Software Dependent Differences in HIV-1 Drug Resistance Determination.

Dimitri Gonzalez[1], Ronan Boulmé[1], Chalom Sayada[1], Ah-Young Sung[2], Boyka Baltadjieva[2], Michael Michalov[2], Lech Mazur[2]

[1] ABL SA, Luxembourg.
[2] ACL Central Laboratory Rosemont, IL USA.

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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*).

Tab. 1: Evaluated HIV-1 drug resistance interpretation software systems.

Software	Supplier	Registration	Guidelines
ViroSeq Genotyping Software	Abbott	FDA-approved	• ViroSeq v3.0.0.32 (VS)
DPM v1.0 (Research use only, RUO)	ABL SA	FDA-registered	• Genotypic-based: ▪ HIVdb v7.0.1 (SD) ▪ Others (>7 algorithms) • Virtual-Phenotypic-based: ▪ Geno2pheno v3.3 (G2P)
ViroScore-HIV® v3.20 (RUO)	ABL SA	CE-IVD / RUO	• Same as DPM v1.0

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*.

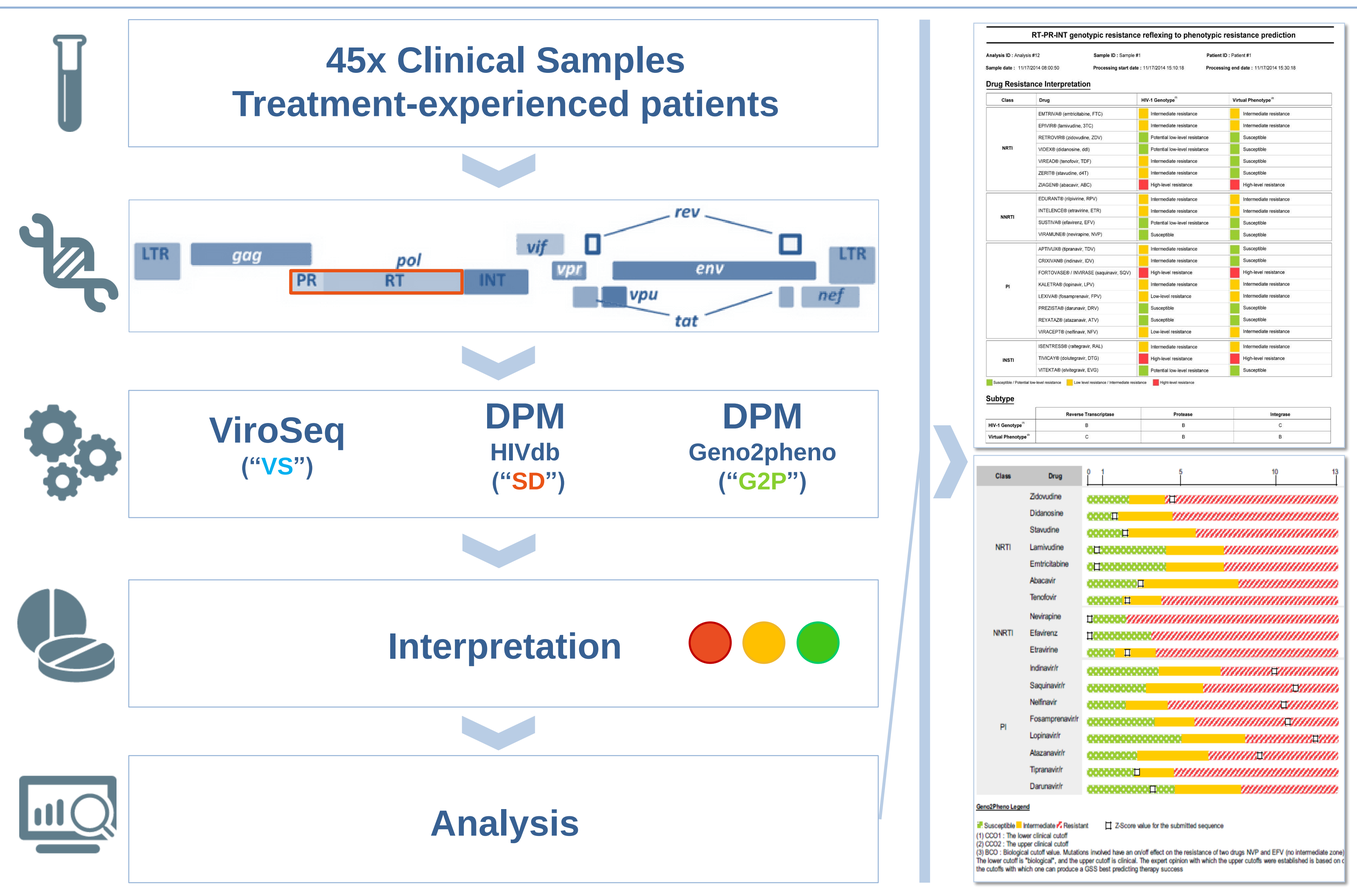

Fig. 1: Samples analysis methodology overview.

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 all 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.

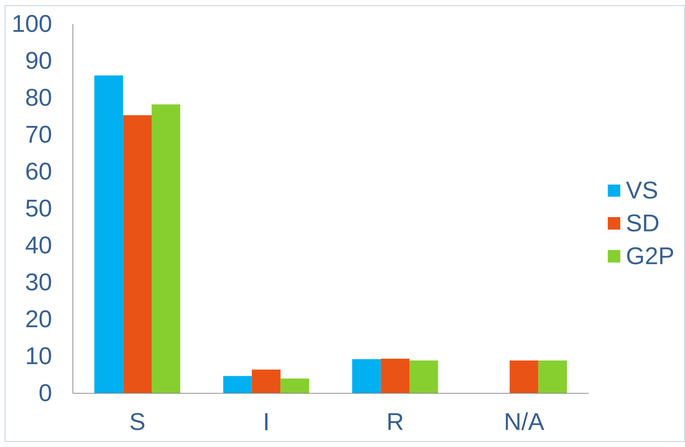

Fig. 2: Comparison of drug resistance interpretations between ViroSeq, HIVdb and geno2pheno.

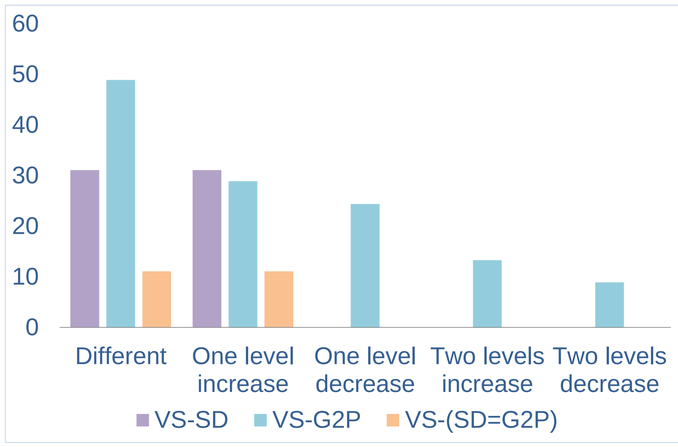

Fig. 3: Percentage of samples showing different drug resistance interpretations.

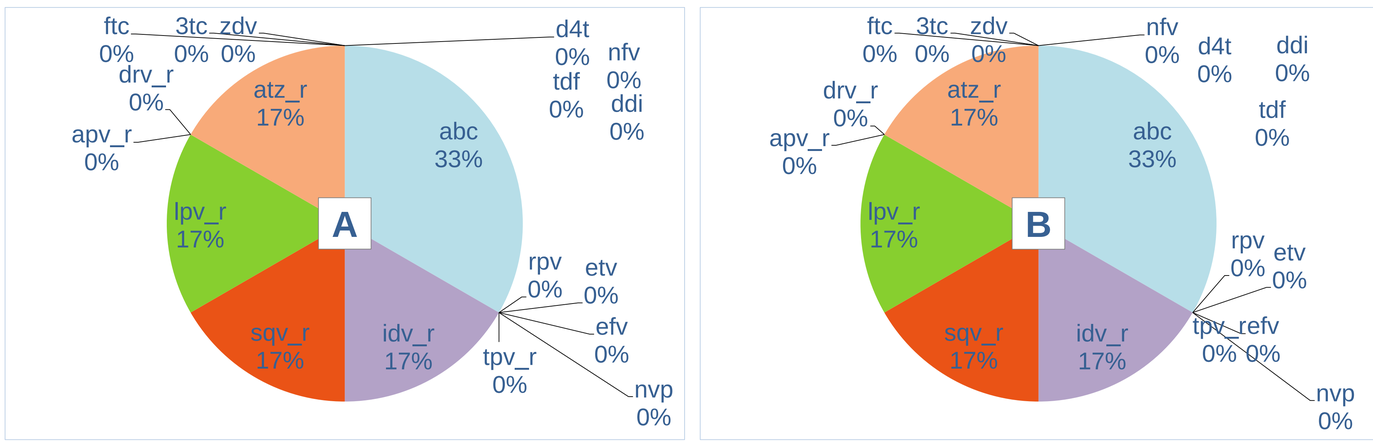

Fig. 4: Repartition per drug of results showing a different interpretation (A) or a one-level increase (B) for VS among specimens showing same interpretation results between SD and G2P.

Conclusions

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