Comparison of HIV-1 drug resistance profiles generated from novel software applications for routine patient care

Background

- Clinical laboratories performing routine HIV-1 genotyping antiviral drug resistance (DR) testing need reliable and up-to-date information systems to provide accurate and timely test results to optimize antiretroviral treatment in HIV-1-infected patients.

Materials and Methods

- Three software applications were used to compare DR profiles generated from the analysis of HIV-1 protease (PR) and reverse transcriptase (RT) gene sequences obtained by Sanger sequencing assay in 100 selected clinical plasma samples from March 2013 through May 2014.

- Interpretative results obtained from the Trugene HIV-1 Genotyping assay (TG; Guidelines v17.0) were compared with a newly FDA-registered data processing module (DPM v1.0, Fig. 1) and the research-use-only ViroScore-HIV (VS) software, both of which use the latest versions of Stanford HIVdb (SD v7.0) and geno2pheno (G2P v3.3) interpretive algorithms (IA, Fig. 2).

- Differences among the DR interpretive algorithms were compared according to drug class (NRTI, NNRTI, PI) and each drug.

- HIV-1 tropism and integrase inhibitor resistance were not evaluated (not available in TG).

Results

- Among 100 selected TG sequences generated at the Mayo Clinic laboratory from March 2013 through May 2014, agreement of DR interpretative results between DPM v1.0 and VS was >99.9%.

- Agreement between TG and SD and between TG and G2P were both only 17%.

- Median % agreement in DR interpretation between TG and SD, TG and G2P, SD and G2P are shown in Table 1.

- Detailed % agreement for each drug or drug combination are shown in Table 2.

- With TG as the reference result, SD and G2P generated:
  - “Positive” minor discordance, defined as susceptible S vs. intermediate I, or I vs. resistant R to ≥ 1 drug, in 66% and 56% of results, respectively;
  - “Negative” minor discordance (I vs. S, or R vs. I) in 32% and 54% major discordance (S vs. R) in 6% and 15% and major discordance (R vs. S) in 1% and 19% of subjects, respectively.

Conclusions

- Substantial discrepancies (<75% agreement) exist among the 3 interpretive algorithms for ETR, while G2P differed from TG and SD for resistance to TDF and TPV/r.

- Use of more than one DR interpretive algorithm using well-validated software applications, such as DPM v1.0 and VS, would enable clinical laboratories to provide clinically useful and accurate DR results for patient care needs.