Agilent Technologies

Agilent Bond Elut Mycotoxin

A collection of citations to advance your research

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Food testing and agriculture

[Development of a liquid chromatography–tandem mass spectrometry with ultrasound-assisted extraction and auto solid-phase clean-up method for the determination of Fusarium toxins in animal derived foods](#)

Journal of Chromatography A, **1311,** 21-29 (2013)
Dongmei Chen *et al.*

Tags
Bond Elut Mycotoxin, food testing and agriculture, mycotoxins

Abstract
Agilent Bond Elut Mycotoxin was identified as the best choice for analyzing fusarium toxins, being simpler to operate and cheaper than non-Agilent SPE. Published by Elsevier B. V.

[Development, validation and application of a multi-mycotoxin method for the analysis of whole wheat plants](#)

Mycotoxin Research, **28**, 135-147 (2012)
Judith Schenzel *et al.*

Tags
Bond Elut Mycotoxin, food testing and agriculture, mycotoxins and biotoxins

Abstract
The authors chose Agilent Bond Elut Mycotoxin for cleanup of 26 different mycotoxins. Published by Springer.

[Population analysis of the *Fusarium graminearum* species complex from wheat in China show a shift to more aggressive isolates](#)

Hao Zhang *et al.*

Tags
Bond Elut Mycotoxin, ZORBAX Extend-C18,
1200 Infinity Series, food testing and agriculture,
mycotoxins and biotoxins

Abstract

A large number of *Fusarium* isolates was collected from blighted wheat spikes originating from 175 sampling sites, covering 15 provinces in China. Species and trichothecene chemotype determination by multilocus genotyping (MLGT) indicated that *F. graminearum* s. str. with the 15-acetyl deoxynivalenol (15ADON) chemotype and *F. asiaticum* with either the nivalenol (NIV) or the 3-acetyl deoxynivalenol (3ADON) chemotype were the dominant causal agents. Bayesian model-based clustering with allele data obtained with 12 variable number of tandem repeats (VNTR) markers, detected three genetic clusters that also show distinct chemotypes. High levels of population genetic differentiation and low levels of effective number of migrants were observed between these three clusters. Additional genotypic analyses revealed that *F. graminearum* s. str. and *F. asiaticum* are sympatric. In addition, composition analysis of these clusters indicated a biased gene flow from 3ADON to NIV producers in *F. asiaticum*. In phenotypic analyses, *F. asiaticum* that produce 3ADON revealed significant advantages over *F. asiaticum* that produce NIV in pathogenicity, growth rate, fecundity, conidial length, trichothecene accumulation and resistance to benzimidazole. These results suggest that natural selection drives the spread of a more vigorous, more toxigenic pathogen population which also shows higher levels of fungicide resistance. © The Authors.

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