isolation, as required by microbiological criteria, was not possible because a second sputum sample was unavailable.

*M. sherrisii* is a relatively new species (6), closely related to *M. simiae*. Although most of the rare *M. sherrisii* infections reported since 2004 (online Technical Appendix Table 1, http://wwwnc.cdc.gov/EID/article/21/11/14-1809-Techapp1.pdf) were diagnosed in Europe or the United States, about half of the strains were isolated from patients in Africa. Because *M. sherrisii* infection probably is further underestimated by being misidentified as *M. simiae* infection by the commercially available line probe assays, the hypothesis that *M. sherrisii* infection is not so infrequent in the African setting seems therefore reasonable. In addition, the strategy recommended by World Health Organization and based on use of immunochromatographic tests (7), does not enable NTM identification. A leitmotiv of most *M. sherrisii* infections reported to date is HIV co-infection, which leads to dissemination of the mycobacterial disease.

This report, although it adds to the record of patients in Africa, does not support the association with HIV infection. Our findings are consistent with the view that the pathogenic potential of *M. sherrisii* is comparable to that of other well-known NTM species (e.g., MAC) responsible for disease both in HIV-positive and HIV-negative patients. The retrospective determination of the MICs of antimicrobial agents potentially active against slowly growing mycobacteria (online Technical Appendix Table 2) confirmed, for the 4 strains of *M. sherrisii*, the well-known multidrug resistance of the species (8). The therapeutic failure was thus not surprising because clarithromycin was the only drug among those administered during the treatment that had been shown to be active in vitro. This report provides evidence that conducting appropriate microbiological investigations is essential before initiating a treatment with second-line TB drugs (9).

References


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### Histoplasmosis in HIV-Infected Persons, Yaoundé, Cameroon

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To the Editor: In HIV-infected persons in Cameroon (Central Africa), histoplasmosis is still misdiagnosed as tuberculosis because of clinical similarities (1,2). These patients are automatically given presumptive antituberculous therapy, although tuberculosis is not confirmed. The patients subsequently die of probable disseminated histoplasmosis (DH), and the fungal infection might finally be detected in postmortem tissue samples (3). In this context, 3 cases of DH were detected in HIV-infected patients within a 1-year period (2007–2008) in Yaoundé, Cameroon. We initiated this study to investigate the occurrence of histoplasmosis in HIV-infected patients in 4 medical centers for AIDS treatment in Yaoundé from December 2008 through December 2011.

We recruited patients with known HIV status who agreed to participate in the study. Inclusion criteria were CD4 cells <200/mm³, fever and cough of ≥2 weeks’ duration, and a positive Histoplasma capsulatum skin test. The skin test was performed according to the manufacturer’s instructions (Statens Serum Institut, Copenhagen, Denmark). Positive reactions (≥5-mm induration) were observed in 211 patients (124 HIV-infected persons and 87 non-HIV-infected persons). DH was considered to be present if patients developed fever, cough, night sweats, and weight loss. In 20 of the 124 HIV-infected patients, histoplasmosis was diagnosed during the study period. In 17 of these patients, the diagnosis was based on the detection of Histoplasma capsulatum in respiratory samples. After DH diagnosis, patients were treated with fluconazole (100 mg orally twice daily) for 6 months. Additionally, 9 patients received an antiretroviral regimen. None of these patients died. These results confirm that DH is an important cause of death in HIV-infected patients in Cameroon. Therefore, a high index of suspicion is required to diagnose DH and to initiate effective therapy.

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duration, weight loss, asthenia, and histoplasmosis-like skin manifestations (i.e., ulcerative lesions and/or umbilicated papules or nodules and/or pustules). Patients under effective antituberculous therapy or antimicrobial drugs for any skin or pulmonary infectious disease were excluded from the study. CD4 cell counts were performed in all patients. Histoplasmosis was diagnosed in sputum, bronchoalveolar fluid (BALF), and bronchial and skin biopsies by direct staining with Gomori’s methenamine silver and periodic acid Schiff stains and by culture of sputum and BALF samples on Sabouraud medium. Tuberculosis and bacterial infections were detected in sputum and BALF by using Ziehl-Neelsen and Gram staining and culture on Lowenstein-Jensen and Streptococcus pyogenes media. All laboratory examinations were performed at the Centre Pasteur du Cameroun in Yaoundé. Data were collected on an anonymous questionnaire. Means (and SDs) were calculated for quantitative variables, and frequencies were calculated for qualitative variables. The National Ethics Committee, the Ministry of Health of Cameroon, and the medical centers where the study took place approved the study. Patients approved and signed the informed consent form at the time of recruitment.

Our study comprised 56 patients. Histoplasma capsulatum was detected in 7 (13%) patients on 6 of 7 skin biopsies and 1 of 3 bronchial biopsies. The median CD4 cell count of H. capsulatum–positive patients was 40 cells/mm³. Similarly, some authors have reported diagnosis of severe DH by using direct staining of skin samples (4); in low-income countries, skin involvement is the main presentation of DH because of limited laboratory facilities and/or late diagnosis. In Cameroon until recently, all DH cases in HIV-infected persons were diagnosed by skin biopsy or by chance on peripheral blood smear, thus revealing AIDS at the terminal stage (3,5). We did not detect H. capsulatum infection in sputum or BALF. These results are congruent with findings in Abidjan, Côte d’Ivoire, in 1999 (6). African histoplasmosis was not detected in any sample; although this type is endemic to areas with high rates of HIV infection, it is infrequently associated with AIDS patients (7).

We detected Mycobacterium tuberculosis in 18 (32%) patients and Candida albicans in 14 (25%) patients; 3 (0.5%) patients were co-infected with M. tuberculosis and C. albicans. M. tuberculosis was detected in sputum of 9 (21%) of 42 patients and in BALF of 9 (53%) of 17 patients; we detected C. albicans in sputum of 13 (31%) patients. Our detection of M. tuberculosis in 32% of patients confirms tuberculosis as the main AIDS-defining illness in Cameroon. We did not find tuberculosis and histoplasmosis co-infection, even though it occurs frequently in low-income countries (1,8).

The limitation in our study was the unavailability of validated sensitive and specific tools for diagnosing histoplasmosis in Cameroon (e.g., detection of the H. capsulatum circulating antigen in body fluid using an enzyme immunoassay) (9). Thus, using direct staining methods and culture of biopsies and body fluid samples could possibly lead to false-negative results.

Our detection of H. capsulatum in 13% of the HIV-infected patients in this study suggests that histoplasmosis is an unknown public health problem in Cameroon that is misdiagnosed as tuberculosis. Accounting for the endemicity of tuberculosis, which is the main HIV-defining illness in Cameroon, and the fatal outcome of DH in HIV-infected patients, practitioners need a high index of awareness to differentiate between tuberculosis and histoplasmosis. A recent report showed major clinical and biologic factors discriminating between these infections (10). Knowing these factors may lead practitioners to early diagnosis and treatment of histoplasmosis and in turn reduce the death rate among HIV-infected patients.

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References
Divergent Gemycircularvirus in HIV-Positive Blood, France

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To the Editor: Gemycircularviruses are a group of recently discovered single-stranded DNA viruses, found initially in fungi in 2010 (1). These “myco-like” viruses have a genome ranging from 2.1 to 2.3 kb, containing 2 opposite open reading frames that probably code for a capsid protein (CP) and a spliced replication-associated protein (Rep). Related viruses have been subsequently identified in animal blood and fecal matter, raw and treated sewage, and insects and plant material, suggesting that gemycircularviruses may represent a large group of viruses exhibiting considerable genetic diversity (2–8). The presence of these viruses was recently extended to humans after gemycircularvirus sequences were identified in human blood and brain tissue (multiple sclerosis patient), cerebrospinal fluid, and fecal matter (δ, 9).

While investigating the virome content of an HIV-positive blood donation, we identified several gemycircular-virus-related sequences. The initial metagenomic approach involved an HIV-1–positive plasma sample (B genotype, ≥530 copies/mL) obtained from the French blood agency national plasma bank in Tours, France. A 4-mL aliquot was prepared for metagenomic analysis after filtration, concentration, and nucleases treatment. Next, particle-protected nucleic acids were recovered and used for the preparation of a next-generation sequencing library and its subsequent analysis (online Technical Appendix, http://wwwnc.cdc.gov/EID/article/21/11/15-0486-Techapp1.pdf). Gemycircularvirus sequences identified among reads (1,680 vs. 82,560 reads total; ≈2%) were assembled into a resulting full-length sequence (Gemyc1c) by using CodonCode Aligner version 5.1 (CodonCode Corporation, Centerville, MA, USA). This sequence was verified by using back-to-back specific primers, and the amplicon was cloned and sequenced according to the Sanger method.

The analysis of the Gemyc1c sequence (2,109 nt, GenBank accession no. KP987887) revealed a genome divergent from those already available in databases, despite a similar genomic organization (Figure, panel A) and assignment to gemycircularviruses after BLAST (http://blast.ncbi.nlm.nih.gov/Blast.cgi) analysis of putative CP and Rep proteins. This divergence was demonstrated by the phylogenetic analysis of the deduced CP (Figure, panel B), which exhibited ≈72% and ≈44% aa pairwise identity with the 2 closest gemycircularvirus CP sequences available in GenBank (gemycircularvirus c from mongoose feces [Conceicao-Neto N., unpublished data] and HCBI8.215 from cattle blood, respectively). Moreover, Gemyc1c CP exhibited ≈30% pairwise identity with viral sequences identified previously in humans (BZ1 from feces, SL1 from cerebrospinal fluid, MSS12.225 from blood). The deduced spliced Rep (major Rep1 and minor Rep2), seen in such viruses, contained putative rolling circle motifs I (LFTYS), II (HLHAFVD), and III (YATKD) retrieved from gemycircularviruses (4).

We subsequently investigated the presence of Gemyc1c DNA in 128 HIV-positive plasma samples (French blood agency national plasma bank) along with 256 HIV-negative plasma samples (healthy blood donors, southeastern France; mean donor age 38 years; 136 men; 1 man:1.13 women). Plasma samples were prepared as described previously (10), and extracted nucleic acids were tested for Gemyc1c DNA by using a specific PCR that included negative, positive, and extraction controls (online Technical Appendix).

Application of the above Gemyc1c DNA detection system did not generate any positive signal in the 384 plasma samples in this study, suggesting that the presence...