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ADVANCES IN THE IDENTIFICATION OF EMERGING POWDERY MILDEW FUNGI USING MORPHOLOGICAL AND MOLECULAR DATA

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Recently, the classical morphological criteria and host range data used in the identification of powdery mildew fungi were supplemented with scanning electron microscope (SEM) and molecular phylogenetic analyses. This paper discusses the joint use of these methods in the identification of powdery mildew anamorphs causing new or emerging plant diseases in different parts of the world.

Keywords: identification of powdery mildew fungi

Powdery mildew fungi (Erysiphaceae) are one of the most conspicuous and most studied groups of plant pathogens. These biotrophic fungi can relatively easily be studied as most of them produce white epiphytic or hemiendophytic mycelia on the aerial parts of living plants with large one-celled conidia produced terminally on isolated aerial unbranched conidiophores and with haustoria in the epidermal cells of their hosts. Traditionally, their taxonomy and identification were based largely on the characteristics of the teleomorph, such as the shape of the appendages on the cleistothecium and the number of asci in the cleistothecium [1–3]. However, many powdery mildew fungi do not produce cleistothecia regularly or do not produce them at all, especially when they increase their host ranges or are in geographical areas causing previously unknown plant diseases – so, exactly when there is an urgent need to precisely identify the species involved and also to determine the origin of the inocula. In the absence of the teleomorph (the cleistothecium), based solely on the classical morphological characteristics of the anamorph, it was impossible even in the 1990's to identify conclusively most of the powdery mildew species responsible for new or emerging plant diseases. The lack of an accurate identification of powdery mildew anamorphs causing recent epidemics on tomato [4–6], poinsettia [7] and *Rhododendron* [8] have illustrated this point well. In our studies, the identification of powdery mildew fungi not reported before on bean [9] and on ornamentals like *Crassula ovata* [10] and *Sedum spectabile* [11] was also problematical in the absence of the teleomorphs.

In 1997, Cook et al. [12] showed that surface patterns of powdery mildew conidia and septa, visible especially under the scanning electron microscope (SEM), are important characteristics in the identification of anamorphs. Based on SEM patterns, many powdery mildew anamorphs were well characterized and accurately identified [12]. This approach allows even a presumptive identification of the teleomorph genera. The results of this comprehensive SEM study [12] were subsequently supported by phylogenetic analyses of the nuclear ribosomal DNA (rDNA) internal transcribed spacer (ITS) sequences in the Erysiphaceae which have provided a large data set for molecular identification of many powdery mildew species [13-19]. Therefore, the classical morphological criteria and host range data used in identification [1, 2] can now be supplemented with both SEM and molecular methods. This confluence of methods giving mutually supporting results has triggered a complex revolution in powdery mildew taxonomy [3, 20, 21].

In our laboratory, we have applied the recently developed SEM and molecular phylogenetic analyses to identify conclusively the powdery mildew anamorphs infecting tomato worldwide. These fungi caused serious economic damage during the past 10-15 years in all continents where tomatoes are grown [4-6]. The published data on their classical morphological characteristics were often contradictory making their identity and host range questionable [5]. Based on the joint use of morphological, SEM and rDNA ITS data, we found that all the recent tomato powdery mildew epidemics outside Australia were caused by one single species, *Oidium neolycopersici*, while in Australia an other taxon, *O. lycopersici*, was responsible for this disease [6]. Currently, rDNA ITS sequence data and SEM patterns are being used in our laboratory to precisely identify little known powdery mildew anamorphs responsible for recently emerged infections on hornbeam (*Carpinus betulus*), snowberry (*Symphoricarpos albus*) and privet (*Ligustrum vulgare*) in different European countries.

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