

论著

我国代表地区须癣毛癣菌复合体的分子鉴定与分型研究

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摘要: 目的 对我国代表地区的须癣毛癣菌菌株进行分子再鉴定和分型研究。方法 选取我国南北方8个省市地区经表型鉴定的须癣毛癣菌菌株47株,通过再培养形态观察、生理试验;PCR扩增核糖体DNA(rDNA)的内转录间隔区(ITS)和核糖体大亚基(LSU)D1-D2区,测序后利用数据库进行序列比对,对须癣毛癣菌复合体进行再鉴定;PCR扩增rDNA非转录间隔区(NTS)的三个串联重复亚单位S0、S1和S2区,进行种内分型,并比较不同部位来源菌株型别的差异性。结果 我国南北方8个省市地区47株须癣毛癣菌中3株鉴定为断发毛癣菌,6株鉴定为无性型苯海姆节皮菌,其余均鉴定为万博节皮菌中的亲人型趾间毛癣菌;三对不同引物扩增38株趾间型毛癣菌和2株苯海姆节皮菌NTS区,共产生28种特征性带型。带型和菌株来源及发生部位无相关性。结论 我国分离自人类须癣毛癣菌复合体的主要组成菌种为趾间毛癣菌;ITS区结合LSU D1-D2区测序有助于鉴定须癣毛癣菌复合体至种水平;NTS区的三个串联重复亚单位所产生的特征性指纹图提供了一种快速、稳定的分子生物学种内分型方法,可应用于趾间毛癣菌感染的流行病学研究。

关键词: 须癣毛癣菌复合体 rDNA内转录间隔区 核糖体大亚基D1-D2区 rDNA非转录间隔区

Study on molecular identification and typing of *Trichophyton mentagrophytes* complex from the representative regions in China

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Abstract: Objective To study molecular identification and typing of *Trichophyton mentagrophytes* complex from the representative regions in China. Methods A total of 47 strains of *Trichophyton mentagrophytes* (*T. mentagrophytes*) identified by phynotype characteristic from 8 different regions of China were re-identified by sequence analysis of the rRNA gene internal transcribed spacer regions(ITS) and the D1-D2 domain of the large-subunit rRNA gene(LSU D1-D2), and typed by PCR fingerprinting analysis of *Trichophyton mentagrophytes* using polymorphic subrepeat loci in the rDNA nontranscribed spacer(NTS). The relationship between type and origin of strains was studied. Results Three strains of *Trichophyton tonsurans*, 6 strains of *A. benhamiae*, and 38 strains of *T. interdigitale* were identified. Combining PCR fingerprints from each of the three polymorphic loci produced a total of 28 individual strain profiles. No relationship was observed between profiles and the origin and location of strains. Conclusions *Trichophyton interdigitale* was the most common species from human beings in China. Sequence analysis of ITS combining LSU D1-D2 are helpful for identification and the typing method using NTS is rapid, reproducible and discriminatory for fragments interpreting. PCR fingerprint analysis of variable tandem repeat loci in the *T. mentagrophytes* NTS is valuable for future epidemiological investigations.

Keywords: *Trichophyton mentagrophytes* complex internal transcribed spacer D1-D2 domain of the large-subunit rRNA gene nontranscribed spacer

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