

中国杨树上壳囊孢及其相关有性型的形态 鉴定和系统发育分析*

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摘要: *Cytospora* Ehrenb.及其相关有性型 (*Valsa* Fr., *Leucostoma*(Nitschke) Höhn., *Valsella* Fuckel., *Valseutella* Höhn.) 是常见的木本植物习居菌, 该类真菌内包括多种可造成植物茎腐和枝枯(即烂皮)的病原菌。杨树, 作为该类真菌的主要寄主植物之一, 深受 *Cytospora* 及其性型真菌的侵害。杨树由于其在中国巨大的生态和经济价值, 在我国东北、华北、西北、西南等大部分地区均有分布。我国是世界上杨树人工林面积最大的国家, 而寄生于其上的 *Cytospora* 及其有性型种类多样, 且分类地位混乱, 在许多情况下阻碍了病理学的发展, 同时也不利于杨树烂皮病的防治。本研究广泛收集中国杨树上的 *Cytospora* 及其相关有性型真菌, 在依据子座和腔室排列为主要特征的形态学鉴定基础上, 结合 rDNA 内转录间隔区间的序列同源性进行系统发育分析。82 个来自中国杨树上的分离株序列与世界其他国家多个寄主上的 *Cytospora* 及其相关有性型进行比较, 得到至少 30 个具有明显碱基差异的菌株序列, 分别存在于 12-14 个已知组内和 3 个单系起源的独立分支。在寄主材料和培养基上的显微形态特征观察, 结果表明, 依据最新腔室排列方式定义, 共发现 1 种子座类型 leucostomoid, 4 种分生孢子器主要类型, 分别是 cytosporoid (rosette cytosporoid, labyrinthine cytosporoid)、unilocular、torsellioid、leucotorellioid。利用 MP 和 MrBayes 方法进行的系统发育分析良好地支持了上述形态类型的鉴定。综合鉴定我国杨树壳囊孢真菌的种 13 个, 包括: *Cytospora chrysosperma*(Pers.) Fr., *C. nivea*(Hoffm) Fr., *C. kantschavelii* Gvrit, *C. cacculus*(Schwein.) Gvrit, *C. eriobotryae* Curzi & Barbaini, *C. atrocirrhata* Gvrit, *Leucostoma persoonii* Höhn., *L. translucens* (De Not.) Höhn., *L. niveum* (Hoffm.) Höhn., *Valsa sordida* Nitschke, *V. Salicina*(Pers.)Fr., *V. ceratosperma*(Tode) Maire, *Valsella melostoma* (Fr.) Sacc., 其中 *C. chrysosperma* 为广布优势种类, 在东北地区、华北地区、西北地区频繁获得; *C. kantschavelii*、*C. eriobotryae*、*C. atrocirrhata* 为中国的新记录种。结果表明, 杨树上的 *Cytospora* 及其相关有性型真菌具有大量的碱基差异明显的 DNA 序列, 同源性分析与形态学观察结果相吻合, 分生孢子器结构的显微特征及菌落颜色、生长温度、放线菌酮抗性等培养学特征可用于各个

种的形态学描述。该篇研究有助于理解和认识 *Cytospora* 及其有性型系统发育地位，尤其是界定该类真菌在中国杨树上的分类地位，杨树上与烂皮病有关的 *Cytospora* spp.菌的正确鉴定，为杨树产业中抗病树种、杂交种、无性系的选择提供重要依据，期望在最小程度上减少烂皮病爆发的可能性，为该类病原真菌的防治提供有用的线索。

关键词： *Cytospora* spp.; 杨树; 烂皮病; 系统发育

Morphology and phylogeny of *Cytospora* spp. and related telemorphs from *Populus* in China

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Abstract: *Cytospora* Ehrenb. species and their related telemorphs(*Valsa* Fr., *Leucostoma*(Nitschke) Höhn., *Valsella* Fuckel., *Valseutella* Höhn.) are common inhabitants of woody plants and some of these have associated with stem canker and die back diseases. *Populus* L., as one of the main host plant, are suffered a great deal of these pathogens. *Populus* is widely distributed in most of the Northeast China, North China, Northwest China and Southwest China because of enormous ecological and economic value. China is the largest country of poplar plantation in the world, however *Cytospora* species and their telemorphs parasitized in *Populus* are various, furthermore the taxonomy of this fungi has been confused for a long time, which hindering pathology studies and prevention of stem canker in some cases. This study was based on extensive collection of *Cytospora* and their telemorph species from different Poplar factions in China, and the isolate was identified based on morphology including locule forms(*Cytospora* spp.) and stroma features(telemorphs) and DNA sequence homology of the intertransgenic spacer ribosomal DNA. Eighty-two isolates from *Populus* in China, yielding 30 genetically distinct sequences, were compared for homology to *Cytospora* species from other hosts. Phylogenetic analysis clustered isolated into 12-14 known groups and 3 unique monophyletic branches. Microscopic structure of the fungi was examined on natural substrates and in culture with the latest descriptive terms of locule form, in order to identify distinctive characters linked to phylogenetic

analyses. So far, The isolate was grouped into 1 ascostromata and 4 conidiomata corresponding to confusing locule arrangement. including leucostomoid, cytosporoid(rosette cytosporoid, labyrinthine cytosporoid), unilocular, torsellioid, leucotorellioid. Phylogenic analysis by MP and Mrbayes methods was well supported the result of morphylogy observation. Based on morphology and DNA sequence comparisons, there were toally 13 species identified among *Cytospora* spp. and their related telemorphs, as follows, *Cytospora chrysosperma*(Pers.) Fr., *C. nivea*(Hoffm) Fr., *C. kantschavelii* Gvrit, *C. cacculus*(Schwein.) Gvrit, *C. eriobotryae* Curzi & Barbaini, *C. atrocirrhata* Gvrit, *Leucostoma personii* Höhn., *L. translucens* (De Not.) Höhn., *L. niveum* (Hoffm.) Höhn., *Valsa sordida* Nitschke, *V. Salicina*(Pers.)Fr., *V. ceratosperma*(Tode) Maire, *Valsella melostoma* (Fr.) Sacc., *C. chrysosperma* was a widely distributed and dominant species, frequently acquired from most area of Northeast China, North China, Northwest China meanwhile, several species were new records for China, such as *C. kantschavelii*、*C. eriobotryae*、*C. atrocirrhata*. The result showed that numerous genetically distinct lineages of *Cytospora* spp. and their telemorph occur on *Populus*, homology analysis was well with mophylogy, pycnidium structure and cultural characteritics including colony colour, cardinal temperatures are useful for species describing. This wide-ranging study should contribute to a better understanding of the taxamony of *Cytospora* spp. and their telemorphs, especially the taxonomic placement on *Populus* in China. Correct identification of species *Cytospora* spp. and related telemorphs associated with cankers on *Populus* will play a important role in selecting *Populus* species, hybirds, or clones for plantation development, and minimise the likelihood of serious disease outbreaks. It is also hoped this study will created a new clue to recognise these pathogen fungi and improved management strategies in the long term.

Key words: *Cytospora* spp., stem canker, *Populus*, Phylogeny