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CASE REPORT

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Scedosporium boydii pulmonary infection in an immunocompetent patient with COPD confirmed by next-generation metagenomic sequencing and culture: a case report

Jiaqing Ye[1,2†], Suli Jin[3†], Yahua Li[2], Weili Gao[4], Cuiying Zheng[2], Huifen Zuo[5], Chenfeng Zhang[2], Minghui Song[2], Jiahao Hao[2], Yuxin Liu[6], Zhongjun Feng[2], Hong Zhang[4], Zhenjun Zhao[5*], Yumei Guo[4*] and Lijie Zhang[2*]

Abstract

Scedosporium boydii infections pose diagnostic challenges due to their nonspecific clinical manifestations and slow growth characteristics in conventional cultures. This paper highlights the diagnostic value of molecular technology combined with targeted prolonged culture for rare fungi. Unitl now, only one case was identified using metagenomic next-generation sequencing (mNGS). This case represents the first report of a 20-day delayed culture confirmation of *S. boydii* guided by mNGS results in a non-immunocompromised chronic obstructive -with history of COPD who was admitted with fever and cough. Despite two weeks of antibacterial treatment, chest computed tomography (CT) showed worsening infection. To clarify the pathogen, mNGS and bacterial culture of bronchoalveolar lavage fluid (BALF) were performed. Subsequent culture and Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry (MALDI-TOF MS) confirmed the growth of *Scedosporium* species. Based on clinical presentation, chest CT findings, mNGS results, pulmonary Scedosporiosis was diagnosed, and an antifungal treatment regimen (200 mg BID orally) was initiated. Subsequent culture confirmed *S. boydii* growth and antifungal susceptibility results were also obtained. After six weeks of voriconazole treatment, he was discharged from the hospital and continued to take oral medication for three months. He was fully recovered without recurrence after six months of follow-up. The present case suggests that mNGS findings can unveil cryptic pathogens like *Scedosporium*. Use mNGS results to trigger intentional, extended targeted cultivation– challenging standard incubation times – especially in non-immunocompromised hosts with underlying lung disease. Seamless clinician-laboratory collaboration is paramount for treatment success.

†Jiaqing Ye and Suli Jin contributed equally to this work and share first authorship.

*Correspondence:
Zhenjun Zhao
zzjhospital@sina.com
Yumei Guo
325069675@qq.com
Lijie Zhang
zhanglijie@hebmu.edu.cn

Full list of author information is available at the end of the article

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Background

The nomenclature and classification of *Scedosporium* species have undergone multiple revisions [1–4]. *Scedosporium apiospermum* was originally considered the sexual stage of *Pseudallescheria boydii*, with both included under *Scedosporium.* According to the latest classification, *S. apiospermum* and *Scedosporium boydii* are now classified as separate species, with the latter's asexual stage referred to as *S. boydii* [2]. The genus name *Scedosporium* has replaced *Pseudallescheria* [5].

Scedosporium species have been reported as the second most common filamentous fungi causing clinical infections after *Aspergillus* in Spain and Australia [6]. Scedosporiosis is an emerging fungal infection caused by species of the *Scedosporium* complex species [7]. The main fungal pathogens belong to the *S. apiospermum* species complex, includes *S. apiospermum*, *S. boydii*, *Scedosporium ellipsoideum*, *Scedosporium angustum*, *and Scedosporiu*m fusoideum [8]. In Asian countries such as India, Japan, and Malaysia, *S. apiospermum* is the most common pathogen within this genus, followed by *S. boydii* and *S. aurantiacum* [7]. *Scedosporium* is a genus of saprophytic fungi widely distributed in soil and contaminated water sources [9]. Among these species, *S. boydii* is an opportunistic pathogen that frequently causes invasive fungal infections in immunocompromised individuals.

We present the case of a 61-year-old male with a documented history of chronic obstructive pulmonary disease (COPD) who exhibited no clinical improvement following a two-week course of antibacterial therapy. Pulmonary infection with *S. boydii* was definitively diagnosed through metagenomic next-generation sequencing (mNGS), Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF MS), and fungal culture. The patient subsequently achieved complete resolution of infection following treatment with voriconazole.

Case presentation

A 61-year-old male, with a history of COPD, presented with fever for 3 days and cough for 1 day. He was admitted to Respiratory Department with a diagnosis of pulmonary infection on December 15, 2023. Laboratory tests revealed an Hs-CRP level of 23.94 mg/L, a WBC count of 6.71 × 10^9/L, and a NEUT% of 48.90%. Chest CT on December 15, 2023, showed a high-density shadow in the anterior segment of the right upper lobe, along with multiple small nodules, linear opacities, and emphysema in both lungs (Fig. 1A). Based on clinical findings, empirical treatment with cefuroxime (3 g IV bid) and moxifloxacin (0.4 g PO daily) was initiated on December 16, 2023. Meanwhile, respiratory samples were obtained for microbiological culture. After one weeks of treatment, Sputum culture initially identified *Pseudomonas aeruginosa*, prompting a change in antimicrobial therapy to piperacillin-tazobactam (4.5 g IV q8h) combined with aztreonam (2 g IV q8h) on December 21, 2023. After 10 days of treatment, follow-up chest CT showed disease progression. Although the extent of pulmonary infection had slightly decreased compared to previous imaging, inflammatory resolution remained slow, with partial consolidation of patchy shadows in the right upper lobe (Fig. 1B). Because empirical treatment is not effective, the patient was advised that bronchoscopy could be performed to determine whether coinfection with other pathogens was present.

To establish a definitive diagnosis, bronchoalveolar lavage fluid (BALF) was obtained from the patient on December 29, 2023 for mNGS and bacterial culture. The mNGS identified 15,470 sequences of *S. boydii* on December 30, which was highly suspected as the causative pathogen. We uploaded the sequencing results of the strain to NCBI with the accession number PRJNA1102500 (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1102500/). Based on the mNGS results, the clinical microbiology laboratory staff extended the incubation period. We found that *S. boydii* grew within 1 to 7 days (Table 1). However, in this case, it took up to 20 days for colony growth. After 20 days of incubation of BALF samples, *S. boydii* was cultured and identified by MALDI-TOF MS. Colonies grew on sabouraud dextrose agar (SDA) at 25 °C (Fig. 2A). The surface texture of colony was spreading, white and cottony on blood agar plates (Fig. 2B). Colony morphology after 31 days of cultivation was shown (Fig. 2C). Fine, transparent and separated hyphae were observed in the 10% KOH and gossypol blue stained smears, and most of the conidia were oval-shaped, with a size of about 4–9 μm (Fig. 2D-E). Further inquiry revealed that the patient had been working in the basement many times in the past six months, where the air was humid, dusty and musty. It was speculated that he might have inhaled the pathogen at that time. *Scedosporium* can colonize respiratory secretions in patients with chronic lung diseases such as COPD, so the patient was at higher risk of fungal infection. Overall, combined with the patient's imaging findings, the diagnosis was pulmonary *S. boydii* infection. In this case, the isolated strain showed an itraconazole MIC minimum inhibitory concentration value ≤ 0.002 μg/mL, voriconazole MIC value ≤ 0.002 μg/mL and an amphotericin B MIC

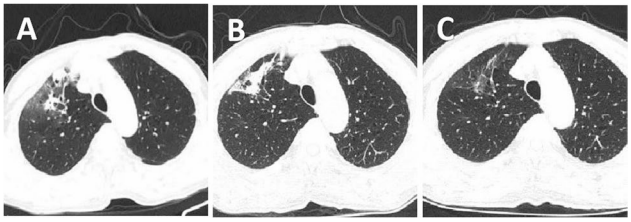

Fig. 1 **A** Chest CT showed a high-density shadow in the anterior segment of the right upper lobe, along with multiple small nodules, linear opacities, and emphysema in both lungs; **B** After two weeks of treatment, chest CT showed deterioration of the condition, with partial consolidation of patchy shadows in the right upper lobe; **C** Following six weeks of antifungal treatment, chest CT showed a reduction in the extent and density of the high-density shadow in the anterior segment of the right upper lobe

value ≥ 32 μg/mL. Then the patient was treated with antifungal therapy with voriconazole (200 mg BID po).

Following six weeks of antifungal treatment with voriconazole (until February 17, 2024), the CT scan showed a reduction in the extent and density of the high-density shadow in the anterior segment of the right upper lobe (Fig. 1C). The patient's symptoms of cough and expectoration resolved, and no significant abnormalities were found in the laboratory examination. Upon discharge, the patient continued with oral voriconazole treatment for 3 months. After six months of follow-up, the patient was fully recovered with no recurrence.

Discussion

S. boydii infections are uncommon, particularly in immunocompetent individuals. This case represents only the second reported instance of *S. boydii* detected via mNGS, emphasizing the utility of advanced molecular diagnostics in identifying slow-growing or fastidious pathogens. Typically, *S.boydii* colonies grow within 1–7 days; however, under the guidance of mNGS, incubation was extended for 20 days before colonies finally emerged;

Table 1 Search on pubmed for case reports related to infections caused by *S. boydii* (2016–2025). Abbreviations: COPD, chronic obstructive pulmonary disease; MALDI-TOF, matrix-assisted laser desorption/ionization time-of-flight

Reference	Country/Age/gender	Predisposing factors	Site of infection	Treatment	Outcome	Strain identification methods	Culture time(day)	
Vanzzini-Zago V, 2016	Mexico/69/male	Diabetes mellitus type 2 and prior surgery on the right femur is described	Eye	-	Enucleation of the eyeball	Morphological characteristics, DNA sequencing (Sanger sequencing)	-	[10]
Viñuela L, 2019	España/56/famale	Multiple fractures in a road accident	Skin	Voriconazole, Ketoconazole, amphotericin B	-	Morphological examination and MS MALDI-TOF	-	[11]
Jiang Y, 2020	USA/53/male	Coronary artery disease, stage V chronic kidney disease on hemodialysis, hypertension, diabetes mellitus, warm autoimmune hemolytic anemia, hypercholesterolemia, and gout	Brain, heart, thyroid, lung	Vancomycin, primaxin, doxycycline, micafungin	Died	DNA sequencing (ITS2-28 S rRNA PCR sequencing), Histopathologic Study	-	[12]
Jackson JS, 2022	USA/67/female	Left ankle grade 3 open trimalleolar fracture	Marrow	Voriconazole	Recover well	Culture	-	[13]
Gao S,2022	China/30/female	Systemic lupus erythematosus	Brain	Voriconazole	Died	Culture, DNA sequencing (mNGS)	1	[14]
Ramadán S, 2023	Argentina/58/male	COPD, heart transplant	Brain, heart, lung	Voriconazole, Amphotericin B	Died	Culture, DNA sequencing (ITS/β-tubulin sequencing)	7	[8]
Xiao Y, 2024	China/24/female	Foot infection for ten years	Foot	Voriconazole	Recover well	Culture, DNA sequencing (rDNA ITS sequencing)	2	[6]
Jackson DL,2024	USA/52/male	Hypertension, smoking, alcohol abuse, and marijuana use	Brain, heart	Ceftriaxone, Doxycycline, Cefepime, vancomycin, steroids	Died	DNA sequencing (Targeted Next-Generation Sequencing)	-	[15]
Jiaqing Y, 2025	China/61/male	COPD	lung	Voriconazole	Recover well	DNA sequencing (mNGS), culture, MALDI-TOF	20	This Study

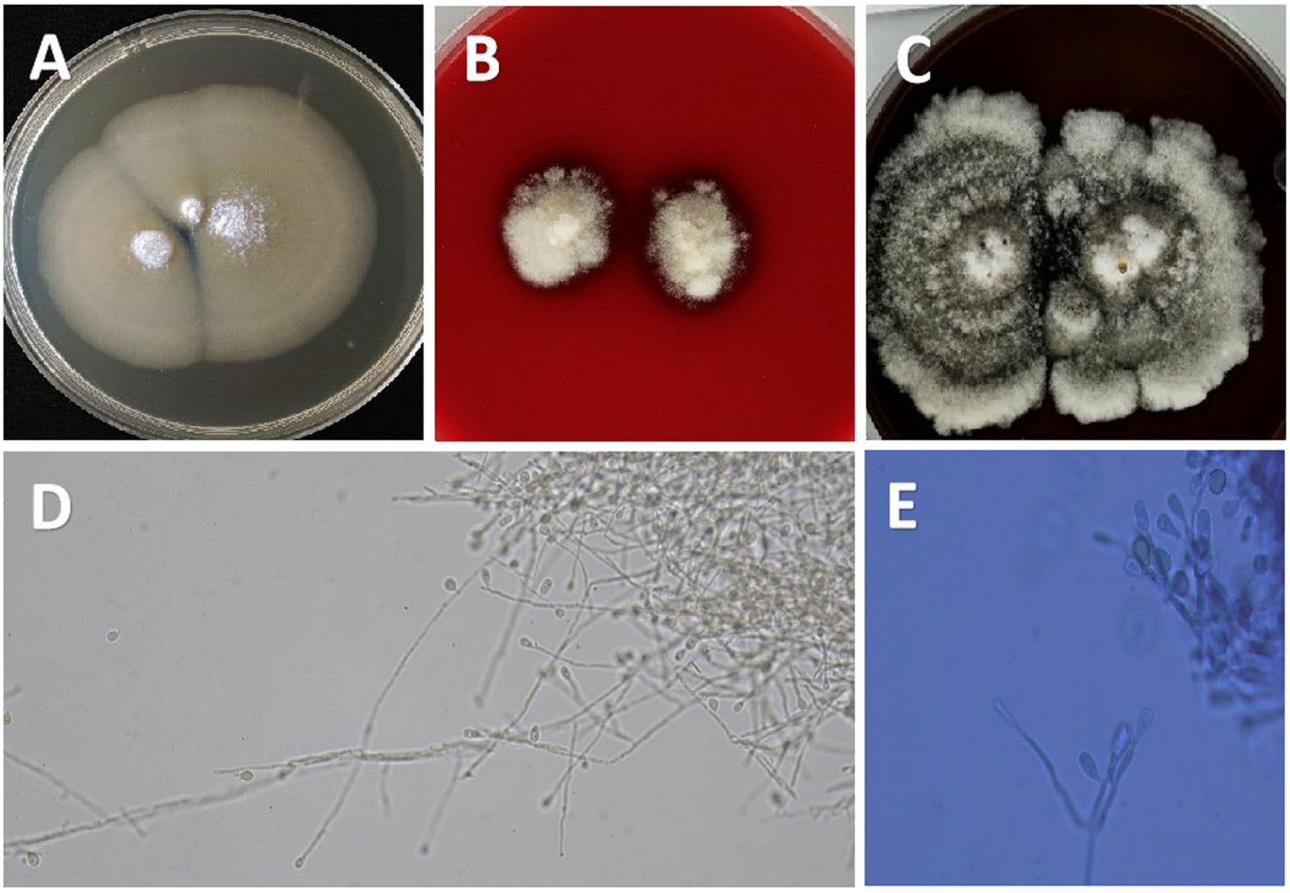

Fig. 2 **A** After 20 days of incubation of BALF samples, *S. boydii* was cultured and colonies grew on SDA; **B** The surface texture of colony was spreading, white and cottony on blood agar plates; **C** Colony morphology after 31 days of cultivation; **D**,**E**: Fine, transparent and separated hyphae were observed in the potassium hydroxide wet mount and gossypol blue stained smears, and most of the conidia were oval-shaped, with a size of about 4–9 μm

however. This case provides a detailed morphological atlas of *S. boydii*, including its dynamic growth characteristics on Sabouraud dextrose agar and blood agar over 20 and 31 days, as well as microscopic features of hyphae and conidia. The diagnostic-therapeutic process of this case was implemented as follows: mNGS detection → Microbial culture incubation extension (20days) →MALDI-TOF MS confirmation →Antifungal susceptibility-guided therapy (Fig. 3). mNGs findings can unveil cryptic pathogens like *Scedosporium*, Use these results totrigger intentional, extended targeted cultivation - challenging standard incubation timesespecially in non-immunocompromised hosts with underlying lung disease. Seamlessclinician-laboratory collaboration is paramount for success.

Due to changes in the bacterial nomenclature, we conducted a search on PubMed and found only 8 case reports of infections caused by *S. boydii* from 2016 to 2025(Table 1) [6, 8, 10–15], with this article being the 9th. Among these, only one report used mNGS for strain identification [14], making this the second case. Most of the patients (6/8) were over 50 years old, and infections predominantly occur in individuals with compromised immune function. The infection sites were quite extensive, involving the brain, heart, lungs, and even bone marrow. Voriconazole was used as a first-line treatment, with half of the patients receiving this medication. The duration of strain culture varied from 1 to 7 days, and clinical identification typically combined morphological analysis with DNA sequencing.

S.boydii infections frequently cause invasive fungal infections in immunocompromised patients, include post-transplant status, trauma, postoperative surgery, history of corticosteroid use, near-drowning, and idiopathic autoimmune diseases [6]. *Scedosporium* infections can affect any organ, with common sites being the lungs (27%), skin (23%), eyes (8%), and central nervous system (13%) [9]. Pulmonary infections caused by *Scedosporium* species most commonly present with cough (60.0%), followed by hemoptysis or blood-streaked sputum (50.0%) and fever (35.0%). When microbiological confirmation is unavailable but imaging findings strongly suggest fungal infection, management strategies should be adjusted based on host factors and radiological features.

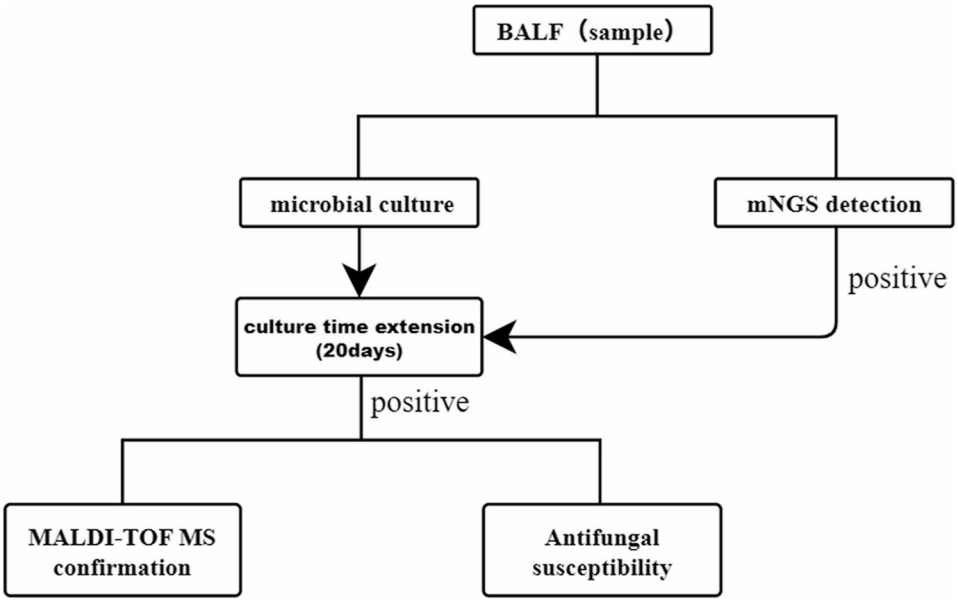

Fig. 3 *S. boydii* diagnostic flow chart

Characteristic CT findings of *Scedosporium* infections include consolidation, nodules, infiltrates, cavitary lesions with surrounding infiltrates, necrotizing pneumonia, abscesses, and pleural effusion [16, 17]. A small proportion of patients may develop fungal balls [18]. Imaging findings in *Scedosporium* infections lack specificity, making accurate etiological diagnosis particularly important.

Among the detection methods, clinical microbial culture has the advantage of being the gold standard for accurate strain identification and being cost-effective. However, its disadvantages include being time-consuming, potentially delaying diagnosis, and being prone to false negatives/misidentification. Species confirmation can be achieved through ITS and β-tubulin gene sequencing or other molecular methods [19]. MALDI-TOF MS offers the advantage of being economical and efficient, enabling species-level identification within minutes. However, its limitations include the requirement for prior pathogen isolation and culture, as well as insufficient database coverage for rare species, leading to reduced identification accuracy. mNGS has the advantage of detecting pathogens directly from clinical samples without the need for culture, enabling broad-spectrum detection of bacteria, fungi, viruses, and parasites. It provides results relatively quickly, typically within 24–48 h. However, its disadvantages include high cost, difficulty in distinguishing infection from colonization, and potential false positives due to environmental or human DNA contamination.

Infection with *S. boydii* is clinically rare and nonspecific, making early diagnosis particularly challenging. Currently, most diagnoses rely on molecular methods [19]. In this case, after *S. boydii* was detected in BALF by mNGS, the laboratory staff intentionally paid attention to extending the cultivation time. However, it took up to 20 days for colony growth. The possible reasons may be the difference in metabolic rate between different species and different isolates of *Scedosporium*, and poor culture conditions: temperature, humidity or oxygen partial pressure deviating from the optimal range may inhibit growth. It is worth noting that *S. boydii* had a higher initial positive rate in the first generation culture under 37℃5% CO_2 environment. Under typical conditions, *Scedosporium* spp colonies grew within 3–7 days at 37 °C on SDA medium, reaching a diameter of 60–70 mm after 10 days [7, 19]. Unlike what was described in the relevent literature, the strain in this case grew extremely slowly and did not grew until 20 days later. It can be said that the fungus might not have been cultivated if the culture time was not deliberately extended. This case once again highlights that compared to microbial culture, mNGS offers broader pathogen coverage, higher detection rates, improved accuracy, and shorter turnaround times, which are particularly advantageous for detecting unknown species, slow-growing, or intractable pathogens [14, 20]. Later, the fungus was cultured and drug sensitivity results were obtained. This case is a perfect combination of mNGS with traditional cultivation techniques and MALDI-TOF MS pathogen identification technology.

The initial antimicrobial treatment of the patient was unsatisfactory mNGS indicated that *S. boydii* might be the causative pathogen. The patient's past medical history was questioned and it was found that the patient had been exposed to a musty basement environment in the past six months and had a history of COPD.

Scedosporium species can colonize the lungs of individuals with chronic lung disease [15]. 20 days later, the strain isolated from BALF was identified as *S. boydii*, which was consistent with mNGS, further confirming that the pathogen was *S. boydii*. After six weeks of treatment with voriconazole, the patient's clinical symptoms, chest CT results, and laboratory examination showed significant improvement, indicating the effectiveness of the antifungal therapy.

Based on current case reports and treatment guidelines, voriconazole monotherapy is the first-line treatment for *Scedosporium* infections, with surgical debridement recommended if necessary to reduce pathogen burden reduction [21]. Although the epidemiological breakpoint for *Scedosporium* has not yet been established, an MIC value of voriconazole below 2 μg/mL may suggest a favorable treatment outcome [8]. Isavuconazole, posaconazole, or itraconazole monotherapy may be used as second-line treatment [22]. If Scedosporiosis progresses or shows poor response to initial antifungal therapy, guidelines recommend either posaconazole or voriconazole alone, or a combination of voriconazole or echinocandin [22, 23]. In immunocompromised hosts, pathogen clearance efficacy is highly dependent on systemic immune reconstitution and management of underlying comorbidities. The study by Neoh et al. indicated that most infections caused by *Scedosporium* species responded to antifungal therapy during a 3-to-6-month follow-up period, suggesting that extended treatment for at least 6 months may be required.

Conclusion

Given the rarity of *S. boydii* infections, this study aims to enhance clinical awareness of *S. boydii.* Promote the application of molecular techniques such as mNGS and MALDI-TOF MS in diagnosing these infections. For rare and uncommon fungi, extending the incubation time for cultures from BALF is crucial, thereby aiding early diagnosis and improving patient outcomes.

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Authors' contributions
JY, SJ and YL collected the data and drafted the manuscript. WG, CZ and HZ analysed the data. MS, JH, CZ and YL collected the data. ZF, HZ, ZZ, YG and LZ reviewed and edited the manuscript. All authors approved the submitted version.

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Data availability
The sequencing results of the strain was uploaded to NCBI with the accession number PRJNA1102500 (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1102500/). The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request.

Declarations

Ethics approval and consent to participate
As a case report, our paper did not require any referral to our institutional clinical ethics committee.

Consent for publication
Written informed consent was obtained from the patient for publication of this report and any accompanying images.

Competing interests
The authors declare no competing interests.

Author details
[1]Jiaxing Hospital of Traditional Chinese Medicine Affiliated to Zhejiang Chinese Medical University, Jiaxing, China
[2]Hebei Medical University Third Hospital, Shijiazhuang, China
[3]First Hospital of Hebei Medical University, Shijiazhuang, China
[4]Hebei Key Laboratory of Intractable Pathogens, Shijiazhuang Center for Disease Control and Prevention, Shijiazhuang, China
[5]Hebei Yiling Hospital, Shijiazhuang, China
[6]Fourth Hospital of Hebei Medical University, Shijiazhuang, China

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