

What makes HIV-positive gay men disclose their disease status?

HIV-positive men tend to weigh the consequences of disclosure before confiding to friends and family that they are infected with the virus, a US study suggests. This finding is at odds with the popular “disease progression” theory that HIV-infected men generally reveal that they have HIV only when the physical manifestations of the disease make the diagnosis difficult to conceal.

Julianne Serovich, director of the Marriage and Family Therapy Programme at Ohio State University (Columbus, OH, USA), who examined the two hypotheses in a study of 138 HIV-positive gay men, concludes that “disease progression may not play a role in the decision to disclose an HIV diagnosis” (*AIDS Educ Prev* 2001; 13: 355–64). The participants, 55% of whom had disclosed their HIV status to their families and 63% had told friends, were asked to rate the importance to themselves of 18 possible consequences of disclosure to a specific person. Serovich suggests that improved therapies for HIV have influenced decisions on whether or not to disclose the infection. “Early in the HIV/AIDS epidemic the progression of disease was unambiguous, but advances in HIV therapies now keep the virus under control in many cases.” Thus, “disease progression may no longer be a component of the disclosure process”.

“Disclosure could be a pivotal factor in reducing the behaviours that continue the spread of HIV”, says Serovich, in whose study 76% of participants had been infected through unsafe sex. Reasons for disclosure included wanting to keep family and friends safe from HIV, seeking understanding and emotional support, and feeling that others had a right to know. The main reasons for non-disclosure were to avoid fights, blame, and losing relationships. “If the positive consequences of disclosure outweighed the negative repercussions the chances were good that a man told his friends and family”, Serovich adds. “But the same doesn’t seem to hold for sexual partners, and we’re not sure why.”

Gary Marks (Centers for Disease Control and Prevention, Atlanta, GA, USA) argues that “it is too early to discard the disease-progression hypothesis on the basis of this one relatively small

study”. “In reality, both hypotheses are likely to be valid, and both are likely to account for some of the variance in disclosure to family and friends.”

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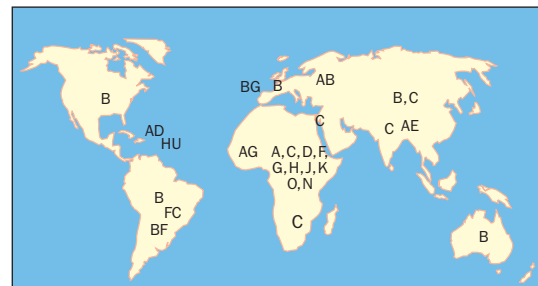
New Argentine HIV variants

Spanish scientists have discovered six different recombination variants of the BF intersubtype of HIV-1 (*J Gen Virol*, 2001; 83: 107–19), raising questions about what new biological or drug-resistance properties the virus might be acquiring.

Until recently, the HIV viruses circulating in Argentina were all thought to belong to the B subtype. The BF intersubtype, which now appears to be spreading rapidly in that country, must have arisen from the recombination of B with that of an F subtype virus in co-infected individuals. This probably occurred through contact with infected people from neighbouring Brazil, where the F subtype is involved in 10–15% of all HIV infections.

The new BF recombination variants were discovered when Michael Thomson, Elena Delgado, and colleagues of the Department of Viral Pathogenesis at Madrid’s Carlos III Institute of Health, amplified and sequenced almost complete viral genomes taken from eight BF-infected people. In previous work, the team had found 40% of infected Argentines to harbour the BF subtype, and 60% the B subtype, but saw no non-recombinant F subtype cases (*AIDS*, 2000; 14: 897–99). This contradicted the work of other authors who found up to 40% of F cases and only 5% of BF cases. The Spanish team began to look at the whole genome rather than just the short, standard pieces normally inspected. What they found was a mosaic of recombination variants of BF (especially in the *pol*

gene) in which different parts of the B and F genomes had been exchanged. The Argentinean viruses earlier reported to be of the F subtype were almost certainly BF, the team concludes, simply not enough of their genomes had been checked. “What this means is that if you want to know what’s really happening, you have to look at the whole genome”, commented Rafael Nájera, co-author of the report and team leader.



Geographical distribution of HIV subtypes.

Rafael Nájera

The researchers believe that 65% of Argentines carrying HIV harbour the BF subtype, and that none have the straight F form. To have spread so successfully, some BF recombinations must have an advantage over B and F subtypes. Already, BF cases have cropped up in Uruguay, Bolivia, and Spain. “Recombination is not just a process that affects the replication or the molecular biology of the virus”, said Nájera, “it also has an impact on its epidemiology”. Such recombinations might provide the virus with greater virulence, greater drug resistance, or replicative capacity etc. “It’s likely that different subtypes and their recombinants have different susceptibilities to antiviral medication”, added Thomson.

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