

Molecular epidemiology of HIV type 1 in Chile: Differential geographic and transmission route distribution of B and F subtypes

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We examined the genetic makeup of 221 HIV-1 strains from Chilean persons living with HIV/AIDS by HMA and DNA sequencing of the env gene: 143 cases were infected by sexual contact with an already-infected partner, 76 were infected by mother-to-child transmission, and 2 were transfusion related. We found env HIV-1 subtype B in 202 cases (91.4%) and subtype F in 19 cases (8.6%). Subtype B strains were found throughout the country whereas subtype F viruses were predominantly found in cases from the metropolitan/central to the northern regions of Chile ($p < 0.01$). Chilean F subtypes clustered in two different groups: viruses from the central region clustered with F subtypes from Argentina, Uruguay, and Brazil, and viruses from the northern region, which independently segregated from other South American and European F strains. All of the 59 men having sex with men (MSM) were infected with B subtype strains whereas 7 (9.2%) and 12 (15.8%), respectively, of heterosexually infected females and