Epidemiology of dermatophytosis in northeastern Iran; A subtropical region

Maryam Ebrahimi¹, Hossein Zarrинфar², Ali Naseri³, Mohammad Javad Najafzadeh⁴, Abdulmajid Fata³,⁴, Mahmoud Parian⁵, Imaneh Khorsand⁵, Monika Novak Babič⁶

¹ Department of Biology, Damghan Branch, Islamic Azad University of Damghan, Damghan, Iran
² Allergy Research Center, Mashhad University of Medical Sciences, Mashhad, Iran
³ Department of Parasitology and Mycology, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
⁴ Cutaneous Leishmaniasis Research Center, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
⁵ Department of Biology, Biotechnical Faculty, University of Ljubljana, Ljubljana, Slovenia

Article Info

Article type: Original article

Article History:
Received: 09 January 2019
Revised: 20 March 2019
Accepted: 15 May 2019

* Corresponding author: Hossein Zarrинфar
Allergy Research Center, Laboratory of Parasitology and Mycology, Ghaem Hospital, Mashhad University of Medical Sciences, Mashhad, Iran.
Email: Zarrинфar@mums.ac.ir

Background and Purpose: Dermatophytes as the causative agents of dermatophytosis (ringworm) are widely spread around the world. Accurate identification of dermatophytes in one area can be particularly important for epidemiological studies. Regarding this, the aim of the present study was to describe the species spectrum of dermatophytes, isolated from patients in Mashhad city, Iran, using the molecular-based method.

Materials and Methods: This study was conducted on 79 dermatophyte isolates obtained from the human skin, hair, and nail specimens. Species identification was performed by the polymerase chain reaction-restriction fragment length polymorphism analysis of ribosomal DNA internal transcribed spacer regions using MvaI restriction enzyme.

Results: The identified species included Trichophyton mentagrophytes, T. interdigitale species complex (n=37, 46.8%), Epidermophyton floccosum (n=12, 15.2%), T. rubrum (n=8, 10.1%), Microsporum canis (n=8, 10.1%), T. violaceum (n=5, 6.3%), T. tonsurans (n=4, 5.1%), Nannizzia gypsea (n=3, 3.8%), T. benhamiae (n=1, 1.3%), and T. verrucosum (n=1, 1.3%). The clinical forms of infection were tinea corporis (n=26, 32.8%), tinea cruris (n=22, 27.8%), tinea capitis (n=10, 12.6%), tinea unguium (n=7, 9%), tinea manuum (n=6, 8%), tinea pedis (n=5, 6.3%), and tinea faciei (n=3, 3.5%).

Conclusion: As the findings indicated, T. mentagrophytes/T. interdigitale species complex had the highest prevalence, and T. benhamiae appeared to be a new emerging agent of dermatophytosis in Mashhad, northeastern Iran.

Keywords: Dermatophyte, Dermatophytosis, PCR-RFLP, Subtropical, Iran

Introduction

Dermatophytes are a group of keratinophilic molds with a global distribution that can invade the keratinous materials in the outer layer of the skin and its appendage structures, such as the hair, nails, hooves, feathers, and claws, in humans and animals. These molds cause a spectrum of infections known as dermatophytosis (i.e., ringworm or tinea) [1]. Based on the most recent introduced taxonomy, this group consists of more than 50 species distributed in the genera of Trichophyton, Microsporum, Epidermophyton, Nannizzia, Arthroderma, Lophophyton, Paraphyton, and Guarromyces [2].

Over the past century, the distribution of dermatophytes isolated from clinical specimens has undergone a significant change. The spectrum of species varies significantly from country to country [3]. A number of factors are responsible for the distribution of dermatophytes, including high population density and social activities in rural and urban areas, low living standards, and the growth of immigrant populations [4]. The ecological changes, migration, international travel, and socioeconomic alterations can evolve the epidemiological aspects [5]. Dermatophytes account for human and animal infections with diverse clinical manifestations and can be transmitted via various routes.

Although the infection is not life-threatening, it can sometimes be serious, as in the case of deep dermatophytosis [6]. Identification and differentiation of dermatophyte species are important from an epidemiological point of view. The wide use of empirical antifungal agents in clinical practice has resulted in a varied pattern of antifungal susceptibility among particular dermatophyte species [7].
this, the identification of the causative agents and potential sources of dermatophytosis is an issue of significant importance facilitating the accurate control and treatment of this infection [8]. The spread of dermatophyte species in all parts of the world, especially the Middle East, has not been fully understood yet.

Currently, the identification of dermatophytes in the majority of the medical mycology laboratories in Iran is mostly based on the macroscopic and microscopic characteristics of the isolated colonies, which render imprecise results that are not identical to the current taxonomy of dermatophytes [9, 10]. With his background in mind, the present study was conducted to characterize the mycological and clinical aspects of dermatophytosis in Mashhad, a subtropical region of northeastern Iran, using the molecular-based method.

Materials and Methods

This study was approved by the Ethics Committee of Mashhad University of Medical Sciences, Mashhad, Iran (Ethics Committee code: IR.MUMS.REC. 1392.34). This research was conducted on the skin, hair, and nail clinical specimens collected from the patients (suspected of dermatophytosis) referred to the medical mycology laboratories of Ghaem and Imam Reza University hospitals in Mashhad during 2014-2015. The samples were examined using 15% potassium hydroxide and cultured on Sabouraud dextrose agar with chloramphenicol and cycloheximide medium (Conda, Spain). The cultures were then incubated at 28-30°C for 21-28 days, which resulted in the achievement of 79 dermatophyte colonies from the patients with dermatophytosis.

For DNA extraction, a small piece of fresh dermatophyte colony was placed in a 1.5-mL Eppendorf tube, containing glass beads (0.5 mm) and lysis buffer (200 mM Tris-HCl, pH of 7.5, 25 mM EDTA, 0.5% w/v SDS, and 250 mM NaCl), and then homogenized using a homogenizer (SpeedMill Plus, Jena, Germany) according to the manufacturer’s protocol. In the next stage, the genomic DNA was purified by the phenol-chloroform method [5]. The internal transcribed spacers (ITS) 1 and 2 regions, and the 5.8S ribosomal DNA subunit were amplified using two universal fungal primers, namely ITS1 (5´-TCCGTAGGTGAACCTGCGG) and ITS4 (5´-TCCTCCGCTTATTGATATGC) [11, 12]. The amplification of DNA was accomplished using polymerase chain reaction (PCR) as previously described by Rezaei-Matehkolaei et al. [11]. The PCR products were digested by MvaI FastDigest restriction enzyme (Fermentas Life Sciences, Lithuania) at 37°C for 10 min [11].

The restriction products were separated by electrophoresis in 2% agarose gels, and the size of DNA fragments was compared with those reported in the previous studies [11]. To confirm the accuracy and efficacy of PCR-restriction fragment length polymorphism (RFLP) results in dermatophyte identification, 11 isolates were randomly subjected to ITS sequencing. The PCR products were cleaned from primers, nucleotides, polymerases, and salts by means of a QIAquick purification kit (Qiagen GmbH, Hilden, Germany), and then sequenced on an ABI PrismTM 3730 genetic analyzer (Applied Biosystems, Foster City, CA, USA) with the ITS1/ITS4 primers. The obtained sequences were identified at the species level using the validated Online Dermatophyte Database of the Westerdijk Fungal Biodiversity Institute at Utrecht, the Netherlands (www.westerdijkfungaldb.org).

Results

The results of direct examination were positive for all of the 79 dermatophyte colonies collected from the patients with suspected dermatophytosis regardless of the presence of septate hyphae and/or arthroconidia. The clinical specimens consisted of 62, 10, and 7 skin, hair, and nail samples, respectively. Among the patients with dermatophytosis, 66% of the cases were male (n=52). The patients were within the age range of 1-98 years with the highest frequency (21.5%) in the age group of 21-30 years (Table 1). The spectrum of clinical presentations included tinea corporis, tinea cruris, tinea capitis, tinea unguium, tinea manuum, tinea pedis, and tinea faciei. Table 2 presents the clinical presentations and their causative agents.

The electrophoresis of the PCR-RFLP products revealed different banding patterns that were confirmed to belong to nine various dermatophyte species after ITS sequencing. These dermatophyte species included T. mentagrophytes/T. interdigitale species complex, E. floccosum, T. rubrum, M. canis, T. violaceum, T. tonsurans, N. gypsea, T. benhamiae, and T. verrucosum (Table 2). On the other hand, because T. mentagrophytes and T. interdigitale had the same ITS electrophoretic pattern after digestion with MvaI, they could not be differentiated by ITS RFLP. As a result, all of the isolates with such patterns were reported.

### Table 1. Prevalence of different clinical forms of dermatophytosis among various age groups in Mashhad, Iran

| Age Group | Total (%): | P-value |
|-----------|------------|---------|
| 1-10 years| 26 (32.8)  | 0.713   |
| 11-20 years| 4 (5.1) | 0.106 |
| 21-30 years| 22 (27.8) | <0.001 |
| 31-40 years| 10 (12.6) | 0.171 |
| 41-50 years| 7 (9) | 0.602 |
| 51-60 years| 6 (8) | 0.028 |
| > 61 years| 2 (3.5) | 0.455 |

Except for tinea capitis and tinea pedis, the clinical forms of dermatophytosis have the same distribution across different age groups.
as *T. mentagrophytes*/*T. interdigitale* species complex. The results of the complete ITS region sequences of the isolates were submitted to the GenBank under the accession numbers of MF850250/53 and MH790392/98.

**Discussion**

Dermatophytes are an important group of the skin, hair, and nail pathogens that can cause some serious problems as a result of deficient sanitation. The distribution of dermatophyte species varies across different geographical regions. Regarding this, the accurate identification of dermatophyte species in a particular region can clarify the epidemiological aspects. In the current study, the cutaneous specimens obtained from the patients with suspected dermatophytosis were examined in Mashhad.

Based on the evidence, the causative agents of dermatophytosis correspond to a group of nearly 7 different genera with more than 50 species, 11 cases of which are most commonly reported in humans [2]. However, *T. mentagrophytes*/*T. interdigitale* species complex and *T. rubrum* are together responsible for more than 80% of all cases of dermatophytosis around the world [13, 3]. Over the past two decades, tremendous changes have taken place in the classification, taxonomy, and nomination of dermatophytes [2]. However, in some parts of the world, the dermatophytes are still identified by the conventional phenotypic methods, which mostly present unreliable results [14].

The identification of dermatophytes based on phenotypic techniques not only requires experienced technologists but also is often labor-intensive with prolonged turnaround time. Moreover, these methods cannot be used for the complete differentiation of species within the genus or subspecies. In some recent investigations carried out in Iran, the identification of these fungi has been accomplished by the sequence-based methods [5, 8]. However, to the best of our knowledge, there are no data regarding the mycological aspects of dermatophytosis in Mashhad based on the DNA-based method [14]. Regarding this, the present study involved the characterization of the identity of dermatophytes causing dermatophytosis in Mashhad by means of this method.

The distribution of dermatophyte species varies depending on the climate and geographical location. Moreover, it seems that overcrowding, human-animal interaction patterns of children, and poor economic conditions are the significant underlying factors for this infection [15]. For example, in the United States, *T. rubrum* was reported as the major causative agent of dermatophytosis, while *T. violaceum* has been introduced as the dominant etiological agent in most of the African countries [16, 17]. However, in many parts of the world, there has been a lot of changes in the spread of certain species.

For instance, the incidence of dermatophytosis due to *M. canis* has strongly increased in Europe during recent years [3]. There is also a discrepancy between the results of a study conducted in Mashhad by Naseri *et al.* [14] and those of the current study about the major causative agents of dermatophytosis. In the current study, the prevalence of *T. mentagrophytes*/*T. interdigitale* was higher than that of other species, while in the study by Naseri *et al.*, *E. floccosum* was the dominant dermatophyte. The difference in the prevalence rate can be due to several factors, including changes in the living conditions and cultures, increased prevalence of migration and travel, and use of new identification methods.

Dermatophytes can affect both genders and all age groups in different regions; nonetheless, based on the local and international scientific reports, dermatophytosis occurs predominantly in males [5, 18-20]. In the same vein, the results of the current study indicated a higher incidence of dermatophytosis among the male patients (66%). This could be due to the higher involvement of men in outdoor activities. In this regard, it seems that the individuals who deal with domestic animals and soil are more likely to be infected with these fungi [21].

One of the limitations of this study was the lack of comprehensive information on the occupational status of the patients; in addition, this study had a small sample size. The clinical forms of dermatophytosis vary across the studies conducted in Iran and around the world [8, 22]. Even the severity of clinical symptoms can be different due to the species and strain of the dermatophytes causing the infection [23]. In the present study, the most common clinical form was tinea corporis, followed by tinea cruris, which is in

| Dermatophytes | Clinical forms | Total (%) |
|---------------|---------------|-----------|
|               | *T. floccosum*| E. floccosum | 12 (15.2) |
|               | *M. canis* | 2 (7.7) | 8 (36) | 0 | 1 (20) | 1 (16.7) | 0 | 0 | 8 (10.1) |
|               | *N. gypse*  | 0 | 0 | 1 (10) | 1 (16.7) | 0 | 0 | 0 | 3 (3.8) |
|               | *T. benhamiae* | 0 | 0 | 0 | 1 (16.7) | 0 | 0 | 0 | 1 (1.3) |
|               | *T. mentagrophytes*/*T. interdigitale* | 17 (65) | 9 (41) | 4 (40) | 1 (16.7) | 3 (42) | 3 (60) | 2 (67) | 37 (46.8) |
|               | *T. rubrum* | 3 (11.9) | 2 (9.1) | 0 | 2 (33.2) | 2 (29) | 0 | 1 (33) | 8 (10.1) |
|               | *T. tonsurans* | 0 | 2 (9.1) | 1 (10) | 0 | 0 | 0 | 0 | 4 (5.1) |
|               | *T. verrucosum* | 0 | 1 (4.8) | 0 | 0 | 0 | 0 | 0 | 1 (1.3) |
|               | *T. violaceum* | 2 (7.7) | 0 | 1 (10) | 0 | 0 | 1 (20) | 0 | 5 (6.3) |

**Table 2.** Frequency of different clinical forms of dermatophytosis in association with causative agents in Mashhad, Iran

**Curr Med Mycol, 2019, 5(2): 16-21**
agreement with the previous reports conducted in Iran and other countries [5, 24-27].

Currently, tinea corporis is reported as the dominant clinical form of dermatophytosis in the Middle East [5, 22]. This form is often acquired by close person-to-person contact. Accordingly, some specific social relationships can exert a great influence on the distribution of this infection in this region. However, the lesions caused by geophilic and zoophilic dermatophytes can produce a more intense inflammatory response than those caused by anthropophilic species [28]. Unlike many worldwide reports introducing T. rubrum as the predominant cause of infection [3], T. mentagrophytes/T. interdigitale species complex were the dominant agents of dermatophytosis in Mashhad. This is in accordance with the results of the most recent DNA-based studies performed in Tehran, Alvaz, Mazandaran province, and Isfahan in Iran [5, 8, 29, 30], as well as those of the other reports [22, 31].

T. rubrum, T. violaceum, E. floccosum, and M. canis were identified as the other agents of tinea corporis among dermatophyte isolates. This is contrary to the reports from Europe where most of the tinea corporis cases were due to Microsporum species, especially M. canis [13, 32]. In the past, M. canis was one of the most prevalent agents of scalp infection in Iran [34]; however, recently, this infection has been reported to be caused by species other than M. canis (e.g., T. mentagrophytes and T. tonsurans) [5, 22]. The growing trend of keeping pets (e.g., dogs and cats) at home can be one of the main causes of the increased incidence of M. canis in this area.

The second most common clinical form among the patients with dermatophytosis was tinea cruris (groin) or jock itch, which is in agreement with the results reported in other studies conducted in Iran [5, 22, 34]. Although according to some reports, the patients with tinea cruris often have concurrent dermatophyte infections of the feet, in the present study, those cases were not accounted [35]. Based on the evidence, the infection usually affects adult men [5, 36]; likewise, in this study, 80% of the patients were male. The type of dermatophyte species causing the infection varies in different geographical regions around the world. While E. floccosum and T. rubrum are reported as the common dermatophytes [37], in the current study, the most causative agents were T. mentagrophytes/T. interdigitale species complex and E. floccosum, respectively. This difference can be due to various factors, including the number of samples, geographical area, population density, and climate conditions.

In the current study, tinea pedis had the lowest frequency (7%) in comparison to the other clinical forms. However, Toukabri et al. (22.5%) and Vena et al. (20.4%) reported higher incidence rates for this clinical form [38, 39]. The prevalence of the infection is expected to undergo a dramatic increase owing to the increasing urban population and sports activities.

On the other hand, the relevant environmental factors, such as pH and CO₂ concentration, may be effective in this regard [40]. In the current study, T. mentagrophytes/T. interdigitale complex was the main causative agent of most of the clinical forms, probably due to the high prevalence of the fungus in this area. On the contrary, T. rubrum has been reported as the main species implicated in tinea pedis in previous global studies [3,41-42].

As our results indicated, T. benhamiae had the lowest prevalence, compared to the other species, and was reported in Mashhad for the first time. This fungus is rarely reported (or reported at a low frequency) in other studies conducted in Iran and the Middle East [5, 22]. One of the reasons can be the use of traditional identification methods and the subsequent misdiagnosis. This species was isolated from tinea manum in our research. In a study carried out by Rezaei-Matehkolaei [5] in Khuzestan, Iran, the species was also isolated from tinea manuum, tinea corporis, and tinea capitis. Given that the zoophilic species of T. benhamiae is a new strain that is recently derived from T. mentagrophytes complex, the lack of reports on this species can be justified. Our study was one of the first studies in Mashhad that used a molecular approach to identify the causes of dermatophytosis. The findings of the current research showed no significant difference in the distribution pattern of dermatophytosis and their causative agents between northeast Iran and the rest of the area.

Conclusion

As the results of the present study indicated, T. mentagrophytes/T. interdigitale species complex and E. floccosum had the highest prevalence, compared to the rest of the dermatophytes. In addition, tinea corporis and tinea cruris were the most common clinical forms in the patients with dermatophytosis. Based on the findings, T. benhamiae appears to be a new emerging agent of dermatophytosis in the area under investigation. However, our findings should be confirmed by the implementation of further studies with a larger cohort.

Acknowledgments

We extend our gratitude to the staff of Medical Mycology and Parasitology Laboratory in Ghaem and Imam Reza Teaching hospitals affiliated to Mashhad University of Medical Sciences. This work was derived from as a Master’s thesis and financially supported by the Deputy of Research of Mashhad University of Medical Sciences (grant No. 910900).

Author’s contribution

M. E. performed the project. H. Z. and A. F. designed and planned the study. I. K., M. P., and A. N. collected specimens and performed the project. A. M. undertook the statistical analysis. H. Z. and M. N. interpreted the data. M. N. and M. E. prepared the
manuscript. All authors read and approved the final manuscript.

Conflicts of interest
The authors declare that they have no conflict of interest.

Financial disclosure
The authors declare no financial interests related to the materials of the study.

References
1. Weitzman I, Summerbell RC. The dermatophytes. Clin Microbiol Rev. 1995; 8(2):240-59.
2. de Hoog GS, Dukik K, Monod M, Packeu A, Stubbe D, Hendricks M, et al. Toward a novel multilocus phylogenetic taxonomy for the dermatophytes. Mycopathologia. 2017; 182(1-2):5-31.
3. Seebacher C, Bouchara JP, Mignon B. Updates on the epidemiology of dermatophyte infections. Mycopathologia. 2008; 166(5-6):335-52.
4. Svejgaard EL. Epidemiology of dermatophytes in Europe. Int J Dermatol. 1995; 34(9):525-8.
5. Rezaei-Matehekolaie A, Rafiei A, Makimura K, Graser Y, Gharhamani S, Sadeghi-Nejad B. Epidemiological aspects of dermatophytosis in Khouzestan, southwestern Iran, an update. Mycopathologia. 2016; 181(7):547-53.
6. Lanternier F, Pathan S, Vincent QB, Liu L, Cypowyj S, Prando C, et al. Deep dermatophytosis and inherited CARD9 deficiency. N Engl J Med. 2013; 369(18):1704-14.
7. Adimi P, Hashemi SJ, Mahmoudi M, Mirhendi H, Shidfar MR, Emmami M, et al. In-vitro activity of 10 antifungal agents against 320 dermatophyte strains using micro dilution method in Tehran. Iran J Pharm Res. 2013; 12(3):537-45.
8. Rezaei-Matehekolaie A, Makimura K, de Hoog S, Shidfar MR, Zaini F, Eshraghian M, et al. Molecular epidemiology of dermatophytosis in Tehran, Iran, a clinical and microbiological survey. Med Mycol. 2013; 51(2):203-7.
9. Ahmadi B, Mirhendi H, Shidfar MR, Noirpour-Sisakht S, Jalalzad N, Geramishoar M, et al. A comparative study on morphological versus molecular identification of dermatophyte isolates. J Mycol Med. 2015; 25(1):29-35.
10. Heidemann S, Monod M, Gräser Y. Signature polymorphisms in the internal transcribed spacer region relevant for the differentiation of zoophilic and anthropophilic strains of Trichophyton interdigitale and other species of T. mentagrophytes sensu lato. Br J Dermatol. 2010; 162(2):282-95.
11. Rezaei-Matehekolaie A, Makimura K, Shidfar MR, Zaini F, Eshraghian M, Jalalzad N, et al. Use of Single-enzyme PCR-restriction digestion barcode targeting the internal transcribed spacers (ITS rDNA) to identify dermatophyte species. Iran J Public Health. 2012; 41(3):82-94.
12. White TJ, Bruns T, Lee S, Taylor JL. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR Protocols. 1990; 18(1):315-2. 
13. Havlickova B, Czaka VA, Friedrich M. Epidemiological trends in skin mycoses worldwide. Mycoses. 2008; 51(Suppl 4):2-15.
14. Naseri A, Fata A, Najažadeh MJ, Shokri H. Surveillence of dermatophytosis in northeast of Iran ( Mashhad) and review of published studies. Mycopathologia. 2013; 176(3-4):247-53.
15. Hainer BL. Dermatophyte infections. Am Fam Physician. 2003; 67(1):101-8.
16. Theel ES, Hall I, Mandrekar J, Wengenack NL. Dermatophyte identification using matrix-assisted laser desorption ionization-time of flight mass spectrometry. J Clin Microbiol. 2011; 49(12):4067-71.
17. Nweeze E, Eke I. Dermatophytes and dermatophytosis in the eastern and southern parts of Africa. Med Mycol. 2017; 56(1):13-28.
18. Heidrich D, Garcia MR, Stopiglia CD, Magagnin CM, Daboti TC, Vetrocato G, et al. Dermatophytosis: a 16-year retrospective study in a metropolitan area in southern Brazil. J Infect Dev Ctries. 2015; 9(8):865-71.
19. Neji S, Makni F, Cheikhrouhou F, Sellami A, Sellami H, Marrekkchi S, et al. Epidemiology of dermatophytoises in Sfax, Tunisia. Mycoses. 2009; 52(6):534-8.
20. Bhagra S, Ganju SA, Kanga A, Sharma NL, Guleria RC. Mycological pattern of dermatophytoises in and around shimla hills. Indian J Dermatol. 2014; 59(3):268-70.
21. Alsemayehu A, Minwuyelet G, Andualem G. Prevalence and etiologic agents of dermatophytosis among primary school children in Harari Regional State, Ethiopia. J Mycol Med. 2016; 26(4):351-4. 
22. Abastabar M, Rezaei-Matehekolaie A, Shidfar MR, Kordbacheh P, Mohammadi R, Shokooohi T, et al. A molecular epidemiological survey of clinically important dermatophytes in Iran based on specific RFLP profiles of beta-tubulin gene. Iran J Public Health. 2013; 42(9):1049-57.
23. Achtermann RR, White TC. Dermatophyte virulence factors: identifying and analyzing genes that may contribute to chronic or acute skin infections. Int J Microbiol. 2011; 2012:358305.
24. Mahmoudabadi AZ. A study of dermatophytosis in South West of Iran (Ahvaz). Mycopathologia. 2005; 160(1):21-4.
25. Mathur M, Shrestha S. Intravenous iron sucrose therapy in iron deficiency anemia in antenatal and postnatal patients. NJMA Nepal Med Assoc. 2015; 53(198):108-12.
26. Nenoff P, Krüger C, Ginter-Hanselmayer G, Tietz HJ. Mycology-an update. Part 1: dermatomycooses: causative agents, epidemiology and pathogenesis. J Dtsch Dermatol Ges. 2014; 12(3):188-209.
27. Heidrich D, Garcia MR, Stopiglia CD, Magagnin CM, Daboti TC, Vetrocato G, et al. Dermatophytosis: a 16-year retrospective study in a metropolitan area in southern Brazil. J Infect Dev Ctries. 2015; 9(8):865-71.
28. Shimamura T, Kubota N, Shibuya K. Animal model of dermatophytosis. J Biomed Biotechnol. 2012; 2012:125384.
29. Didehdar M, Shokohi T, Khansarinejad B, Ali Asghar Sefidgar S, Abastabar M, Haghani I, et al. Characterization of clinically important dermatophytes in North of Iran using PCR-RFLP on ITS region. J Mycol Med. 2016; 26(4):345-50.
30. Mohammadi R, Abastabar M, Mirhendi H, Badali H, Shadzi S, Chadeganpour M, et al. Use of restriction fragment length polymorphism to rapidly identify dermatophyte species related to dermatophytosis. Jundishapur J Microbiol. 2015; 8(6):e17296.
31. Ghoghoji A, Falahati M, Paghel As, Abastabar M, Ghasemi Z, Ansari S, et al. Molecular identification and epidemiological aspects of dermatophytosis in Tehran, Iran. Res Mol Med. 2015; 3(3):11-6.
32. Ameen M. Epidemiology of superficial fungal infections. Clin Dermatol. 2010; 28(2):197-201.
33. Omidinaya E, Farshchian M, Sadjadi M, Zamanian A, Rashidpouraie R. A study of dermatophytooses in Hamadan, the governmentship of West Iran. Mycopathologia. 1996; 133(1-3):13.
34. Zaman S, Saleghi G, Yazdinia F, Moosa H, Pazooki A, Ghafariania Z, et al. Epidemiological trends of dermatophytosis in Tehran, Iran: a five-year retrospective study. J Mycol Med. 2016; 26(4):351-8.
35. Weinstein B, Berman T. Topical treatment of common superficial tinea infections. Am Fam Physician. 2002; 65(10):2095-102.
36. El-Gohary M, van Zauren EJ, Fedorowicz Z, Burgess H, Doney L, Stuart B, et al. Topical antifungal treatments for tinea cruris and tinea corporis. Cochrane Database Syst Rev. 2014; 8:CD009992.
37. Bassiri-Jahromi S, Khaksari AA. Epidemiological survey of dermatophytosis in Hamadan, the governmentship of Iran (Ahwaz). Mycopathologia. 2005; 160(1):21-8.
38. Ctries. 2015; 9(8).
arthroconidia production in common species of Trichophyton genus and Epidermophyton floccosum. J Biol Sci. 2009; 9(6):561-6.

41. Hayette MP, Sacheli R. Dermatophytosis, trends in epidemiology and diagnostic approach. Curr Fungal Infect Rep. 2015; 9(3):164-79.

42. López-Martínez R, Manzano-Gayosso P, Hernández-Hernández F, Bazán-Mora E, Méndez-Tovar L. Dynamics of dermatophytosis frequency in Mexico: an analysis of 2084 cases. Med Mycol. 2010; 48(3):476-9.