

## **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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### **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.

### **Methods**

Patients included had failed a previous regimen and started using either abacavir or ddi for the first time and had a genotype and viral load at baseline. The following interpretation systems were evaluated: ANRS-V12, Detroit Medical Center-3, Stanford HIV RT and PR Sequence Database-8 (SHIVD-8) and Rega-6.3 for both drugs and CHL-4.4, Retrogram-1.6, Sao Paulo-2 and VGI-5.0 for abacavir. For each system and each drug, a regression model was fitted of week 8 change in viral load with sensitivity as covariate: Resistant group (R) as a base versus intermediate (I) and sensitive (S). Models were also adjusted for baseline viral load and number of other drugs in the new regimen to which virus was sensitive.

### **Results**

Data were obtained from 9 sources\*, with 583 and 400 patients included in the abacavir and in the ddi analysis respectively. For abacavir, the median baseline viral load was 4.4 log<sub>10</sub> copies/ml, with a change by week 8 of -1.6 log<sub>10</sub> copies/ml. The percentage of R viruses ranged from 7.3% (ANRS) to 31.9% (VGI). In univariate analysis, for 3 of the systems, there was no significant association between change in viral load and sensitivity. Among the other systems, all but one showed a larger response for I viruses than for S viruses. These results remained the same after adjustment. For that one system, the difference between I viruses (n=76) and R viruses (n=42) was +0.72 (95% CI: +0.25;+1.20) and for S viruses (n=465) +0.79 (95% CI: +0.39;+1.19). For ddi, the median baseline viral load was 4.2 log<sub>10</sub> copies/ml, with a change of -1.8 log<sub>10</sub> copies/ml. The percentage of R viruses ranged from 8.0% (ANRS, Rega-6.3) to 13.5% (SHIVD-8). In univariate analysis, for all 4 systems assessed, there was no significant association between change in viral load and sensitivity.

### **Conclusion**

These results raise the question of external validation of existing interpretation systems and emphasize the need for collaborative work to improve existing systems both by increasing the sample size and by developing innovative statistical approaches.

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