INTRODUCTION

Globally, 2.7 million people are co-infected with HIV and HBV. Little is known regarding the prevalence and genotype distribution of HBV in HIV-infected subjects in the Mesoamerican region. As the HBV epidemic evolves, it is important to understand the dynamics of HIV/HBV co-infection in the region. In this study, we analyze HBV prevalence, genotype distribution, and treatment resistance prevalence in 6 countries of the Mesoamerican region.

MATERIALS AND METHODS

HIV-infected antiretroviral treatment-naïve persons were enrolled after written informed consent, as part of a multicenter study evaluating HIV pretreatment drug-resistance and HBV co-infection in Mesoamerica. Participants were selected by convenience sampling from key HIV clinics and research centers in the region. Serology for HBsAg was performed for all participants and HBV was genotyped using an in-house amplification method in those testing positive. HBV sequences were reviewed for quality and a consensus was generated for each participant. Treatment resistance was evaluated with a web-based application. For genotyping consensus sequences for each participant were compared phylogenetically to reference HBV sequences from NCBI using MEGA, PhyML and Nexstrain.

RESULTS

Major drug mutations to Lamivudine and Telbivudine were observed in 17 (8%) of the sequences, and to Entecavir in 19 (9%) (n=202).

DISCUSSION

HBV/H ancestry suggest the global distribution occurred out of Mexico. Additionally, the very slight deviation between sequences may suggest formation of new clades. Given further evolution time, new sub genotypes of HBV/H may exist.

CONCLUSIONS

HBV coinfection in persons living with HIV in Mesoamerica was under the global prevalence of 7.4% (except for Belize), but over 4%, suggesting middle to high prevalence in the region. Sexual transmission, including heterosexual, remains the leading risk factor for co-infection, warranting focused interventions. Drug resistance prevalence approached 10% for most drugs, underscoring the importance of baseline drug resistance tests and warranting continuous surveillance.