

WETENSCHAPPELIJK INSTITUUT VOLKSGEZONDHEID INSTITUT SCIENTIFIQUE DE SANTÉ PUBLIQUE



Presentation for the 'Belgische Vereniging voor Menselijke en Dierlijke Mycologie' 14th November 2013





Background

- David Triest
- PhD at the Scientific Institute of Public Health Brussels
- Department of Mycology & Aerobiology
- Belgian fungal collection BCCM/IHEM
- Fusarium



BCCM/IHEM collection

BELGIAN CO-ORDINATED COLLECTIONS OF MICRO-ORGANISMS



http://bccm.belspo.be/about/ihem.php

- Gathered 'clinical' strains over the last 30 years
- Many Fusarium strains
- Lots of taxonomical changes
- Profound re-identification at species level



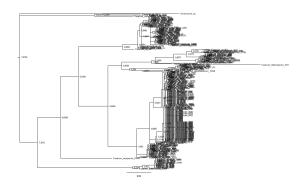
Re-identification

- Sequence analysis
- ITS-5.8S, BT, TEF1α, LSU
- Position in a Bayesian phylogenetic tree
- Morphological examination

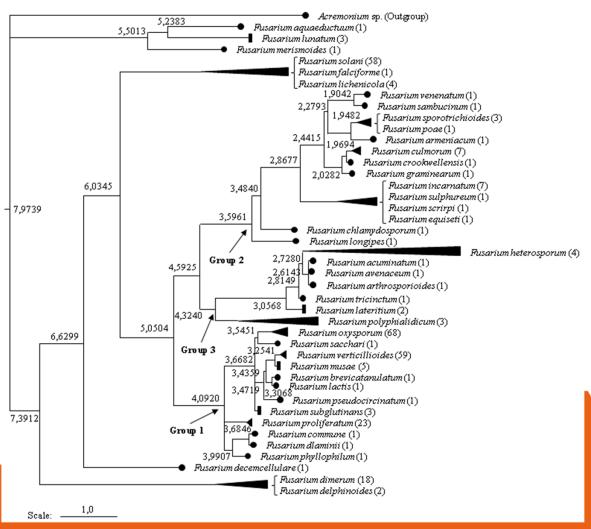
→ Dataset of 295 validated Fusarium strains



A valuable dataset



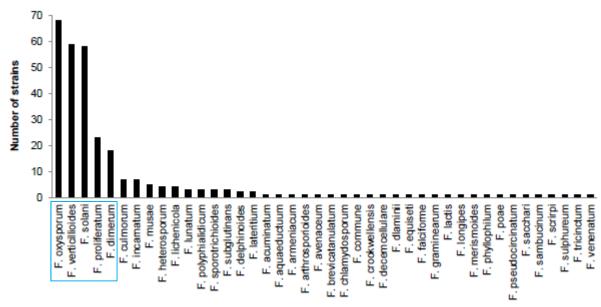
- 42 ≠ species
- 16 with more than 1 strain





Epidemiological information

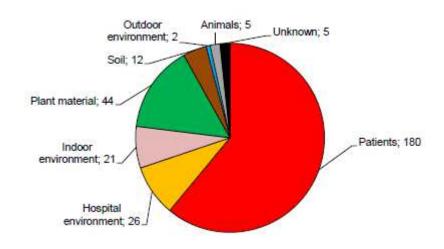
All clinically important species represented



Source and date of strain's isolation available



Antifungal susceptibilities



- Strains isolated from patients
- EUCAST E.DEF 9.1 broth microdilution method
- FLC, ITR, KTZ, POS, VOR, 5FC, TER, AMB

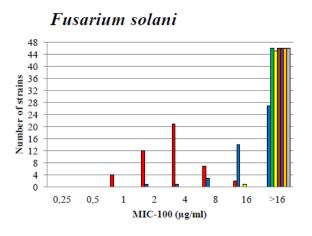


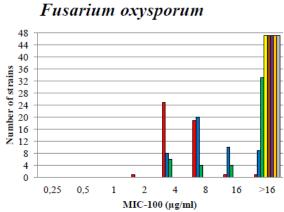
Need to identify Fusarium sp.?

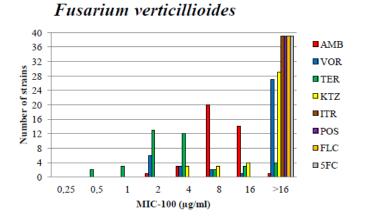
- One of most antifungal drug-resistant fungi
- Azole-resistance, especially F. solani
- Recommended treatment is amphotericin B, as it has activity against all Fusarium species
- Species identification by morphology is difficult, molecular techniques require time
- Bother about the ID of a Fusarium infection?

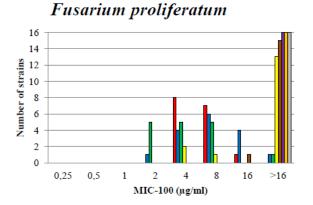


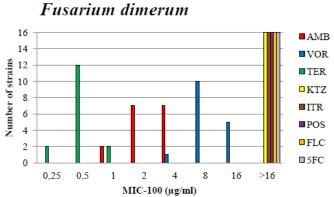
Variable susceptibility profiles









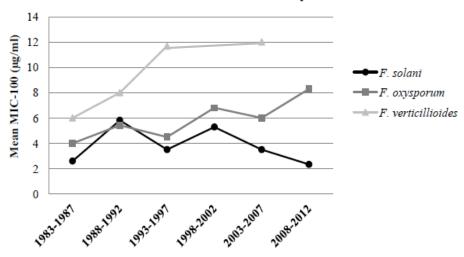




Yes, ID is important !!!

 AMB is drug of choice when ID of the fusariosis is unknown, but not always most effective

Evolution of the amphotericin B MIC-values over 30 years





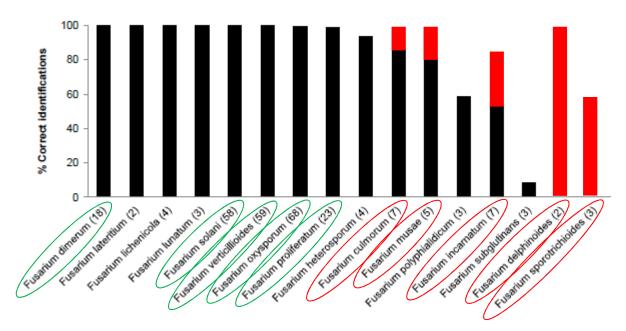
Identity by MALDI-TOF MS?

- Blood/Biopsy cultures often + (Nucci et al., 2007)
- Morphology = difficult, sequencing = time, costs
- MALDI-TOF as ID-tool: generates strain specific proteomic spectrum, compared with database
- All validated strains in own database and screen
- Protein extraction (Cassagne et al., 2011)
- Previous studies lack in-depth analysis



94,4% correct identifications

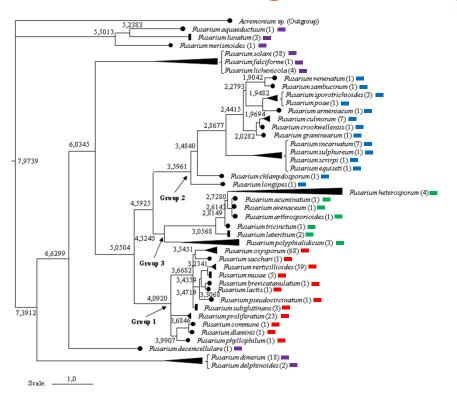
Spectra construction succeeded for 295 strains

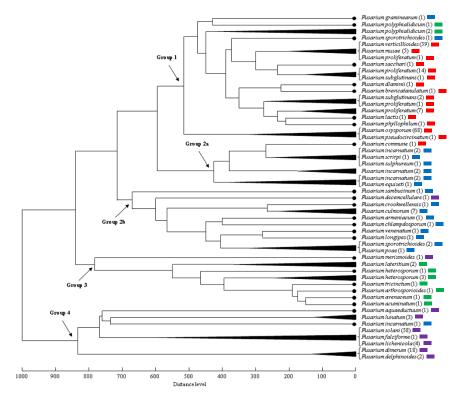


POP database with new isolates = good quality



Interesting similarity





- Phylogenetic tree versus spectral distance matrix
- 57,5% single-strain sp. identified as related sp.



Conclusion

- ID is important for therapy of Fusarium infections
- MALDI-TOF MS has the capacity as ID-tool



Acknowledgments

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Dr. Koen De Cremer



Promoter: Prof. Dr. Denis Piérard



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