**INTRODUCTION**

Although the incidence of AIDS cases in Puerto Rico has declined, Puerto Rico continues to have one of the highest incidences of HIV-1 infection in the United States. After the advent of highly active antiretroviral therapy (HAART), the mortality of HIV-1/AIDS was substantially reduced, but the genetic diversity and mutation rate of the virus combined to produce numerous resistant strains, resulting in reduced treatment efficacy.

As of 2003, 28,301 cases of HIV/AIDS had been reported in Puerto Rico. More than 10,000 persons live with HIV/AIDS in Puerto Rico. HIV/AIDS was the major cause of death (47.7%) among drug users in Puerto Rico in 1998. HIV infection in Puerto Rico is characterized by patients with a median age of 35 years, mostly Hispanic (98.8%) men, women (77.7%), and the major risk for infection is drug abuse (54.3%). Increased risk behaviors have been associated with alcohol abuse and homelessness.

HIV therapy typically includes a combination of reverse transcriptase inhibitors (RTI) and protease inhibitors (PI). The activity of HIV-1 reverse transcriptase is essential for viral replication and is required for the conversion of single-stranded genomic RNA into double-stranded viral DNA, which is later integrated into the host genomic DNA. For this reason, HIV-1 RTIs are powerful inhibitors of HIV-1 replication and represent an important class of antiretroviral agents. HIV-1 protease cleaves viral Gag and Gag-Pol polyproteins into structure and replication proteins that are necessary for the virus to become infectious and, therefore, PI are important for HIV therapy.

A continuing challenge to maintaining the efficacy of drugs designed to impede viral reproduction is the presence of amino acid polymorphisms. Amino acid polymorphisms may occur as the result of mutations associated with drug resistance. Numerous mutations with specificity for the RTIs and PIs have been identified and well characterized.

As the need to assess the prevalence of resistant mutations became evident, HIV-genome sequence data have been collected and analyzed since 2000. In this study, we determined the prevalence of genotypic mutations in a sample of Puerto Ricans infected with HIV-1 and analyzed sex differences in mutation expression profiles. Although clinical and demographic data, other than sex, were not compiled in the study, the data provide a starting point for more complex studies in which more variables can be measured. Since these data are relevant for mutation prevalence, especially details about exposure to antiretroviral therapy, which is directly related to the development of mutations, we are working with physicians to expand the data obtained by the study.

The purpose of the study is to establish a HIV-1 resistance-monitoring system in Puerto Rico. Furthermore, the information obtained is also important to determine if the virus found in the island differs from the virus in the continental United States. As drug resistance is a major factor in treatment success, and data from Puerto Rico are scarce, the development of the database will assist physicians in determining treatment regimens specific for the island.