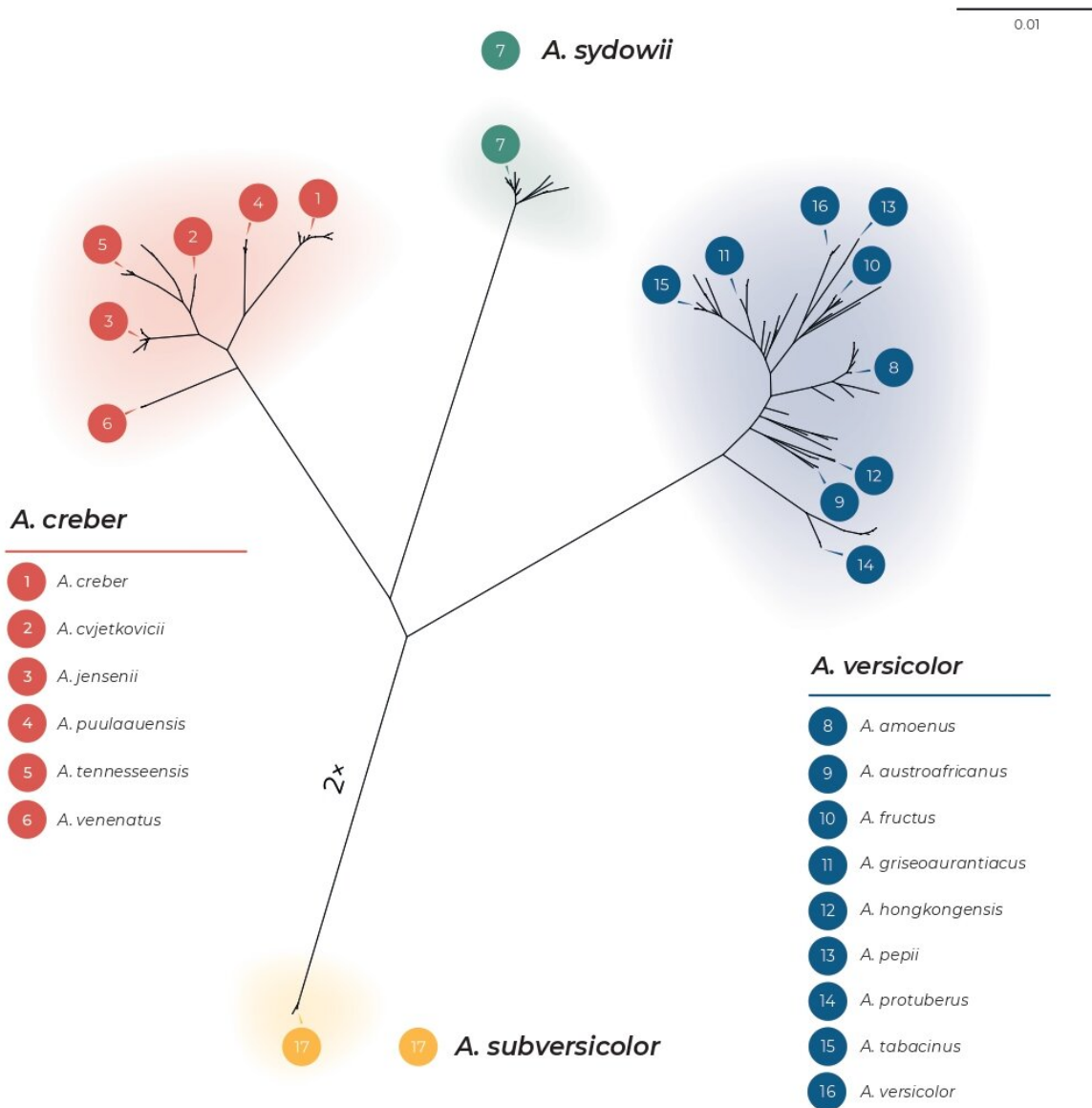


Working against the mainstream in fungal systematics

February 23 2023



One of the examples of the resolution of species boundaries in *Aspergillus versicolor* and related species, where the number of accepted species has been reduced from 17 to only 4 (the names of accepted species are indicated in larger letters and underlined, and synonyms are indicated in smaller letters). Credit: Authors of the studies

Developments in the current systematics of fungi are largely directed towards the division of existing species into smaller, narrowly defined species. But as demonstrated by scientists from the Faculty of Science, Charles University, Prague, and the Institute of Microbiology of the Academy of Sciences of the Czech Republic on the *Aspergillus* genus model, such a division is often not justified and only complicates or makes the correct identification of species impossible.

The findings of the scientists show that the [species](#) category for fungi is significantly wider than expected, and as a result, their number in the investigated groups was considerably reduced. Since a number of desirable and undesirable properties of organisms tend to be tied to the species level, these findings have implications for practice, where these species are known as producers of mycotoxins, enzymes, bioactive substances and [organic acids](#), or as the cause of human and animal infections and food spoilage fungi.

The results were published in a series of three papers in *Studies in Mycology*.

Species like *Aspergillus niger* and *A. versicolor* are relatively well known. They are important in the biotechnological industry as producers of enzymes and organic acids (e.g. citric) or are used in food and beverage fermentations, especially in Asia. At the same time, however, they often spoil food, produce unwanted mycotoxins (e.g. ochratoxin,

fumonisin, or sterigmatocystin), worsen the air quality in buildings, and cause serious infections in humans and animals.

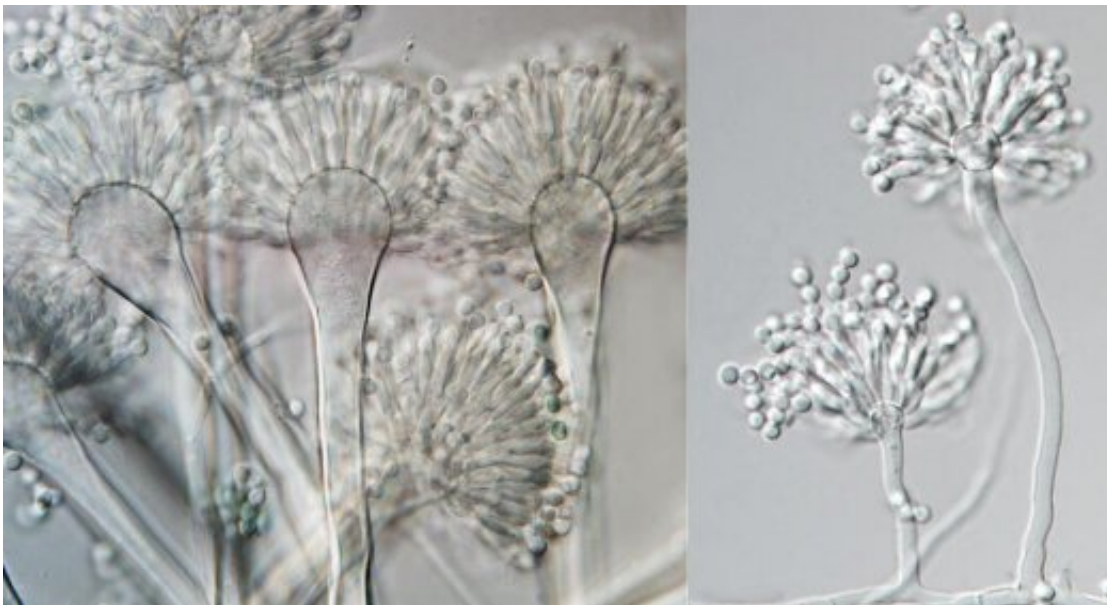


Variability of colonies within a species *Aspergillus versicolor* on 8 different

culture media. Credit: Authors of the studies

Species identification in fungi and other organisms is important because a number of specific properties are often associated with it, such as the aforementioned production of mycotoxins or pathogenicity. The current taxonomy of fungi, based largely on molecular-genetic data, is mainly moving towards the division of existing species into smaller ones.

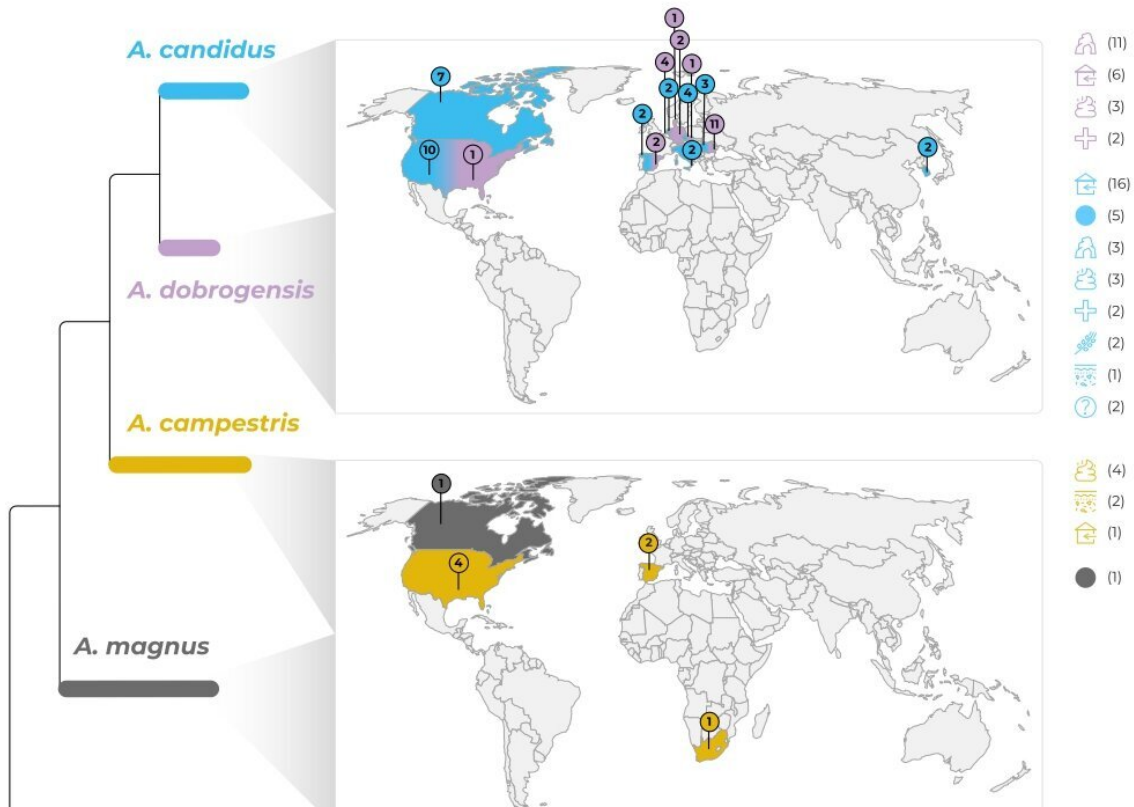
The consequence is the introduction of new names for so-called cryptic species (indistinguishable from one another by the appearance of colonies, microscopic and other features), which complicates or even makes their precise identification in clinical mycology, food science, and other fields impossible.



Conidiophores producing spores (conidia) in the examined representatives of *Aspergillus*. Credit: Authors of the studies

"The reason for the excessive number of described species in mycology is partly the ignorance of the characteristics of the species as such in its entire breadth, whether we are talking about variability in morphological, physiological, or genetic characters. This is due to the fact that new species are often described on the basis of a small number of obtained strains from one or more substrates and localities. Examining only a small number of variable individuals within a species can then easily be interpreted as finding an undescribed species. Another reason is the generally prevailing direction of taxonomists' thinking toward the description of new species, rather than the opposite direction. This gives scientists a better opportunity to publish their results because describing new species is more attractive than merging them. Also, it is generally easier to create a species description based on a smaller number of interesting strains than to collect a large dataset revealing the entire variability of a species," says Vít Hubka from the Faculty of Science, Charles University.

"For our study, we chose as a model a ubiquitous representatives of *Aspergillus*, e.g. *A. niger*, *A. versicolor*, or *A. candidus*, and collected hundreds of samples from different continents and substrates. Thanks to the fact that we applied a wide range of methods, including modern phylogenetic methods based on data from a large number of genes, or genomes, we have been able to assess the true diversity within a species. This has led to the discovery that species are much more variable than we thought, at many levels—colony appearance, microscopic characters, genetic variability, mycotoxin production, etc.," says team member František Sklenář.



Geographic distribution of selected *Aspergillus* members based on available DNA data. The numbers in the location pointers correspond to a total number of reliably identified strains reported from a specific country; the numbers following icons of substrates represent a total number of strains reported from this substrate. Credit: Authors of the studies

"The result of the studies was a significant reduction in the number of species in the intensively researched species complexes of the genus *Aspergillus*, which will greatly simplify their complicated identification in the applied sphere and diagnosis in clinical mycology. A new view of the breadth of species boundaries in microscopic fungi will allow scientific interest to be focused on more important questions, rather than on the unrelenting effort to distinguish or describe 'unrealistically defined cryptic species' using different methods. As the genus

Aspergillus largely sets trends in taxonomy and other disciplines, we expect comparable conclusions also for other groups of fungi when similar methodological approaches will be applied," concludes Miroslav Kolařík, head of the laboratory of fungal genetics and [metabolism](#) from the Institute of Microbiology of the Academy of Sciences of the Czech Republic.

More information: C. Bian et al, Reducing the number of accepted species in *Aspergillus* series *Nigri*, *Studies in Mycology* (2022). [DOI: 10.3114/sim.2022.102.03](https://doi.org/10.3114/sim.2022.102.03)

F. Sklenář et al, Taxonomy of *Aspergillus* series *Versicolores*: species reduction and lessons learned about intraspecific variability, *Studies in Mycology* (2022). [DOI: 10.3114/sim.2022.102.02](https://doi.org/10.3114/sim.2022.102.02)

K. Glässnerová et al, A monograph of *Aspergillus* section *Candidi*, *Studies in Mycology* (2022). [DOI: 10.3114/sim.2022.102.01](https://doi.org/10.3114/sim.2022.102.01)

Provided by Charles University

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