review of death certificates, 5 case reports were obtained from other health departments, and 23 cases were identified through other special projects during the study period. In addition, the sensitivity study, conducted between October 1997 and July 1998, identified 43 persons with AIDS who were seen at the selected sites during the study period but had not been reported by either system. The completeness of reporting was 92% \[= (55 + 964)/(1068 + 43)\] by the active system and 5% \[= (55 + 1)/(1068 + 43)\] by the passive system. The completeness of reporting for the first study year was 90% for the active reporting and 6% for the passive reporting, and for the second study year, 94% and 3%, respectively. The median time between date of diagnosis and report was 2 months by the active system and 1 month by the passive system. The proportion of cases reported within 6 months of diagnosis by the active and the passive systems was 82% and 84%, respectively.

Our study demonstrates that although timeliness of reporting by the passive system at the selected sites was comparable with the active system, the completeness of reporting was very poor. The current AIDS surveillance system in San Francisco is predominately an active system that relies heavily on health department personnel to collect data on AIDS cases. This has not only ensured the completeness and timeliness of AIDS case reporting but also greatly enhanced the quality and quantity of AIDS surveillance data. Given that a large proportion of reported cases in San Francisco were diagnosed at the active surveillance sites, our findings suggest that if we were to rely on passive reporting, the completeness of reporting would be considerably jeopardized. Our data are consistent with other studies that have shown that active reporting results in more complete surveillance of other infectious diseases (3,4) as well as AIDS (5–8).

Our estimates of the completeness of passive reporting may be low because selected individuals who were responsible for case reporting knew about the concurrent active surveillance as well. However, participants agreed to participate, received training and monetary compensation, and knew that a passive reporting system, if successful, could save money. In addition, the decline in completeness of passive reporting in the second study year suggests that although there was an initial willingness to report, this diminished over time. Although passive reporting is significantly less expensive, it would result in substantial loss of valuable AIDS surveillance information in San Francisco.

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Evidence of HIV-1 Genetic Diversity Among Pregnant Women With AIDS or Infected With HIV-1 in Central Brazil

To the Editor: The first AIDS cases officially reported in Brazil date back to 1982 in the northeastern part of that country (São Paulo and Rio de Janeiro). The epidemic has since spread throughout the country with a cumulative total of 163,355 AIDS cases registered by May 1999 and an estimated 500,000 HIV-infected people. Initially, the epidemic was observed mainly among men who have sex with men, later injecting drug use played an important role, and at present transmission by heterosexual contact is increasing over time. Thus, during the past decade, women of childbearing age who are infected with HIV-1 have comprised an increasing proportion of patients in Brazil (1). Brazil is a country with almost 200 million inhabitants who live in five different geographic regions (South, Southeast, Central West, North, and Northeast). Goiânia city is the capital of Goiás, one of three states and the federal capital district (i.e., Brasília) that comprise the Central West region. This state accounts for 2851 (1.75%) of the total AIDS cases in Brazil (2). Genotypic studies in Brazil have indicated infection derived primarily from HIV-1 subtype B (74.6%), followed by subtypes F (6.3%), C (3.2%), and D (0.5%), and samples in which the subtype could not be determined through heteroduplex mobility assay (HMA; 15.4%; unpublished data). Most of these studies have been performed in patients from the southern region of the country (3). For the first time, we have characterized the genetic diversity of HIV-1 circulating among HIV-1–infected pregnant women in central Brazil.

Pregnant women were recruited on a volunteer basis at the only regional referral AIDS program (Hospital de Doenças Tropicais [HDT-SUS]), located in Goiânia city, between April 1997 and December 1998. Information about pregnancy outcome, mode of delivery, and neonatal birth data was obtained from the regional maternity center for HIV-positive/AIDS patients and their newborns (Hospital Materno Infantil [HMI-SUS]). For newborns, death certificates were reviewed to verify the relation between the cause of death and AIDS-associated illness.

Table 1 presents the baseline characteristics of pregnant
TABLE 1. Individual characteristics of pregnant women who are HIV-positive or have

<table>
<thead>
<tr>
<th>Case no.</th>
<th>Age (y)</th>
<th>Time interval between HIV-positive/AIDS diagnosis—pregnancy (mo)</th>
<th>HIV-positive (POS)/AIDS status</th>
<th>CD4 count (cells/μl)</th>
<th>RNA load (copies/ml)</th>
<th>Survival of newborns (days)</th>
<th>Subtypes</th>
</tr>
</thead>
<tbody>
<tr>
<td>01</td>
<td>16</td>
<td>0</td>
<td>POS</td>
<td>473</td>
<td>5273</td>
<td>310</td>
<td>B</td>
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<td>0</td>
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<tr>
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<td>36</td>
<td>AIDS</td>
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<td>&gt;750000</td>
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<td>C</td>
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<tr>
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<td>27</td>
<td>5</td>
<td>AIDS</td>
<td>205</td>
<td>166</td>
<td>Alive</td>
<td>B</td>
</tr>
</tbody>
</table>

*a,b* Indicate the two patients who became pregnant twice during the study period.

0, Simultaneous.

*women who tested positive for HIV or were diagnosed with AIDS. Their median age was 25 years old; in half the cases, HIV infection or AIDS was diagnosed during pregnancy. All patients who were referred had had sexual partners with known HIV-positive status and had practiced unsafe sex. Heterosexual contact alone was the prevailing reported route of transmission (71.4%). The HIV/AIDS ratio was 4:10. Prophylactic intravenous zidovudine treatment during labor was provided to 75% of the patients and vaginal delivery occurred in 68.8% of the cases. Two patients became pregnant twice during the study period, yielding 16 singleton live births (6 girls and 10 boys) with a median weight in these newborns of 2.8 kg. Four infant deaths occurred within 16 to 310 days postpartum, of which 3 had resulted from AIDS-associated conditions. The variation in number of HIV-1 RNA copies (Amplicor HIV-1 Monitor, Roche, Branchburg, NJ, U.S.A.) ranged from <50 to 41,934 copies/ml among HIV-positive patients and from 80 to >750,000 copies/ml among patients with diagnosed AIDS. Median CD4 counts (FACSCalibur, Becton Dickinson, San Jose, CA, U.S.A.) for HIV-positive persons and persons with AIDS were 781.0 cells/μl and 323.0 cells/μl, respectively.

Our HMA (4) results demonstrated the presence of the following subtypes: B (n = 12), C (n = 1), and B/A (n = 1). The B/A sample showed fast heteroduplex bands when annealed with both A and B reference strand fragments. Four B, the C, and the B/A subtype samples were sequenced in the C2V3 region of the *env* gene. In addition, the B/A sample was sequenced in part of the protease gene. Three of four sequenced B subtypes showed the amino acid sequence of the apex of the principal neutralizing determinant in the tip of the V3 loop of the HIV-1 *env* gene as GPG. One of four sequenced B subtypes presented this motif as GWG, which corresponded to the so-called B*, which is highly prevalent among subtype B as reported in different regions in Brazil (5,6). Sequence analysis of the *env* gene from the subtype C sample confirmed the detection of this subtype. Sequence analysis of the HIV-1 *env* and protease genes from the B/A isolate showed that its sequence belongs to HIV-1 subtypes B and A, respectively. The amino acid sequence of this isolate showed the GPG motif in the tip of the V3 loop in the *env* gene. The prevalence of the subtype B is in keeping with its predominance in other parts of Brazil (3).

HIV-1 subtype C was detected in a patient with recent history of migration from southern Brazil. This subtype has been detected in that region of Brazil (7), where it accounts for almost 20% of the subtyped samples (unpublished data). More recently, this subtype has been reported in the southeastern (3) and northeastern (8) parts of the country. HIV-1 subtype C has been reported as the most prevalent subtype worldwide (9). In India and in several African countries, it has been detected among patients who contracted the disease through heterosexual transmission group as the most commonly transmitted subtype at this time (9–11).

To our knowledge, this is the first molecular evidence of the introduction of HIV-1 subtype A in Latin America. Concerning the B/A sample, we could consider it as a double infection or as a recombination event according to the HMA result. Simultaneous circulation of various HIV-1 subtypes increases the probability of dual infections and the appearance of mosaic genomes due to intersubtype recombination events (12). HIV-1 subtype A is the most prevalent strain in Africa and a prospective study in Senegal indicated that this subtype might be less pathogenic with slower rate of disease progression (13).

Different HIV-1 subtypes have been considered as markers of the spread of the epidemic. Our findings point out the importance of current patterns of population migration and national and international travel in the introduction and spread of new subtypes into a population. Despite the small sampling size in our study, it was possible to demonstrate the presence of different subtypes in Central West region of Brazil. The demonstration of noteworthy HIV-1 subtype diversity among pregnant women in Central Brazil with the potential spreading by vertical and horizontal transmission strengthen the need of a large and systematic sampling for HIV-1 diversity surveillance.
A better understanding of the molecular pattern of the epidemic is valuable to AIDS prevention and control programs in Brazil.

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