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Molecular phenotyping of intestinal epithelial cells exposed to mycotoxins

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Introduction: Mycotoxins are natural food contaminants that display a wide variety of toxic effects (cytotoxic, genotoxic, endocrine disruption, …). Characterization of their toxicity is hence cumbersome, so the development of high-throughput, comprehensive tools to depict their toxicity is needed. One possibility would be the use of the molecular profiling methodology ICM-MS (Intact Cell MALDI-TOF Mass Spectrometry). This technique is based on the acquisition of MS profiles from whole cells. An ICM-MS profile represents a specific molecular cell phenotype, which can be later combined in machine-learning algorithms for the construction of diagnostic/predictive models. Our hypothesis is that the ICM-MS profiles of cells exposed to characterized, known mycotoxins could be used to build a toxicity-predictive model, that could be valuable for toxicity screening of uncharacterized mycotoxins, toxin combinations, etc. Our **objective** was to verify if the ICM-MS profile of intestinal cells exposed to known mycotoxins was toxin-specific as a first step to test the potentiality of this technique applied to toxicological screening. The **methodology** followed involved a short exposition of differentiated Caco-2 cells to low concentrations of several mycotoxins (deoxynivalenol, zearalenone, aflatoxin-B1, Fumonisin-B1, patulin, ochratoxin-A). Cells were then analyzed using ICM-MS and profiles were compared. **Results** showed that ICM-MS intestinal cells phenotyping was specific enough to differentiate the response to different mycotoxins, with cross-validation and recognition values higher that 80%. The molecular phenotype changed in response to concentration changes and different exposition times. In **conclusion**, ICM-MS shows a promising potential to become a toxicity screening tool.

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