



POSTER PRESENTATION

Open Access

# Mutations in the V1 domain of Thai CRF01-AE viruses that confer sensitivity/resistance to broadly neutralizing antibodies

S O'Rourke<sup>2\*</sup>, G Tatsuno<sup>2</sup>, B Yu<sup>2</sup>, P Phung<sup>1</sup>, K Mesa<sup>2</sup>, B To<sup>2</sup>, K Limoli<sup>1</sup>, T Wrin<sup>1</sup>

From AIDS Vaccine 2012

Boston, MA, USA. 9-12 September 2012

## Background

Antibodies to the V1/V2 domain of gp120 have recently been identified as a correlate of protection in the RV144 clinical trial. To better understand the specificity of broadly neutralizing antibodies to the V1/V2 domain of Thai CRF01\_AE viruses, we analyzed the specificity of antibodies in HIV+ elite neutralizer (EN) sera by swarm analysis.

## Methods

Swarm analysis makes use of the swarm of closely envelope variants that evolve in each HIV-1 infected individual, as a source of naturally occurring and biologically relevant mutations that confer neutralization sensitivity/resistance. Envelopes from clade B and CRF01\_AE viruses were tested for neutralization sensitivity/resistance with sera from ENs infected with clade B and CRF01\_AE viruses.

## Results

We found five mutations in the V1 domain that affected neutralization sensitivity/resistance of CRF01\_AE viruses. This differed from clade B viruses in which mutations altering neutralization sensitivity/resistance clustered in the V2 domain. Structural studies have shown that the V1/V2 domain of gp120 consists of a four-stranded  $\beta$ -sheet structure. We found that mutations affecting neutralization sensitivity/resistance in Thai CRF01\_AE viruses clustered around the exposed turn at the junction of the A-B strands. In contrast, the mutations that altered neutralization sensitivity/resistance in clade B viruses clustered around exposed turns at the junction of the B-C and the C-D strands.

## Conclusion

The present studies suggest that there is a major difference in the antigenic structure of the V1/V2 domain between clade B and CRF01\_AE envelope proteins. These results suggest that antibodies to the V1 domain of CRF01\_AE envelope proteins should be evaluated as a correlate of protection in the RV144 trial. For this purpose, studies using novel proteins and scaffolds, that replicate the structure of conformation- and glycoform- dependent epitopes in the V1/V2 domain, are under investigation.

## Author details

<sup>1</sup>Monogram Biosciences, San Francisco, CA, USA. <sup>2</sup>Monogram Biosciences, San Francisco, CA, USA.

Published: 13 September 2012

doi:10.1186/1742-4690-9-S2-P106

Cite this article as: O'Rourke et al.: Mutations in the V1 domain of Thai CRF01-AE viruses that confer sensitivity/resistance to broadly neutralizing antibodies. *Retrovirology* 2012 **9**(Suppl 2):P106.

Submit your next manuscript to BioMed Central and take full advantage of:

- Convenient online submission
- Thorough peer review
- No space constraints or color figure charges
- Immediate publication on acceptance
- Inclusion in PubMed, CAS, Scopus and Google Scholar
- Research which is freely available for redistribution

Submit your manuscript at  
[www.biomedcentral.com/submit](http://www.biomedcentral.com/submit)



<sup>2</sup>Monogram Biosciences, San Francisco, CA, USA

Full list of author information is available at the end of the article