HIV-1, which has many different clades, has claimed more than 25 million lives in the last thirty years. Clade B is most common in the United States and Europe, while non-clade B is more common in other parts of the world, especially sub-Saharan Africa. Non-clade B strains are responsible for >80% of HIV infections.

During binding of HIV-1, the third hypervariable loop of the gp120 protein is expressed. This loop has different amino acids in clade B and non-clade B.

Phage panning and selection

The random variable chain fragments are tested sequentially against clade B and non-clade B V3 loop. The amount of peptide is decreased each time to make the process more selective.

Results of library variant binding

Phage variants were tested for clade B and non-clade B V3 loop binding using ELISA. Those colonies that bound well were sequenced to determine the amino acid sequence.

Conclusion

- This technique did yield single chain variable fragments of antibodies that seem to bind better than the wild-type KD-247 to non-clade B.
- Neutralization and other CDR regions should be tested.

Acknowledgments

- Special thanks to: Yee Ong, Dandan Liu, Dallas Pineda and Stefan Sarafianos!
- Research supported by: This work was supported, in whole or in part, by National Institutes of Health grants AI076119, AI074389, AI076119-S1, A107619-02S1, A1100890, A1099284, and GM103368 (S. G. S.) and AI079801 (M. A. P.).
- Student support: An endowment established by IDEXX-RADIL.