A new view on the global diversity of the toxin-producing *Aspergillus flavus*

Popular science article by Dr. Valter P. Pfliegler (NFCSO)

A newly published scientific article from the University of Debrecen (Hungary) and the National Food Chain Safety Office (NFCSO) of Hungary in collaboration with the North Carolina State University (USA) analyzed world-wide genomic data on one of the most important toxigenic mold species, Aspergillus flavus, and on the koji fungus.
The article was published in the mycological journal IMA Fungus.

Aspergillus flavus can cause human disease and contaminate crops, while its close relative *A. oryzae* is safely used to make foods like soy sauce and sake. Scientists have long been unsure how these two fungi are related and how *A. oryzae* was domesticated. By comparing the genomes of 639 fungal samples from around the world, our latest study shows that their evolutionary history is more complex than expected. These fungi fall into several distinct groups, with many strains showing mixed ancestry, and *A. oryzae* appears to have been domesticated more than once. Some disease-causing strains are genetically similar to food-fermentation strains, suggesting that domestication and mixing between groups have influenced pathogen diversity. These findings blur current species boundaries and help explain how these fungi evolved, with important consequences for human health, food safety, and monitoring fungal risks. The group also called attention on under-sampled regions, including Africa and Europe, where the diversity of the species is not well known.

The published study was led by Dr. Valter P. Pfliegler and Prof. Dr. István Pócsi of the Department of Molecular Biotechnology and Microbiology at the University of Debrecen and the National Food Chain Safety Office (NFCSO) of Hungary.

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Funded by the European Union

Funded by the European Union (project 101181208, MYMATCH). Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union. Neither the European Union nor the granting authority can be held responsible for them.