Extremely high prevalence and genetic diversity of hepatitis C virus infection among HIV-1 infected injection drug users in Taiwan

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摘要

Abstract

Background. An outbreak of human immunodeficiency virus (HIV) type 1 infection among injection drug users (IDUs) occurred in Taiwan, and thereafter, injection drug use became the most frequent risk factor for HIV infection in Taiwan. We sought to study the prevalence of and genotypes causing hepatitis C virus (HCV) infection among HIV-infected IDUs in Taiwan. Methods. A multicenter, longitudinal cohort study of 990 HIV-infected IDUs was conducted from 1993 through 2006. Blood samples were collected and analyzed for the presence of antibody to HCV and to determine the genotype of HCV. Results. The overall prevalence of HCV infection among HIV-infected IDUs was 96.6%. The annual prevalence increased from 65.5% before 2002 to 98.6% in 2006. The main circulating HCV genotypes were la (accounting for 29.2% of samples), 6a (23.5%), and 3a (20.2%), whereas 1b, the most predominant genotype circulating in the general population in Taiwan, accounted for only 13.2% of samples. Genotypes 2b (accounting for 6.6% of samples), 6k (2.9%), 2a (1.6%), 6g (1.6%), and 3b (1.2%) were present in only a few IDUs. Multivariate logistic regression analysis revealed that duration of injection drug use and a travel history to China or Southeast Asia were significantly associated with infection due to HCV genotypes la, 3, and 6. Conclusions. Our study demonstrated a high prevalence of HCV infection among HIV-infected IDUs in Taiwan, with a predominance of infection due to genotypes la, 6a, and 3a, as a result of the impact of IDUs' behavior and their drug trafficking route. Our study revealed that HCV infection in IDUs originated from a geographically large transmission network that was mainly distinct from that associated with other HCV-infected individuals; this transmission network has also been documented in association with HIV infection in IDUs..

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