

TAXONOMY OF PLANT PATHOGENIC FUNGI: CAN WE MERGE THE PAST WITH THE FUTURE?

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Lists of actionable quarantine organisms, i.e. name lists of plant pathogenic fungi, play an important role in global trade, and in guaranteeing free market access. Various studies support the estimate that there could be at least 1.5 M fungal species on earth. Of the currently known 100 000 species, only around 16% have to date been deposited in genetic resource centres; approximately 11.5% of these species are known from nucleotide sequence data (Hawksworth D.L., 2004 *Studies in Mycology* 50: 9-18). In plant pathology, species definitions and their genetic circumscriptions remain paramount to quarantine decisions and disease control practices. The potential problems entailed by this system are intensified by the fact that the best known pathogenic fungal species concepts are “old names” for which no ex-type cultures are available. When multiple strains of many of these plant pathogens are subjected to nucleotide sequence analysis, it becomes clear that, in most cases, they harbour several morphologically similar but genetically diverse cryptic species. Future global trade is inevitable, and plant pathologists will have to develop new tools to deal with this challenge. The bulk of our current taxonomic knowledge is based on the phenotype, while the genotype is clearly seen as the future of taxonomy. Major new taxonomic initiatives include assembling the fungal tree of life (AFToL), aimed at resolving phylogenetic relationships, and the European Consortium for the Barcode of Life (ECBoL.org and Mycobol.org), aimed at using DNA barcodes to accurately and quickly identify fungal taxa. Other components of an accessible, quality-controlled taxonomic system are data repositories for descriptions and new names (Mycobank.org), DNA banks (e.g. NL-Bank at CBS), electronic access to specimens (e.g. BPI, H-CBS, etc.) and open access to data (e.g. free online journals). Plant pathology journals need to take a standpoint pertaining to these developing vouchering and access standards, and also need to be able to link to the new data sets so that the reader (or user) is empowered to merge the taxonomic concepts of the past with the nucleotide data of the future.

CURRENT STATUS OF PLANT VIRUS TAXONOMY

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Viruses are elementary biosystems that have some of the properties of living organisms, as they possess a genome, are able to replicate, and to adapt to changing environments. Thousands of viruses have been described since their discovery at the end of the 19th century, thus making it compulsory the development of a specific taxonomy, i.e. a practical system for partitioning their world into distinguishable, universally recognized entities. “Classification” is the arrangement of biological entities into taxonomic categories (taxa) on the basis of similarities and/or relationship, whereas “nomenclature” is the assignment of names to taxa, according to international rules. To apply these (apparently) simple concepts to viruses, the International Committee on Taxonomy of Viruses (ICTV) was created in 1966. Regardless of the host (plants, vertebrates, invertebrates, bacteria, fungi, algae) viruses are currently classified with a system based on the hierarchy of family, genus, and species. A virus species, is defined as “*a polythetic class of viruses that constitute a replicating lineage and occupy a particular ecological niche*”. Parameters used in taxonomy are: (i) virion properties (morphology, physico-chemical and physical characteristics), (ii) genome structure (iii) replication strategy; (iv) phylogenetic relationships; (v) antigenic properties (serological relationships); (vi) biological properties (host range, epidemiology, pathogenicity, cytopathology). To give an idea of how dramatically virus taxonomy has grown, the first ICTV Report (1971) consisted of 82 pages whereas the 8th Report (2005) exceeds 1250 pages. Currently the “classified” plant virus world consists of 1 order, 1 dsDNA family, 2 ssDNA families, 3 dsRNA families, 2 (-)ssRNA families, 2 ssRNA reverse transcribing families, 9 (+)ssRNA families. Recognized plant virus genera are 81, most of which are assigned to families. Names of definitive virus species are in English, written in italics (e.g. *Tobacco mosaic virus*), the same as the names of species in other kingdoms. Names of taxa have different ending: orders end in *-ales* (e.g. *Mononegavirales*), families in *-idae* (e.g. *Tombusviridae*), and genera in *-virus* (e.g. *Potexvirus*).

TAXONOMY AND PHYLOGENY OF PHYTOPATHOGENIC BACTERIA

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Historically, phytopathogenic bacterial species were classified using pathogenicity tests. Many could not be differentiated biochemically and were omitted from the 1980 list of approved names. To save these epithets, the subspecific term, “pathovar” was proposed. The standard for species revival under the Code is DNA/DNA relatedness of $\geq 70\%$. Taxonomy of *Xylella* and citrus pathogenic xanthomonads are discussed. *Xylella fastidiosa* (XF) infects many hosts and encompasses considerable genetic diversity, but is classified as a single species. Based on DNA relatedness assays (T_m -15 C and -8), we propose reordering XF strains among subspecies: subsp. *fastidiosa* infecting grape, alfalfa, almond, and maple; subsp. *multiplex* infecting peach, plum, almond, elm, and sycamore; and, subsp. *pauca* infecting citrus (Schaad et al., 2004). Phylogenetic studies using gene sequencing show subspecies *fastidiosa* and *multiplex* diverged 16,000 years ago. Vauterin et al. (1995), based on phenotypic and optically-based DNA relatedness assays, proposed naming the xanthomonads causing the five forms of citrus canker (A, B, C, D, and E) as *Xanthomonas axonopodis* pathovars: “citri” (A), “aurantifolia” (B, C, D), and “citrumelo” (E). However, S_1 nuclease assays at T_m -15 C showed $\leq 41\%$ relatedness between the citrus xanthomonads and *X. axonopodis* (Schaad et al., 2005). Furthermore, these citrus pathogenic pathovars are related at $\geq 70\%$ to three species-level taxa: including *X. campestris* pathovars “malvacearum”, “phaseoli var. fuscans”, and “alfalfae”. Based on T_m -8 C relatedness and/or phenotypic and pathogenic characters, we suggest the three citrus pathogens be named subspecies of *X. citri* subsp. *citri*, *X. fuscans* subsp. *aurantifolii*, and *X. alfalfae* subsp. *citrumelonis*.

