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Poster Abstract - F.06

MOLECULAR TRACEABILITY OF FUSARIUM SPECIES ALONG BREAD PRODUCTION CHAIN

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The grain contamination with mycotoxigenic *Fusaria* is of great economic concern to cereal producers and to the grain processing industry and is of great relevance for the quality and safety of the final products, like human food and animal feed. The predominant toxin produced by fungal species associated with Fusarium Head Blight in wheat is deoxynivalenol (DON), a thricotecene that has been shown to cause both acute or chronic toxic effects in human and animals.

Several analytical methods are available to assess the degree of mycotoxin contamination in cereals belonging to two classes: instrumental methods like GC-MS and HPLC and fast methods, like TLC and immunoassays. DNA-based methods for *Fusaria* species detection have been developed for studies on epidemiology and chemical control, as well as for risk assessment, as alternative to morphological approaches, that require taxonomical expertise and longer time.

The first goal of our work was to develop a real-time qPCR based approach for the detection and quantitation of *Fusarium graminearum* and *Fusarium culmorum* presence in cereal samples. This assay has been applied for the quantitative detection of the presence of these micotoxigenic fungi on a panel of DNA samples extracted from the grains of two bread wheat cultivars grown on different locations of Po valley. This same assay has been repeated even on wholemeal, flour and bread obtained from these grains.