Extensive Dermatophytosis Caused by Terbinafine-Resistant *Trichophyton indotineae*, France

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Extensive dermatophytosis caused by terbinafine-resistant *Trichophyton indotineae* harboring Phe397Leu and Leu393Ser substitutions in the squalene epoxidase enzyme was diagnosed in France. Analysis of internal transcribed spacer sequences revealed the wide spread of this species in Asia and Europe. Detection of *T. indotineae* isolates from patients suggests their possible role as reservoirs.

In recent years, dermatologists in India have alerted the medical community to the wide spread of recalcitrant extensive dermatophytosis across the country. Clinically, extensive dermatophytosis is characterized by tinea cruris, tinea corporis, or both, of the glabrous skin (1). The spread of this condition is thought to be a consequence of ill-advised use of over-the-counter corticosteroid-antifungal combinations, resulting in the emergence of terbinafine-resistant *Trichophyton* strains in India (2). *T. mentagrophytes* and *T. interdigitale* were suspected, but the correct identity of the etiologic agent of this outbreak was debated (3,4). Genomic data showed that India terbinafine-resistant isolates form a distinct clade from *T. interdigitale* and *T. mentagrophytes* (5). Recently, the clinical, mycological, and molecular features of 2 highly resistant *T. interdigitale* isolates from patients in Nepal and India, harboring mutations in the squalene epoxidase (SQLE) gene, have been analyzed and identified as a new species named *T. indotineae* (6).

The taxonomy of the *T. mentagrophytes/T. interdigitale* complex, including *T. indotineae*, has been revised based on multigene phylogeny revealing that analysis of the high-mobility group gene clearly demarcates the species, as suggested elsewhere (5,7). *T. indotineae* appears to be the primary contributor to terbinafine resistance (8). Migration and travel enable the spread of nonautochthonous pathogens in nonendemic areas. Terbinafine-resistant *T. indotineae* isolates have been recently identified in Europe (9–11). We present a series of extensive dermatophytosis cases in France caused by terbinafine-resistant *T. indotineae* and document the worldwide spread of *T. indotineae* using results from internal transcribed spacer (ITS) sequence-based screening.

**The Study**

Ten patients in 4 hospitals in France with clinical manifestations of tinea cruris or tinea corporis were diagnosed with extensive dermatophytosis caused by *T. mentagrophytes* (Table 1; Appendix Figure 1, https://wwwnc.cdc.gov/EID/article/28/1/21-0883-App1.pdf). The first case was observed in 2017, and the involvement of *T. indotineae*, confirmed in 2019, revealed that the condition was probably introduced into France several years earlier. Patients were 9 men and 1 woman (mean age 30 years, range 16–53 years). All but 1 patient came from or had visited Bangladesh (Table 1), a commonality probably related to a 2016 increase in migrants from Bangladesh applying for asylum in France (12). Source of infection was difficult to determine. Patients 3 and 10 reported clinical symptoms after a journey in Bangladesh. Patients 6 and 9 reported that symptoms started before arriving in France after a

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DOI: https://doi.org/10.3201/eid2801.210883

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stay in refugee camps in Turkey and Bangladesh. For patients 1, 4, and 8, skin lesions had appeared after living in France for 3–4 years, suggesting that human-to-human transmission could have occurred in France. All patients declared no contact with animals.

Eight out of 10 patients received oral treatment with terbinafine. Clinical cure or treatment failure were recorded when skin lesions disappeared after treatment; clinical improvement was recorded when patient reported a reduction of clinical symptoms (itching and inflammatory lesions).

Table. Characteristics of extensive dermatophytosis case-patients diagnosed with *Trichophyton indotineae* in France*

<table>
<thead>
<tr>
<th>Patient no.</th>
<th>Year</th>
<th>Country of origin</th>
<th>Treatments†</th>
<th>Clinical outcome‡</th>
<th>Follow up</th>
<th>ITS genotype§</th>
<th>TRB MIC, µg/mL</th>
<th>SQLE# substitution</th>
<th>ITR MIC, µg/mL</th>
<th>VOR MIC, µg/mL</th>
<th>AMO MIC, µg/mL</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2017</td>
<td>India</td>
<td>Oral cream TRB 1 mo</td>
<td>Clinical cure; negative MyE</td>
<td>No relapse after 6 mo</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>2</td>
<td>2018</td>
<td>Bangladesh</td>
<td>TRB 1 mo</td>
<td>Improvement§ after 1 mo</td>
<td>Lost to follow-up</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>3</td>
<td>2019</td>
<td>Bangladesh</td>
<td>TRB 2 mo</td>
<td>Clinical cure</td>
<td>No relapse 1 y later</td>
<td>T. indotineae</td>
<td>0.06</td>
<td>None</td>
<td>0.125</td>
<td>0.125</td>
<td>0.125</td>
</tr>
<tr>
<td>4</td>
<td>2019</td>
<td>Bangladesh</td>
<td>TRB 3 mo, GRS 3 mo, ECZ 3 mo</td>
<td>No improvement after 9 mo; positive MyE</td>
<td>Lost to follow-up</td>
<td>T. indotineae</td>
<td>2</td>
<td>Leu393Ser</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>5</td>
<td>2020</td>
<td>Bangladesh</td>
<td>TRB 2 mo</td>
<td>No improvement after 2 mo; positive MyE</td>
<td>Lost to follow-up</td>
<td>T. indotineae</td>
<td>&gt;8</td>
<td>Phe397Leu</td>
<td>0.06</td>
<td>0.06</td>
<td>0.06</td>
</tr>
<tr>
<td>6</td>
<td>2020</td>
<td>Myanmar</td>
<td>CCL 1 mo</td>
<td>Clinical cure</td>
<td>No relapse 1 y later</td>
<td>T. indotineae</td>
<td>0.06</td>
<td>Ala448Thr</td>
<td>0.125</td>
<td>0.125</td>
<td>0.06</td>
</tr>
<tr>
<td>7</td>
<td>2020</td>
<td>Bangladesh</td>
<td>TRB 3 wk, BFN 3 wk</td>
<td>Improvement after 6 wk</td>
<td>Relapse 2 mo later</td>
<td>T. indotineae</td>
<td>2</td>
<td>Leu393Ser</td>
<td>0.016</td>
<td>0.03</td>
<td>0.06</td>
</tr>
<tr>
<td>8</td>
<td>2020</td>
<td>Bangladesh</td>
<td>OMC 1 mo, MCN 1 mo</td>
<td>Improvement after 2 mo</td>
<td>Lost to follow-up</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>2021</td>
<td>Bangladesh</td>
<td>TRB 2 mo</td>
<td>Improvement after 1 mo; negative MyE</td>
<td>Lost to follow-up</td>
<td>T. indotineae</td>
<td>0.06</td>
<td>None</td>
<td>0.06</td>
<td>0.06</td>
<td>0.125</td>
</tr>
<tr>
<td>10</td>
<td>2021</td>
<td>Bangladesh</td>
<td>TRB 6 mo, GRS 6 mo</td>
<td>No improvement after 1 y; positive MyE</td>
<td>ITR 2 mo improvement</td>
<td>T. indotineae</td>
<td>2</td>
<td>Phe397Leu &amp; Ala448Thr</td>
<td>0.25</td>
<td>0.5</td>
<td>0.01</td>
</tr>
</tbody>
</table>

*AMO, amorolfine; BFN, bifonazole; CCL, ciclopiroxolamine; ECZ, econazole; GRS, griseofulvin; ITR, itraconazole; ITS, internal transcribed spacer; MCN, miconazole; MyE, mycologic exam; ND, not determined; OMC, omouconazole; SQLE, squalene epoxidase enzyme; TRB, terbinafine; VOR, voriconazole.

†Treatments: oral TRB (250 mg/d); oral GRS (1 g/d); 1% ECZ cream; 1% CCL cream; 1% BFN cream; 1% OMC cream; 2% MCN cream; oral ITR 400 mg/d.

‡Clinical cure was recorded when skin lesions disappeared after treatment; clinical improvement was recorded when patient reported a reduction of clinical symptoms (itching and inflammatory lesions).


¶TBR resistance was defined by a MIC₅₀ >0.25 µg/mL (15).

#For SQLE sequencing, the amplified fragment was cut in 2 using a total of 4 primers because it was >1,000 nt long, (Appendix Table). Registered under GenBank accession no. M2318454–9.
Phe397Leu, or Phe397Leu/Ala448Thr substitutions. Three terbinafine-susceptible isolates exhibited no substitutions or an Ala448Thr substitution alone. We determined low MICs for itraconazole, voriconazole, and amorolfine for 6 isolates (Table 1).

Using an ITS sequence-based screening of sequences stored in GenBank and a review of literature up through March 2021 (Appendix Table 2), we investigated the epidemiologic characteristics of T. indotineae. Information was available about the origin of the infection for 526/537 sequences found. Human-to-human transmission was predominant because 98.8% of the sequences identified were of human origin; however, 6 sequences indicated an animal origin. Two sequences detected during a survey that included 760 calves came from Egypt, 1
detected in an infected dog came from India, and 3 came from Poland but with no specific animal host indicated. These results suggest that animals can be reservoirs of *T. indotineae* and zoonotic transmission must be considered.

We obtained geographic information for all 537 sequences and temporal information for 486 sequences. Our study revealed that *T. indotineae* was present in India, Australia, Iran, and Oman during 2004–2013 (Figure 1, panel A). After 2014, a substantial increase in reported cases was observed, related to the outbreak in India. Since 2019, the number of reported *T. indotineae* cases has increased in Europe, confirming its spread. Currently, 76% of the known sequences have been identified in India, 12.8% in the Middle East, 9.6% in Europe, and 1.1% in other countries (Figure 1, panel B). Cases reported in Europe are supposed to have been introduced by migrants or travelers from India, Bangladesh, Pakistan, Bahrain, Libya, Saudi Arabia, or Thailand, suggesting the presence of *T. indotineae* in those countries. The cases imported from Bangladesh that were reported in France, together with those reported in Germany (9), suggest that *T. indotineae* transmission could be endemic in Bangladesh. Results obtained in this study were limited to data obtained from sources available in GenBank; *T. indotineae* distribution is probably greater than what is documented here.

The epidemiology of terbinafine-resistant *T. indotineae* isolates was difficult to assess because studies recording available molecular analysis and in vitro antifungal susceptibility testing were scarce. In India, 71.3% (n = 279) of reported isolates were resistant to terbinafine, but in Iran, 71.8% (n = 32) were susceptible. Of the isolates from this study, 50% (n = 29) from Germany and 57.1% (n = 7) from France were resistant. Isolates from India showed 11 different single or combined missense mutations of the SQLE gene with a large range of terbinafine MICs (Figure 2). Of note, Phe397Leu and Leu393Phe substitutions, associated with terbinafine resistance, were predominant in isolates from India and Germany, probably related to population movements between the 2 countries. Leu393Ser substitution was predominant in France in the isolates from Bangladesh.

Figure 2. *Trichophyton indotineae* susceptibility to terbinafine reported from 4 countries. A) Relationships between terbinafine MIC and codon changes reported in isolates from different countries. Grey line shows terbinafine susceptibility threshold of 0.2 μg/mL. Available MICs were determined using the Clinical Laboratory and Standards Institute (https://clsi.org) or EUCAST (https://eucast.org) methods. Data show mean values. B) Prevalence of substitution points in the gene encoding SQLE. Sources shown in the Appendix (https://wwwnc.cdc.gov/EID/article/28/1/21-0883-App1.pdf). SQLE, squalene epoxidase enzyme.
Conclusions
The medical community and organizations receiving migrants and travelers should be aware that extensive dermatophytosis linked to terbinafine-resistant *T. indotineae* has reached France. Efficient systems to promptly identify terbinafine-resistant *T. indotineae* isolates must be implemented to halt the progression of this pathogen throughout Europe.

Acknowledgments
We thank technical staff of the parasitology-mycology and dermatology departments from the hospitals included in this study.

About the Author
Dr. Jabet was a final-year resident at La Pitié-Salpêtrière Hospital (now a medical mycologist at La Pitié-Salpêtrière Hospital and Saint Antoine Hospital) in Paris, France. His primary research interests are dermatophytosis infections and emerging fungal pathogens. Dr. Brun is a medical mycologist working at Avicenne Hospital in Bobigny, France, and is particularly interested in dermatophytosis and fungal infections observed in migrants.

References

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Appendix

### Appendix Table. PCR primers used in this study and annealing temperatures*

<table>
<thead>
<tr>
<th>DNA portion</th>
<th>Primer</th>
<th>Sequence</th>
<th>Annealing temperature</th>
</tr>
</thead>
<tbody>
<tr>
<td>ITS</td>
<td>ITS1</td>
<td>TCCGTTAGGTGAACCTGCGG</td>
<td>55°C</td>
</tr>
<tr>
<td></td>
<td>ITS3</td>
<td>GCATCGTGAAGAAGACGACG</td>
<td></td>
</tr>
<tr>
<td></td>
<td>ITS4c</td>
<td>TCCTCCGCTTATTGATATGC</td>
<td></td>
</tr>
<tr>
<td>Squalene epoxidase</td>
<td>Erg1–2_F</td>
<td>CCAGACGTGATGGCAAGCAAGA</td>
<td>60°C (used only for sequencing)</td>
</tr>
<tr>
<td></td>
<td>Erg1–2_R</td>
<td>ATAAGCTCCAGGCCCCAGAA</td>
<td></td>
</tr>
<tr>
<td></td>
<td>TrSQLE_F1</td>
<td>ATGGTTGTAGAGGCTCCTCCC</td>
<td></td>
</tr>
<tr>
<td></td>
<td>TrSQLE_R1</td>
<td>CTAGCTTTGAAGTCGGCAAA</td>
<td></td>
</tr>
</tbody>
</table>

* Primers were previously described by Yamada et al. (1). ITS, internal transcribed spacer.

### Appendix Figure 1. Clinical presentation of extensive dermatophytosis diagnosed in France. A–B) The various lesions consisted in multiple and large erythematous or brown, round to oval macular lesions on the abdomen, legs, arms and inguinal folds, slightly scaly, with a raised inflammatory edge. Patients reported peripheral spreading but no central clearing. C) An atypical clinical presentation was observed in one patient (patient 9) with large and brown annular macular lesions and no inflammatory edge.
Appendix Figure 2. Terbinafine susceptibility screening using the solid plate method. Photos show antifungal susceptibility to terbinafine determined using the growth method involving Sabouraud-chloramphenicol-cycloheximide medium (SCC) with or without terbinafine at 0.2 μg/mL (lower and upper photos respectively). A–F) Patients 3, 5, 6, 7, 9, 10, respectively. Terbinafine susceptibility using this method could be determined for 6 isolates (loss of viability for isolate 4). Isolates from patients 5, 7, 10 were able to grow in terbinafine-containing solid medium.

Reference

**Additional Sources**


