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Molecular identification of *Sporothrix* clinical isolates in China

中国地区孢子丝菌临床分离株的分子鉴定

Key words: Internal transcribed spacer (ITS), Diagnosis, *Sporothrix globosa,* Taxonomy, Phylogeny

关键词：ITS、球形孢子丝菌、分类学、系统发育学

S. schenckii had long been believed to be the unique causal agent of sporotrichosis. Recently, *S. schenckii* was demonstrated to be a complex of at least six cryptic species, comprising currently four clinical relevant species, i.e., *S. schenckii s. str.*, *S. brasiliensis*, *S. globosa* and *S. luriei*.

Studies revealed the existence of the correlation between geographical distribution and genotypes in *Sporothrix* complex. The virulence and antifungal susceptibility were suggested to be associated with different species of *Sporothrix*.

Previously, based on calmodulin (CAL) sequence analysis, five Chinese environmental isolates received as *S. schenckii* had been clustered into the clade of *S. globosa*, together with six clinical isolates of *Sporothrix* using ITS region analysis, and a total of 11 (100%) Chinese isolates were confirmed to be *S. globosa*.

64 clinical isolates from China

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DNA extraction

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β-tubulin and ITS amplification

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Sequencing

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Sequence alignment

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Phylogenetic analysis

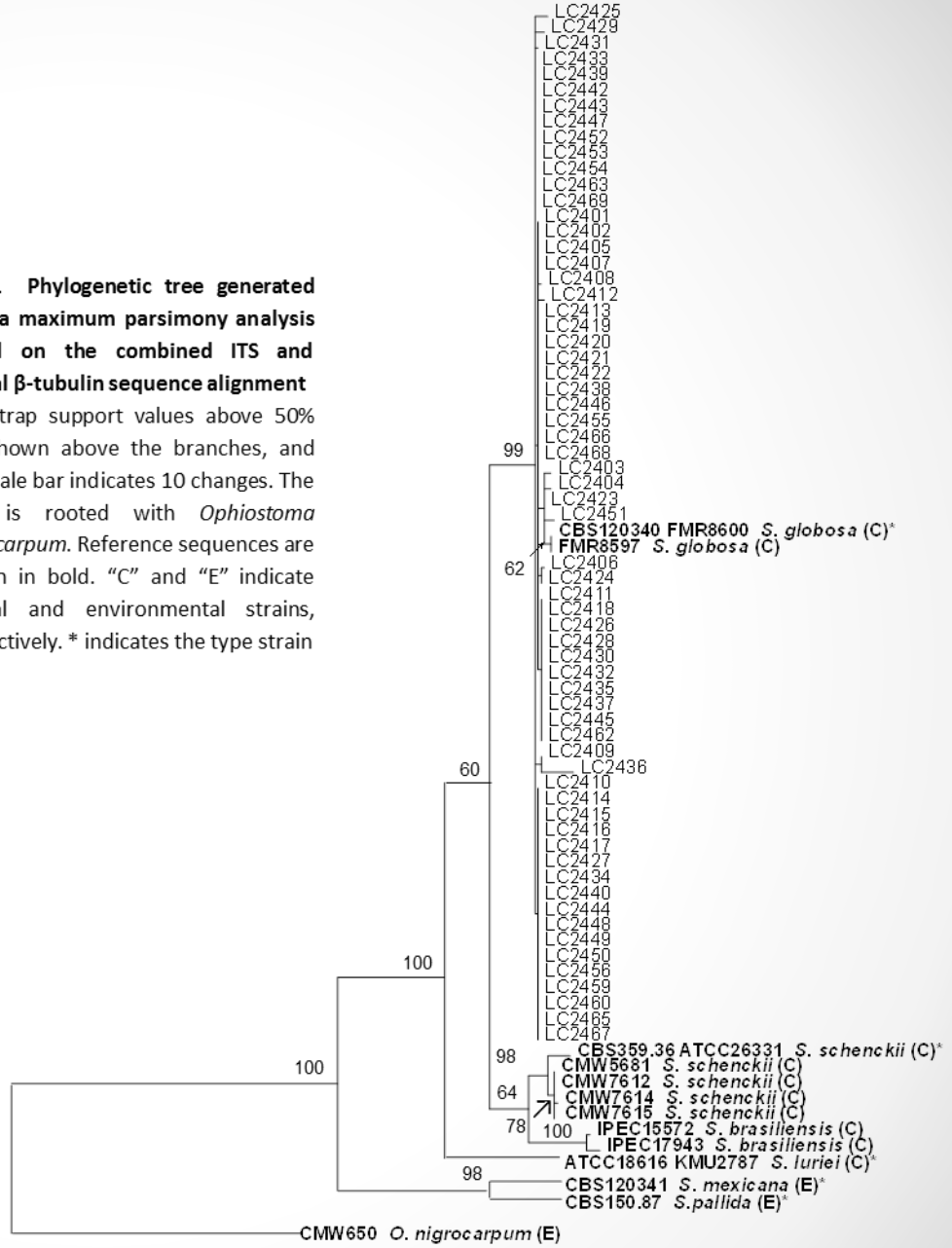


Fig. 1 Phylogenetic tree generated from a maximum parsimony analysis based on the combined ITS and partial β-tubulin sequence alignment Bootstrap support values above 50% are shown above the branches, and the scale bar indicates 10 changes. The tree is rooted with *Ophiostoma nigrocarpum*. Reference sequences are shown in bold. "C" and "E" indicate clinical and environmental strains, respectively. * indicates the type strain

Results showed that all of the isolates were clustered in a distinct clade with a type of *Sporothrix globosa*. Our analysis showed that *S. globosa* is the causal agent of the tested sporotrichosis in China, rather than *S. schenckii*.

ITS and β-tubulin are also efficient to distinguish species in *S. schenckii* species complex.

With the increasing multilocus sequence data in this group, efficient molecular diagnosis protocols using specific primers should be developed to enable a rapid and accurate identification of clinical *Sporothrix* species.