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

1. Hoefsloot W, van Ingen J, Andrejak C, Angeby K, Bauriaud R, Bemer P, et al. The geographic diversity of nontuberculous mycobacteria isolated from pulmonary samples: an NTM-NET collaborative study. Eur Respir J. 2013;42:1604–13. http://dx.doi.org/10.1183/09031936.00149212
2. Badoum G, Saleri N, Dembele MS, Ouedraogo M, Pinsi G, Boncoungou K, et al. Failing a re-treatment regimen does not predict MDR/XDR tuberculosis: is "blind" treatment dangerous? Eur Respir J. 2011;37:1283–5. http://dx.doi.org/10.1183/09031936.00144710
3. Tortoli E, Pecorari M, Fabio G, Messinò M, Fabio A. Commercial DNA-probes for mycobacteria incorrectly identify a number of less frequently encountered species. J Clin Microbiol. 2010;48:307–10. http://dx.doi.org/10.1128/JCM.01536-09
4. Crump JA, van Ingen J, Morrissey AB, Boeree MJ, Mavura DR, Swai B, et al. Invasive disease caused by nontuberculous mycobacteria, Tanzania. Emerg Infect Dis. 2009;15:53–5. http://dx.doi.org/10.3201/eid1501.081093
5. Griffith DE, Aksamit T, Brown-Elliott BA, Catanzaro A, Daley C, Gordin F, et al. An official ATS/IDSA statement: diagnosis, treatment, and prevention of nontuberculous mycobacterial disease. Am J Respir Crit Care Med. 2007;175:367–416. http://dx.doi.org/10.1164/rccm.200604-571ST
6. Selvarangan R, Wu WK, Nguyen TT, Carlson LDC, Wallis CK, Stiglich SK, et al. Characterization of a novel group of mycobacteria and proposal of *Mycobacterium sherrisii* sp. nov. J Clin Microbiol. 2004;42:52–9. http://dx.doi.org/10.1128/JCM.42.1.52-59.2004
7. World Health Organization. Use of liquid TB culture and drug susceptibility testing (DST) in low and medium income settings. Geneva: the Organization; 2007.
8. van Ingen J, Tortoli E, Selvarangan R, Coyle MB, Crump JA, Morrissey AB, et al. *Mycobacterium sherrisii* sp. nov.; a slow-growing non-chromogenic species. Int J Syst Evol Microbiol. 2011;61:1293–8. http://dx.doi.org/10.1099/ijs.0.024752-0
9. Miotto P, Saleri N, Dembele M, Ouedraogo M, Badoum G, Pinsi G, et al. Molecular detection of rifampin and isoniazid resistance to guide chronic TB patient management in Burkina Faso. BMC Infect Dis. 2009;9:142. http://dx.doi.org/10.1186/1471-2334-9-142

Address for correspondence: Enrico Tortoli, San Raffaele Scientific Institute–Emerging Bacterial Pathogens Unit, via Olgettina 60, 20132 Milano, Italy; email: tortoli.enrico@hsr.it

Histoplasmosis in HIV-Infected Persons, Yaoundé, Cameroon

Christine E. Mandengue, Antoinette Ngandjio, Paul J.A. Atangana

Author affiliations: Université des Montagnes, Bangangté, Cameroon (C.E. Mandengue); Centre Pasteur du Cameroun, Yaoundé, Cameroon (A. Ngandjio, P.J.A. Atangana)

DOI: http://dx.doi.org/10.3201/eid2111.150278

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/mm^3, fever and cough of ≥2 weeks'

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/mm^3. 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.

Acknowledgments

We thank Omer Njajou for statistical analysis of data.

This study was financially supported by the Réseau International des Instituts Pasteur.

References

1. Couppié P, Aznar C, Carme B, Nacher M. American histoplasmosis in developing countries with a special focus on patients with HIV: diagnosis, treatment, and prognosis. Curr Opin Infect Dis. 2006; 19:443–9. http://dx.doi.org/10.1097/01.qco.0000244049.15888.b9
2. Jeong HW, Sohn JW, Kim MJ, Choi JW, Kim CH, Choi SH, et al. Disseminated histoplasmosis and tuberculosis in a patient with HIV infection. Yonsei Med J. 2007;48:531–4. http://dx.doi.org/10.3349/ymj.2007.48.3.531
3. Mandengue CE, Lindou J, Mandeng N, Takuefou B, Nouedoui C, Atangana P, et al. Fatal miliary tuberculosis in an HIV-infected Cameroon woman: disseminated histoplasmosis due to *Histoplasma capsulatum capsulatum* [in French]. Med Trop (Mars). 2011;71:615–7.
4. Couppié P, Clyti E, Nacher M, Aznar C, Sainte-Marie D, Carme B, et al. Acquired immunodeficiency syndrome–related oral/or cutaneous histoplasmosis. a descriptive study of 21 cases in French Guiana. Int J Dermatol. 2002;41:571–6. http://dx.doi.org/10.1046/j.1365-4362.2002.01590.x
5. Mandengue Ebenye C. A case of disseminated histoplasmosis detected in peripheral blood smear staining revealing AIDS at terminal phase in female patient from Cameroon. Case Rep Med. 2012;2012:215207.
6. Adou-Bryn KD, Ouhon J, Assoumou A, Kassi EA, Kone M, Therizol-Ferly M. Champignons et parasites isolés à l'examen de 142 liquides d'aspiration bronchique à Abidjan (Côte d'Ivoire). Med Afr Noire. 1999;46:362–5.
7. Loulergue P, Bastides F, Baudouin V, Chandenier J, Mariani-Kurkdjian P, Dupont B, et al. Literature review and case histories of *Histoplasma capsulatum* var. *duboisii* infections in HIV-infected patients. Emerg Infect Dis. 2007;13:1647–52. http://dx.doi.org/10.3201/eid1311.070665
8. Agudelo CA, Carlos A, Restrepo CA, Molina DA, Tobón AM, Kauffman CA, et al. Tuberculosis and histoplasmosis co-infection in AIDS patients. Am J Trop Med Hyg. 2012;87:1094–8. http://dx.doi.org/10.4269/ajtmh.2012.12-0292

9. Adenis AA, Aznar C, Couppié P. Histoplasmosis in HIV-infected patients: a review of new developments and remaining gaps. Curr Trop Med Rep. 2014;1:119–28.
10. Adenis A, Nacher M, Hanf M, Basurko C, Dufour J, Huber F, et al. Tuberculosis and histoplasmosis among human immunodeficiency virus–infected patients: a comparative study. Am J Trop Med Hyg. 2014;90:216–23. http://dx.doi.org/10.4269/ajtmh.13-0084

Address for correspondence: Christine E. Mandengue, Department of Internal Medicine (Dermatology), Université des Montagnes, Cliniques Universitaires des Montagnes, PO Box 208, Bangangté, Cameroon; email: cmmandengue@udesmontagnes.org

Divergent Gemycircularvirus in HIV-Positive Blood, France

Rathviro Uch, Pierre-Edouard Fournier, Catherine Robert, Caroline Blanc-Tailleur, Vital Galicher, Romain Barre, François Jordier, Philippe de Micco, Didier Raoult, Philippe Biagini

Author affiliations: Centre National de la Recherche Scientifique, Marseilles (R. Uch, P.-E. Fournier, C. Robert, C. Blanc-Tailleur, V. Galicher, R. Barre, F. Jordier, P. de Micco, D. Raoult, P. Biagini); Institut Hospitalo-Universitaire Méditerranée-Infection, Marseille, France (R. Uch, P.-E. Fournier, C. Robert, C. Blanc-Tailleur, R. Barre, F. Jordier, P. de Micco, D. Raoult, P. Biagini); Aix-Marseille Université, Marseille (R. Uch, P.-E. Fournier, C. Robert, C. Blanc-Tailleur, V. Galicher, R. Barre, F. Jordier, P. de Micco, D. Raoult, P. Biagini); Unité Mixte de Recherche 7268 ADES, Marseilles (R. Uch, V. Galicher, R. Barre, F. Jordier, P. de Micco, P. Biagini); Etablissement Français du Sang, Marseilles (R. Uch, V. Galicher, R. Barre, F. Jordier, P. de Micco, P. Biagini); Unité de Recherche sur les Maladies Infectieuses et Tropicales Emergentes, Marseilles (P.-E. Fournier, C. Robert, C. Blanc-Tailleur, D. Raoult)

DOI: http://dx.doi.org/10.3201/eid2111.150486

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 (*8,9*).

While investigating the virome content of an HIV-positive blood donation, we identified several gemycircularvirus-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., unpub. 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, MSSI2.225 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