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# ABL InSight

## HIV-1 Subtype Determination in Routine Clinical Samples from 5 Countries Using an Internet-Based Subtyping Tool

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

**OBJECTIVE** : To assess the prevalence of HIV subtypes in different countries by using sequences obtained from the resistance genotyping routine.

**DESIGN** : HIV-1 subtypes were determined by submitting 1806 protease (PRO) [LU: 625, DE: 436, FR: 428, BE: 252 and BR: 65] and 1779 reverse transcriptase (RT) sequences [LU: 586, DE: 450, FR: 428, BE: 250 and BR: 65] from the clinical routine resistance genotyping to the previously validated ABL HIV i-Subtyping tool located at <http://www.ablnetworks.com>.

**RESULTS** : In most countries subtype B remains predominant, varying from 93.6% (PRO) respectively 96% (RT) in Germany, 90.4% (PRO) and 99.3% (RT) in France, 81.4% (PRO) and 81.1% (RT) in Luxembourg, 80% (PRO) and 95.4% (RT) in Brazil, down to 47.6% (PRO) and 48% (RT) in Belgium. Most common non-B subtypes differ also from country to country and were subtypes D (2.2%) and circulating recombinant form (CRF)-01-AE (1.7%) in Germany, CRF-02-AG (1.6%) and D (1.4%) in France, F1 (4.8%) and C (3.2%) in Luxembourg, D (12.3%) and F1 (4.8%) in Brazil, and A (13.2%) and C (8.7%) in Belgium.

**CONCLUSION** : HIV-1 subtype determinations starting from sequences obtained in the clinical resistance genotyping routine are feasible with easy-to-use internet-based tools, thus allowing to create simple surveillance systems for subtype distributions in most countries. The prevalence of subtypes vary largely from one country to another, even in Europe. However, these results are influenced by the patient material submitted for genotyping (patient selection) and the primers for amplification and sequencing which may not equally detect all subtypes. In addition, internet-based subtyping tools do not always correctly recognize recombinants others than the common CRFs.

## Abstracts