

# **Development of resistance mutations in Human Immunodeficiency Virus type 2 (HIV-2)**

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# Clinical follow-up of HIV-2 infected patients

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## DETERMINATION OF PLASMATIC VIRAL LOAD

No commercial system at present

Development of a **quantitative real-time PCR** assay:

Quantification by SYBR-Green  
External standard curve made with a RNA-standard produced *in vitro*.

Optimised on reference strains, now tested on patients.

Viral load rise may indicate failure of antiviral therapy

**Sequencing** of appropriate genome regions before and after V.L. breakthrough under treatment

Contacts with clinical departments





Relationships established with other **clinical parameters**:  
CD4 count, stage of disease, treatment, duration of treatment, ...

# Development of resistance mutations: *in vitro* study




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Study of appearance of mutations under drug pressure: selection of resistant strains

Evaluation of viral replication *in vitro* in presence of drugs: determination of IC50 values

-  ELISA p26 Ag
-  Strong CPE on MT-2 cells with ROD strain
-  MT-4 cell line/MTT assay: quantitative evaluation of CPE
-  Quantitative real-time PCR

If IC50 value increase, a phenotype of resistance is observed

-  Sequencing of appropriate region of the viral genome
-  Comparaison with results obtained in patients
-  Correlation between phenotype and genotype

Very few data's available about resistance to drugs for HIV-2: this work should be a first step towards description of genotypic resistance.

This study should help to design drug regimens specifically for HIV-2: at present patients are treated when needed by analogy to HIV-1.