# NATURAL TOXINS IN PLANTS AND FOODS: FROM TARGET ANALYSIS TOWARDS METABOLOMICS

**<u>Rudolf Krska</u>[1*], Franz Berthiller[2], Michael Sulyok[3], Rainer Schuhmacher[4]**

[1,2,3,4] BOKU, IFA-Tulln, Austria
*Corresponding author - E-mail: rudolf.krska@boku.ac.at , Phone: +43227266280401

Despite huge research investment on mycotoxins (poisonous, low molecular weight, secondary metabolites of moulds), prevention and control remains difficult and the food industry continues to be vulnerable to problems of contamination. Continued research has led to some understanding of fungal metabolism, but has also highlighted the complexity of fungal/plant interactions. When analytical work is undertaken to monitor foods, a significant fraction of bound or masked mycotoxins can remain undetected. The toxicological fate of these substances is largely unknown. Recognising these significant gaps in current knowledge there are great efforts underway to investigate the metabolism of mycotoxins by plants, microbes and animals. In addition, during the last couple of years, research interests have increasingly shifted towards the role of specific gene modifications as a means to understand pathogen-plant interactions at a molecular level and to consquently reduce the level of contamination of foods with natural toxins such as mycotoxins. Mass spectrometry based analytical methods (GC-MS, Q-TOF, LC-MS/MS) have been key for the quantification of natural toxins in plants and foods and for the investigation of the metabolism of these toxic compounds in body fluids such as serum and urine. Metabolite profiling represents an extremely useful tool that finds applications in many aspects of drug discovery, food safety issues and disorders of cells and organisms. One example is a multi-analyte method which has recently been developed capable of quantifying 270 fungal metabolites, respectively, in cultures and grains. Metabolomics or metabolome analysis has been introduced to designate the set of all low-molecular-mass compounds, i.e. metabolites, synthesized by an organism. In contrast to mere metabolite profiling, metabolomics always shows fitness for a functional genomics context. An example for successful research in this area was the finding that the ability of wheat to detoxify the relevant mycotoxin deoxynivalenol into its non-toxic glucosidic form can directly be linked to recently identified resistance genes. This paper will summarize the expertise as well as the required latest state-of-the-art analytical instrumentation available to successfully perform high-level research in the area of mycotoxins and other fungal and plant metabolites relevant to the food and agricultural industry.

*Keywords: mycotoxins, fungal/plant metabolism, metabolomics, masked mycotoxins, mass spectrometry*