# CHANGES IN THE HIV-1 3'-PPT IN PATIENTS FAILING DOLUTEGRAVIR IN BRAZIL

Jeroen J. van Kampen<sup>1</sup>, David A. van de Vijver<sup>1</sup>, Thibault Mesplède<sup>1</sup>, Rob A. Gruters<sup>1</sup>, Jolanda C. Voermans<sup>1</sup>, Daniel R. Kuritzkes<sup>2</sup>, Saye Khoo<sup>3</sup>, Atze Das<sup>4</sup>, Ben Berkhout<sup>4</sup>, James Hunter<sup>5</sup>, Mauro Schechter<sup>6</sup>, Ricardo S. Diaz<sup>5</sup>.

<sup>1</sup> Erasmus University Medical Center, Rotterdam, The Netherlands. <sup>2</sup> Brigham and Women's Hospital, Boston, MA, United States. <sup>3</sup> University of Liverpool, Liverpool, United Kingdom. <sup>4</sup> Amsterdam University Medical Centers, Amsterdam, The Netherlands. <sup>5</sup> University of Sao Paulo, Sao Paulo, Brazil. <sup>6</sup> Federal University of Rio de Janeiro, Brazil.

## **BACKGROUND**

The 3'-polypurine tract (3'-PPT) is a 15 nucleotide long region of the HIV genome. *In vitro* studies showed that mutations in 3'-PPT can cause high-level resistance to dolutegravir and other INSTIs. Whether mutations in the 3'-PPT also lead to INSTI resistance in HIV-1 infected patients is still under debate. Here, we determined the 3'-PPT sequences of HIV-1 infected patients failing DTG-containing cART in Brazil.

Consensus 3'-PPT	A AAA GAA AAG GGG GG
Patient 12	AAGR GAAAAG GGG GG
Patient 19	AAGAGAGGGGGG
Patient 29	AAGAGAGAGGGGG
Patient 31	AAAA GAA <u>C</u> AG GGG GG
Patient 34	AAAAGAAACG GGG GG
Patient 45	AAAA GAA MAG GGG GG

#### **METHODS**

- 67 samples from patients failing DTG-containing cART were selected from the biobank of the University of Sao Paulo. Here we report the results of the first 51 patients.
- 3'-PPT sequences of HIV-1 from patients failing DTG containing cART were obtained by Sanger sequencing of total nucleic acid isolated from EDTA whole blood.
- Phylogenetic analysis was used to rule-out cross contamination in the 3'-PPT sequencing procedure.
- For all 3'-PPT sequences that deviated from the consensus 3'-PPT sequence, we calculated the frequency of the observed mutations in 3123 HIV-1 sequences from the Los Alamos database (2018, all subtypes). The binominal distribution was used to calculate the probability of obtaining a particular number of mutations given the frequency obtained from Los Alamos.

### **RESULTS**

• In 6 of the 51 patients, we detected mutations in the 3'-PPT.

#### CONCLUSIONS

- In 3 patients we observed a A → G transition at the 3<sup>rd</sup> position of the 3'-PPT, which is a polymorphic mutation.
- In the remaining 3 patients we observed mutations in the 3'-PPT at relatively conserved positions.
- The phenotypic effect of the 3'-PPT changes detected here on INSTI susceptibility and HIV-1 replication capacity is still unknown and will be further investigated in our project.

## **ACKNOWLEDGEMENTS**

Research reported in this publication was supported by the National Institute Of Allergy And Infectious Diseases of the National Institutes of Health under Award Number R01Al147330. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health

patient	RAL pretreatment	Subtype integrase	RAMs in integrase
Patient 12	yes	В	_
Patient 19	no	В	R263K
Patient 29	yes	В	
Patient 31	no	В	
Patient 34	yes	В	
Patient 45	yes	В	_

Mutation	Position in 3'-PPT	Frequency in Los Alamos database	P-value
$A \rightarrow G$	3rd	7%	0.23
$A \rightarrow G$	4th	0.2%	0.08
$A \rightarrow C$	8th	1.1%	0.07
$A \rightarrow C$	9th	0.2%	0.08