

## **Proposed changes to the classification of Basidiomycota and Microsporidiomycota, and a proposal to recognize the Dikarya:**

The following items describe proposed modifications to the classification of Basidiomycota that were received in response to the first draft classification (items 1-13, below), distributed in July 2005, as well as additional comments regarding Dikarya and Microsporidiomycota (items 14-15). The names of the individuals who proposed the changes are not listed. Comments that did not suggest a change are not included. Discussion among the AFTOL classification group regarding each suggestion is summarized, as well as the final (interim?) decision of the group.

The purpose of this document is to provide background on the discussions that have led up to the current draft classification, and to provide a framework for future discussion. If it is appropriate, please refer to the numbered items below in correspondence regarding the draft classification.

### **1. Reclassify “Urediniomycotina” as “Pucciniomycotina”, and raise current Subclasses to Class.** Thus, the new classification would be (present names in parentheses, unchanged names not indicated):

- Pucciniomycotina (Urediniomycotina)
  - Pucciniomycetes (Urediniomycetidae)
    - Puccinales (Uredinales)
  - Cystobasidiomycetes (Erythrobasidiomycetidae)
  - Agaricostilbomycetes (Agaricostilbomycetidae)
    - Agaricostilbales
  - Microbotryomycetes (Microbotryomycetidae)
  - Atractiellomycetes (Atractiellales)
    - Atractiellales
  - Classiculomycetes (Classiculales)
    - Classiculales
  - Cryptomycocolacomycetes (Cryptomycocolacales)
    - Cryptomycocolacales
  - Mixiomycetes (Mixiales)
    - Mixiales

Discussion: Positive aspects of this proposal include elimination of the higher-level redundancy of Urediniomycotina/Urediniomycetes in the July 2005 classification. However, some correspondents objected to the change from the *Uredo* basionym, which would cause confusion among plant pathologists and others. It has been pointed out that there is nothing in the *Code* that prevents using an anamorph name as a basionym. Consequently, we decided to continue to call this subphylum the Urediniomycotina.

The Classiculomycetes, Cryptomycocolacomycetes, and Mixiomycetes may eventually be recognized as classes, but these would be redundant names

for very small orders, which could prove to be included in other higher taxa. Alternatively, we suggest that these groups should be placed as orders *incertae sedis* among the Urediniomycotina.

The revised classification is as follows (all classes and orders indicated):

Urediniomycotina

- Urediniomycetes
  - Uredinales
  - Helicobasidiales
  - Platyglloeales
  - Septobasidiales
- Cystobasidiomycetes
  - Cystobasidiales
  - Erythrobasidiales
- Agaricostilbomycetes
  - Agaricostilbales
- Microbotryomycetes
  - Heterogastridiales
  - Leucosporidiales
  - Microbotryales
  - Sporidiobolales
- Atractiellomycetes
  - Atractiellales
- Orders incertae sedis*
  - Classiculales
  - Cryptomyocolacales
  - Mixiales

**2. Include Wallemiomycetes as a class incertae sedis among the Basidiomycota.**

Discussion: Zalar et al. in *Antonie Van Leeuwenhoek* 87:311-328 (2005) present analyses of nuc-ssu rDNA data that strongly support *Wallemia* (a group of xerophilic, conidiogenous fungi) as a member of the Basidiomycota (bootstrap=98%). Also included were Ustilaginomycetes (bootstrap=97%), Tremellomycetes (bootstrap=80%), and Dacrymycetes (one species). The Dacrymycetes+Tremellomycetes clade was supported at 67%. Based on these results, Zalar et al. suggested that *Wallemia* represents a new order and class of Basidiomycota. However, these analyses were based on a single gene and a limited sampling of taxa. We decided to include Wallemiales as an order *incertae sedis* among the Basidiomycota.

**3. Divide Ustilaginomycotina into three classes, eliminate subclasses. Thus:**

- Ustilaginomycotina
  - Ustilaginomycetes
  - Entorrhizomycetes
  - Exobasidiomycetes

(with orders remaining as in the draft classification)

Discussion: We adopted this proposal.

**4. Place Sebaciales and Auriculariales as *incertae sedis* within Agaricomycotina.**

Discussion: An unpublished five-locus analysis (*rpb2*, *tef1*, 18s, 25S, 5.8S rDNA) by Brandon Matheny supports the monophyly of the Agaricomycetes (i.e., the Agaricomycotina excluding the Dacrymycetes and Tremellomycetes) with bootstrap support of 100% and posterior probability of 1.0. Consequently, we decided not to make the proposed change.

**5. Place Geastrales as *incertae sedis* within Agaricomycotina (i.e., remove Geastrales from Phallomycetidae).**

Discussion: There is strong support for inclusion of *Geastrum* in the Phallomycetidae. In Lutzoni et al. (2004, fig. 2), the Phallomycetidae, including *Geastrum saccatum*, was supported with a bootstrap score of 100% and a posterior probability of 1.0. Kentaro Hosaka's recent analyses also support inclusion of *Geastrum* in Phallomycetidae. Consequently, we decided not to make the proposed change.

**6. Reduce Atheliales to family rank as Atheliaceae, and place as *incertae sedis* among Agaricomycetes (i.e., remove Atheliales from Agaricomycetidae).**

Discussion: Brandon Matheny's five gene analysis, referenced above, supports Agaricomycetidae with a bootstrap score of 96% and a posterior probability of 1.0, with Atheliales outside of Agaricales (75%, 1.0) and Boletales (100%, 1.0). Recent analyses by Larsson et al. (2004) and Binder et al. (2005) are consistent with this placement. We did not adopt the proposed change.

**8. Elevate Cantharellales to subclass rank as Cantharellomycetidae; recognize orders Cantharellales, Tulasnellales, Ceratobasidiales.**

Discussion: The Cantharellales, as delimited here, is strongly supported as monophyletic, but many nodes within this clade are still not well resolved. In part this is a consequence of the high rate of evolution of the nuclear rDNA in some lineages, particularly *Tulasnella* and Cantharellaceae.

Brandon Matheny's five-gene analysis, cited above, shows conflict among the rDNA and protein-coding genes with regard to the placement of *Tulasnella*. In analyses that include rDNA, the Tulasnellaceae(-ales) is the sister group of a clade that contains *Cantharellus* and *Craterellus* (Cantharellaceae), with strong bootstrap and posterior probability support. However, analyses that exclude the rDNA suggest that *Hydnum*, *Clavulina*, and *Sistotrema* are more closely related to *Cantharellus*-*Craterellus* than *Tulasnella*. The analysis of Binder et al. (2005) also suggests that *Hydnum* is the sister group of *Cantharellus*-*Craterellus*. That study (Binder et al. 2005) also found strong support for monophyly of *Tulasnella* (four isolates), which could be regarded as Tulasnellaceae(-ales), as well as a clade that

includes *Ceratobasidium*, *Uthatabasidium*, and *Thanatephorus*, which would be equivalent to Ceratobasidiales s.str.

In summary, there is strong support for several clades within the Cantharellales(-omycetidae) that could be recognized as orders, including Cantharellales (*Cantharellus*, *Craterellus*, *Hydnum*), Tulasnellales (*Tulasnella*), and Ceratobasidiales (*Ceratobasidium*, *Uthatabasidium*, *Thanatephorus*). However, that leaves taxa such as *Sistotrema*, *Multiclavula*, *Clavulina*, and *Botryobasidium* unplaced. At this time, we have not made the change that has been proposed, preferring instead to retain this clade as the Cantharellales, as in the Dictionary of the Fungi 9<sup>th</sup> ed.

### **9. Elevate Russulales to subclass rank as Russulomycetidae with multiple orders (not specified).**

Discussion: This situation is similar to that in the Cantharellales-Cantharellomycetidae. Relationships within the Russulales are poorly resolved at present (see Larsson and Larsson 2003 and Binder et al. 2005). At this time, there are three well supported clades that are candidates for elevation to order within "Russulaes" s.lat., based on the provisional names used by Larsson and Larsson, including Russulales s.str. (i.e., *Russula*, *Lactarius*, their gasteroid derivatives, and resupinate relative), Stereales, and Peniophorales. That leaves many taxa unaccounted for (e.g., *Amylostereum*, *Bondarzewia*, "*Gloeocystidiellum*", *Albatrellus*, *Hericium*, *Lentinellus*, *Auriscalpium*, etc).

At this time, we have not made the proposed change, for the sake of simplicity and consistency with the *Dictionary*. However, it would be good to know what the large community of workers in this area thinks.

### **10. Change Corticiaceales to Vuilleminiaceae (or Vuilleminiales, but better to place it at a low rank because of the small size of the clade).**

Discussion: This group is strongly supported and appears not to be nested in any other clade recognized at the ordinal rank, so retaining ordinal rank seems appropriate. The name Corticiales is as valid as Vuilleminiales and is more familiar. The proposed change has not been made.

### **11. Multiple taxa placed in Tremellales should be placed elsewhere, including (suggested placements in parentheses):**

*Ceratosebacina* (Agaricomycetes incertae sedis)

*Tremellochaete* (syn. of *Exidia*, Auriculariales)

*Tremellodon* (syn. of *Pseudohydnum*, Auriculariales)

*Tremelloscypha* (Sebacinales)

*Tremiscus* (Auriculariales)

Discussion: These changes have been made.

### **12. The Phallomycetidae should be classified as a single order, Phallales, with current orders Geastrales, Gomphales, Hysterangiales, and Phallales reduced to families (and therefore not treated in this classification).**

Discussion: In principal, this is a similar argument to those raised with regard to the Cantharellales and Russulales. Nevertheless, arguments for classifying this group as the Phallomycetidae include the following: 1) This clade includes four distinct clades that contain considerable phylogenetic and species diversity; 2) Retaining Phallomycetidae promotes the use of ordinal names that have longer usage than Phallales sensu Dict of Fungi 9th ed; 3) Retaining Phallomycetidae uses all available names in Botanical nomenclature to name well supported nodes, and 4) Retaining Phallomycetidae does not promote of compression of unnamed nodes towards the tips of the tree.

Finally, Kentaro Hosaka has recently completed a major analysis of the "Phallomycetidae" that employs the classification that was proposed in the July 2005 draft classification, and which is retained here.

**13. Brandon Matheny noted that the tree for Basidiomycota that was sent out was not as well resolved as it could have been, given our current understanding of the phylogeny. Specifically, he notes that there is strong evidence that 1) Ustilaginomycotina and Agaricomycotina are sister groups; 2) Dacrymycetes is the as sister group of Agaricomycetes; 3) Thelephorales and Polyporales are sister groups; 4) Russulales and Agaricomycetidae are sister groups; 5) Exobasidiomycetidae is paraphyletic.**

Discussion: I have grouped these comments together because Brandon is not actually suggesting that we create taxa for the clades that he indicates (1-4), or erect an alternative classification for Exobasidiomycetidae (5). Items 1-4 do not contradict any aspects of the proposed classification, but they would add names for groups that are not presently included. Do others feel that we should name these nodes? If so, what names should be used, and at what rank?

**14. Create a subkingdom taxon for the clade that includes the Ascomycota and Basidiomycota. Call this Dikarya.**

Discussion: An alternative name would be Dikaryofungi. Comments would be welcome. At present, the name Diakrya is used.

**15. Revise the classification of Microsporidia to reflect the recent phylogenetic analysis of nuc-ssu rDNA sequences in 125 species of Microsporidia by C. R. Vossbrinck and B. A. Debrunner-Vossbrinck (Folia Parasitologica 52: 131-142, 2005). The Vossbrinck and Debrunner-Vossbrinck classification includes three classes, Aquasporidia, Marinosporidia, and Terresporidia.**

Discussion: The trees presented by Vossbrinck and Debrunner-Vossbrinck show that the Aquasporidia is not monophyletic. One possible classification that reflects the groupings resolved by the Vossbrinck and Debrunner-Vossbrinck analysis, but which uses suffixes in a manner that is consistent with the rest of the classification of Fungi, and avoids naming non-monophyletic groups, is as follows:

Microsporidiomycota  
    Microsporidiomycetes

Aquasporidiales s.str.  
Marinosporidiales  
Terresporidiales  
Metchnikovellidales

Taxa placed in Aquasporidiales, but not in the main group (with clades I and II in the publication) could be left as Microsporidiomycetes *incertae sedis*. One remaining problem with this classification is that there is no order "Microsporidiales." This classification is present in the current draft classification, but this should be regarded as very provisional, requiring comment from experts.