Disseminated Blastomycosis Mimicking Tuberculosis, China

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Blastomycosis is endemic in central and southern North America but rare in China. It can mimic community-acquired pneumonia, tuberculosis, or cancer. We describe a patient who initially had tuberculosis diagnosed and later had blastomycosis diagnosed through metagenomic detection, which aided diagnosis and treatment. Clinicians should consider blastomycosis in differential diagnoses for respiratory diseases.

Blastomycosis is a dimorphic fungal infection endemic to North America but rarely reported in China. (*1*). The pathogen is not directly transmissible between persons (*1*). Disseminated blastomycosis should be considered in cases with multisystemic involvement, even when typical symptoms such as cutaneous or central nervous system lesions are absent (*2*). Clinical manifestations of blastomycosis often mimic those of tuberculosis (TB), malignancy, or bacterial pneumonia, complicating diagnosis. *Blastomyces percursus*, a novel species phenotypically and epidemiologically distinct from *B. dermatitidis*, has been linked to infections in patients from Israel, South Africa, and other regions in Africa (*3*,*4*). We report an unusual case of *B. percursus* infection in China that was initially diagnosed as pulmonary tuberculosis.

A 38-year-old man from Xinxiang, Henan Province, China, sought care after 4 months of cough, hemoptysis, and weight loss. He had been treated empirically with antimicrobial drugs at a local hospital without substantial improvement. He had no history

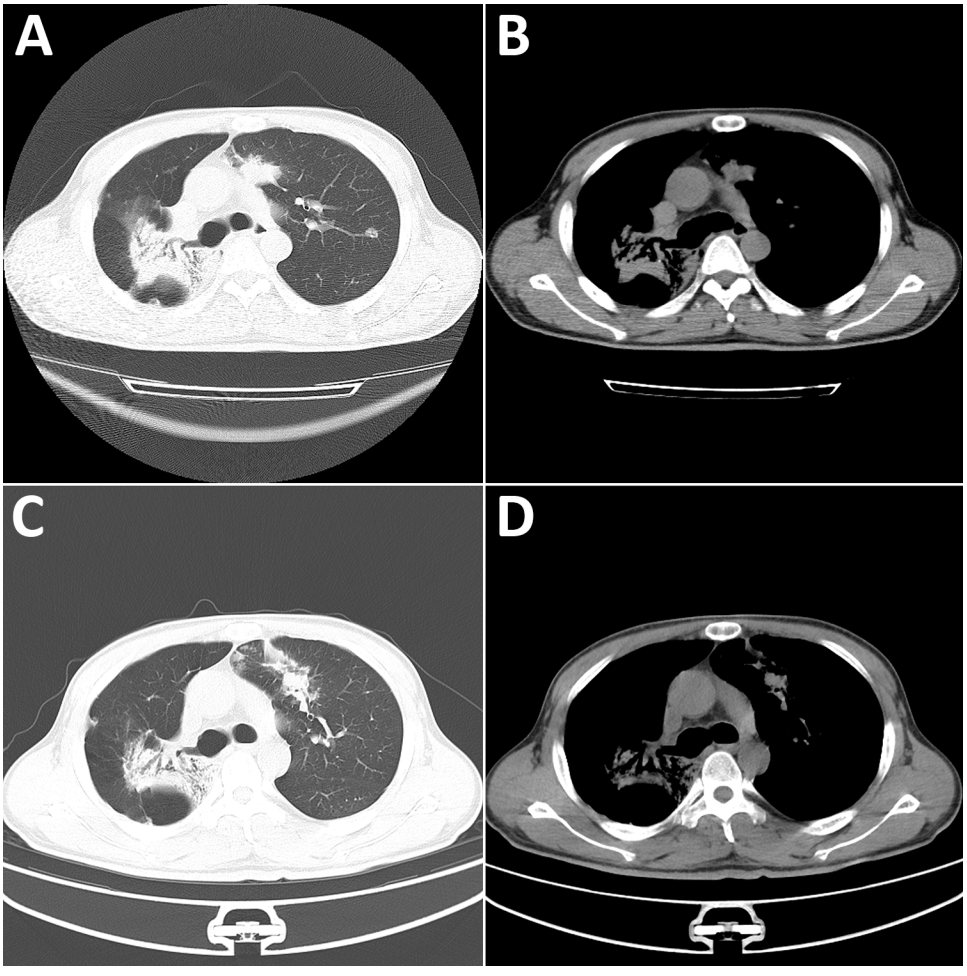

Figure 1. Chest computed tomography (CT) images from a patient with disseminated blastomycosis mimicking tuberculosis, China. A, B) Chest CT at first admission revealed bilateral lobar infiltrates (A) and patchy opacities (B). C, D) Chest CT taken 2 months later showed resolution of left lung lesions but progression of right lung lesions.

of incarceration, foreign travel, or known immunosuppression. He worked as a truck driver and had lived locally for years.

Chest computed tomography scans revealed bilateral lobar infiltrates and patchy opacities (Figure 1, panels A, B). Tests for *Aspergillus galactomannan*, β-D-glucan, and respiratory viruses were negative. Bronchoscopy revealed noncaseating granulomatous inflammation, and all stains and cultures for mycobacteria and fungi were negative. Because of clinical suspicion, we started the patient on a 4-drug TB treatment regimen (rifampin 600 mg, isoniazid 300 mg, ethambutol 1,000 mg, and pyrazinamide 1,500 mg daily).

Two months later, the patient was readmitted with new cutaneous lesions on his abdomen and lower limbs, which were nodular and verrucous (Figure 2). Laboratory studies showed leukocytosis (leukocyte count 14,160/μL) and 85.9% neutrophils. Results of ELISA testing for HIV were negative, and results for tumor markers and autoimmune antibody panels were unremarkable. Repeat chest computed tomography scans demonstrated resolution of left lung lesions but progression on the right (Figure 1, panels C, D).

Repeat bronchoscopy was performed. GeneXpert MTB/RIF (Cephalid, https://www.cepheid.com) testing of bronchoalveolar lavage fluid was negative. However, 1 week later, metagenomic next-generation sequencing of bronchoalveolar lavage fluid identified *B. percursus*.

The patient received intravenous liposomal amphotericin B (3 mg/kg/d) for 2 weeks, then oral itraconazole (200 mg 2×/d) for 1 month. After treatment, both pulmonary and cutaneous lesions resolved. Itraconazole remains a preferred agent for treating mild-to-moderate pulmonary and disseminated blastomycosis (*8*).

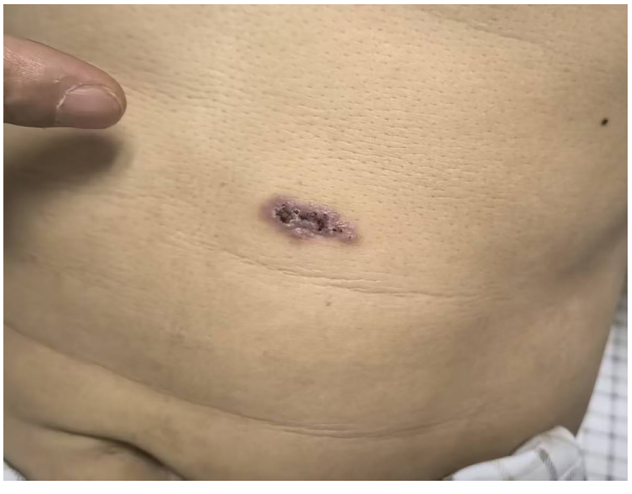

Figure 2. Cutaneous lesion on the abdomen from a case of disseminated blastomycosis mimicking tuberculosis, China. Two months after treatment for tuberculosis, new cutaneous lesions developed on the patient's abdomen and lower limbs; molecular methods on bronchoalveolar lavage fluid detected *Blastomyces percursus*.

Blastomycosis can involve virtually any organ and often masquerades as TB, leading to frequent misdiagnoses. In this case, the patient was treated with multiple drugs for TB, delaying accurate diagnosis by ≥1 month. Ultimately, metagenomic sequencing identified *B. percursus*. Metagenomic approaches increasingly have been applied to clinical microbiology for detecting pathogens in respiratory infections (*5*), bloodstream infections (*6*), and central nervous system infections (*7*). Those methods make unbiased, broad-spectrum detection possible even when conventional tests fail.

The delay in diagnosis led to unnecessary drug exposure and progressive dissemination, including cutaneous lesions. Medications for TB carry substantial risks, including hepatotoxicity and bone marrow suppression. The lack of reliable rapid diagnostic tests for *B. percursus* remains a barrier to timely treatment. Comprehensive physical examination, especially of the skin, is crucial, because cutaneous findings can aid in early recognition. In this case, clinicians adhered to a TB diagnosis despite a lack of microbiological evidence, and skin lesions developed in the patient while he was receiving empirical TB therapy only. Earlier consideration of alternative etiologies, such as blastomycosis, nocardiosis, or actinomycosis, might have expedited appropriate care.

This case illustrates how blastomycosis, although rare in China, can mimic pulmonary TB and lead to delayed diagnosis and treatment. Clinicians should include blastomycosis in the differential diagnosis of unexplained pulmonary infections. Increasing awareness of endemic mycoses and integrating metagenomic tools into routine diagnostics could improve the precision and timeliness of care.

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Crimean-Congo Hemorrhagic Fever Virus Circulation in Wild European Rabbits, Portugal, 2018–2023

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Crimean-Congo hemorrhagic fever virus is considered a public health risk in southwestern Europe. We surveyed serum samples from 667 European rabbits across Portugal, a rabbit species known to host immature *Hyalomma lusitanicum* ticks. We found low levels of virus antibodies (>1%), with a localized cluster reaching 5.77% in southern populations.

Crimean-Congo hemorrhagic fever virus (CCHFV) is a highly pathogenic tickborne pathogen able to cause severe hemorrhagic fever that has a high case-fatality rate in humans (*1*). Since the virus' first detection in southwestern Europe in 2010 (*2*), CCHFV has emerged as a formidable public health risk. Reports from Spain have identified *Hyalomma lusitanicum* ticks as reservoirs and vectors of CCHFV (*2*–*4*) and have suggested circulation and maintenance of the virus at local levels to be related to animal abundance (*5*). Mammals infected by tick bites become viremic for 2–10 days and develop a persistent immune response (*4*), making serologic surveys an effective tool for monitoring CCHFV dynamics (*2*,*4*–*6*).

Wild lagomorphs, and particularly European rabbits (*Oryctolagus cuniculus*), are key hosts of immature stages of *H. lusitanicum* ticks (*7*) and are expected to play a critical role in CCHFV epidemiology (*8*). However, prior reports have not established clear evidence of natural exposure of lagomorphs to CCHFV in Europe (*8*). Our study aimed to fill this gap through a serologic survey of rabbit populations from Portugal.

During May 2018–December 2023, we sampled 667 wild rabbits across 20 sites throughout mainland Portugal (average 33.4 ± 46.1 [standard deviation] rabbits per site) (Figure). We selected 8 longitudinal sites on the basis of their high rabbit abundance.