MYTOXPLEX PROJECT MARCH 2012 – MARCH 2014

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OUTLINE OF THE PRESENTATION

- MytoxPlex background
- Condensed material and methods
- Results for unprocessed cereals, feed and food
- Implications

MYTOXPLEX BACKGROUND

- EFSA call on T-2 and HT-2 complex
- Up-and-coming Fusarium species in Belgium
- Focus on food, but also unprocessed grains and feed
- Partners:

















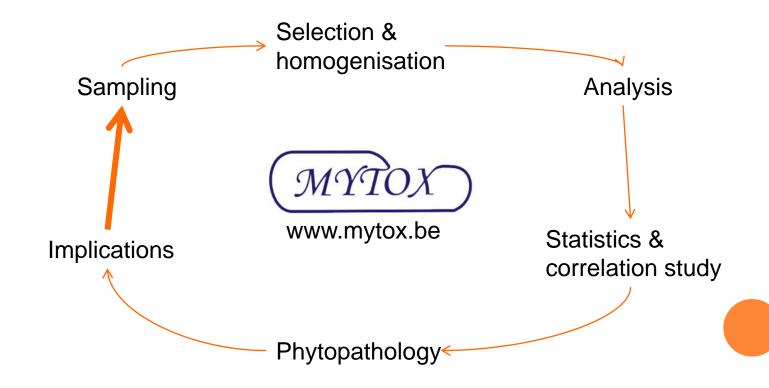


MYTOXPLEX BACKGROUND

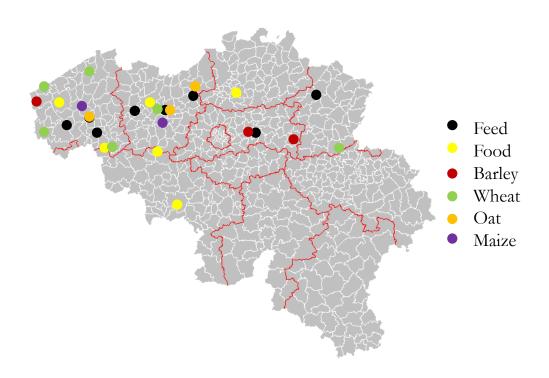
MYTOX = valuab

) = valuable combination of interests:

development of new analytical techniques monitoring of toxin levels in grains, food and feed phytopathology behind the occurence of mycotoxins



MATERIAL AND METHODS: SAMPLING



MATERIAL AND METHODS: SELECTION & HOMOGENISATION

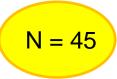
Unprocessed grains: ground with mixer
 Barley, wheat, triticale, maize

N = 178

Feed samples: pulverizing of +/- 200 grams
 Oat feed, mixed feed (diverse origins)

N = 26

Food samples: pulverizing of +/- 100 grams
 Breads and breakfast cereals



MATERIAL AND METHODS: ANALYSIS

- Extraction of mycotoxins from the ground cereal matrix: acetonitril extraction
- Detection of 12 mycotoxins in 11 minute run:
 DON, DON-3G, 3-ADON, 15-ADON, FUS-X
 NEO, DAS, T-2, HT-2
 ZEN, A-ZEL, B-ZEL
- LOQ T-2: 18-22 μg/kg; HT-2: 10-18 μg/kg
- Analysis of fungal DNA on the same samples: detection of 9 different *Fusarium* species

RESULTS: UNPROCESSED CEREALS

Barley (N = 65):

T-2: 2 positive samples (mean = $18,5 \mu g/kg$)

HT-2: 2 positive samples (mean = $16 \mu g/kg$)

No F. langsethiae, but F. sporotrichioides in 2nd sample

 \circ Wheat (N = 93):

T-2: 0 positive samples

HT-2: 1 positive sample (17 µg/kg)

No F. sporotrichioides, highest detected load of F. langsethiae

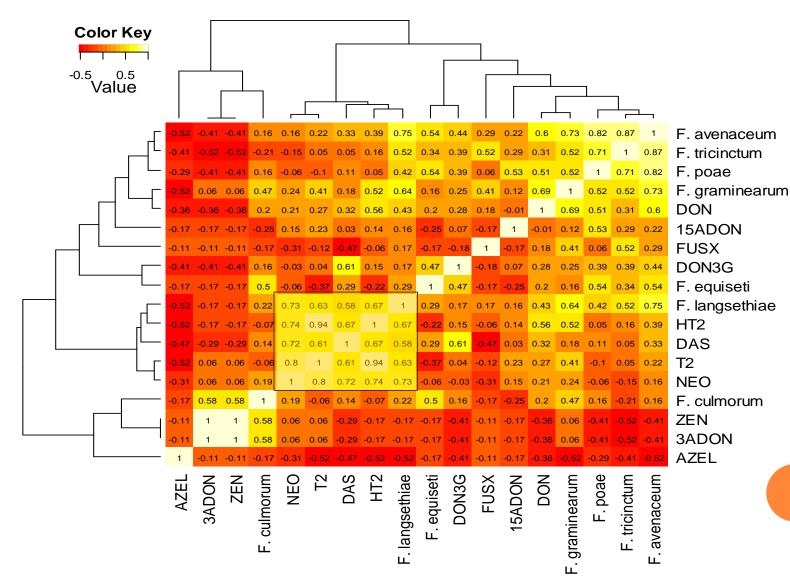
- Triticale (N = 10): no positive samples
- Maize (N = 10): no positive samples

No conflicts with 2013/165/EU

RESULTS: FEED

- o 16 mixed feed samples:
 - Show a mycotoxin and fungal profile very similar to wheat, barley and triticale field samples
- o 10 oat feeds:
 - T-2: detected in 9 samples (19 190 μg/kg)
 - HT-2: detected in every sample (34 405 µg/kg)
 - No F. sporotrichioides detected in the samples, but F. langsethiae in every sample

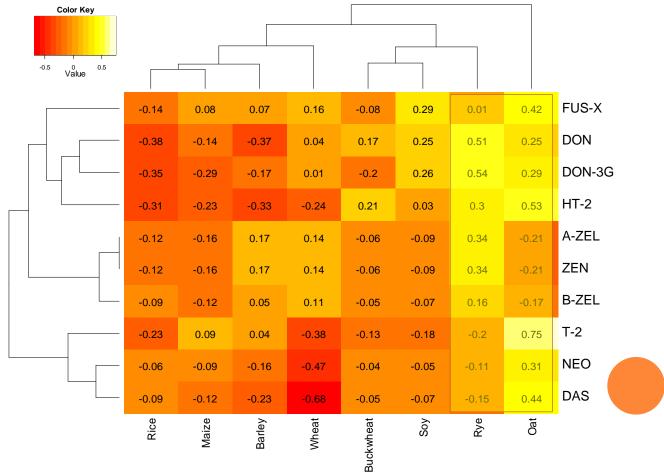
RESULTS: OAT FEED



- 25 analyzed breads:
 - T-2: detected in 2 samples (mean = 24 μg/kg)
 - HT-2: detected in 12 samples (19 21 μg/kg)
 - No F. langsethiae, no F. sporotrichioides
 - Degradation of DNA during production process?
 - 16 breads were advertised as "whole-wheat"
 - 2 positive T-2 samples
 - 10 of the 12 positive HT-2 samples

- 20 analyzed breakfast cereals:
 - T-2: detected in 7 samples (24 59 μg/kg)
 - HT-2: detected in 6 samples (20 92 μg/kg)
 - No F. sporotrichioides, but F. langsethiae detected in all positive samples

 Division of all food samples according to cereal ingredients:



MycoMask project (Marthe De Boevre):

- 1. Probabilistic risk assessment on T-2 + HT-2 intake
 - Extensive survey on cereal-based food products (2010-2011)
 - Detailed information on consumer habits in Belgium
 - TDI for T-2 + HT-2: 100 ng/kg b.w.
 - Fiber-enriched bread: 16.60 % > TDI
 - Bran-enriched bread: 1.89 % > TDI
 - Oatmeal: 0.02 % > TDI
 - All cereal based foods: 4.11 % > TDI

→ De Boevre et al. (2013), Toxicology Letters

MycoMask project (Marthe De Boevre):

- 2. Fate of DON and DON-3G during baking of bread
 - Simulation of breadmaking process:
 - Flour → white bread: no effect on DON and DON-3G
 - Flour/bran (85/15) → grey bread: increase in DON and DON-3G

What (enzymatic) reactions lead to this increase?

→ an interesting case for future research!

IMPLICATIONS

- Origins of T-2 and HT-2 complex in the field are rather unclear
- T-2 and HT-2 in oat (feeds) are caused by F.
 langsethiae but do not exceed indicative levels
- Rye and oats in food samples may lead to increased risk for T-2 and HT-2 contamination
- Co-occurence of T-2 and HT-2 with NEO and DAS: other toxic "type A trichothecenes"!

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