



HIV-1 Subtype Characterization Using Automated Internet-Based Resources

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BACKGROUND : HIV-1 subtype related genetic variations influence molecular diagnostic assays and possibly impact on disease progression.

METHODS : We assessed the characterization of HIV-1 subtypes with two internet-based subtyping tools [Stanford HIV-SEQ (<http://hiv-4.stanford.edu>) and ABL HIV i-Subtyping (<http://www.ablnetworks.com>)] by submitting protease (PRO) and reverse transcriptase (RT) sequences of known subtypes from the Los Alamos database. For both programs we obtained a list of sorted similarity percentages comparing the submitted sequence to a set of reference sequences. We evaluated the characterization of strains into "B/non-B" (BNB), and also into the correct clade for non-B strains. Then, we assessed on a much larger data set the occurrence of mismatches using the ABL system.

RESULTS : For BNB characterization, 40 clade B and 40 non-B PRO and RT sequences (subtypes A, C, D, F1, F2, G, H, J, K, N, O, and recombinants) were submitted. All clade B strains were correctly identified by both systems. For non-B clades, using only the highest similarity percentage, the correct response was found in 89,5% and 87% (ABL) and in 75% and 58% (Stanford), for PRO and RT respectively. The correct subtype was found among the results with the five highest similarity percentages in the PRO in 92% for ABL and 81% for Stanford. Main differences between the systems were observed in recombinant isolates. In a second step, 2482 PRO and 224 RT sequences from the Los Alamos database were submitted to ABL HIV i-SubtypingTM and concordance with Los Alamos was found in the PRO in 97% and in the RT in 91%.

CONCLUSIONS : Both systems perform well for the detection of non-B clades. PRO sequences allow a better characterization of non-B clades than RT sequences. The ABL HIV i-Subtyping system seems to be more accurate because of the better recognition of recombinant isolates.

Abstracts