

# Initiatives for developing and comparing genotype interpretation systems Step 1: External validation of existing rules-based algorithm for abacavir and ddI evaluated on virologic response

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The Forum for Collaborative HIV Research is a coalition including government, industry, academia, advocacy and foundations, with the mission to enhance and facilitate HIV research.

## Objective

- The Forum for Collaborative HIV Research has set up an initiative to investigate the relationship of baseline genotype interpreted by different algorithms with virologic outcome for ddI and abacavir.
- An analysis plan was developed and investigators contributed data to create a large database.

## Analysis plan

- Change from baseline in viral load at 8 weeks (4-12 weeks) accounting for the censoring of VL measurements due to assay lower limits by use of a program designed for parametric survival analysis models (PROC LIFETEST in SAS, using the DIST=NORMAL option)
- For each interpretation system, a regression model was fitted with the following covariates:
  - Baseline VL
  - Sensitivity (S, I, R with R as the base)
  - Baseline VL
  - Number of other drugs in the new regimen to which viruses are sensitive using either ANRS or Rega or HIVDB
- See analysis plan at ([http://www.hivforum.org/analysis\\_collab.html](http://www.hivforum.org/analysis_collab.html))

## Inclusion criteria

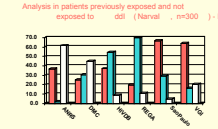
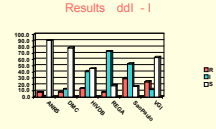
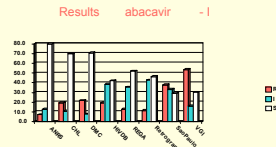
- Drug experienced people starting a new regimen including the drug under consideration (being used for the first time) were eligible for inclusion if
  - Virologically failed the previous regimen
  - <12 weeks before start of the new regimen while on the previous regimen
  - genotype resistance test
    - VL >500 copies/ml
  - VL measured between 4-12 weeks from the start
  - No changes in therapy
  - No evidence of inadequate adherence

## Data Sources

- 9 sources
  - Adult AIDS Clinical Trials Group, USA;
  - British Columbia Cohort, Canada;
  - IsaacsDA, Europe;
  - ICO.NA, Italy;
  - Narval ANRS 88, France;
  - Swiss HIV Cohort Study, Switzerland;
  - Stanford HIV Database, USA;
  - Catholic University Sacro Cuore (UCSC), Italy;
  - UK National Resistance Database, UK;
- Abacavir: N=583
  - change in VL: -1.6 log<sub>10</sub> copies/ml
- ddI: N=400
  - change in VL: -1.8 log<sub>10</sub> copies/ml

## Interpretation systems evaluated

- For both ddI and abacavir
  - ANRS V12, Detroit Medical Center-3 (DMC-3), Stanford HIV RT and PR Sequence Database-8 (HIVDB-8), Rega 6.3, Sao Paulo 4.0, VGI V10.0
- For abacavir
  - CHL 4.4, Retrogram 1.6



### Results abacavir - II

	R	I	S	P value IR and SR
ANRS	0.00	+0.64 (-0.16-1.71)	+0.66 (-0.21-1.21)	0.0070.001
DTC	0.00	+0.21-0.09	+0.20-0.08	<0.0010.10
DMC	0.00	+0.24-0.09	+0.26-0.07	0.000.19
HIVDB	0.00	+0.24-0.09	+0.26-0.07	<0.0010.62
REGA	0.00	+0.23-0.09	+0.21-0.07	<0.0010.20
Sao Paulo	0.00	+0.23-0.09	+0.11-0.03	0.420.71
VGI	0.00	+0.23-0.09	+0.40-0.21	0.460.15
VGI	0.00	+0.18-0.07	+0.47-0.07	0.020.88

### Results ddI - II

	R	I	S	P value IR and SR
ANRS	0.00	-0.10 (-1.16-1.00)	+0.38 (-0.20-1.77)	0.950.256
DMC	0.00	-0.11 (-0.68-0.47)	-0.12 (-0.70-0.51)	0.710.0.618
HIVDB	0.00	-0.11 (-0.70-0.47)	-0.12 (-0.70-0.51)	<0.910.0.665
REGA	0.00	+0.20 (-0.29-0.68)	-0.07 (-0.62-0.48)	0.420.0.816
Sao Paulo	0.00	+0.20 (-0.29-0.68)	-0.07 (-0.62-0.48)	0.171.0.550
VGI	0.00	+0.17 (-0.28-0.52)	+0.02 (-0.30-0.34)	0.450.0.890

### Analysis in patients previously exposed and not exposed to ddI (Narval, n=300) - II

	R	I	S	P value IR and SR
ANRS	0.00	-0.68 (-1.39-0.21)	+0.36 (-0.53-0.75)	0.114.0.035
DMC	0.00	+0.68 (-0.34-0.51)	+0.45 (-0.04-0.85)	0.700.0.032
HIVDB	0.00	+0.67 (-0.13-0.82)	+0.44 (-0.11-0.61)	0.007.0.161
REGA	0.00	+0.10 (-0.30-0.45)	+0.39 (-0.20-0.18)	0.810.0.197
Sao Paulo	0.00	+0.56 (-0.21-0.81)	+0.52 (-0.24-1.28)	0.000.0.180
VGI	0.00	+0.10 (-0.43-1.28)	+0.13 (-0.03-0.81)	<0.001.0.038

## Impact of specific differences in mutations between interpretation systems

Among the 465 patients classified as 'S' by ANRS

- if 'R' for ANRS and number of RT mutations >= 14/15
  - 1 These patients with the minor response probably because of nonadherence
- if 'I' for ANRS and number of RT mutations <= 11 (N=170)
  - 1 Most mutation TAM8 (R, G, G, G) 184/191
  - 1 These patients probably represent a true abacavir low resistance
- if 'S' for ANRS but 'I' for Rega and number of RT mutations <= 14 (n=150)
  - 1 Most mutation TAM8 (R, G, G, G) with 184/191
  - 1 These have better response than R and are classified by Rega as intermediate resistance to abacavir
  - 1 Indeed the presence of >= 5 TAM8 or 184/191 -> TAM in Rega is a rule for intermediate resistance
- In contrast, in ANRS the rule is to have 4 among 41, 67, 74, 144, 210 and 215 on 70 and 219 are not considered.

Our results seem to suggest that it is better to have 70 and 219 out of the rule for intermediate resistance and in general to give less weight to TAM8 = 184

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- To all data providers
- To all interpretation system providers

### Project Structure

- Chairs: D. Kuritzin and V. Miller
- Sub-group planning committee chairs:
  - Genetic, bioinformatics: Francois Brun-Vesinet and Andrew Zolberg
  - Epidemiology: David Ho and Jean-Francois Delfino
  - Technology and standardization: Lisa Demeter and Rob S. Visman
- Advisors: Victor Galvan, Dominique Costagliola and Andrew Zolberg

Forum for Collaborative HIV Research

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