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Determination of peptaibol trace amounts in marine sediments by liquid chromatography/electrospray ionization-ion trap-mass spectrometry

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Abstract:

Extraction followed by reverse phase liquid chromatography (LC)/electrospray ionization-ion trap-mass spectrometry (ESI-IT-MS) analysis has been successfully developed for the determination of peptaibols, fungal toxic metabolites, in marine sediments. Spiking experiments showed that the mean recovery of target compounds exceeded 85% at a spiking level of 10 ng/g of sediment (wet weight). Detection and quantification limits were 250 and 830 pg/g of sediment, respectively. The method developed constituted the first sensitive assay for quantification of peptaibol trace amounts in a natural environment. A concentration of 5 ng/g in sediment samples collected from Fier d'Ars was found.

Keywords: Fungal peptide metabolites; Trichoderma sp.; Marine fungal contamination; Electrospray ionization-ion trap-mass spectrometry (ESI-IT-MS); Matrix matched calibration

1. Introduction

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Fungal production of mycotoxins in the marine environment is proposed as a possible cause for episodes of unexplained toxicity observed in shellfish populations during the last decade. Within this framework, numerous strains of toxigenic saprophytic fungi were isolated from shellfish, sediment and seawater samples collected in shellfish farming areas [1]. Among them, different strains of *Trichoderma* sp., grown in marine-like culture conditions, produced peptaibols, peptidic metabolites, which are toxic for different larval models (diptera or crustacean larvae) [2].

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45 Peptaibols constitute a constantly growing family of linear peptide antibiotics of 46 fungal origin. They are characterized by a molecular mass from 500 to 2200 u, an acetyled N-47 terminus, a C-terminus amino alcohol and a high content of a non proteinogenic amino acid, 48 α -aminoisobutyric acid (Aib or U) [3]. Peptaibols are exclusively produced by filamentous 49 fungi mainly belonging to the genera Trichoderma, Acremonium, Paecilomyces, Emericellopsis and Gliocladium. They have been classified into subfamilies according to their 50 51 amino acid chain lengths (ranging from 5 to 20 residues) and their chemical characteristics [4]. These fungal metabolites exhibit a variety of biological activities resulting from their 52 membrane-modifying and pore-forming properties. Thus antibacterial, antifungal and 53 54 occasionally antiviral and antiparasitic activities have been reported [5-8].

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56 A previous experimental contamination has shown that peptaibols can be accumulated 57 in filter-feeder molluscs (Mytilus edulis) when present in sea-water as soluble compounds [9]. 58 The presence of such compounds in the marine environment could lead to health risks for 59 shellfish and their consumers. Different peptaibols were recently detected in sediments in a marine area devoted to shellfish farming (Fier d'Ars, Atlantic coast, France) [10]. These 60 61 sediment samples displayed high toxicity for mussel larvae in the absence of significant 62 contaminations (metals, PCBs, HAPs, pesticides, antibiotics) or eutrophication [11]. 63 Developing analytical methods allowing the precise determination of these fungal metabolites 64 in the marine environment is therefore of great interest in order to establish a causal relationship between peptaibol concentrations and biological effects. Certain methods, that 65 use radioactivity or capillary electrophoresis coupled with UV and ESI-TOF-MS, have 66 already been described for the quantification of peptaibols isolated from fungal cultures 67 68 [12,13]. However, they are not sensitive enough for determining trace amounts. The aim of this work is to develop a process for extracting peptaibols from marine sediment matrices and 69 70 a sensitive assay for the determination of trace amounts by using LC/ESI-IT-MS. The method 71 developed focuses on long-sequence peptaibols, including 18 to 20 amino acid residues, 72 because of their high bioactivity [6] and their predominance in peptaibol family [14].

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75	2.	Experimental
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- 77 2.1. Chemicals
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79 Methanol and dichloromethane were purchased from Carlo Erba (Val de Reuil, France) and distilled before use. Ethanol was purchased from APC (Aubervilliers, France). 80 81 Trifluoroacetic acid (TFA) was obtained from Fluka Chemical (Buchs, Switzerland), 82 hydrochloric acid from Acros organics (Geel, Belgium) and acetic acid from Sigma Aldrich 83 (Saint-Quentin Fallavier, France). For mass spectrometry analysis, HPLC-grade methanol was 84 obtained from Baker (Deventer, Holland). Water was purified to HPLC-grade quality with a 85 Millipore-Q RG ultrapure water system from Millipore (Milford, CT, USA). Alamethicin F50 86 was obtained from Sigma Aldrich (Ref. A4665).

- 87
- 88 2.2. Sediment samples
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90 Sediment samples used for optimizing extraction and purification procedures were 91 collected from La Rochelle (France) in January 2000. They were transported from the site to 92 the laboratory in isothermic containers and frozen at -20°C.

93 Sediment samples used to estimate environmental contamination were collected from 94 different sites on the French Atlantic coast. Surface sediment samples (oxic fraction, 1st cm) were collected from four sites: the Bay of Marennes-Oléron (45° 55' N 1° 13' W), Auray 95 River (47° 38' N 2° 58' W) and the Bay of Veys (49° 22' N 1° 08' W) in June 2004 (in the 96 97 framework of the French program "MOREST"), and from Fier d'Ars (Ré Island – 46° 13' N 98 1° 29' W) in March 2006. All the samples were transported from the site to the laboratory in 99 isothermic containers and frozen at -20°C until analysis. Each sample (approximately 10 g 100 wet weight) was subjected to extraction, purification and LC/ESI-IT-MS analysis.

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102 *2.3. Optimization of the extraction procedure*

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104 The efficiency of the extraction procedure was checked by recovery experiments. The 105 nature of the extraction solvents was the decisive parameter for which optimization was 106 required. Approximately 10 g wet weight (ww) of sediments were spiked with 100 ng of 107 alamethicin F50 and extracted with 3×25 mL of different organic solvents. According to the 108 preliminary experiments, five different mixtures of solvents were selected for definitive tests: 109 (a) dichloromethane/methanol (1:1, v/v), (b) methanol/TFA 0.1% (v/v), (c) ethanol/acetic acid 110 1% (v/v), (d) acetone/acetic acid 1% (v/v) and (e) acetone/hydrochloric acid 0.02% (v/v). At 111 each extraction step, the sample was sonicated for 15 min and centrifuged at 700 g for 5 min. 112 Two procedures were used in order to eliminate salts. The supernatants obtained with mixtures (a), (b) and (c) were evaporated to dryness and redissolved in 50 mL of 113 114 dichloromethane/methanol/water (2:2:1). The aqueous phase containing salts was washed 115 twice with dichloromethane. The organic phases were then combined and evaporated to 116 dryness. The supernatants obtained with solvent mixtures (d) and (e) were simply filtered and 117 evaporated to dryness (crude extracts).

- 118
- 119 2.4. Purification of extracts
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Purification of crude extracts was performed by vacuum liquid chromatography (VLC) on a diol-silica gel column (10 x 40 mm) (Supelco, Bellefonte, PA, USA). The column was prepared with 2 g of sorbent and rinsed with 10 mL of dichloromethane prior to sample 124 loading. For this step, two deposit modes were investigated. In mode 1, the extract was redissolved and deposited with 3 mL of three successive solvent mixtures in the purification 125 126 column: dichloromethane/ethanol (100:0, 90:10 and 50:50, v/v). Mode 2 corresponded to a 127 dry deposit. The crude extract was dissolved in 10 mL of dichloromethane/ethanol mixture 128 (50:50, v/v) and mixed with a quarter of the sorbent phase. This mixture was evaporated to 129 dryness and loaded in the column. Elution was performed with 40 mL of successive 130 dichloromethane/ethanol mixtures (100:0, 98:2, 90:10 and 50:50, v/v). The fractions obtained 131 (A, B, C and D, respectively) were evaporated to dryness and redissolved in methanol (500 132 μ L) prior to analysis by using the hyphenated LC/MS technique.

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134 2.5. LC/MS analysis

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136 The samples were analyzed on a modular HPLC system consisting of a Spectraphysics 137 Spectra System P2000 pump, an AS 100XR autosampler (Thermo Separation Products, San Jose, CA, USA) equipped with a Kromasil C-18 5- μ m reverse-phase 2.0 \times 250 mm column 138 139 (Interchim, Montluçon, France) heated to 40°C and coupled with a Finnigan Matt LCQ[™] 140 ESI-IT-mass spectrometer (Thermo Separation Products). The mobile phase consisted of a 141 methanol/H₂0 (85:15, v/v) mixture delivered at a constant flow rate of 0.2 mL/min (isocratic mode). The sample injection volume was 5 µL. All mass analyses were performed in positive 142 mode. To ensure optimal detection, perfusion of a methanolic solution of alamethicin F50 (50 143 144 ng/mL) into the flow of LC using a micrometrically automated 250-µL syringe (Hamilton, 145 Reno, NV, USA) at a flow rate of 3 µL/min was performed to optimize the mass spectrometer parameters. The spray voltage was set to 4.50 kV, the capillary temperature to 266°C and the 146 147 capillary voltage to 42 V. Nitrogen flow rates were 89 and 37 (arbitrary units), respectively, 148 for sheath and auxiliary gas. The parameters of ion optic transmission were adjusted to 55 V 149 for Tube Lens Offset, -3.50 V for Multipole 1 Offset, -6 for Multipole 2 Offset and 400 V for Multipole RF Amplifier (peak to peak). 150

151 MS^n spectra acquisitions were carried out with a collision energy of 32% and an isolation 152 width of 1 u.

All spectra acquisitions and reworks were done using LCQ Xcalibur 1.3 software (ThermoFisher Scientific).

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156 2.6. Calibration and quantification

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External and matrix matched calibrations were compared. A commercial solution of alamethicin F50 was used as external standard and characterized by LC/MSⁿ analysis. This product contains four individual components which have been identified as alamethicin F50/5, F50/6a, F50/7 and F50/8b with molecular masses of 1962, 1976, 1976 and 1990 u respectively, according to Kirschbaum *et al.* [15].

The two main components, alamethicin F50/5 (m/z 1004.3, t_R 8.8 min) and F50/7 (m/z164 1011.3, t_R 10.6 min), which represented a constant proportion of 90.5 % in the reference 165 solution, were used for the calibration performed by using LC/ESI-IT-MS. This proportion 166 remained constant after the extraction and purification steps. For external standardization, a 167 calibration curve was prepared using 8 concentrations of alamethicin F50 in methanolic 168 solution (1 to 100 µg/L). To consider the matrix effects, matrix matched calibration samples 169 were prepared by adding different concentrations of alamethicin F50 to sediment extracts 170 obtained after purification. 100 μ L of alamethicin F50 reference solution at 12.5, 25, 50, 100 171 and 200 μ g/L were added to 100 μ L of each purified fraction C and D. LC/MS analysis of 172 each concentration level was performed 6 times for both external and matrix matched 173 calibrations. The accuracy and precision of the matrix matched calibration method were 174 calculated for each concentration level.

The accuracy of the method developed was determined by the analysis of three sediment samples spiked with 100 ng of alamethicin F50 solution. All the percentages of recovery were determined relative to the standard samples.

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- 179 2.7. Statistical treatment
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181 Mann Whitney U-tests were carried out to compare the percentages of recovery of 182 alamethicin F50 and impurity masses obtained during the optimization of the extraction and 183 purification steps. Pearson's correlation was used to test the linearity of the quantification 184 data.

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- 189 **3. Results and discussion**
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192 *3.1. Selection of extraction conditions of peptaibols from sediments*

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194 To achieve the efficient extraction of the target compounds, recovery experiments with 195 alamethicin F50 spiked sediments were carried out. Five solvent mixtures were evaluated and 196 the results are shown in Table 1. Extraction using mixtures of dichloromethane/methanol, 197 methanol/TFA and ethanol/acetic acid did not provide satisfactory recovery of alamethicin 198 F50, since the values were below 10%. Methanol was generally used in the extraction 199 procedures of peptaibols from fungal cultures (qualitative analysis) [16,17]. In spite of its 200 high eluotropic strength, this solvent was not strong enough to remove peptaibols from a 201 complex sedimentary matrix. Acetone/hydrochloric acid mixture (e) provided a higher 202 recovery of alamethic n F50 with a mean of $64 \pm 9\%$. Satisfactory extraction efficiency ($86 \pm$ 203 20%) was obtained using acetone/acetic acid mixture (d) (significant differences with (a), (b) 204 and (c) at the 95% level). An additional extraction test was performed with acetone 100% and 205 resulting in 47% recovery (results not shown), a value lower than those obtained for acidified acetone mixtures. Acid conditions were essential for the extraction of molecules of interest 206 207 from sedimentary particles. The acetone/acetic acid 1% (v/v) mixture was therefore chosen as 208 the best solvent for further studies.

209

210 **TABLE 1**

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- 213 *3.2. Purification of analytes*
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The crude extracts thus obtained contained a high level of impurities. Hence it was 215 216 essential to proceed to further purification steps on extracts to minimize chromatographic 217 interferences and ions suppression. Silica [5,18] and diol-silica gel columns [2,19] were 218 generally used to purify the peptaibols (fungal cultures). In this study, the sediment extracts 219 were purified on diol-silica gel and alamethicin F50 was eluted by fractions C and D 220 (dichloromethane/ethanol 90:10 and 50:50 v/v, respectively). Because of partial dissolution of 221 the extract in dichloromethane, it was necessary to optimize the deposit mode. Thus, two 222 different procedures were tested: mode 1 - solubilization of the extract in three successive 223 solvent mixtures; mode 2 - dry deposit.

The recovery of alamethicin F50 was not significantly different depending on modes 1 and 2 as shown in Fig. 1a (Mann-Whitney, p-value = 0.042). However, there were significantly fewer impurities eluted when using mode 2 than when eluted with mode 1, as shown in Fig. 1b (Mann-Whitney, p-value = 0.05). Moreover, repeatability was better with mode 2 than with mode 1. The dry deposit mode (mode 2) was therefore chosen for the purification of sediment extracts because of less interference from impurities and better repeatability.

- 231
- **FIGURE 1**
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- 235 *3.3 LC/MS identification of peptaibols*
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237 Analysed under neutral conditions and positive mode by ESI-IT-MS, long-sequence 238 peptaibols mainly appeared as doubly charged sodium adduct ions [M+2Na]²⁺ with a peptidic 239 isotopic profile (Fig. 2a). In LC/MS, their detection was performed through three scan events 240 repeated throughout the chromatographic separation: a total current ion scan (fullscan) from m/z 150 to 2000 and two enhanced resolution scans (zoomscan) from m/z 870 to 890 and from 241 m/z 985 to 1015. An additional analysis in MS² mode was performed during a second run on 242 the sodium adduct ions observed previously. This generated a spectrum containing mainly the 243 a_n and y_n ion series as classically reported by others authors [20], while b_n ions, predominant 244 in the acid medium, were also detectable but in lower abundance [21,22]. Peptide 245 identification was based on the production of N- and C-termini fragments resulting from 246 preferential breaking of the Aib–Pro bond [23-25]. MS^2 analysis of m/z 1004.3 (alamethicin 247 248 F50/5) is depicted in Fig. 2b which shows a predominant doubly charged ion $[M-H_20+2Na]^{2+}$ 249 at m/z 995.8 corresponding to a loss of a water molecule on the amino alcohol located at the 250 C-terminus. The N-terminus $[a_{13}+Na]^+$ at m/z 1183.8 and the C-terminus $[y_7+Na]^+$ at m/z251 796.6 could be easily identified. An Aib residue can be visualized between fragments 252 $[a_{12}+Na]^+$ at m/z 1098.7 and $[a_{13}+Na]^+$ at m/z 1183.8.

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FIGURE 2

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3.4. LC/MS quantification of peptaibols

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259 External and matrix matched calibrations were compared for peptaibol quantification. 260 To investigate the matrix effect, matrix matched calibration was performed using sediment extracts spiked with the alamethicin F50 reference solution after purification (e.g. for fraction 261 262 D, Fig. 3a, b, c). Both external and matrix matched calibration curves, obtained by summing 263 the peak areas of the two alamethicin components F50/5 and F50/7, were observed to be linear up to a concentration of 100 μ g/L with correlation coefficients higher than 0.98. The 264 comparison of matrix matched calibrations performed with sediments from different origins 265 (La Rochelle and Fiers d'Ars) showed a significant and variable matrix effect with a signal 266 267 decrease varying from 20 to 52 % compared to the signal of alamethicin F50 in methanolic 268 solution. Matrix matched calibration requires at least two LC/MS runs per analysis: one for 269 the sample extract and one for the sample extract spiked with a known quantity of the 270 reference peptaibol. However, it permitted the correction of signal quenching and taking into 271 account the variability of sedimentary matrices.

272

273 **FIGURE 3**

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275 The analytical method was validated considering the linear range, limit of detection (LOD) and precision. The limit of quantification (LOQ) was determined using the method of 276 277 Vial and Jardy [26] with a pre-established value of area relative standard deviation (RSD) of 278 10%. For the reference peptaibol in methanolic solutions, LOD and LOQ were respectively 279 0.5 and 1.7 µg/L. For matrix matched calibration samples, the signal intensity of alamethicin F50 was decreased by coeluted substances originating from the sediments. Consequently, 280 LOD and LOQ were increased, reaching respectively 2.5 and 8.3 µg/L, corresponding to a 281 282 detection of 250 pg/g and a quantification of 830 pg/g of sediment (ww).

Intra-day statistics of accuracy and precision were determined for matrix matched calibration method (Table 2). The accuracy, expressed in terms of bias (deviation from true values) was between 29% for the lowest concentration (below LOQ), and 2% for a concentration of 9.4 ng/g of sediment. The precision, given by relative standard deviations, was from 10% for a concentration of 0.6 ng/g to 2% for a concentration of 9.4 ng/g.

The whole procedure, from sample treatment to instrumental quantification, provided a satisfactorily accurate result with a recovery of $86 \pm 4\%$ determined using spiked sediment samples at a concentration of 10 ng/g (Fig. 1a).

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- 294 **TABLE 2**
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- *3.5. Application to environmental samples*

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The method developed (acetone/acetic acid extraction; dry deposit; LC/MS analysis using three scan events; matrix matched calibration) was applied to natural sediment samples collected from different sites along the French Atlantic coast. Long-sequence peptaibols were identified and quantified in samples collected from Fier d'Ars but they were not observed in sediment samples collected from the Bay of Marennes-Oléron, Auray River and the Bay of Veys.

306 In the Fier d'Ars samples, after chromatographic separation, four doubly charged ions 307 with a peptidic isotopic profile were observed at m/z 991.2, 991.7, 998.2 and 998.7 (e.g. for 308 m/z 991.7, Fig. 4a, b). The molecular masses and retention times of these compounds are shown in Table 3. To confirm their peptaibolic nature, MS² fragmentation was carried out. 309 Fragmentation profiles were obtained for the two main ions m/z 991.7 and 998.7 and were 310 311 similar in both cases to the fragmentation pattern of long-sequence peptaibols (e.g. for m/z312 991.7, Fig. 4c). An identical N-terminus fragment at m/z 1163.8 was identified for these two 313 peptaibols. Two different C-termini parts were observed, respectively, at m/z 773.5 and 787.5. Peptides with molecular masses of 1937.4 and 1951.4 u and showing these N- and C-termini 314 315 fragments showed numerous similarities with longibrachins and trichokonins, 20-residue 316 peptaibols isolated from Trichoderma species [27-31]. The quantification of peptaibols 317 observed in Fier d'Ars samples allowed establishing a concentration of 5.2 ± 2.1 ng/g of 318 sediment (ww) (n=2).

319

FIGURE 4

321

- **TABLE 3**
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325 **4. Conclusion**

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327 The method described using LC/ESI-IT-MS allows both the identification of 328 peptaibols and, for the first time, their quantification in the pg/g range in complex matrices. 329 LOD and LOQ were respectively 250 and 830 pg/g in marine sediments. Several sediment 330 samples were analysed to evaluate the environmental contamination and the possible 331 implication of these fungal metabolites in toxicity episodes observed in populations of 332 bivalves along the Atlantic coast. The presence of long-sequence peptaibols was shown in 333 sediments collected from Fier d'Ars and trace amounts were determined in these samples. The adaptation of this analytical method to shellfish matrices is under consideration. Further 334 335 investigations will permit studying the relationship between environmental concentrations and 336 the toxicity of these compounds for marine organisms.

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340 Acknowledgements

341	
342 343 344 345	Samples from the Bay of Marennes-Oléron, Auray River and the Bay of Veys were collected in the framework of the French program "MOREST" coordinated by IFREMER. We would like to express our thanks to C. Robiou du Pont, N. Berthet and M. Le Goff for their technical participation.
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350	Re	ferences
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406	Figure captions
407	
408	
409	Fig. 1. Influence of the purification mode of crude extracts
410 411	Mode 1: extract deposited with three successive fractions: dichloromethane/ethanol 100:0, 90:10 and 50:50 (v/v);
412	Mode 2: dry deposit
413 414 415	(a) Cumulative recovery of alamethicin F50(b) Cumulative percentage of eluted impurities
416	
417	Fig. 2. Mass spectra of alamethicin F50/5
418 419 420	 (a) Zoomscan mode (b) MS² spectrum of ion at <i>m/z</i> 1004.3 [M+2Na]²⁺ The main fragments corresponding to a_n and y_n ion series are shown.
421	
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423 424	Fig. 3. LC/ESI-IT-MS analysis of surface sediment samples collected from Fiers d'Ars - chromatograms of fraction D spiked with alamethicin F50 reference solution (25 μ g/L)
425 426 427 428	 (a) Total ion current (b) Detection on the range [1003.9-1004.9]: peak of alamethicin F50/5 (c) Detection on the range [1010.9-1011.9]: peak of alamethicin F50/7
429	
430	Fig. 4. LC/ESI-IT-MS analysis of surface sediment samples collected from Fiers d'Ars
431 432 433 434	 (a) Chromatogram (detection on the range [991.2-992.2]) (b) Mass spectrum corresponding to peak at t_R = 6.11 min (c) MS² spectrum of ion at m/z 991.7 [M+2Na]²⁺ The main fragments corresponding to a_n and y_n ion series are shown.
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TABLES

Table 1

Influence of the solvent mixture on alamethicin F50 extraction from sediments spiked at 10 ng/g.

Tested solvents	Mean recovery (%) \pm SD (n=3)
a: dichloromethane / methanol (1:1, v/v)	8.7 ± 0.0
b: methanol / TFA (0.1%, v/v)	1.9 ± 0.0
c: ethanol / acetic acid (1%, v/v)	5.8 ± 0.0
d: acetone / acetic acid (1%, v/v)	86 ± 20
e: acetone / hydrochloric acid (0.02%, v/v)	64 ± 9.0

- 1 -

Table 2 12

13 14 15 Matrix matched calibration: repeatability and accuracy.

Alamethicin Theoretical (ng/g of sediment)	Mean (ng/g of sediment) ± SD (n=6)	RSD (%)	Bias (%)
0.6	0.8±0.1	10	29
1.2	1.1±0.1	7	-8
2.3	2.2 ± 0.2	9	-4
4.7	3.8±0.2	4	-18
9.4	9.5±0.2	2	2

16

19 Table 3

Spectral and chromatographic characteristics of peptaibols observed in surface sediment samples from Fier d'Ars 20

21 22 23

Observed ions $[M+2Na]^{2+}(m/z)$	Calculated M (u)	t _R (min)
991.2	1936.4	8.90
991.7	1937.4	6.11
998.2	1950.4	10.06
998.7	1951.4	6.98