Comparison of HIV-1 Drug Resistance Interpretations Software

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 distinct software (Tab. 1).

METHODS

- HIV sequencing data from 45 clinical samples belonging to treatment-experienced patients were analysed using ViroSeq (VS) Genotyping Software v3.0.0.32.
- VS results were compared to the FDA-registered DPM product and to the RUO ViroSeq-HIV® system from Advanced Biological Laboratories which 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 the lowest differences 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 76.3% 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.

CONCLUSIONS

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

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