Recent Change in the Nomenclature of *Phellinus pini*: What is *Porodaedalea*?

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The white-rot genus *Phellinus* contains many important forest pathogens and saprotrophs, including those that produce heartrot, saprot, and root-rot or butt-rot. One of the most notorious species is *Phellinus pini*, the causal agent of "red ring decay" or "white fleck," which primarily affects older stands of conifers, including Douglas fir, larch, pine and spruce. The fungus produces a white pocket rot, creating wood that is highly desirable for paneling and other wood crafts but otherwise low in value due to strength loss during advanced decay (Tainter and Baker, 1996). *Phellinus pini* initially infects through branch stubs and spreads into extractive-rich heartwood. The pathogen is also able to attack and spread in killed sapwood. Decay may continue shortly after death of the host but the fungus is not an important saprotroph of slash (Tainter and Baker, 1996). Trees may be subject to breakage at the points of decay (Dunster, 1996), so the presence of *P. pini* conks, especially if large and in high numbers, is an important criterion in hazard assessment protocols (Bakken, 1995; Dunster, 1996; Toupin et al., 2008).

Since the 19th Century, researchers have worked to define individual species of fungi and arrange those species in groupings (or taxa) based on similar aspects of gross physical appearance and habit. With the development of the concept of evolution by natural selection, mycologists attempted to form natural groupings that reflect evolutionary pathways while still being based on simple, visible characteristics. Through the 20th Century, microscopic and chemical features were added to further refine and in many cases segregate or split off taxa. As more was learned about differences and similarities in fungi, taxonomy moved into biosystematics, the delineation of taxa at all levels (e.g., species, genera, families) into monophyletic groups - groups that have a single ancestral lineage.

The names of fungal taxa have also reflected concepts of what makes two fungi similar or different. With the advent of molecular analytical tools in the 1990s that more directly assess ancestral relatedness, the status of many fungal groups, including the genus *Phellinus*, has been radically revised. This has led to confusion by plant pathologists who frequently encounter forest fungi and their effects. The confusion can also be shared by researchers who are developing the underlying concepts of relatedness.

What is the current name of a particular fungus? Why do the names keep changing? Classification systems based strictly on morphology and physiology are often misleading because of convergent evolution. Thus morphological or physiological features, such as the structure of the hymenium (pores, gills, teeth or a flat surface) or decay mechanism (white-rot versus brown-rot) have evolved independently. The Latin binomal of a fungus can provide much

information about the fungus, giving an instant "genealogy" to one familiar with current classification systems. The genus identifies a closely related group of species, as compared to those in a different genus, and can give one insight into physiologies, decay mechanisms, and disease-inducing potential shared by species in the genus (Glaeser and Lindner, in press.).

The genus *Phellinus* has traditionally been used to describe brown, poroid, white-rot fungi that produce perennial fruiting bodies with a dimitic hyphal system of skeletal and simple-septate generative hyphae. Many species form hymenial or tramal setae or setal hyphae that darken in KOH (Gilbertson and Ryvarden, 1987). It is a large, cosmopolitan genus with host specific species, such as *Phellinus robineae* on black locust, and nonspecific saprotrophs, such as *Phellinus gilvus* (Larsen and Cobb-Poulle, 1990). The genus *Phellinus* was erected in 1886 by Quélet (1886). Murrill (1907) split *Phellinus* into several smaller, restricted genera, most of which were largely ignored for the next 77 years. In 1984, Fiasson and Niemela (1984) reassessed the European species of *Phellinus* using a combination of conventional morphological criteria, numerical taximetric analyses, chemotaxonomy, protein electrophoresis, nuclear condition and cultural studies. They reintroduced five of Murrill's generic names and created two new genera. Gilbertson and Ryvarden (1987) were aware of this revision but elected to retain *Phellinus* as a single genus in their landmark work, "Polypores in North America" (Gilbertson and Ryvarden, 1986; 1987).

Phellinus is placed in the Order Hymenochaetales (Oberwinkler, 1977) and the Family Hymenochaetaceae (Donk, 1964) along with its close relative *Inonotus*, a white-rot genus that produces annual, monomitic fruiting bodies (Gilbertson and Ryvarden, 1987). Analyses of DNA sequences confirmed the placement of *Phellinus* and *Inonotus* in the Hymenochaetales (Wagner and Fischer 2001; Larsson et al., 2006). Additional polyporoid, toothed, agaric and corticioid fungi, including *Trichaptum*, *Oxyporus*, and *Hyphodontia*, are also member of this order (Kim and Jung, 2000; Hibbett and Thorn, 2001; Larsson et al., 2006; Redhead et al, 2002). To date, the Hymenochaetales is defined only by molecular analysis and does not have a single unifying morphological feature, although the ultrastructure of the septum may be an ancestral state (Larsson et al., 2006).

Molecular phylogenetic analyses demonstrate that *Phellinus* is not a monophyletic group. This revelation was not surprising given the large distribution and myriad forms of the genus. Wagner and Fischer (2001; 2002) analyzed the nuclear encoded large subunit ribosomal DNA (LSU rDNA) and found support for Fiasson and Niemela's 1984 division of *Phellinus* and *Inonotus* into a number of smaller genera based on morphological and chemical characteristics. The eleven genera recognized were: *Phellinus* sensu stricto *(i.e.* "in a narrow sense;" s.str.), *Inonotus* s.str., *Inocutis*, *Fomitiporella*, *Aurificaria*, *Phylloporia*, *Fulviformes*, *Mensularia*, *Pseudoinonotus*, *Fomitiporia*, *Porodaedalea*, *Onnia*, *Fuscoporia*, and *Inonotopsis*. Subsequent molecular studies supported these results but called for a revision of *Onnia*, *Phellinidium* and *Pseudoinonotus* (Larsson et al., 2006). The systematics of *Phellinus* and *Inonotus* and allied taxa are still in state of flux. Proposed combinations that are of interest to forest pathologists include: *Porodaedalea pini (*syn. *Phellinus pini)*, *Porodaedalea chrysoloma (*syn. *Phellinus chrysoloma)*, *Porodaedalea cancriformans (*syn. *Phellinus cancriformans)*, *Onnia tomentosa (*syn. *Inonotus*

*tomentosus), Phellinidium sulphurascens (*syn. *Phellinus sulphurascens*), *Phellinidium weirii (*syn. *Phellinus weirii), Fulviformes robiniae (*syn. *Phellinus robiniae),* and *Pseudoinonotus dryadeus (*syn. *Inonotus dryadeus).* Jin et al (2005) detected 13 different evolutionary lineages and several unresolved species within *Phellinus* and the related genera of *Inonotus*, *Hymenochaete*, and *Onnia* using a combination of ITS and mitochondrial small subunit ribosomal DNA (mt-ssu-rDNA). These lineages were divided into two major groupings that correlated with nuclear condition, i.e. binucleate versus oligonucleate. The Hymenochaetales, or hymenochaetoid clade, is obviously quite complex and needs more work to be fully resolved.

The fungus that has been known to us as *Phellinus pini* has had many names. It was first named *Boletus pini* by Thore in 1803 and was subsequently placed in the genera *Daedalea*, *Polyporus*, *Trametes*, *Fomes*, *Ochroporus*, *Xanthochrous*, *Porodaedalea*, *Fomes*, *Inonotus*, and *Cryptoderma* (Larsen and Cobb-Poulle, 1990). *Phellinus pini* was erected in 1941 by Bondartsev and Singer (Bondartsev and Singer, 1941), although many foresters learned about *Fomes pini* well into the 1970s. The epithet *Porodaedalea pini* was first published by Murrill in 1905 (Murrill, 1905) and is the nomenclatural type of the genus.

The test of any taxonomic change is whether other mycologists and plant pathologists will accept it and start to use the new epithets. This can sometimes take years to resolve. Changing the name of well known fungal pathogens is always difficult, as was shown in the renaming of the chestnut blight fungus in the 1980s (Anagnostakis, 1987) and the breakup of *Armillaria mellea* into different species in the 1990s (Burdsall and Volk, 1993). In the era of molecularly based phylogenetics, we are able to trace evolution as never before. Most fungal groups are being reevaluated and reassessed. In the end, we will know much more about relationships within the fungal world and gain better understandings of fungal physiology and pathology. A better understanding of relationships among fungi has the potential to improve the practice of forest pathology.

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