

Poster presentation

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## PI2-II. Resistance to the CD4 mimetic mini protein M48-U1 induces changes in a highly conserved region on the HIV-1 gp120 envelope protein

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### Background

HIV-1 prevention methods, like a prophylactic vaccine and/or microbicides, are urgently needed. Since the ideal immunogen is as yet undefined and given the role of the envelope protein (Env) in the entry process, investigation of the Env structure-function relation is necessary. In this context resistance towards a promising candidate microbicide M48-U1, a CD4 mimetic mini protein, was evaluated.

### Methods

Resistance to M48-U1 was obtained by culturing virus in the presence of increasing concentrations of the compound. When the degree of resistance was considered sufficient (fold change in IC<sub>50</sub> of >10000), genotyping was performed. Additionally, phenotyping was done by testing the sensitivity towards other CD4 binding site (CD4bs) inhibitors in a TZM-bl based assay. Furthermore, the 3D structure of Env's of resistant viruses was modelled using the software application PyMol.

### Results

Resistance to M48-U1 was induced in three subtype B viruses (BaL, SF162 and a biological cloned virus VI943-3). All resistant viruses differ in only one amino acid from their respective controls: S375, situated in the highly conserved Phe43 cavity of the CD4bs, is mutated into an arginine. Arginine, as a complex amino acid, is predicted to fill the Phe43 cavity, thereby abrogating the binding of

M48-U1 yet still allowing binding of the CD4 receptor. Interestingly, although the viruses belong to the same subtype and exhibit the same mutation, their phenotypic outcomes are different. Cross-resistance towards some CD4bs inhibitors is observed, but with a different spectrum for the different viruses. Also, the earlier, less potent mini protein M48, is still active against some but not all of these viruses.

### Conclusion

In all viruses the same mutation (S375 R) was induced by M48-U1. However, it is clear that the active site is not the sole determinant of the phenotype, as viruses with the same mutation exhibit different cross-resistance patterns.