Introduction

• Software for HIV-1 genotypic drug resistance testing is routinely used to generate clinical drug resistance interpretations. In this study we compare the differences found in the results obtained with 3 distinct software (Tab. 1).

Methods

• HIV sequencing data of forty five (45) clinical samples belonging to treatment-experienced patients were analyzed using ViroSeq (VS) Genotyping Software v3.0.0.32.

• All (VS) results were compared to the FDA-registered DPM product and to the RUO ViroScore-HIV® system: both products from Advanced Biological Laboratories.

• ViroScore® include several knowledge databases i.e. Stanford HIVdb v7.0.1 [SD] or the virtual-phenotypic-based algorithm from Geno2pheno v3.3 (G2P) – Fig. 1.

Results

• Overall, G2P was the algorithm showing fewer interpretations classified as “Resistant” (8.9%, compared to 9.4% with SD and 9.2% with VS) and VS was the one showing the highest percentage of “Susceptible” interpretations (86.1%, compared to 75.3% with SD and 78.3% with G2P) – Fig. 2.

• For 41 of the samples we retrieved resistance interpretations for 19 drugs with three algorithms, allowing us to compare 779 drug resistance results between algorithms. In 34.1% of the samples, VS reported different resistance interpretations for at least one drug when compared to SD, with a 1-level lower resistance value (from Resistant [R] to Intermediate [I] or from I to Susceptible [S]).

• When considering only the interpretations where SD was in agreement with G2P (714), VS reported 1-level lower resistance values for at least one drug in 12.2% of the samples – Fig. 3.

• At the drug level, differences were observed as shown in Fig. 4.

Conclusions

• Laboratories performing DR testing should be aware of alternative interpretive systems which could be used to supplement their existing DR reports.