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GENETIC DIVERSITY OF HIV TYPE 1 IN RURAL EASTERN CAMEROON

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INTRODUCTION: To monitor the presence of genotypic HIV-1 variants circulating in eastern Cameroon.

METHODS: Blood samples from 57 HIV-1-infected individuals attending three local health centers in the bordering rural villages with Central African Republic (CAR) were collected and analyzed phylogenetically.

RESULTS: Out of the 40 HIV-1 strains with positive polymerase chain reaction (PCR) profile for both *gag* and *env*-C2V3,12 (30.0%) had discordant subtype or CRF designation: 2 subtype B/A (*gag/env*), 1 B/CRF01, 2 B/CRF02, 1 CRF01/CRF01.A, 2 CRF11/CRF01, 1 CRF13/A, 1 CRF13/CRF01, 1 CRF13/CRF11, and 1 G/U (unclassified). Twenty-eight strains (70.0%) had concordant subtypes or CRF designation between *gag* and *env*: 27 subtype A and 1 F2. Out of the remaining 17 HIV-1 strains negative for PCR with the *env*-C2V3 primers used, 10 (58.8%) had discordant subtype or CRF, and 7 (41.2%) had concordant one based on *gag/pol/env*-gp41 analysis. Altogether, a high proportion (22/57, 38.6%) of the isolates were found to be recombinant strains. In addition, an emergence of new forms of HIV-1 strains, such as subtype B/A (*gag/env*), B/CRF01 and B/CRF02, was identified. The epidemiologic pattern of HIV-1 in eastern Cameroon, relatively low and high prevalence of CRF02 and CRF11, respectively, was more closely related to those of CAR and Chad than that of other regions of Cameroon, where CRF02 is the most predominant HIV-1 strain.

CONCLUSIONS: These findings strongly suggest that this part of Cameroon is a potential hotspot of HIV-1 recombination, with a likelihood of an active generation of new forms of HIV-1 variants, though epidemiologic significance of new HIV-1 forms is unknown.

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