

# Mycokey

Integrated and innovative key actions for mycotoxin management in the food and feed chain

Lay summaries

Knowledge transfer to stakeholders

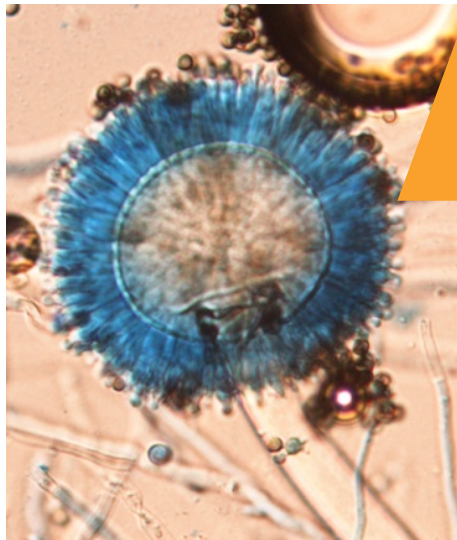
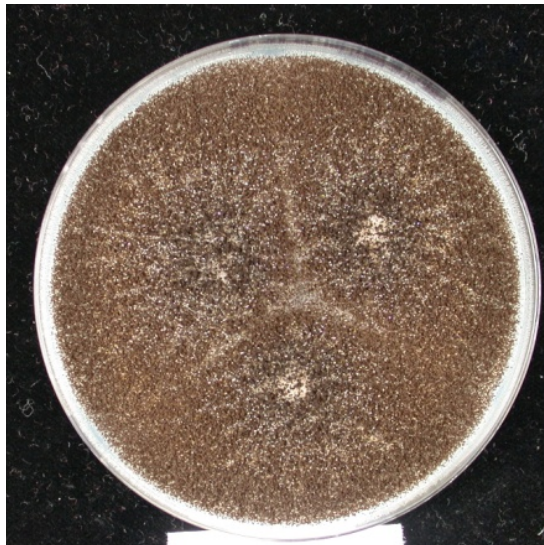


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# Variation in Fumonisin and Ochratoxin Production Associated with Differences in Biosynthetic Gene Content in *Aspergillus niger* and *A. welwitschiae* Isolates from Multiple Crop and Geographic Origins

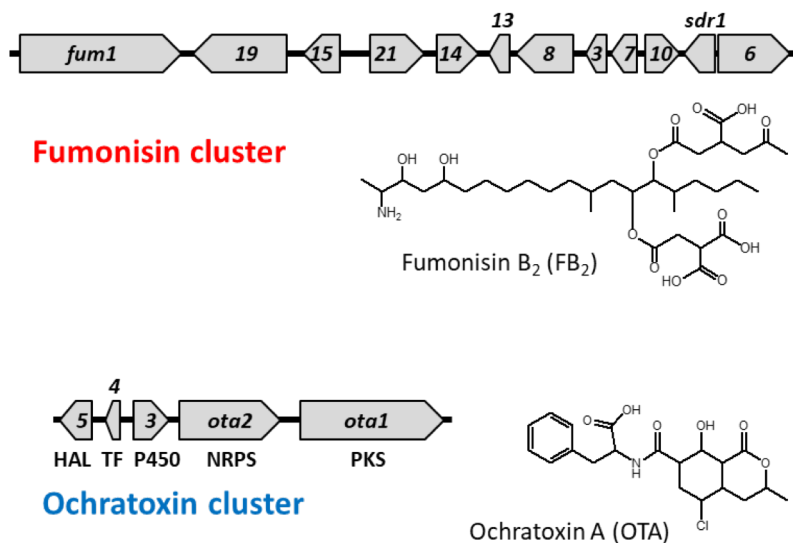
The black aspergilli *A. niger* and *A. welwitschiae* are used in fermentation of food and beverages. However, concerns about the safety of these fungi have been raised with the discovery that some isolates can produce the mycotoxins FBs and OTA. Both species exist as mixed populations of FB-producing or FB-nonproducing individuals, as well as OTA-producing or OTA-nonproducing individuals. Differences in homologs of the *ota* and *fum* clusters in *A. niger* and *A. welwitschiae* were analyzed.



# APPROACH

A strategy to reduce the impact of mycotoxins in the food and feed chains is to monitor mycotoxicological risks during the growing season in field and on-line way at farm level.

Genotype characterization of mycotoxin gene clusters in producing and nonproducing fungi is the basic step for development of on-site detection kit specific for toxigenic fungi.



Characterization of  
mycotoxins  
biosynthetic genes

Identification of  
DNA markers

Development of  
detection kits for  
toxigenic fungi

Keep track of  
mycotoxicological  
risks

research

Identification of strategy

exploitation

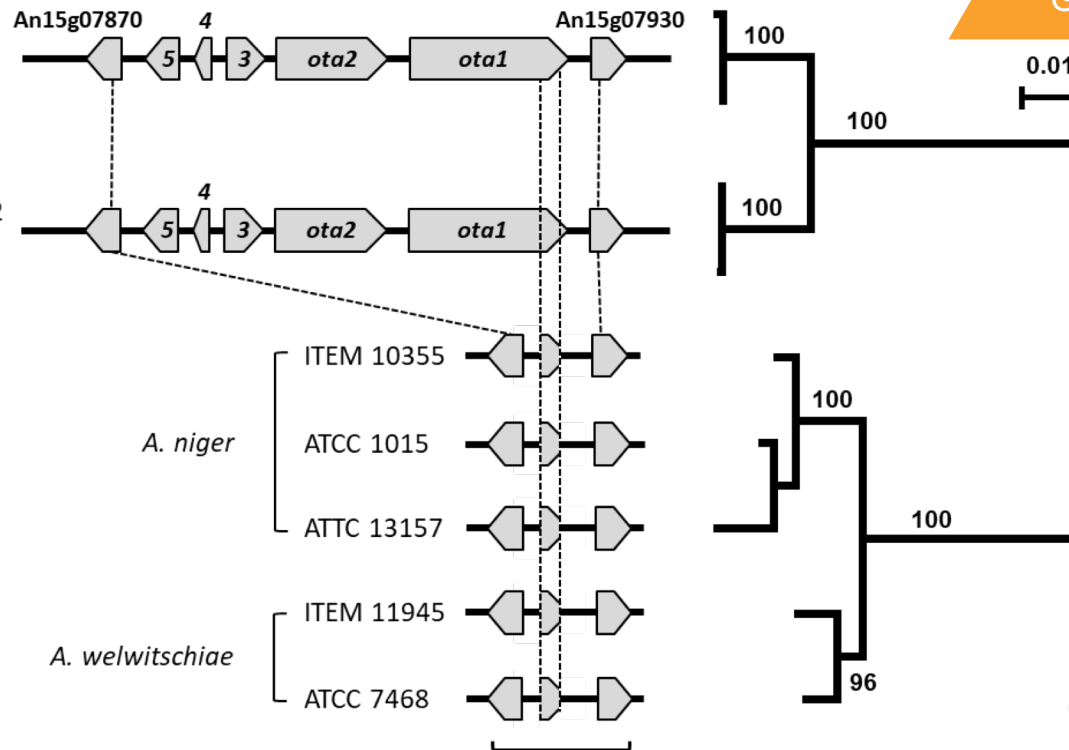
# OUTCOMES

## DNA-based Detection Methods

### Genetics and Biodiversity of toxigenic fungi

*A. niger* CBS 513.88  
and ATCC 13496

*A. welwitschiae* ITEM 4552  
and ITEM 6142



### Feasibility of data

- Development of A loop-mediated isothermal amplification (LAMP) assay for rapid detection of fumonisin producing *Aspergillus* species



### Genetics and Biodiversity

- Genome sequence data indicate that *fum* cluster is partially deleted in FB-nonproducing isolates of *A. welwitschiae*, whereas the *fum* cluster is intact in FB-nonproducing isolates of *A. niger* (which might produce FBs under conditions other than those employed in the current study and other studies)
- Genome sequence data indicate deletion of DNA within the *ota* cluster region is almost identical in OTA-nonproducing strains of *A. niger* and *A. welwitschiae*.