Emergence of Terbinafine Resistant *Trichophyton mentagrophytes* in Iran, Harboring Mutations in the Squalene Epoxidase (SQLE) Gene

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Introduction

Dermatophytois or tinea is known as the most common superficial mycosis in dermatological practice. It involves skin, nails and hair. Dermatophytosis is caused by a group of fungi, called dermatophytes. The dermatophytes are cosmopolitan and encompass more than 50 species from the genera *Trichophyton*, *Microsporum*, *Epidermophyton*, *Arthroderma*, *Nannizzia*, *Lophophyton*, and *Paraphyton*.1 Most skin infections by dermatophytes, especially by *Trichophyton* spp., are successfully treated by using terbinafine (TRB), an allylamine compound which is the first-line oral medication for the treatment of such infections.2 The drug blocks the formation of ergosterol, the major component of fungal membrane, by inhibiting squalene epoxidase enzyme (SQLE) and subsequently inhibits the fungal growth.3 However, an increasing number of difficultly treated cases is being documented.4,5 This phenomenon can be connected in part with relapses because of poor adherence to antifungal treatment regime.6 However, the most important part is emergence of

This study documented a step in the global spread of resistance mechanisms in *T. mentagrophytes*. However, treatment alternatives for resistant isolates were available.

Keywords: *Trichophyton mentagrophytes*, SQLE, terbinafine, antifungal drug resistance, Iran
recalcitrant dermatophytosis due to verified in vivo/in vitro resistance to TRB. In the first decade of the 21st century, terbinafine resistance in dermatophytes was found to be rare and primarily limited to T. rubrum isolates.

Nonetheless, recent reports from India and some other Asian and European countries indicate that clinical/microbial TRB resistance now involves T. interdigitale and T. mentagrophytes. Since these fungi are essentially conspecific, they can be treated together as the T. mentagrophytes/T. interdigitale species group (TMTISG). In most mentioned reports, clinical therapeutic failures have been correlated with nonsynonymous point mutations in the SQLE gene. But, there has been no report on TRB resistance and molecular mechanisms underlying reduced susceptibility to this antifungal agent in Iranian TMTISG isolates.

Our study aimed to assess antifungal susceptibility of Iranian TMTISG isolates. We described five T. mentagrophytes strains, harboring some known point mutations in SQLE gene, which probably were responsible for high terbinafine MICs and proposed treatment alternatives for TRB resistant cases.

Materials and Methods

Clinical Isolates

A total of 141 clinical TMTISG isolates from different provinces of Iran were included in the study. These isolates were a part of a recent investigation on the epidemiological aspects of infections due to the TMTISG in Iran over a two-year study during 2016–2018. The study was approved by the Ethic Committee of Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran (approval ID: IR.AJUMS.REC.1398.851).

Molecular Identification of the Isolates

Identification of all isolates was performed by sequencing of the internal transcribed spacer region of ribosomal DNA (ITS). Briefly, the isolates were sub-cultured on Sabouraud dextrose agar (SDA; BD Diagnostics, USA) and incubated at 28°C for one week. Genomic DNA was isolated from the mycelium of each strain by mechanical homogenization in lysis buffer, consisting of 200 mM Tris-HCl [pH 8.0], 0.5% sodium dodecyl sulfate, 250 mM NaCl, and 25 mM EDTA with the use of SpeedMill device (Analytik Jena, Germany), followed by purification with phenol-chloroform-isoamyl alcohol (25:24:1) and precipitation with ethanol. ITS region was amplified in each isolate by V9G (5′-TTACGTCCCTGCCCTTTTGA3′) and LS266 (5′-GCATTCCCAAAACTCAGACTC-3′) primers. The amplification program could be schematically represented in the following way: 6 min 94°C; 35 × [30 s 94°C, 30 s 58°C, 1 min 72°C]; 10 min 72°C. The amplified products were sequenced with the use of mentioned primers and the BigDye Terminator Kit version 3.1 (Applied Biosystems, USA), in an ABI Prism 3130XL Genetic Analyzer (Applied Biosystems, USA). The obtained raw sequences were imported to MEGA software ver. 7.0 and quality-checked. Each isolate was identified down to the species level by BLAST search of respective ITS sequence against annotated sequences, deposited in the Westerdijk Fungal Biodiversity Institute (CBS) database (http://www.cbs.knaw.nl).

Antifungal Susceptibility Testing

In vitro AFST against TMTISG isolates was done by the Clinical and Laboratory Standards Institute broth microdilution method, according to CLSI M38-A2 document. The following drugs were tested: terbinafine (TRB; Combi Blocks, USA), itraconazole (ITC; Sigma-Aldrich, USA), griseofulvin (GRE; Wako Pure Chemical, Japan), clotrimazole (CLT; Sigma-Aldrich, USA), efinaconazole (EFN; Nihon Nohyaku, Japan), luliconazole (LUZ; Funakoshi, Japan), amorolfine hydrochloride (AHC; LKT Laboratories, USA) and ciclopirox olamine (CPO; LKT Laboratories, USA). The final concentration of each antifungal agent was as follows: 0.001–0.5 µg/mL for TRB, 0.016–8 µg/mL for ITC, 0.015–8 µg/mL for GRE, 0.0625–32 µg/mL for CLT, 0.001 to 0.5 µg/mL for EFN, 0.00006–0.315 µg/mL for LUZ, 0.03–16 µg/mL for AHC and 0.004–2 µg/mL for CPO. To promote conidiation, we cultured the strains for a week at 28°C on Petri dishes containing modified Sabouraud Glucose agar, diluted 10-fold (peptone 0.2%, KH₂PO₄ 0.1%, MgSO₄·7H₂O 0.1%, glucose 0.1%, agar 1.5%). The sterile saline containing 0.05% (w/v) Tween 80 was added to the surface of each mature colony and inoculum suspension was prepared by rubbing with a sterile scraper. Conidial suspension was harvested by a sterile syringe and transferred to a sterile filter (0.4 µm) to eliminate the hyphal masses. After gentle shaking conidial suspension was diluted to achieve 65–70% light transmission at wavelength of 530 nm. To obtain final density of 1 × 10⁸ to 3 × 10⁸ CFU/mL, the conidial suspension was diluted in RPMI 1640 medium, with the ratio of 1:50. For each isolate, the dermatophyte-free and antifungal-free controls were used and microplates were incubated at 30°C. To check the performance accuracy of AFST, the CLSI...
reference strains of *Candida parapsilosis* ATCC 22019 and *C. krusei* ATCC 6258 were used as control for every new batch of tested isolates. The minimal inhibitory concentrations (MICs) for all used antifungals were defined as the lowest concentration that led to complete inhibition of observable growth after 96 hrs.

**Sequencing of Squalene Epoxidase (SQLE) Gene and Analysis**

In order to determine whether a mutation in the *SQLE* gene could be potentially involved in elevated TRB MICs, the partial *SQLE* gene in five resistant isolates, and also in five susceptible isolates for comparison, was amplified and sequenced with the TrSQLE-F1 (5'-ATGGTGTAGAGGCTCTCC-3') and TrSQLE-R1 (5'-CTAGCTTTGAAGTTCGGCAAA-3') primer pair. 11

A PCR machine was run according to a program, modified from Singh et al: 5 min 95°C; 34 × [30 s 95°C, 30 s 60°C, 3 min 72°C]; 10 min 72°C. The predicted amino acid sequences of SQLE in all tested *T. mentagrophytes* isolates were compared with the reference sequence for *T. mentagrophytes* and *T. interdigitale* (GenBank accession number KU242352).

**ITS Typing**

Given that some recent reports correlated in vitro/in vivo TRB resistance in the TMTISG with a distinct ITS genotype (Type VIII), the nucleotide sequences for ribosomal ITS1-5.8S-ITS2 region in all isolates were used for typing by a script ([https://github.com/Ivan-Pchelin/genotyping-by-sequencing](https://github.com/Ivan-Pchelin/genotyping-by-sequencing)). All point mutations and indel events strictly within the borders of ITS region were considered significant. 21

**Results**

By ITS sequencing, 96 isolates were identified as *T. interdigitale* and 45 isolates as *T. mentagrophytes*. The *T. interdigitale* isolates originated from tinea pedis (*n* = 71), tinea unguium (*n* = 20) and tinea corporis (*n* = 5) infections, while the majority of *T. mentagrophytes* isolates were from tinea corporis (*n* = 43), followed by tinea capitis (*n* = 1) and nail infection (*n* = 1).

Table 1 summarizes MIC ranges, geometric means (GMs) of MICs, and the MIC50/MIC90 ratios of 8 antifungal drugs used against 141 TMTISG isolates. GM MIC values of LUZ and EFN against *T. interdigitale* isolates were 0.0016 and 0.0057 µg/mL while these values for *T. mentagrophytes* isolates were 0.0024 and 0.009 µg/mL, respectively. Whereas GRE had the highest GM MIC value (1.1 µg/mL) for *T. interdigitale* isolates, CLT showed the highest GM MIC value (3.25 µg/mL) against *T. mentagrophytes* isolates. In view of susceptibility to TRB, all *T. interdigitale* isolates were susceptible to this agent (MICs range = 0.003–0.25 µg/mL and MIC90 = 0.0125 µg/mL) while the MICs of TRB for *T. mentagrophytes* isolates were in the range 0.007–32 µg/mL. We found 5 *T. mentagrophytes* isolates with TRB MICs ≥32 µg/mL (resistant). From a total of 45 *T. mentagrophytes* isolates, 28 isolates harbored ITS type VIII and all five TRB resistant strains were from this genotype (5/28; 18%).

The partial *SQLE* sequence was successfully amplified in all 5 sensitive and 5 resistant strains. The obtained sequences were deposited in GenBank under accession numbers MN893286 and MN901902–MN901905 for susceptible and MN901906–MN901910 for resistant strains. All *T. mentagrophytes* resistant isolates harbored missense mutations in *SQLE*, corresponding to amino acid substitution Ala448Thr in combination with Leu393Ser (isolate

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**Table 1** MIC Values (µg/mL) of 8 Antifungal Agents Against 141 *Trichophyton interdigitale* and *T. mentagrophytes* Isolates

| Species                  | Antifungal MICs | TRB  | ITC  | EFN  | LUZ  | CLT  | AHC  | CPO  | GRE  |
|--------------------------|-----------------|------|------|------|------|------|------|------|------|
| *T. interdigitale* (*n*=96) |                 |      |      |      |      |      |      |      |      |
| MIC50                    | 0.038           | 0.36 | 0.0057 | 1.43 | 0.92 | 0.45 | 1.1  |      |      |
| MIC90                    | 0.062           | 0.5  | 0.007 | 0.003 | 1    | 0.5  | 1    |      |      |
| MIC range                | 0.125           | I    | 0.015 | 0.001 | 4    | 2    | 2    |      |      |
| MIC range                | 0.003–0.25      | 0.062–8 | 0.001–0.125 | 0.25–16 | 0.125–4 | 0.062–1 | 0.062–4 |      |      |
| *T. mentagrophytes* (*n*=45) |                 |      |      |      |      |      |      |      |      |
| MIC50                    | 0.12            | 0.32 | 0.009 | 0.0024 | 3.25 | 0.92 | 0.56 | 1.8  |      |
| MIC90                    | 0.625           | 0.25 | 0.0075 | 0.003 | 4    | 1    | 0.5  | 2    |      |
| MIC range                | >32             | 0.5  | 0.031 | 0.001 | 16   | 2    | 1    | 4    |      |
| MIC range                | 0.007–0.32      | 0.062–2 | 0.001–0.125 | 0.5–32 | 0.125–4 | 0.062–1 | 0.25–4 |      |      |

Abbreviations: TRB, terbinafine; ITC, itraconazole; EFN, efinaconazole; LUZ, luliconazole; CLT, clotrimazole; AHC, amorolfine hydrochloride; CPO, ciclopirox olamine; GRE, griseofulvin.
Discussion
The antifungal susceptibility profile of Iranian TMTISG isolates, described in our results (Table 1), was comparable to that ones from other Iranian and foreign studies. The MIC values of EFN against TMTISG isolates from Japan, Canada, US and Iran in three studies all in all ranged from 0.001 to 0.03 µg/mL. They did not differ significantly from the MIC values for EFN in the current study (MICs = 0.001–0.125 µg/mL). Similarly, LUZ inhibitory concentrations against our TMTISG isolates ranged from 0.0004 to 0.015 µg/mL and were comparable with 0.0001–0.004 µg/mL for this imidazole against TMTISG strains in two previous reports from US and Iran. In two other investigations, LUZ has also had the most pronounced in vitro effect against TMTISG isolates from India and Iran, when compared with other antifungals, though the MIC values were higher (0.016–0.25 µg/mL) than in the current study. In our study, all TRB resistant isolates belonged to T. interdigitale (wild type).

In two other investigations, the antifungal susceptibility profile of dermatophytes from the Iran and other countries, including India, Switzerland, Japan, Finland, Denmark, Bahrain, and Germany, the TRB MIC values in resistant TMTISG isolates from Iran and other countries varied in the range ≥1–≥32 µg/mL. In the current report, similar to some other studies, all TRB resistant isolates belonged to T. mentagrophytes species and ITS type VIII (5/28; 18%). Despite this, careful analysis of the literature revealed resistant Type II strains (Table 3). Hence, more data are needed to clarify whether in the TMTISG there is an association between genotypes and a potential to develop antifungal drug resistance. Among amino acid substitutions in SOLE, leading to TRB resistance, the most commonly encountered are Phe397Leu and Leu393Phe (Tables 2 and 3). The substitution Leu393Ser or other less common substitutions were also correlated with a high MIC value (≥32 µg/mL) of TRB. In some cases, in vitro resistance could not be explained by the presence of any mutation in SOLE (wild type). Then, mechanisms other than Phe397Leu and Leu393Phe substitution should still be considered as alternatives for TRB treatment failure. For example, Santos et al, recently showed that TRB resistance in T. rubrum can be mediated by multiplication of salicylate 1-monooxygenase (salA) gene.

Conclusion
Overall, in both T. mentagrophytes and T. interdigitale, the potencies of LUZ and EFN against TMTISG isolates were apparently greater than those of other agents. Here, for the first time in Iran, we described TRB resistance in TMTISG isolates with its molecular mechanisms. The emergence of high level of in vitro TRB resistance with proven mutation in

Table 2 MIC Values (µg/mL) of Used Antifungal Agents Against 10 Terbinafine Resistant/Susceptible T. mentagrophytes Isolates and Corresponding GenBank Accession with Consequential Amino Acid Substitutions in SOLE Gene

| Amino Acid Substitution | Resistant | Sensitive |
|-------------------------|-----------|-----------|
| SQLE accession number   | MN901906–MN901910 | MN901902–MN901905, MN893286 |
| Phe397Leu/Ala448Thr     | 4         | 0         |
| Leu393Ser/ Ala448Thr    | 1         | 0         |
| Ala448Thr               | 0         | 3         |
| Wild type               | 0         | 2         |

| MIC Values (µg/mL) | TRB | ITC | EFN | LUZ | CLT | AHC | CPO | GRE |
|-------------------|-----|-----|-----|-----|-----|-----|-----|-----|
| Resistant          | ≥32 | 0.125–2 | 0.002–0.008 | 0.008–0.004 | 1–8 | 1–4 | 1–4 |
| Sensitive          | 0.125–0.25 | 0.25–2 | 0.008–0.125 | 0.008–0.015 | 2–16 | 0.5–2 | 0.5–1 | 1–4 |
Table 3  Number of Terbinafine (TRB) Resistant Isolates Showing Mutations in the Squalene Epoxidase (SQLE) Gene in Regards to the ITS Genotypes and TRB MIC Values in Different Studies

| Row | Species         | ITS Genotype | Country of Origin | MIC Rates of Resistant Isolates (μg/mL) | Number of Resistant Isolates | Amino Acid Substitution Found in Resistance Isolates | Study                   |
|-----|----------------|--------------|-------------------|----------------------------------------|----------------------------|-----------------------------------------------------|-------------------------|
| 1   | *T. interdigitale* | ND           | Switzerland       | 3.2                                    | 1                          | Phe397Leu                                           | Yamada et al., 2017     |
| 2   | *T. interdigitale* | II           | Japan             | 2                                       | 1                          | Wild type                                           | Hiruma et al., 2018     |
| 3   | *T. mentagrophytes* | VIII      | India             | 1–32                                    | 20                         | Phe397Leu/Leu393Phe                                  | Singh et al., 2018      |
| 4   | *T. interdigitale* | ND           | India             | 4–16                                    | 4                          | Phe397Leu                                           | Rudramurthy et al., 2018|
| 5   | *T. interdigitale* | ND           | India             | 4–32                                    | 13                         | Phe397Leu                                           | Khurana et al., 2018    |
| 6   | *T. interdigitale* | II           | Denmark           | 4–8                                     | 2                          | Phe397Leu                                           | Saunte et al., 2019     |
| 7   | *T. mentagrophytes* | VIII     | Finland           | 4–8                                     | 4                          | Phe397Leu                                           | Järv et al., 2019 TIMM  |
| 8   | *T. mentagrophytes* | ND           | Switzerland       | ≥1                                      | 1                          | Gin408Leu                                           | Hsieh et al., 2019      |
| 9   | *T. mentagrophytes* | VIII     | Bahrain           | –c                                     | 1                          | Phe397Leu                                           | Sull et al., 2019       |
| 10  | *T. mentagrophytes* | VIII     | India             | –c                                     | 1                          | Phe397Leu                                           | Burmester et al., 2019  |
| 11  | *T. mentagrophytes* |           | Iran              | ≥32                                     | 5                          | Phe397Leu/Ala448Thr                                   | Current study            |

Notes: *No ITS sequence accession numbers were mentioned. *The TRB resistant isolates were reported as *T. interdigitale* but the true identity of isolates based on ITS-sequencing is *T. mentagrophytes*. *Resistance was not determined by the broth microdilution method, but by the agar diffusion method using Sabouraud’s dextrose agar containing 0.2 μg/mL terbinafine.

Abbreviation: ND, not determined.

SQLE gene in Iranian *T. mentagrophytes* isolates is unpromising and warrants the genotyping of isolates primarily resistant to TRB.

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Disclosure
The authors declare that they have no competing interests in this work.

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