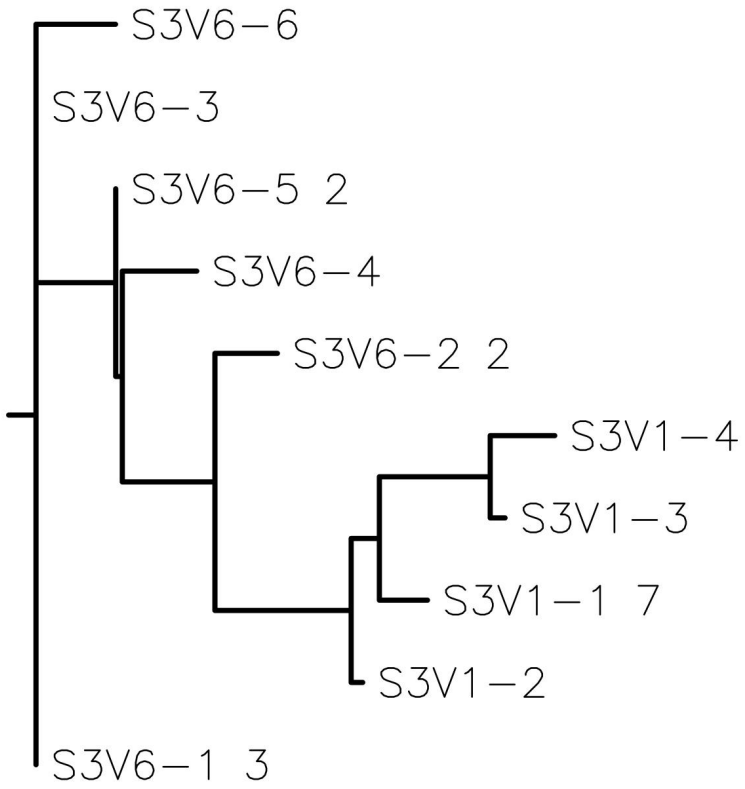
Sequence alignment of rapid progressors shows large number of mutations from first to last

Sequence alignment of non progressors shows less mutations per number of clones than rapid progressors from first to last visits.



Sequence alignment of non progressors shows less mutations per number of clones than rapid progressors from first to last visits.





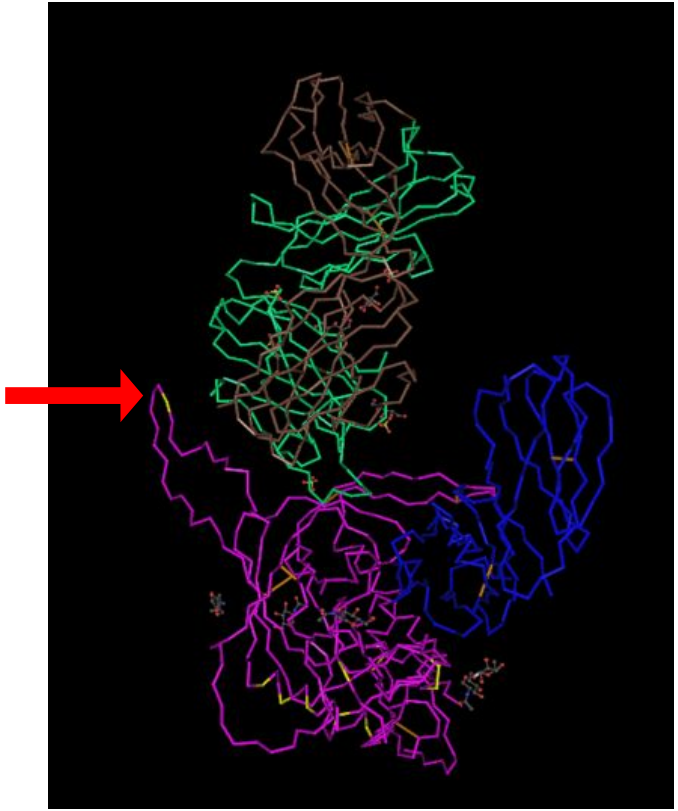
Rooted trees of each subject's first and last visits were unhelpful in identifying diversity changes over time.

ClustIdist shows higher rate of diversity among rapid progressors than non-progressors by comparing the distances of mutations from the first visit to the last per subject.

Progressor Type	Subject	Distance between first and last visit
Rapid	3	0.010
Rapid	10	0.137
Non	12	0.010
Non	13	0.021

Mutations are identified and located using structure of gp120 that Kwong et al. discovered.

- Subject 10's mutations can be visible in yellow
- One mutation can be seen in the V3 loop



The types of mutations may affect how the protein function would differ.

Subject	Number of major mutations	Number of minor mutations	Number of clones
3	4	5	10
10	14	10	17
12	7	4	12
13	3	2	10

Data suggests higher diversity among rapid progressor amino acid sequences than non-progressors, but a larger sample size is needed to confirm results

- Using more subjects would create a larger sample size
- More data points per subject could increase statistical evidence

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References

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