**BACKGROUND**

The implementation of national HIV-1 treatment programs on a global scale has saved hundreds of thousands of lives, but widespread ARV use did not begin until the last decade. Although both acquired and transmitted HIV-1 drug resistance are public health concerns, transmitted resistance has the potential to more rapidly reverse the effectiveness of frontline ARV therapy at the population level. Surveillance of transmitted resistance can supply information to support the rational use of ARV drugs by treatment programs, clinicians, and policy makers. During the past decade, the authors of about 200 studies of ARV resistance in broadly untreated populations have submitted the reverse transcriptase (RT) and protease (PI) sequences from well-characterized representative populations of HIV-1-infected individuals or from selected subsets of patients from a larger untreated population. RT ± protease sequences from well-characterized representative populations of HIV-1-infected individuals from Sub-Saharan Africa (SSA) and from countries in South/South East Asia (SSEA) in which widespread ARV use did not begin until the last decade.

**RESULTS**

Genotypic drug resistance definition: Genotypic drug resistance was defined as the presence of drug-resistant mutations determined using the Stanford University HIV Drug Resistance Database. The authors were supported in part by a grant from the NIH-NHGRI 5U01GM072950. The authors thank the large number of researchers who made this analysis possible by their contribution to the published literature and by their submission of sequence data to the Stanford database.

**CONCLUSIONS**

Determining the prevalence of transmitted drug resistance is challenging because the occurrence of even minimally polymorphic drug-resistance mutations (i.e., mutations occurring at levels between 0.1% and 0.5% in viruses not subject to ARV selection pressure) and of unrecognized ARV exposure may lead to elevated estimates of transmitted resistance. Studies of transmitted resistance should therefore be designed and interpreted with caution. Moreover, our study suggests that aggregate data from multiple studies provides an indirect indicator of regional trends in the proportions of HIV-1 infected individuals with transmitted drug resistance.

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