Retrovirology

Poster presentation

P20-09. Worldwide epitope prevalence of crystallographically resolved anti-V3 antibodies

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Background

The diversity of HIV-1 viruses, especially the multiplicity of epitopes presented by the sequence variable loops of different strains, is a major obstacle to developing a successful vaccine.

Methods

In order to estimate the worldwide prevalence of V3 epitopes recognized by several monoclonal antibodies (mAbs) which have been crystallographically resolved in complex with V3 peptides bound, we used our recently published method in which the entire LANL HIV sequence database was searched for the occurrence of each epitope motif recognized by selected broadly neutralizing anti-V3 mAbs [Cardozo T et al., AIDS Res Hum Retroviruses, 2009. 25: 441]. The occurrence of these epitopes was then corrected using updated estimates of global HIV-1 subtype distribution [Hemelaar J et al., AIDS, 2006, 20: W13].

Results

We estimated the epitope prevalence in worldwide HIV-1 strains for each of the epitopes recognized by the following anti-V3 loop mAbs: 2219 (66.91%, present in all subtypes), 3074 (82.72%, present in all subtypes), 3791 (64.25%, present primarily in non-B subtypes), 447 (12.36%, present primarily in subtype B), and 268 (3.75%, present mostly in subtype B).

Conclusion

The results illuminate the disconnect between epitope-based classification of HIV-1 strains (described here) and traditional genotype-based classification. Furthermore, the results demonstrate that certain neutralizing epitopes (e.g. that recognized by mAb 3074) are present in almost all circulating HIV-1 strains despite their location in sequence variable loops.