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Isolation and molecular identification of *Trichophyton mentagrophytes* from patients with dermatophytosisHana K Maikhan¹, Shwan K Rachid² and Khalid A Habeb³¹University of Garmian, Iraq²Charmo University, Iraq³University of Baghdad, Iraq

Out of 30 clinical specimens isolated from patients with dermatophytosis in the Dermatology unit of the General Hospital in Kalar district\ Sulaimania province\ North region of Iraq, five clinical isolates showed positive results for dermatophytes, four of them were identified as *Trichophyton mentagrophytes* characterized by the production of white colonies at the surface and brown color at the reverse. Primarily, the colonies appeared with cottony texture and after two weeks changed to powdery-granular colonies. Microscopic examination appeared numerous single-celled, spherical shaped microconidia were seen as clustered on both sides of hyphae. Multiseptate cigar shaped macroconidia and spiral hyphae were seen during the formation of granular colonies. *Trichophyton mentagrophytes* was positive for urease and hair perforation tests. Molecular identification according to the conventional PCR by using set primers ITS1 and ITS4 resulted in PCR product about 700bp in all isolates. PCR-RFLP by using *Bst*NI digestion enzyme revealed four pattern bands 250, 180, 150 and 120bp. Sequencing of the ITS region in one of the isolates, *Trichophyton mentagrophytes* revealed similarity of about 86% with *Trichophyton mentagrophytes* isolate ATCC11481 regarding the following parameters: internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence. 2) Sequencing Results: Sequencing of the ITS region in one of the isolated *T.mentagrophytes* revealed similarity about 86% with *Trichophyton mentagrophytes* isolate ATCC11481 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

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