

Section 1. Fungal diseases

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Introduction to the fungal pathogens

Changing status on taxonomy of fungi

More than half of all rice diseases are caused by fungal pathogens. Before we proceed to discuss individual fungal diseases and their causal pathogens, a brief introduction on the changes in fungal systematics in recent years is given here. These changes are the consequences of recent advances in molecular biology including gene sequencing, which have been employed in phylogenetic studies of different organisms. Fungi are no longer considered to be closely related to plants but more to animals. Fungi had been divided into two unique groups. One of these is the so-called “true fungi”, which represents a distinct kingdom that is more closely related to animals (Rossman and Palm-Hernandez 2008), and is now taxonomically placed under Kingdom Fungi. The stramenopiles or heterokonts, which include diatoms, golden algae, brown algae, and oomycete, are grouped under Kingdom Chromista, while the various kinds of slime molds are placed under Kingdom Protozoa. Under this new classification scheme, many rice diseases caused by fungal pathogens belong to the “true fungi” under Phylum Ascomycota or Ascomycetes in traditional mycology.

Oomycetes, which include fungi of water molds, white rusts, and downy mildews, historically classified under Phycomycetes that consisted of major groups of plant pathogens such as *Phytophthora*, *Pythium*, and fungi causing downy mildews, have been found to be closely related to the yellow-brown algae or the heterokont algae under Kingdom Chromista, Phylum Heterokonta (Rossman and Palm-Hernandez 2008). The Oomycota are differentiated from the true fungi based on sexual reproduction, the nuclear state of their vegetative mycelium, cell wall (composed of glucans, small amount of hydroxyproline and cellulose), the type of flagella, and the mitochondria.

Most rice fungal pathogens fall under the “true fungi”, of which there are five groups (Blackwell et al 2006). The two major phyla, Ascomycota and Basidiomycota, comprise most the rice pathogens discussed in this online resource. Although rice is a semi-aquatic plant, the largest group of rice fungi belongs to Ascomycota followed by Basidiomycota. There are a few rice fungal pathogens that belong to Phylum Oomycota (Oomycetes), exemplified by downy mildew and feeder root fungi.

Members of the Kingdom Fungi produce mycelium and the cell walls contain glucans and chitin, but the cells lack chloroplasts. The two phyla of interest to rice pathologists are Ascomycota and Basidiomycota. Phylum Ascomycota includes ascomycetes or fungi that produce sacs. They have a sexual state (teleomorph) and an asexual state (anamorph). They produce sexual spores called ascospores, which generally form a group of eight within an ascus. The asexual spores (conidia) they produce are on free hyphae or in asexual fruiting structure such as pycnidia and acervulli. Phylum Basidiomycota includes basidiomycetes, the club and mushroom fungi. Members produce sexual spores called basidiospores externally on a club-like, one- or four-celled spore-producing structure called basidium.

Organisms in Kingdom Chromista are uni- or multi-cellular, filamentous or colonial, and are primarily phototrophic microorganisms. Some of them form tubular flagellar ap-

pendages and/or chloroplasts inside the rough endoplasmic reticulum. Members of this kingdom include the brown algae, diatoms, oomycetes, and some other similar organisms. The cell walls of members of this group of “fungi” are composed of glucans, small amounts of hydroxyproline, and cellulose.

Rules on naming of fungi

Taxonomy, nomenclature, and phylogeny, discussed in the introduction for the bacterial diseases section, are all components of systematics, which relates to the study of biological diversity. A taxon is a taxonomic group of any rank, e.g., order, family, genus, species, and subspecies. Taxonomy aims to describe, to classify and to name (nomenclature) organisms. Nomenclature is the branch of systematics that determines the correct scientific name for a taxon.

Since 1950, the rules on naming fungi are based on a set of basic principles governed by the International Code of Botanical Nomenclature (ICBN). ICBN is under the “Botanical Nomenclature” because it had been assumed, historically, that fungi and plants were closely related. The naming of animals is governed by a different set of rules set by The International Code of Zoological Nomenclature, while bacteria and other prokaryotic organisms are named according to The International Code of Nomenclature of Prokaryotes (ICNP) (see An Introduction to Bacterial Pathogens).

A large part of the following discussion is based on a review by Rossman and Palm-Hernandez (2008).

The basic principles in naming fungi include: the first scientific name applied to a species or other taxon has priority; and each name must be based on a type that represents that entity. In the case of a species, the type is a specimen; for a genus, the type is a species; for a family, the type is a genus, etc.; a name must be published in a specific manner, i.e., with a Latin description and a type designated, and the publication must be widely distributed; and a species can have only one correct scientific name except in the case of fungi that have alternate states ([Article 59, ICBN](#)). The ICBN also governs how to transfer a species name from one genus to another as the concept of the genus or species changes.

Each scientific name for a species consists of two or more portions, minimally a genus and a species epithet. A specific name is placed in a defined hierarchy that usually includes the family, order, class, phylum, and kingdom. Species may also be given a subspecific designation such as variety or subspecies. The subspecific taxon *forma specialis* or *form species*, which is common in many plant pathogens, is used to indicate a physiological difference based on adaptation to a different host.

Example: naming of the rice blast fungus

Because the name of rice blast fungus has changed frequently in recent years, we use it in the following discussion to illustrate how the ICBN rules are applied.

A brief historical account:

- *Pyricularia grisea* was first mentioned in the literature as *Trichothecium griseum* Cooke by Cooke and Ellis (1879).
- Saccardo (1880) described the genus *Pyricularia*, citing *P. grisea* as the type species.
- The generic description fulfills the requirement for a description of the species (according to [Article 42, ICBN](#)), thus the first official name of *P. grisea* was dated from this publication.
- The author’s citation for *P. grisea* is “Cooke in Cooke & Ellis ex Sacc.”

- *Pyricularia oryzae* Cavara was described and illustrated on the label of specimens issued in 1892 by Cavara as Fungi Longobardiae #49.
- These specimens were issued under the name “*Piricularia oryzae*”, which is the correct Latin spelling of the genus name.
- However, according to ICBN Article 73, the genus must be spelled as originally published by the author, thus, the correct spelling of this genus is *Pyricularia*.

Advances since the discovery of the sexual state of the fungus: The teleomorph of *Pyricularia oryzae* was described as *Ceratosphaeria grisea* by Hebert (1971). Later, this name was transferred to the genus *Magnaporthe* by Barr (1977). Yaegashi and Udagawa (1978), who produced the sexual stage from crosses of *Pyricularia* isolates from several graminaceous hosts including *Oryza*, independently placed the teleomorph in the genus *Magnaporthe*. Their publication, however, only appeared after Barr’s new combination had been published. Besides Yaegashi and Udagawa, many other subsequent authors had also placed the teleomorph of *Pyricularia oryzae* in *Magnaporthe* as *M. grisea*. The new rule of ICBN allows more than one species name to be conserved. Some suggested that *Pyricularia oryzae* should be conserved under the new ICBN rules (Kirk 1983). Rossman et al (1990) argued that, although *P. oryzae* is widely used, a well-known name, the earlier name, *P. grisea*, is not altogether obscure. It has been used in the literature for this fungus on hosts other than *Oryza*.

There are other considerations when using the rules in naming a plant pathogenic fungus:

- According to [Article 59, most recent ICBN](#) (Greuter et al 1988), a fungus must be referred by the name of the holomorph, i.e., the whole fungus in all its morphs and phases (Hawksworth et al 1995).
- In cases where both the teleomorph and anamorph are known, one generally uses the name of the teleomorph.
- However, if the teleomorph is known but rarely encountered or is not relevant to the discussion, i.e., the research is dealing only with the anamorphic state of the fungus, it is acceptable to use only the name of the anamorph in the publication.
- In the case of *Pyricularia grisea*, the teleomorph is rarely encountered in nature but the sexual state is known experimentally.
- However, it is the asexual stage of the fungus that is widely distributed in nature and that causes the damage that most scientists are dealing with.
- Therefore, it is acceptable to refer to the fungus as either *Magnaporthe grisea* (Hebert) Barr or *Pyricularia grisea* Sacc.

The controversy: The proposal to change *P. oryzae* to either *M. grisea* or *P. grisea* was met with disagreement from some rice pathologists notably Kato et al (2000). They believed that the rice blast fungus should be considered as a separate species, under the genus *Magnaporthe* for the teleomorphic state and *Pyricularia* for the anamorphic state. They pointed out that RFLP analysis revealed that the fungus belongs to the cultivated cereals (CC) group, which is distinct from isolates of crabgrass. The CC group consists of isolates from *Oryza*, *Setaria*, *Panicum*, *Eleusine*, *Triticum*, and *Eragrostis* and possess at least one of the three criteria for species recognition—biological, morphological, and phylogenetic species recognition.

Members of the CC group are inter-fertile but reproductively isolated from other isolates including *Digitaria* thus qualify for the recognition of CC as biological species. Morphologically, they are indistinguishable from one another but distinguishable from

Digitaria isolates; the macroconidia are slightly slender compared with those of the CC group, thus, qualifying its recognition as a morphological species. They also form a single clade on the dendrograms constructed from single copy of RFLP data (Kato et al 2000) and rDNA data (Kusaba et al 1999), thus, qualifying its recognition as phylogenetic species. Following these findings, Kato et al (2000) suggested that the CC group should be referred to as *P. oryzae* for the rice blast fungus.

Is it final? The proposal of Kato et al (2002) was not seriously considered until Couch and Kohn (2002). Based on multilocus gene genealogy concordant with host preference, Couch and Kohn (2002) provided evidence that isolates from *Oryza*, *Setaria*, and *Eleusine* are distinct from *M. grisea* and they proposed a new species, *M. oryzae*, for these blast pathogen isolates. This proposal was further confirmed by Tosa et al (2004). Henceforth, the rice blast fungus is accepted as *P. oryzae* with the teleomorph, *M. oryzae*. The anamorphic name, *Pyricularia oryzae*, which is used is based on reasoning discussed above. Following the rule of ICBN, either *Magnaporthe oryzae* or *Pyricularia oryzae*, which ever is a more familiar name among rice researchers is the accepted name to be used in publication. In practice, *M. oryzae* is now accepted by the community of rice pathologists.

Naming of plant diseases based on symptoms

We mentioned briefly how fungi are named. But how are plant diseases, in general, named and recognized? We have borrowed an expression from Wheeler (1976) that “Plant disease is more readily recognized than defined” to express our experience based on long-years of working on rice disease in the rice fields of South and Southeast Asia. Even if only one agent may be involved in causing a disease, a number of changes in the plant in response to the infection may occur to form symptoms. Symptoms are the basis in naming a disease. Thus, a plant disease is named based on a symptom on the primary host. Symptom(s) may form a symptom-picture that is known as a syndrome. Names of symptoms are recognized by the process of their development on the host plant.

Plant pathologists (Wheeler 1976 and others) have recognized the following possible changes that occur once a host plant is infected.

- Death of the tissues or necrosis: necrotic lesions, leaf spot, stripe, streaks, scald, blotch.
- Abnormal increase in the tissues: an increase in size (hypertrophy or gall) and/or in number (hyperplasia or grassy stunt).
- Failure to attain normal size or development (hypoplasia): dwarf (e.g., yellow dwarf in rice).
- Change in color: yellowing or chlorosis are common (orange leaf, red stripe).
- Wilting: caused by interference with the normal movement of water within the plant (e.g., bacterial blight of rice).
- Unusual development or transformation of organs: smut (e.g., false smut).
- Disintegration of tissues: rot (wet rot or dry rot; in rice diseases, seedling rot and foot rot, both caused by bacterial pathogens).
- Excessive gum formation (more often in trees).

The symptoms of rice diseases caused by fungal pathogens are composed of all the above except disintegration of tissues and excessive gum formation. Among the known fungal diseases, death of plant (foliar) tissues or necrosis is, by and large, the most common symptom reported. Among these diseases, blast and brown spot are typical. Even though the necrotic foliar tissue is common after infection, the shape of necrosis varies.

In some rice fungal diseases, the pathogen grows or produces various structures on the surface of rice plant, which may include mycelium, sclerotia, or other fruiting bodies,

which are called signs. Signs are unique structures of the invaded pathogens that are distinct from symptoms, which refer to the appearance of the infected plants or plant parts. Thus, in fungal diseases of rice, such as sheath blight or stem rot, even though sclerotia are produced by the invading fungal pathogens on infected host tissues, the size, color, and location are unique from each other. Signs are a useful diagnostic feature of the disease and its causal organism.

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