

中国鞘锈菌的分类学和分子系统学研究

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摘要: 鞘锈菌属 (*Coleosporium*) 引起的松针锈病作为一种重要的病原主导性森林病害, 广泛分布于我国及世界各地, 严重危害 10 年生以下幼林和苗木, 造成严重经济损失。全世界已报道有 113 种鞘锈菌, 中国记载有 59 种, 转主寄生在 16 个科寄主植物上。传统的鞘锈菌分类主要以冬孢子寄主植物来划分, 尤其以罹病松树分布地区可能存在的转主寄主植物来确定种, 缺乏可靠的分类依据。而且鞘锈菌对冬孢子寄主植物的选择并不严格, 相近种的寄主有重叠, 造成按传统分类方法定种的混乱局面。因此, 对松针锈病病原菌的系统分类学进行研究具有重要的生物学和病理学意义。

本文对采自全国 23 个省(市、自治区)的 876 份鞘锈菌标本进行了形态学和分子系统学研究。利用光学和扫描电子显微镜, 对鞘锈菌夏孢子和冬孢子的形态学特征进行了传统分类学观察, 分析了不同“形态学种”的形态学特征差异, 以及与寄主植物之间的关系, 并利用数量分析法对这些形态学特征进行了主成分分析和聚类分析。同时, 通过对不同鞘锈菌的 28S rDNA 和 ITS rDNA 片段的系统发育分析, 揭示了其 DNA 多态性与寄主植物进化之间的关系, 并进行了分子水平上的种与形态学种的相关性研究, 构建了中国鞘锈菌属的分子系统学关系。结果如下:

1. 摸清和确立了我国鞘锈菌属的种类及其地理分布, 重新订正了中国鞘锈菌的种类。根据形态学特征和分子系统发育结果, 将中国已记载的 59 种鞘锈菌重新订正为 56 种。详细记录了每个鞘锈菌种生活史的各个孢子阶段的形态学特征、转主寄主植物、地理分布等, 编写了中国鞘锈菌真菌名录, 并编制了中国鞘锈菌的分类检索表。研究结果认为, 羊乳鞘锈菌 *Coleosporium horianum* Hennings 是金钱豹鞘锈 *C.campanumoeae* Dietel 的同种异名; 类叶升麻鞘锈菌 *C.actaea* P Karst. 是升麻鞘锈菌 *C.cimicifugatum* Thüm 的同种异名; 发现寄生在内蒙古蹄叶橐吾 (*Ligularia fischeri* (Ledeb.) Turcz.) 上的鞘锈菌为一个鞘锈新种, 并命名为 *Coleosporium zhuangii* C.M. Tian & C.J. You; 认为原有记录种 *Coleosporium pseudocampanulae* 和 *Coleosporium elongatum* 是错误记载的鞘锈种, 在中国并无分布。

2. 提出了新的有效的可用于种的水平上的形态学分类依据。结果表明: 冬孢子形状、顶端胶质鞘的厚度和夏孢子芽孔分布方式等特征变异较大, 且与其他形态学特征无显著相关性, 而冬孢子大小、冬孢子排列方式、担子底部是否有不孕足细胞、夏孢子大小以及夏孢子表面结构等作为有效的分类学特征, 在种间差异明显。尤其, 夏孢子表面结构和冬孢子排列

方式及底部是否有足细胞可作为稳定的分类依据广泛应用于鞘锈菌在种水平上的分类和鉴定中。同时,根据夏孢子表面纹饰的大小形状和孢子表面有无光滑区或网纹区,将孢子表面有无光滑区或网纹区分为 12 个类型,分别为:刺型(Echinulate),环纹型(Annulate, A1-A7),疣突型(Verrucose, V1-V2),冠型(Coronate)和钉头型(Nailheaded)等。

3. 订正了一些易混淆的鞘锈菌的分类学地位。明确了可区分这些寄生在相近种植物上的鞘锈菌的分类依据:香茶菜鞘锈 *C. plectranthi* Barclay 和紫苏鞘锈 *C. perillae* Kom., 铁线莲鞘锈 *C. clematidis* Barclay 和女娄菜鞘锈 *C. clematidis-apiifolia* Dietel, 风铃草鞘锈 *C. campanulae* (Pers.) Lév.和地笋鞘锈 *C. lycopi* Syd. & P. Syd., 白头翁鞘锈 *C. pulsatillae* (F. Strauss) Fr., 和银莲花鞘锈 *C. anemones* Y. Ono, 橐吾鞘锈 *C. ligulariae* Thüm., 凤毛菊鞘锈 *C. saussureae* Dietel 和具梗鞘锈 *C. pedunculatum* S.Kaneko, 马先蒿鞘锈 *C. pedicularil* 和小米草鞘锈 *C. euphrasiae* (Schumach.) G. Winter 等。

4. 建立了鞘锈菌的分子系统学关系。分别构建了鞘锈菌 28S 和 ITS 序列系统发育树,将其分为了 7 个不同的 28S 类群(Clade)和 6 个 ITS 类群(Clade)。结合形态学观察结果,进行了分子水平上的种与形态学种的相关性研究,表明:分属于不同系统发育分组(Clade)的鞘锈菌具有明显不同的夏孢子表面结构类型和冬孢子形态学特征,但依夏孢子芽孔分布方式和夏、冬孢子数量性状特征如大小形状等所划分的形态学分组与系统发育分组并不十分吻合。

关键词: 松针锈病; 鞘锈; 分类学; 系统发育

Taxonomic and phylogenetic study of a rust genus *Coleosporium* in China

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ABSTRACT: Pine needle rusts caused by *Coleosporium* Lév. (Coleosporiaceae, Basidiomycetes) are among the damaging diseases of young pines in plantations and natural forests worldwide, retarding growth by causing premature defoliation and contributing to tree death. Among the approximately one hundred and thirteen *Coleosporium* species described worldwide, fifty nine species have been reported in China. The uredinial and telial states of *Coleosporium* occur on 16

various families of Angiospermae. Species delimitation in *Coleosporium* remains difficult and confusing. The traditional identifications are mainly based on their telial host plant genera. However, the host plants often tend to overlap in related species, and the teliospore morphological characteristics are very similar. The taxonomy and phylogenetic relationship of *Coleosporium* species in China are also challenging.

A total of 876 uredinio-telial specimens, from 21 provinces, were used for light microscopy, scanning electron microscopy and molecular phylogenetic investigation. The association between the morphological characters of *Coleosporium* species and the telial host families were summarized, then phylogenetic trees were constructed from the 28S region of nuclear large subunit rDNA, and the internal transcribed spacers regions, respectively. We aimed to define the relations between the phylogenetic group and morphological characteristics, and to evaluate the taxonomic the morphological similar species of *Coleosporium*. Main results are as follows:

1. The total number of valid *Coleosporium* species in China is 56. The valid names of species are given together with synonyms, new descriptions for each spore stages, revised or original descriptions, specimens examined, distribution, and remarks. Also the Classification table of *Coleosporium* species is listed. The following specific names in brackets are reduced to synonyms of the former namers: *Coleosporium horianum* Hennings (syn. *C.campanumoeae* Dietel), *C.cimicifugatum* Thüim (syn. *C.actaea* P Karst.), and a new *Coleosporium* species is firstly described, named as *Coleosporium zhuangii* C.M. Tian & C.J. You (Type on *Ligularia fischeri* (Ledeb.) Turcz.). Two wrong recorded *Coleosporium* species, including *Coleosporium pseudocampanulae* and *Coleosporium elongatum*, are moved.

2. The surface structure of urediniospores, and the morphological characters of teliospores have been proved to be more reliable taxonomic characters for the delimitation and circumscription of *Coleosporium* species. Also, the urediniospore-surface structures of 43 *Coleosporium* species were classified into twelve types based on gross shape and size of processes on the spore surface, and they were categorized into five major types: echinulate, annulate, verrucose, coronate, and nailheaded, in particular, the annulate type was further classified into eight subtypes (A1-A7) on the basis of the shape of processes, as well as the presence or absence of a smooth or reticulum-like spot on spore surface, while the verucose type also was classified into two subtypes

(V1-V2), We also discussed the morphological variations of urediniospore-surface structure in relation to putative uredinial host specificity.

3. The circumscription and identification of the following morphologically similar species have been demonstrated to be clear based on morphological characters and phylogenetic study. *C. plectranthi* and *C. perillae*, *C. clematidis* and *C. clematidis-apiifolia*, *C. campanulae* and *C. lycopi*, *C. pulsatillae* and *C. anemones*, *C. ligulariae*, *C. saussureae* and *C. pedunculatum*, *C. pedicularil* and *C. euphrasiae*.

4. Sequence data were obtained from 28S region of nuclear large subunit rDNA, and from internal transcribed spacers. Then, phylogenetic trees were constructed from the 28S and ITS regions, respectively. Those *Coleosporium* species were separated into seven groups by MP trees in 28s region, however, the analyses of ITS trees clearly distinguished six groups. The relations between the phylogenetic groups and morphological characteristics were investigated, and the results showed that the urediniospore surface-structure and the morphological characters reflected the phylogeny, the germ pore arrangement of urediniospores and the shape, size of urediniospores and teliospores did not correspond to the phylogeny.

Key words: Pine needle rust, *Coleosporium*, taxonomy, phylogeny

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