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- ⁴ Multi-mycotoxin Stable Isotope Dilution LC-MS/MS
- 5 Method for *Fusarium* Toxins in Cereals
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24

25 Abstract

A multi-mycotoxin stable isotope dilution LC-MS/MS method was developed for 14 26 Fusarium toxins including modified mycotoxins in cereals (deoxynivalenol, 3-acetyl-27 deoxynivalenol, 15-acetyl-deoxynivalenol, HT2-toxin, T2-toxin, enniatin B, enniatin 28 B1, enniatin A1, enniatin A, beauvericin, fusarenone X, nivalenol, deoxynivalenol-3-29 glucoside, and zearalenone). The chromatographic separation of the toxins with 30 particular focus on deoxynivalenol and deoxynivalenol-3-glucoside was achieved 31 using a C₁₈-hydrosphere column. An expedient sample preparation method was 32 developed that uses solid phase extraction for the purification of trichothecenes 33 combined with zearalenone, enniatins, and beauvericin and provides excellent 34 validation data. Linearity, intra-day precision, inter-day precision, and recoveries were 35 ≥0.9982, 1%–6%, 5%–12%, and 79%–117%, respectively. Method accuracy was 36 verified by analyzing certified reference materials for deoxynivalenol, HT2-toxin, and 37 T2-toxin with deviations below 7%. The results of this method found barley malt 38 samples from 2012, 2013, and 2014 frequently contaminated with high 39 concentrations of enniatin B, deoxynivalenol, and its modified mycotoxin 40 deoxynivalenol-3-glucoside. Samples from 2012 were especially contaminated. 41 Fusarenone X was not detected in any of the analyzed samples. 42

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Keywords trichothecenes; enniatins; stable isotope dilution assay; LC-MS/MS; solid
 phase extraction; barley

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47 Introduction

Fusarium head blight is considered as a devastating fungal disease and has recently 48 gained importance. Similar to other small grain crops, the infection of barley causes 49 enormous losses concerning yield, grade, and end-use guality. Heavy infestation of 50 brewing barley with Fusarium species can induce a severe mycotoxin contamination 51 52 and can impair solving as well as malting and brewing properties. Nevertheless, food and feedstuff infected by fungi can affect human and animal health resulting in 53 headaches, vomiting, visual disturbances, multiple hemorrhages, sepsis, feed refusal 54 by animals, etc. [1]. The wide range of toxins produced by various *Fusarium* species 55 causes diseases. Fumonisins, trichothecenes, zearalenones, and their modified 56 forms constitute the major classes of Fusarium toxins. 57

Zearalenone (ZEA) (Fig. 1), a resorcyclic acid lactone and metabolite of inter alia F. 58 graminearum, is not acutely toxic but is well known for its estrogenic activity [2]. 59 Enniatins (ENNs) and beauvericin (BEA) are cyclic depsipeptides of three D-a-60 hydroxyisovaleric acids alternating with three differing N-methylamino acids (Fig. 1) 61 often produced by F. avenaceum and F. tricinctum [2]. They have general antibiotic 62 and phytotoxic effects and are toxic to insects [2]. Trichothecenes can be classified 63 into four groups: types A, B, C, and D. Types A and B (Fig. 1) play the most 64 important roles in food and feed. Modified mycotoxins such as deoxynivalenol-3-65 glucoside (D3G) can be formed by plant metabolism [3]. D3G can again be cleaved 66 in human and animal gastrointestinal tracts in glucose and DON that presents a 67 potential food safety and health risk. However, modified mycotoxins are not 68 69 detectable using standard approaches.

Moreover, type A trichothecenes and enniatins show little UV absorption. Therefore, LC-MS/MS methods are mainly used in multi-mycotoxin analysis [4-6]. Internal or isotope-labeled standards are highly recommended to compensate for matrix effects [7]. Sufficient removal of disruptive matrix components is another possibility for minimizing matrix interferences such as ion suppression or enhancement. In this regard, cereal-based products are often purified by solid phase extraction to analyze trichothecenes [5, 8].

However, there is no solid phase extraction method available to date for trichothecenes combined with zearalenone, beauvericin, and enniatins. Therefore, this study intended to develop a multi-mycotoxin stable isotope dilution LC-MS/MS method using solid phase extraction for sample purification.

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83 Materials and Methods

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Chemicals and reagents. Acetonitrile, methanol, water (analytical grade), and 85 potato starch were purchased from VWR (Ismaning, Germany). Formic acid (>95%) 86 was bought from Sigma-Aldrich (Steinheim, Germany) and the reference material 87 (DON in maize flour) was acquired from Biopure (Romer Labs, Tulln, Austria). The 88 unlabeled reference compounds (nivalenol (NIV), D3G, deoxynivalenol (DON), 89 fusarenone x (FUSX), 3-acetyl-deoxynivalenol (3-ADON), 15-acetyl-deoxynivalenol 90 (15-ADON), HT2-toxin (HT2), T2-toxin (T2), and ZEA) and some labeled standards 91 ([¹³C]₁₅-DON and [¹³C]₂₂-HT2) were bought from Coring System Diagnostix 92 (Gernsheim, Germany), BEA was obtained from AnaSpec (San Jose, USA), ENN B 93 from Bioaustralis (New South Wales, Australia), and the other enniatins B1, A1, and 94 A from Enzo Life Sciences (Lörrach, Germany). The labeled internal standards 95 ([¹³C]₂-3-ADON, [¹³C]₄-T2-toxin, [¹⁵N]₃-ENN B, [¹⁵N]₃-ENN B1, [¹⁵N]₃-ENN A1, [¹⁵N]₃-96 ENN A, and [¹⁵N]₃-BEA) were synthesized in our laboratory as reported previously [9-97 11]. Certified reference material BRM 003001 (naturally contaminated corn flour) was 98 obtained from Biopure Referenzsubstanzen GmbH (Tulln, Austria). 99

Preparation of standard solutions. Stock solutions of labeled and unlabeled toxins were prepared in concentrations of 10–100 μ g/mL in acetonitrile (trichothecenes, ZEA) or methanol (ENNs) and further diluted to a final concentration of 1 μ g/mL and 0.1 μ g/mL. All solutions were stored at 4°C in the dark.

LC-MS/MS. LC-MS/MS was performed on a Shimadzu LC-20A Prominence system 105 (Shimadzu, Kyoto, Japan) using a Hydrosphere RP-C₁₈ column (150 x 3.0 mm², S-3 106 µm, 12 nm, YMC Europe GmbH, Dinslaken, Germany) with a C₁₈-guard column 107 (Phenomenex, Aschaffenburg, Germany) as stationary phase that was kept at 40°C. 108 The binary gradient system (Electronic Supplementary Material Table S-1 and 109 Table S-2) consisted of (A) 0.1% formic acid and (B) methanol with 0.1% formic acid 110 at a flow rate of 0.2 mL/min. The gradient for the negative ESI mode was started and 111 held at 10% B for 2 min, raised linearly from 10% B to 99% B during the next 6 min, 112 and then maintained at 99% B for 7.5 min. Next, the mobile phase returned to 10% B 113 114 within 2 min and the system was equilibrated for 9.5 min before the next run. The gradient for the positive ESI mode was started and held at 10% B for 2 min, raised 115 linearly from 10% B to 87% B during the next 6 min, held at 87% for 7 min, raised to 116 100% B during the next 5 min, and then maintained at 100% B for 3.5 min. Next, the 117 mobile phase returned to 10% B within 2 min and the system was equilibrated for 9.5 118 min before the next run. The injection volume was 10 µL. 119

The LC was interfaced with a hybrid triple guadrupole/linear ion trap mass 120 spectrometer (API 4000; Applied Biosystems Inc., Foster City, CA, USA). It operated 121 in the negative ESI mode for the analytes NIV, D3G, and ZEA and in the positive ESI 122 mode for the analytes DON, 3-ADON, 15-ADON, FUSX, HT2, T2, ENN B, B1, A1, A, 123 and BEA. The ion source parameters (Electronic Supplementary Material Table S-124 3) for the negative mode were set as follows: curtain gas 20 psi, CAD gas pressure 125 medium, ion spray voltage -4500 eV, spray gas 50 psi, dry gas 65 psi, and 126 temperature 525°C. The ion source parameters (Electronic Supplementary 127 Material Table S-3) for the positive mode were set as follows: curtain gas 20 psi, 128

CAD gas pressure high, ion spray voltage 4500 eV, spray gas 80 psi, dry gas 75 psi, 129 and temperature 450°C. MS parameters were optimized by direct infusion of each 130 standard solution (50 ng/mL to 1 µg/mL) into the source. The mass spectrometer was 131 operated in the scheduled multiple reaction monitoring (MRM) mode for MS/MS 132 measurements at the conditions detailed in Electronic Supplementary Material 133 Table S-4. A waste valve diverted the column effluent to the mass spectrometer from 134 7 to 16 min in the negative mode and from 7 to 24 min in the positive mode. The 135 remainder of the run was diverted to the waste. Data acquisition was performed with 136 Analyst 1.6.2 software (Applied Biosystems Inc., Foster City, CA, USA). 137

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Calibration and quantitation. For the response curves constant amounts of internal 139 standard (S) were mixed with varying amounts of analyte (A) in molar ratios between 140 0.02 and 50 (1:50, 1:20, 1:10, 1:5, 1:2, 1:1; 2:1, 5:1, 10:1, 20:1, and 50:1). All 141 analytes applying SIDA had [¹³C]- or [¹⁵N]-labeled isotopologues and [¹³C]₂-3-ADON 142 was internal standard for 15-ADON. The response curves were calculated from molar 143 ratios [n(S)/n(A)] versus peak area ratios [A(S)/A(A)] after LC-MS/MS measurement. 144 Response functions were obtained using linear regression. The response factors 145 were between 0.75 and 1.30. 146

147 Six matrix calibration points were prepared for the matrix calibration curve. The 148 matrix calibration curves were calculated from concentrations of the analyte [c(A)] 149 versus peak area [A(A)] after LC-MS/MS measurement.

The contents of the analytes in cereal samples were either calculated by the respective response function (DON, 3-ADON, 15-ADON, HT2, T2, ENN B, B1, A1, A, or BEA) or by the respective matrix calibration function (NIV, D3G, ZEA, or FUSX).

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Sample preparation. Finely ground solid samples, e.g. barley, malt, oat, wheat or 154 maize, (1 g) had 10 mL of acetonitrile/water (84/16, v/v) added and were shaken in a 155 laboratory shaker at 225 rpm for 2 h at room temperature. The resulting slurry was 156 filtered through a folded filter (595 1/2, 70 mm diameter, Schleicher & Schuell, 157 Dassel, Germany). Then, 4 mL of the filtrate was spiked with the internal standards 158 (50 μL of [¹³C]₁₅-DON (1 μg/mL), 100 μL of [¹³C]₂-3-ADON (1 μg/mL), 30 μL of 159 $[^{13}C]_{22}$ -HT2 (1 µg/mL), 30 µL of $[^{13}C]_4$ -T2 (1 µg/mL) and 80 µL of $[^{15}N]_3$ -ENN B, $[^{15}N]_3$ -160 ENN B1, [¹⁵N]₃-ENN A1, [¹⁵N]₃-ENN A, and [¹⁵N]₃-BEA, respectively (0.1 µg/mL). The 161 filtrate volume was reduced when necessary to fall into the linear range of the 162 response curves and to minimize standard consumption, but it was restocked to 4 mL 163 with acetonitrile/water (84/16, v/v) before purification. The mixture was vortexed for 164 20 s and was completely applied on a Bond Elut Mycotoxin cartridge (Agilent 165 Technologies, Santa Clara, CA, USA). The liquid was passed through the cartridge 166 by vacuum suction with an elution rate of 2 drops per second, and then the eluate 167 was collected and evaporated until dry. The sample was reconstituted with 200 µL 168 methanol/water (1/1, v/v) and membrane filtered (0.45 µm). The LC-MS/MS analysis 169 170 was performed next.

Starch (1 g) was chosen as the blank matrix for the matrix-matched calibration and was spiked with six different amounts of analytes (70–500 μ g/kg for NIV, 20–500

µg/kg for D3G, 1–300 µg/kg for ZEA, and 15–200 µg/kg for FUSX). After evaporation
of the solvent the same preparation as for samples described above was performed.

175 Method Validation

Limits of detection (LODs) and quantitation (LOQs). Potato starch free of the 176 monitored mycotoxins was chosen as the blank matrix and used to determine LODs 177 and LOQs as suggested by Vogelgesang and Hädrich [12]. Therefore, the blank 178 matrix was spiked with the unlabeled analytes at four different amounts (1.5, 5, 10, 179 and 15 µg/kg for DON; 3, 10, 20, and 30 µg/kg for 3-ADON; 5, 15, 30, and 50 µg/kg 180 for 15-ADON; 0.5, 1, 3, and 5 µg/kg for HT2 and T2; and 0.4, 1, 2, and 4 for the 181 ENNs and BEA), each in triplicate. The LODs and LOQs were determined by signal 182 to noise ratio for those analytes quantified by matrix-matched calibration (NIV, D3G, 183 184 ZEA, and FUSX).

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Precision. Naturally contaminated barley malt with contents of D3G at 340 μ g/kg, DON at 100 μ g/kg, HT2 at 6 μ g/kg, T2 at 4 μ g/kg, ENN A1 at 11 μ g/kg, ENN A at 10 μ g/kg, BEA at 2 μ g/kg, and ZEA at 3 μ g/kg was spiked with FUSX (20 μ g/kg), NIV (350 μ g/kg), 3-ADON (50 μ g/kg), and 15-ADON (100 μ g/kg). This barley malt and wheat flour naturally contaminated with ENN B (70 μ g/kg) and ENN B1 (7 μ g/kg) was used for intra-day (n = 3) and inter-day (n = 3, every week within three weeks) precision measurements.

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194 **Recovery of SIDA and matrix calibration.** Blank samples (potato starch) were 195 spiked in triplicate with different amounts of analytes (50, 100, and 300 μ g/kg for

DON; 50, 100, and 150 µg/kg for 3-ADON and 15-ADON; 50, 100, and 300 µg/kg for
HT2 and T2; 20, 50, and 100 for the ENNS; 50, 100, and 250 µg/kg for BEA; 50, 100,
and 150 µg/kg for FUSX; 350, 400, and 450 µg/kg for NIV; 50, 100, and 300 µg/kg for
D3G; and 50, 100, and 250 µg/kg for ZEA) and analyzed as described previously.
Recoveries were calculated as the ratio of detected and spiked contents.

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Accuracy. Reference materials (474 \pm 30 µg/kg certified content of DON in maize flour and consensus values of 9.57 \pm 1.04 µg/kg HT2, 26.5 \pm 3.4 µg/kg HT2, 8.46 \pm 1.02 µg/kg HT2, 21.1 \pm 3.4 µg/kg HT2, 15.7 \pm 2.6 µg/kg HT2, 4.21 \pm 2.17 µg/kg T2, 7.92 \pm 2.25 µg/kg T2, 3.40 \pm 2.18 µg/kg T2, 6.09 \pm 2.25 µg/kg T2, and 4.58 \pm 2.20 µg/kg T2 in five different oat samples from an inter-laboratory ring test performed under the supervision of the German Federal Office of Consumer Protection and Food Safety BVL) were analyzed as described previously.

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210 Results and Discussion

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212 Method Development

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LC-MS/MS. DON, FUSX, 3-ADON, 15-ADON, HT2, T2, ENNs, and BEA were measured in the positive ESI mode. The protonated molecules were used as precursor ions for type B trichothecenes, ENNs, and BEA. In contrast, sodium adducts of HT2 and T2 gave more intensive and reproducible dissociation patterns. The labeled standards had fragmentation patterns similar to the respective unlabeled compounds. Detailed explanations of MS/MS fragmentation of type A trichothecenes, type B trichothecenes, ENNS, BEA, and their respective labeled analogs have been described elsewhere [9-11]. NIV, D3G, and ZEA were analyzed in the negative ESI mode and the abundant [M-H]⁻ ions were used as precursor ions. To enable optimal MS conditions for all analytes, two chromatographic runs in the positive as well as negative ESI modes were performed for each sample.

D3G had the same fragmentation pattern as DON (Electronic Supplementary 225 Material Fig. S-1) due to in-source fragmentation and loss of glucose from D3G in 226 the positive ESI mode. A chromatographic separation of these analytes was 227 necessary to allow quantification of DON and not the sum of D3G and DON in the 228 positive ESI mode. This was achieved using a Hydrosphere RP-C₁₈ column (YMC 229 Europe GmbH, Dinslaken, Germany) as a stationary phase. We were able to assure 230 231 baseline separation of all other analytes except for BEA coeluting with ENN B1 and 3-ADON coeluting with 15-ADON. The use of a Gemini C₆-phenyl or a Synergi Polar 232 RP column would have avoided a coelution of BEA with ENNs [11, 13] and of 233 acetylated DONs [10]. However, there are several reasons these coelutions on the 234 Hydrosphere RP-C₁₈ column were not critical. First, the potentially increased 235 sensitivity for ENN B1 and BEA is negligible when considering their different 236 fragmentation patterns and the very low LODs and LOQs of our method. 237 Furthermore, the position isomers 3-ADON and 15-ADON are differentiated by their 238 partially different product ions resulting from their common precursor $[M+H]^+$ ion (m/z)239 339.1) and especially by the intensities of the product ions (Fig. 2). The three most 240 important fragments of 3-ADON are m/z 213.1, m/z 231.1, and m/z 137.1 compared 241

with those of 15-ADON, which are m/z 261.1, m/z 137.1, and m/z 231.1. The respective product ions were chosen as quantifiers that were not produced from the other isomer, m/z 213.1 for 3-ADON and m/z 261.1 for 15-ADON. Both ADONs revealed the same qualifiers (3-ADON m/z 231.1 and 15-ADON m/z 137.1) but in completely different intensities. In accordance with Berger et al. [14], Berthiller et al. [5], and our own validation data, quantification of 3-ADON and 15-ADON was possible without chromatographic separation.

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Sample purification. Sample purification using solid phase extraction was designed to reduce labeled internal standard consumption, to maximize analyte sensitivity, and to achieve satisfactory validation results. Moreover, a clean-up step is important to extend the HPLC column lifetime and to maintain performance of the ESI-MS source.

Multifunctional SPE-cartridges usually containing activated carbon have been used 254 for sample purification, especially for trichothecene analysis, as reported in the 255 literature [5, 8, 15]. In contrast, dilute-and-shoot methods [4] are often applied for 256 ENNs and some modified mycotoxins. Therefore, this study presents the first multi-257 mycotoxin stable isotope dilution method for trichothecenes combined with ZEA, 258 ENNs, BEA, and the modified mycotoxin D3G using solid phase extraction for sample 259 purification. The use of a Bond Elut Mycotoxin cartridge (Agilent Technologies, Santa 260 Clara, CA, USA) without activated carbon was mandatory to achieve good recoveries 261 and to prevent adsorption of the non-polar toxins (ZEA, ENNs, and BEA). 262

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Calibration and quantitation. Response functions were obtained using linear regression. The response factors ranged between 0.75 (3-ADON) and 1.30 (ENN B1, A1, and A).. The coefficients of determination exceed 0.9982, and, as confirmed by Mandel test, the calibration curves show linearity for DON and 15-ADON within the molar ratios 0.1–10, 3-ADON and HT2 within 0.02–20, T2 within 0.02–50, ENN B within 0.05–10, ENN B1, A1 and A within 0.05–20, and BEA within 0.05–5.

A wide range of linearity for the matrix-matched calibration results for NIV between 70 and 500 μ g/kg, for D3G between 20 and 500 μ g/kg, for ZEA between 1.5 and 300 μ g/kg, and for FUSX between 15 and 150 μ g/kg.

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274 Method Validation

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LODs and LOQs. The LODs and LOQs for the SIDAs were calculated according to 276 Vogelgesang and Hädrich [12]. The LODs and LOQs for the matrix-matched 277 calibration were calculated from signal (S) to noise (N) ratio (LOD = 3xS/N, LOQ = 278 10xS/N). The blank matrix potato starch free of the monitored mycotoxins was used. 279 The LODs range between 0.1 and 5 µg/kg and the LOQs range between 0.2 and 15 280 µg/kg—except for NIV and D3G, whose LODs and LOQs are 70 and 200 µg/kg and 281 10 and 30 µg/kg, respectively (Table 1). The results for ZEA and types B and A 282 trichothecenes are comparable with recently reported results [4, 10, 16, 17]. The high 283 LOD and LOQ of NIV with 70 and 200 µg/kg, respectively, are due to the low MS/MS 284 sensitivity and are comparable with the limits reported by Njumbe Ediage et al. [18]. 285 The LODs and LOQs of the ENNS and BEA using the method presented here reveal 286

287 2–100 times higher sensitivity than those previously reported [11, 13, 19]. However,
288 Tolosa et al. [20] published a method ten times more sensitive for ENNS, which is
289 clearly attributed to the five-fold sample weight applied.

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Precision. The intra-day (n = 3) and inter-day (n = 3) coefficients of variation are 291 shown in Table 1. The intra-day precision ranges between 1 and 6% and the inter-292 day precision ranges between 5 and 12%. Thus, the precision data for the stable 293 isotope dilution assays presented here are similar to those reported for ENNs by Hu 294 et al. [11] and for trichothecenes by Asam et al. [9, 10]. The matrix-matched 295 calibration results are comparable with those of the SIDAs mentioned and more 296 precise than the methods described by Biselli et al. [21] and Ediage et al. [18]. 297 298 However, when comparing precision, one have to be aware that homogeneity of the samples is a crucial aspect and the precision of our method from one gram of sample 299 was only achievable from thoroughly homogenized samples. 300

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Recovery of SIDA and matrix-matched calibration. The recoveries of the SIDAs 302 and matrix-matched calibration were determined at three different spiking levels for 303 each mycotoxin. The recoveries range between 86 and 109% for the SIDAs with 304 relative standard deviations (RSDs) below 7% (Table 1) and between 79 and 117% 305 for the matrix calibration with maximal RSD of 17% (Table 1). These SIDA and 306 matrix-matched calibration recoveries both correspond to the expected levels of 307 stable isotope dilution assays. Figs. 3 and 4 present the LC-MS/MS chromatograms 308 of spiked barley malt samples in the negative and positive ESI mode, respectively. 309

Accuracy. The accuracy of this method was confirmed by analyzing commercially 311 available reference material (CRM) and samples from inter-laboratory method 312 studies. The CRM consisted of maize flour and has a certified content of 474 ± 30 313 $\mu g/kg$ DON. The SIDA of DON revealed a content of 468 ± 10 $\mu g/kg$ (n = 2) which 314 differs from the assigned value by 1.27% (Table 2). Five different oat samples from 315 inter-laboratory method studies were contaminated with HT2 between 9.57 ± 1.04 316 and $26.5 \pm 3.4 \,\mu\text{g/kg}$ and T2 between 3.40 ± 2.18 and $7.92 \pm 2.25 \,\mu\text{g/kg}$. Results and 317 differences between detected and assigned values of HT2 and T2-are provided in 318 Table 2 and vary between 0.60 and 4.45% and 2.14 and 6.73%, respectively. The 319 maximum difference to the respective certified reference values of 1.27% for DON, 320 4.45% for HT2, and 6.73% for T2 indicates the accuracy for different matrixes using 321 this multi-method. 322

323

Analysis of (modified) mycotoxins in cereals. Barley malt samples collected in various German federal states over a period of three years from 2012, 2013, and 2014 were analyzed with the multi-mycotoxin method presented. The results are summarized in **Table 3**. High contamination frequencies and concentrations of DON, D3G, and ENN B were detected, especially in 2012.

Over 93% of the analyzed barley malt samples are contaminated with ENN B and over 83% with ENN B1. The average ENN B concentration of the three years is 3 mg/kg. The maximum ENN B level of 60 mg/kg is from 2012, which is almost comparable with artificially inoculated barley malt [22]. The contents of ENN A1 and ENN A are lower and at maximal one-fifth of those ENN B reached. ENNs

consistently occur in the decreasing order by incidence and concentration: ENN B,
ENN B1, ENN A1, and ENN A. These results are consistent with other studies [11,
23, 24]. BEA was detected in four samples with low contents below 48 µg/kg over all
three years. In contrast, Mediterranean countries like Morocco or Spain had BEA and
ENN levels of wheat, barley, rice flour, and other cereal products that ranged
between 1 and 800 mg/kg [19, 25].

The samples have little contamination with ZEA, except for one of barley malt with250 μg/kg.

No analyzed samples contain type A trichothecenes from 2012. The other years are
not heavily loaded with HT2 and T2. The highest amounts of HT2 and T2 are found in
2014 at 45 and 40 μg/kg, respectively.

NIV was found in two barley malt samples. One from 2012 has a high content of 464
µg/kg. The contents of 15-ADON are lower than those of 3-ADON, which occurs
most frequently at a 30% rate and content range between 33 and 436 µg/kg in 2012.
FUSX was not detected in any of the analyzed samples.

The other type B trichothecenes, DON, and its modified metabolite, D3G, were found 349 in barley malt at frequencies up to 73% and 53%, respectively. The amount of DON 350 ranges between 31 µg/kg and 10 mg/kg and the amount of D3G between 28 µg/kg 351 and 19 mg/kg. During malting, and particularly during the germination process, DON 352 is exposed to glucosylation and can become D3G [26]. The content of D3G in 68% of 353 analyzed malts exceeds the content of DON up to tenfold, while the other 32% of 354 samples are below LOD or LOQ. Earlier studies reported a wide range between 1 355 µg/kg and 5 mg/kg of DON and D3G in barley, wheat, and brewing malt [17, 27, 28, 356

28]. Moreover, most of the reported malt samples had higher D3G levels than DON
levels [28, 29].

359

360 **Conclusions**

In the EU, the maximum regulatory permitted content of DON is 1250 µg/kg in 361 unprocessed cereals, which is also usually applicable to brewing malt [30]. Two of 362 the analyzed malt samples should not have been placed on the market even if the 363 D3G content is ignored and the official regulatory limits for DON are considered. This 364 mycotoxin contamination is likely transferred into beer as brewing barley malt is not 365 intended for direct human consumption. To which extent the toxins under study are 366 transferred into beer will be the focus of further investigations and adaptation of this 367 method to beer and liquid samples is under way. 368

369

370 Conflict of Interest Statement

The authors declare that they have no conflict of interest.

373 Abbreviations

15-ADON, 15-acetyldeoxynivalenol; 3-ADON, 3-acetyldeoxynivalenol; BEA,
beauvericin; D3G, deoxynivalenol-3-glucoside; DON, deoxynivalenol; ENN, enniatin;
ESI, electrospray ionization; FUSX, fusarenone X; HT2, HT2-toxin; NIV, nivalenol;
SPE, solid phase extraction; T2, T2-toxin; ZEA, zearalenone.

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Tables

	Analysis	LOD	LOQ [µg/kg]	Precision (n = 3) [RSD, %]		Recovery [%]		
Analyte		[µg/kg]		intra-day	inter-day		2x	3x
						spiking level 1	spiking level 1	spiking level 1
DON	SIDA	0.9	2.6	4	7	101 ± 3	101 ± 2	89 ± 2
3-ADON	SIDA	1.7	13.5	2	8	96 ± 1	99 ± 4	95 ± 2
15-ADON	SIDA	4.6	13.5	2	7	86 ± 4	95 ± 5	89 ± 2
HT2	SIDA	0.1	0.2	4	8	95 ± 1	97 ± 2	89 ± 2
T2	SIDA	0.2	0.5	5	9	95 ± 2	99 ± 1	97 ± 2
ENN B	SIDA	0.7	2.1	2	7	104 ± 3	101 ± 4	103 ± 2
ENN B1	SIDA	1.3	3.9	1	9	99 ± 4	96 ± 4	88 ± 4
ENN A1	SIDA	1.4	4.1	5	5	97 ± 2	108 ±3	105 ± 7
ENN A	SIDA	1.1	3.1	5	10	103 ± 3	106 ± 2	104 ± 2
BEA	SIDA	0.3	0.7	3	8	103 ± 4	109 ± 3	109 ± 3
FUSX	MMC	5	15	5	6	100 ± 3	94 ± 5	79 ± 10
NIV	MMC	70	200	2	12	101 ± 17	102 ± 13	91 ± 14
D3G	MMC	10	30	6	10	114 ± 10	117 ± 9	81 ± 12
ZEA	MMC	0.5	1.5	1	7	106 ± 3	100 ± 5	98 ± 9

 Table 1
 Validation data of the stable isotope dilution assay and of the matrix-matched calibration

SIDA = stable isotope dilution assay MMC = matrix-matched calibration

Reference material	Analyte	Assigned value [µg/kg]	Detected value [µg/kg]	Difference [%]
oat sample 1	HT2	9.57 ± 1.04	9.19 ± 0.89	-3.97
oat sample 1	T2	4.21 ± 2.17	4.30 ± 0.28	+2.14
oat sample 2	HT2	26.5 ± 3.4	26.7 ± 1.2	+0.60
oat sample 2	T2	7.92 ± 2.25	8.13 ± 0.24	+2.65
oat sample 3	HT2	8.46 ± 1.02	8.05 ± 0.74	-4.85
oat sample 5	T2	3.40 ± 2.18	3.18 ± 0.04	-6.33
oat sample 4	HT2	21.1 ± 3.4	22.1 ± 0.7	+4.45
	Т2	6.09 ± 2.25	6.50 ± 0.05	+6.73
oat sample 5	HT2	15.7 ± 2.6	15.2 ± 0.7	-3.06
oat sample 5	Т2	4.58 ± 2.20	4.86 ± 0.36	+6.11
maize flour	DON	474 ± 30	468 ± 10	-1.27

Table 2 Analysis of reference materials

Mycotoxin	Year	Positive samples	Median [µg/kg]	Min [µg/kg]	Max [µg/kg]
	2012	6	1730	215	19000
D3G	2013	5	118	28.2 ^{*)}	441
	2014	5	50.0	12.0	86.1
	2012	8	279	8.50	10300
DON	2013	5	65.8	9.86	406
	2014	9	12.0	6.93	59.6
	2012	3	73.6	33.0	436
3-ADON	2013	2	22.1	17.1	27.1
	2014	1	13.1	-	-
	2012	3	52.9	36.9	287
15-ADON	2013	2	70.2	37.4	103
	2014	n.d.	-	-	-
	2012	n.d.	-	-	-
HT2	2013	3	5.48	5.23	6.18
	2014	6	4.12	1.58	44.7
	2012	n.d.	-	-	
T2	2013	n.d.	-	-	-
	2014	3	8.91	6.33	40.7
	2012	10	1930	7.50	60200
ENN B	2013	8	51.7	3.19	1160
	2014	10	198	11.3	2070
	2012	9	278	21.6	1540
ENN B1	2013	6	48.8	6.49	203
	2014	10	87.2	4.78	735
	2012	7	162	28.2	1700
ENN A1	2013	3	50.5	41.3	74.9
	2014	8	103	8.02	286
	2012	4	88.5	37.3	362
ENN A	2013	1	6.80	-	-
	2014	5	18.17	1.43 ^{*)}	25.1

Table 3 Occurrence of mycotoxins in barley malt within 3 years (2012 [n = 10], 2013 [n = 10], and 2014 [n = 10])

2012	1	48.2	-	-
2013	1	7.08	-	-
2014	2	5.36	4.63	6.09
2012	1	464	-	-
2013	1	72.5 ^{*)}	-	-
2014	n.d.	-	-	-
2012	5	42.4	2.19	253
2013	2	7.24	1.26* ⁾	13.2
2014	2	1.41* ⁾	1.19* ⁾	1.63
	2012 2013 2014 2012 2013 2014 2012 2012 2013 2014	2012 1 2013 1 2014 2 2012 1 2013 1 2014 . 2013 2 2014 . 2013 2 2013 2 2014 2	2012 1 48.2 2013 1 7.08 2014 2 5.36 2012 1 464 2013 1 $72.5^{*)}$ 2014 n.d 2012 5 42.4 2013 2 7.24 2014 2 $1.41^{*)}$	2012 1 48.2 - 2013 1 7.08 - 2014 2 5.36 4.63 2012 1 464 - 2013 1 $72.5^{*)}$ - 2014 n.d 2012 5 42.4 2.19 2013 2 7.24 $1.26^{*)}$ 2014 2 $1.41^{*)}$ $1.19^{*)}$

n.d., not detected; *) below LOQ

Figure Legends

Fig. 1 Structures of type A and type B trichothecenes, enniatins, beauvericin, and zearalenone

Fig. 2 Fragmentation spectra of 3-ADON and 15-ADON in the positive ESI mode (DP = 90 V, CE = 20 V, EP = 10 V, and CXP = 10 V)

Fig. 3 LC-MS/MS chromatograms of a spiked barley malt sample in the negative ionization mode

Fig. 4 LC-MS/MS chromatograms of a spiked barley malt sample in the positive ionization mode

Figures

Fig. 1



type B trichothecenes



enniatins and beauvericin







	Analyte	R ₁	R ₂	R ₃
type B trichothecenes	NIV	ОН	OH	ОН
	D3G	Glc	н	ОН
	DON	ОН	н	ОН
	3-ADON	OAc	н	ОН
	15-ADON	ОН	н	OAc
	FUSX	ОН	OAc	ОН
type A trichothecenes	HT2	ОН	OAc	OCOCH ₂ CH(CH ₃) ₂
	T2	OAc	OAc	OCOCH ₂ CH(CH ₃) ₂
enniatins	ENN B	CH(CH ₃) ₂	CH(CH ₃) ₂	CH(CH ₃) ₂
	ENN B1	CH(CH ₃) ₂	CH(CH ₃) ₂	CH(CH ₃)CH ₂ CH ₃
	ENN A1	CH(CH ₃) ₂	CH(CH ₃)CH ₂ CH ₃	CH(CH ₃)CH ₂ CH ₃
	ENN A	CH(CH ₃)CH ₂ CH ₃	CH(CH ₃)CH ₂ CH ₃	CH(CH ₃)CH ₂ CH ₃
beauvericin	BEA	CH ₂ C ₆ H ₅	CH ₂ C ₆ H ₅	CH ₂ C ₆ H ₅
zearalenone	ZEA			









Fig. 4

