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SAPIENZA
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Sapienza University of Rome
Piazzale Aldo Moro 5 · 00185 Roma
Dept. of Chemistry "Stanislao Cannizzaro"
Aula La Ginestra



EUROPEAN FUSARIUM SEMINAR

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Occurrence of fusariotoxins and aflatoxins in maize kernels after harvest in Serbia in 2022

Milica Lucev, Iva Savic, Ana Obradovic and Slavica Stankovic

Maize Research Institute Zemun Polje, Laboratory of Phytopathology, Slobodana Bajica 1, 11185, Serbia; mnikolic@mrizp.rs

This study was carried out in order to investigate the natural occurrence of toxigenic fungal species and levels of fumonisin (FBs), zearalenone (ZEA), deoxynivalenol (DON) and total aflatoxin (AFLA) in the maize kernels, stored immediately after harvesting in 2022. Samples of maize kernels from two locations (Zemun Polje and Zagajica) in Serbia were collected, and analysed for the presence of mycotoxins. After drying and grinding, the samples were homogenized with 25 ml of 70% metanol solution and distilled water (3:1), and then extracted. Quantification of the total content of mycotoxins was performed using the immunoabsorption enzyme method according to the manufacturer's operating instructions (Tecna S.R.L., Italy, Celer Test Kit). The analysis of 100 maize kernels samples was determined by great variability in the concentration of examined mycotoxins. All examined samples were positive for at least one of the examined mycotoxins (fumonisin, aflatoxin, zearalenone or deoxynivalenol). Fumonisin is determined in concentration of 0 to 0.254 ppm, total aflatoxin in concentration of 0.619 to 3.676 ppb, zearalenone in concentration 0 to 9.379 ppb, while deoxynivalenol is detected in concentration 0.006 to 3.307 ppm. In all tested hybrids, mycotoxins analyses showed that the levels of AFLA, DON, ZEA and FBs were below the maximum permissible levels stipulated by the legislation of the European Union and the Republic of Serbia in maize intended for maize and maize products. Continuous monitoring of mycotoxin content is necessary, given that it changes from year to year.

GST mediated mycotoxin detoxification in oatAsta Ronager¹, Alfia Khairullina², Nikola Micic¹, David B. Collinge¹, Birgit Jensen¹ and Nanna Bjarnholt¹¹University of Copenhagen, Dept. of Plant and Environmental Sciences, Frederiksberg, 1871, Denmark, ²Lund University, Division of Pure and Applied Biochemistry, Lund, 221 00, Sweden; ashr@plen.ku.dk

Fusarium graminearum is responsible for *Fusarium* Head Blight (FHB) in cereals, not only causing yield loss, but also threatening foods safety due to accumulation of fungal toxins. The mycotoxin deoxynivalenol (DON) is a *F. graminearum* virulence factor and toxic towards plants and mammals. Plants detoxify DON through conjugation to endogenous molecules, such as sugars. While DON glycosylation confers some resistance in plants, the resulting glycoside is a so-called masked mycotoxin, which can be reactivated upon digestion of contaminated grain. Recently, it was found that DON may also be conjugated with glutathione (GSH), either at the C10-position (DON-C10-GS) or the C13-position (DON-C13-GS) of DON. C10 conjugation reduces the double bond, and thereby the overall toxicity, but the reaction is chemically reversible, and DON-C10-GS is hence a masked mycotoxin. On the contrary, DON-C13-GS conjugation is irreversible and reduces the epoxide group that is key for DON toxicity. FHB resistance in the wild wheat grass *Thinopyrum elongatum*, was found to be conferred by a glutathione transferase (GST) that catalyses DON-C13-GS conjugation. While the responsible gene results from horizontal gene transfer and lacks homologs in plants, some wheat and barley GSTs can catalyse formation of both conjugates, at low activity. We used LC-MS to analyse oat and wheat grains infected with *F. graminearum* in the greenhouse. Wheat contained almost exclusively DON-C10-GS, whereas oat grain contained only DON-C13-GS. On the contrary, in oat spikelets inoculated with DON we detected only traces of DON-C13-GS, but relatively large amounts of DON-C10-GS. DON-C10-GS can be effectively produced in a chemical reaction, and DON-C13-GS cannot. Consequently, we hypothesize that C13-conjugation is enzymatically controlled, and that oat harbours a more effective GST with this activity that is likely induced by *Fusarium* infection. We are currently identifying all GSTs in the recently published oat genome and will present the results. This GSTome is to be used in combination with transcriptomics data to identify GSTs that are upregulated in oat upon *Fusarium* infection.