



Comments by ICPA members on the draft proposal by Taylor et al.

Taylor et al. want, based on nearly the same data as us, to only use *Aspergillus* for only subgenus *Circumdati* (*Flavi*, *Nigri*, *Candidi*, *Circumdati*, *Flavipedes*, *Terrei*). This is a possible solution to the problem, but there are so many arguments against it (I only list some of them):

1. The type for *Aspergillus* has to be changed, but why really? There is little chance that this will be adopted by the next Botanical Congress, and *Aspergillus* would in that way be "in flux" for several years, because there will always be some persons that want to follow Pitt and Taylor
2. The ICPA proposal for the single nomenclature of *Aspergillus* is pretty close to that of Raper and Thom (1965) and only few changes had to be made. If we follow Taylor et al., think about *Emericella versicolor*, *Em. sydowii*, *Em. protuberata*, *Em. creber*, *Em. ochraceosea*, *Eurotium restricta*, *Eur.enicillioides*, *Neosartorya lentula*, etc. etc. etc.
3. I googled *Aspergillus* (used in ca 50.000 publications, and *Eurotium* in ca. 300 or so), so there is a strong preference for *Aspergillus* in the scientific community
4. I do not understand the social arguments from Pitt and Taylor and Taylor et al.. For example we know that aflatoxins are important, but they are also produced by *Emericella* species, so it cannot be restricted to *Aspergillus* in the very narrow sense of Taylor et al. and there are Hülle cells present both in *Circumdati* and *Emericella*. Many other secondary metabolites are present throughout *Aspergillus* in the ICPA sense, and that makes that *Aspergillus* a pretty homogenous genus
5. Enzyme producers are all over our concept of *Aspergillus*, also outside the narrow *Aspergillus* of Taylor et al.
6. Most species have aspergilla, so maybe the *Phialosimplex* morph and the *Polypaecilum* morph are synanamorphs and genome sequencing can help us there.
7. Even in the narrow concept of Taylor et al., there are two different kinds of teleomorphs, just compare *Petromyces* with *Fennelia*
8. Do we really loose information by "abandoning" *Eurotium* etc.? I think we can do as ICPA proposed: If there is a sexual state found, just call it *Aspergillus alliaceus* (*petromyces* morph). Databases should also help scientists in finding the correct name and searching for older names (because of cause to occur in the literature)
9. Many scientists have already adopted *Aspergillus* (instead of *Eurotium*, *Emericella*, *Neosartorya*) or have used *Aspergillus* all the time anyway
10. ICPA had a majority vote for *Aspergillus*
11. There is already a fine list of *Aspergillus* species published in Stud Mycol 2014
12. Aspergilla are seen outside *Aspergillus* sensu Samson et al. (2014), but Penicilli are also seen outside *Penicillium*. Everybody agree on the new concepts of *Penicillium* and *Talaromyces*, but consider how different the anamorphs actually are in those genera from monophialidic species to very complicated penicilli in for example *P. olsonii* in *Penicillium*. So what is the real problem with having several aspergilla-types and even polypaecilli in *Aspergillus*?



13. In the concept of Samson et al. (2014) (“wide *Aspergillus*”), two rather obscure genera (*Phialosimplex*, *Polypaecilum*) lacking an *Aspergillus* morph were merged into *Aspergillus*. This alone should not be the reason to split the genus. There are other examples in the Eurotiales where genera are not split even if there are different reproductive structures present. For example, the genus *Thysanophora* is nested deep into *Penicillium*. In that case, ICPA made the logical decision to keep “wide *Penicillium*” and not to split *Penicillium* into > 25 genera.
14. The far majority of the species in Eurotiales with an *Aspergillus* morph belong to ICPA’s definition of *Aspergillus*. There are a few species that are positioned outside their “wide *Aspergillus*” clade. One example is *Aspergillus paradoxa* which was recently transferred to *Penicillium paradoxum*. This species is, based on molecular and extrolite data, nested in *Penicillium* but has an *Aspergillus* morph. There is no doubt that this species belongs to *Penicillium*. A similar, but reversed, case is found in *Aspergillus. Penicillium inflatum*, a species with *Aspergillus* conidiophores was recently transferred to *Aspergillus* (as *Aspergillus inflatus*). If all species with an *Aspergillus* morph would have to belong to *Aspergillus*, then it is indeed correct that *Aspergillus* (but also *Penicillium*) is not monophyletic.
15. From the various published studies, it can be concluded that the data set of Houbraken & Samson (2011) doesn’t have enough phylogenetic signal to unambiguously show the monophyly of *Aspergillus*. The deeper nodes in the published phylograms based on this data set are not or poorly supported and often a better support is often found below genus level (subgenera, sections). Not finding support for certain nodes does not prove that “wide *Aspergillus*” can’t be applied as it doesn’t show that this is not the case.
16. The most convincing phylogeny was published by Houbraken et al., 2014 showing that (wide) *Aspergillus* and *Penicillium* are sister genera. Important to mention is that there might also be problems at subgeneric level and specifically with subgenus *Circumdati*. In the presentation of Jos Houbraken at the CBS Spring meeting in 2015 he showed that sect. *Nigri* might represent a separate subgenus.
17. Based on the current information it is, in my opinion, too early to make a drastic decisions by changing the type of the genus *Aspergillus*. In my opinion the phylogeny should be leading in making good, well supported decisions. We are not that far at this moment. Many *Aspergillus* genomes are currently generated and this will give insight in the generic and subgeneric classification of the genus.
18. The authors claim that species with aspergillus-like conidiophores cannot form a monophyletic group. Of course they are not. We know that eg. *A. paradoxus* and allies (with aspergillus-like anamorphs) belong to *Penicillium*, or *A. monodii* which does not make conidiophores under the conditions tested, but is still *Aspergillus*. We already discussed these problems in the 2014 SIM paper. Besides, the fact that *Phialosimplex*, *Dichotomomyces*, *Cristaspora* or *Polypaecilum* belong to *Aspergillus* might be due to mutations as also discussed in that paper.
19. Regarding the phylogenetic work, we have doubts about the analysis by Taylor et al. First of all, the authors did not claim how the work was done (i.e. which algorithms, etc.). It is unclear how they got a different tree using the same sequences compared to that of Houbraken and Samson (2011). One explanation is that alignment is an NP-complete problem (ie. in large datasets it is almost impossible to generate the best alignment within a reasonable time), so using the same dataset it is possible to get quite different alignments mainly if different softwares (e.g. Clustal, Muscle or others) are used (but we do not know what they used). Usually manual adjustment is also needed which can be subjective. The choice of outgroup can also affect the results. Using different alignments obviously the resulting phylogenetic trees will also be different, not to mention that phylogenetic tree construction is also an NP-complete problem. For NP-complete problems, see this page: https://en.wikipedia.org/wiki/NP-completeness#Solving_NP-complete_problems. For another possibility (eg. to code gaps which might help to get higher support for the branches), see this: Nagy LG, Kocsubé S, Csanádi Z, Kovács GM, Petkovits T, Vágvölgyi C, Papp T. Re-remind the gap! Insertion - deletion data reveal neglected phylogenetic potential of the nuclear ribosomal internal transcribed spacer (ITS) of fungi. PLoS One. 2012;7(11):e49794. doi: 10.1371/journal.pone.0049794.