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Food Additives and Contaminants



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Matrix effect on paralytic shellfish toxins quantification and toxicity estimation in mussels exposed to *Gymnodinium catenatum*

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Abstract

Paralytic shellfish toxins were quantified in whole tissues of the mussel *Mytilus galloprovincialis* exposed to blooms of the dinoflagellate *Gymnodinium catenatum* in Portuguese coastal waters. A validated HPLC method with fluorescence detection, involving pre-chromatographic oxidation was used to quantify carbamoyl, N-sulfocarbamoyl and decarbamoyl toxins. In order to test for any matrix effect in the quantification of those toxins, concentrations obtained from solvent and matrix matched calibration curves were compared. A suppression of the fluorescence signal was observed in mussel extract or fraction in comparison to solvent for the compounds dcGTX2+3, GTX2+3 and GTX1+4, while an enhancement was found for C1+2, dcSTX, STX, B1, dcNEO and NEO. These results showed that a matrix effect varies among compounds. The difference of concentrations between solvent and matrix matched calibration curves for C1+2 (median=421 ng g⁻¹) exceeded largely the values

for the other quantified compounds (0.09-58 ng g⁻¹). Those differences were converted into toxicity differences, using Oshima toxicity equivalence factors. The compounds C1+2 and dcNEO were the major contributors to the differences of total toxicity in the mussel samples. The differences of total toxicity were calculated in ten mussel samples collected during a 10-week blooming period in Portuguese coastal lagoon. Values varied between 53 and 218 μ g STX equivalents kg⁻¹. The positive differences mean that the estimated toxicity using solvent calibration curves exceed the values taking into account the matrix. For the toxicity interval 200-800 μ g STX equivalents kg⁻¹ an increase was found between 44 and 28%.

Keywords: paralytic shellfish poisoning; phycotoxins; saxitoxin; LC-FLD

Introduction

Paralytic shellfish toxins (PSTs) are responsible for one of the most severe forms of seafood poisoning (Gessner and Middaugh 1980; Sommer and Meyers 1937). At least 20 toxins have been identified (Llewellyn 2006). These toxins are produced naturally by microalgae species of the dinoflagellate genus *Alexandrium*, *Pyrodinium* and *Gymnodinium* (Masó and Garcés 2006). The better documented were grouped in three classes according to their chemical structure: carbamoyl toxins (saxitoxin-STX, neosaxitoxin-NEO and gonyautoxins-GTX1 to GTX4), N-sulfocarbamoyl toxins (B1, B2, C1 to C4), and decarbamoyl toxins (dcGTX1 to dcGTX4, dcSTX and dcNEO) (Figure 1). The mechanism of these compounds consists of the blockage of the sodium channels of nerve membranes, resulting in stoppage of the propagation of neural impulses and the paralysis of neuromuscular systems (Lagos and Andrinolo 2000). Different toxicities result from specific binding affinity to voltage-gated sodium channel

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receptors (Genenah and Shimizu 1981). The toxicity of each compound has been estimated by mouse bioassays and expressed in terms of mouse units. The carbamoyl group contains the most toxic compounds, the N-sulfocarbamoyl group contains the least toxic, and the decarbamoyl group have intermediate toxicities (Oshima 1995).

During the last decades, chemical methodologies for PSTs determination have been under development and validation, attempting to replace the mouse bioassay as the official method (Anon.1990). A liquid chromatography method with fluorescence detection (LC-FLD) involving a pre-column oxidation using hydrogen peroxide and periodate was adopted by the Association of Official Analytical Chemists as an official method for determination of PSTs in shellfish (Anon. 2006). After validation through a collaborative study for STX, NEO, GTX2+3, GTX1+4, dcSTX, B1 (GTX5), C1+2 and C3+4 in shellfish (mussels, clams, oysters and scallops) the method was integrated in European Directives to act as a legal alternative to the mouse bioassay (European Union Commission 2006; Lawrence et al. 2005). Recently, a refinement and extension of the AOAC method including the additional toxins dcNEO and dcGTX2+3 offers possibilities to achieve reliable analytical alternatives (Turner et al. 2009).

The AOAC method, also called "the Lawrence method", includes a C18 oyster cleaned extract as a matrix modifier in the periodate reaction in order to enhance the fluorescence intensity of N-hydroxylated toxins oxidation products (Lawrence and Niedzwiadek , 2001). No added matrix modifier is foreseen for the peroxide oxidation running under aqueous solution due to the adequate detection of the products of oxidation. The method was primarily developed for shellfish samples contaminated by *Alexandrium* spp blooms, having N-sulfocarbamoyl and decarbamoyl toxins, which are quantified after peroxide oxidation and have a lower contribution to the PSTs profile (Lawrence and Menard 1991). A different situation occurs with shellfish contaminated

by *Gymnodinium catenatum* a common bloom in Portuguese and Galician waters. The compounds dcGTX2+3, dcSTX (decarbamoyl) and C1+2, B1 (N-sulfocarbamoyl) emerge as major components of the toxin profiles (Artigas et al. 2007; Franca et al. 1996; Oshima 1990; Vale et al. 2008) and, according to the AOAC method, their quantification can be carried out without a matrix modifier.

This work tested whether the matrix effect is relevant in the quantification of Nsulfocarbamoyl and decarbamoyl toxins, as well as other toxins, in mussels naturally contaminated by *Gymnodinium catenatum* using solvent and matrix matched calibration curves. The impact of this effect on the estimation of the total toxicity is examined.

Materials and methods

Shellfish sample preparation

The shellfish samples used in this work were: (i) uncontaminated mussels (*Mytilus galloprovincialis*) from Viana, west coast of Portugal, used as matrix on toxin determination; (ii) mussels collected weekly during a 10-week period from Aveiro lagoon, west coast of Portugal, exposed to repeated blooms of *Gymnodinium catenatum*, to assessing the repercussion of matrix effect on the toxicity calculation; (iii) uncontaminated oysters (*Crassostrea* spp) from Formosa lagoon, south of Portugal, used as matrix modifier following the Lawrence method (Anon. 2006). Each bivalve was cleaned externally with fresh water, opened and the whole soft tissues removed from the shell, rinsed and drained. Composite mussel samples (n=30 individuals) of soft tissues were blended, mechanically homogenised and stored at -18°C until required for determinations. The same procedure was used for the preparation of the oyster composite sample (n=15).

Extraction, cleanup and oxidation of samples

The extraction, cleanup and oxidation procedures for PSTs determination were based on the AOAC method (Anon. 2006) involving the following steps: (*i*) acid duplicate extraction of the composite shellfish sample with acetic acid solution (first extraction with heating); (*ii*) cleanup using a solid phase extraction (SPE) 500 mg C18 cartridge (Supelclean[®], Supelco, Bellefonte, PA, USA); (*iii*) an aliquot of C18-cleaned extract is added to a SPE ion exchange cartridge (SPE-COOH) (Bakerbond[®], J.T. Baker, Phillipsburg, NJ, USA) being sequentially eluted to obtain three individual fractions (fraction 1 to 3); (*iv*) hydrogen peroxide (10% v/v) is added to 1M NaOH solution and vortex mixed, then a PST standard solution or sample extract after C18 is added, and the mixture thoroughly mixed and allowed to react for 2 min at room temperature; glacial acetic acid is added and vortex mixed; (*v*) a PST standard solution or a sample extract after C18 or SPE-COOH fractionation is added to a matrix modifier solution prepared with PST-free oysters, and then is added the periodate oxidant; the mixture is thoroughly mixed and allowed to react during 1 min., then glacial acetic acid is added and the mixture is allowed to stand for a further 10 min.

Aliquots of C18 extract are used for oxidation of PSTs with peroxide and periodate oxidants, while aliquots of SPE-COOH fractions are used for periodate oxidation, prior to LC analyses.

Liquid chromatography analysis

The LC analysis was carried out by a Hewlett-Packard /Agilent system (Palo Alto, CA, USA) consisted of a 1050 Series quaternary pump, 1100 Series in-line degasser, autosampler, column oven, and 1200 Series fluorescence detector. The Agilent Chemstation[®] software (revision A.10) performed data acquisition and peak integration.

 Separation was performed using a reversed-phase column Supelcosil[®] C18, 15x4.6 mm id, 5 μ m (Supelco, Bellefonte, PA, USA) equipped with a guard column Supelguard Supelcosil[®] C18, 2x4.0 mm id, 5 μ m (Supelco , Bellefonte, PA, USA). Column was kept in a column oven at 30°C. Detection wavelengths were set at 340 nm for excitation and 395 nm for emission. The mobile phase gradient used to elute the PST oxidation products consisted of 2 mobile phases under the following conditions: 0-5 % B (0.1 M ammonium formate in 5 % acetonitrile, pH = 6) in the first 5 min, 5-70% B for the next 4 min and 100% mobile phase A (0.1 M ammonium formate, pH = 6) was used for 5 min before next injection. The flow rate was 1 mL min⁻¹. The injection volumes were 50 μ L and 100 μ L, for the oxidation products of peroxide and periodate reaction, respectively.

Certified calibration solutions for PSTs were purchased from the Certified Reference Materials Program of the Institute for Marine Biosciences, National Research Council, Halifax, Canada (CRM-STX-e, CRM-NEO-b, CRM-GTX2&3-b, CRM-GTX1&4-b, CRM-dcSTX, CRM-dcGTX2&3, CRM-GTX5-b (B1), CRM-C1&2 and CRM-dcNEOb). Working standard solutions were prepared by appropriate dilution of the corresponding stock solution and stored at 4°C during 1 month. All PSTs were identified and quantified by comparison peak areas of sample oxidation products and of working standards. The compounds GTX2+3, GTX1+4, C1+2 and C3+4 were quantified jointly due to the fact that the oxidation process creates the same oxidation product.. Due to the lack of standards for C3+4 and B2 their quantification was not achieved. However, identification was done taking into account their retention time in the LC method (Ben-Gigirey et al. 2007; Lawrence and Niedzwiadek 2001). All chemical and reagents were LC or analytical grade. Acetonitrile, acetic acid, methanol, ammonium formate, ammonium acetate and disodium hydrogen phosphate were

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purchased from Sigma-Aldrich (Steinheim, Germany). Periodic acid, sodium hydroxide, hydrogen peroxide and sodium chloride were from Merck (Darmstadt, Germany). Ultrapure water was obtained by Milli-Q 185 Plus system Millipore (Bedford, MA, USA).

Procedural modification

The procedural modification used in this work is centered on the inversion of reactions sequence of AOAC method (Anon. 2006), the peroxide oxidation being performed before the periodate oxidation. Figure 2 shows a flow diagram highlighting the procedural modification. The reason for this inversion comes from non-N-hydroxylated toxins (B1, C1+2, dcSTX, dcGTX2+3) being the most abundant ones in shellfish samples contaminated by *Gymnodinium catenatum* from Iberian waters. In the AOAC method, these compounds are also quantified in the peroxide oxidation, due to a better detection of the oxidation products, but after a periodate oxidation. The dcNEO toxin was quantified after the periodate oxidation of the C18 extract, avoiding dilution effect during the SPE-COOH fractionation.

To resolve the overlapped areas of dcSTX and dcNEO frequently observed in shellfish samples contaminated by *Gymnodinum catenatum*, dcNEO was quantified by subtracting the dcSTX contribution. This contribution of dcSTX was estimated from the calibration curve oxidized with periodate, using the concentration obtained previously under peroxide oxidation. A similar calculation was applied to quantify (i) GTX1+4 in the extract from fraction 2 followed by periodate oxidation, subtracting the contribution of dcGTX2+3, and (ii) NEO in the extract from fraction 3 followed by periodate oxidation, subtracting the contribution of dcSTX.

Test to matrix effect

To test the matrix effect in the quantification of toxins, two trials of working standard solutions for calibration curves were prepared by dilution of PSTs stock solutions in 0.1 mM acetic acid and in cleaned-up mussel tissue extract and subsequent fractions. Two standard toxin mixtures were prepared: Mix-I containing GTX1+4 and NEO; Mix-II including GTX2+3, dcGTX2+3, STX, dcSTX, B1 and C1+2. The dcNEO was used individually in working standard solutions. The matrix effect in the peroxide oxidation tested in this procedure is not foreseen in the Lawrence method. The oyster C18 cleaned extract is only used in the periodate reaction.

Limits of detection, linearity and recovery

The instrumental limits of detection (LOD) were experimentally determined using a signal:noise ratio of 3:1. The LODs ranged from 12 ng g⁻¹ for B1 and STX to 99 ng g⁻¹ for GTX1+4. These values, expressed in μ g STX equivalents kg⁻¹, were comparable to those quoted in the AOAC method. The linear range of PSTs varied from 67-80 times the respective LOQ (calculated using signal:noise ratio of 10:1) to 100-250 times for GTX2+3, dcGTX2+3, STX, dcSTX, B1 and C1+2. Recoveries of the analytical procedure were assessed through mussel tissues spiked in triplicate, with the addition of two standard mixtures at two levels of contamination. For most of the non-N-hydroxylated compounds and for GTX1+4 and NEO recoveries varied between 77 and 116%. The lower recovery obtained for C1+2 (58%) may be atributed to their thermal instability during spiking procedure. This explanation is supported by results obtained in storage stability tests (Indrasena and Gill 2000).

Results and discussion

Calibration curves in solvent and mussel matrix

Equations for the calibration curves for the calculation of PST concentrations, including the compounds quantified after peroxide and periodate oxidations, showed linear fits with good correlation coefficients for the linearity intervals in solvent and C18-cleaned mussel extract or fractions (Table 1). The mussel extract or fraction exhibited a suppression of the fluorescence signal in comparison to solvent for dcGTX2+3, GTX2+3 and GTX1+4, while an enhancement was obtained for C1+2, STX, dcSTX, B1, dcNEO and NEO. These results corroborate previous findings, indicating that the chromatographic signal associated with matrix effect varied among the compounds (Turner et al 2009). The results of the current study are not fully comparable to ones reported by Turner et al. (2009) since some toxins were quantified in different steps of the analytical procedure.

Figure 3 illustrates three examples of calibration curves in solvent and mussel extract. The GTX2+3 in which the slope in solvent doubled the one in mussel extract, indicated a divergence between the two lines as concentration increases. Consequently, the matrix effect becomes more effective as mussels contain high levels of these compounds. The two lines for C1+2 presented similar slopes and higher Y-intercept value for mussel extract than for solvent. The parallelism of the two lines indicates that matrix effect is similar within the linearity concentration interval. Similar slopes and Y-intercept values were found in solvent and mussel extract for B1, indicating a negligible matrix effect.

PSTs in mussels exposed to toxic algae blooms

Ten composite samples of mussels naturally exposed to blooms of *Gymnodinium catenatum* in Aveiro lagoon were analysed by the above mentioned procedure. Figure 4

illustrates the LC-FLD chromatograms of a selected sample. The peaks obtained after peroxide or periodate oxidation in C18-cleaned extract are shown. Sharp peaks were seen at the response time of working standard solutions used for their quantification. Naturally fluorescent co-extractives had no interference with toxin peaks. The peak areas of quantified compounds in the chromatograms were converted into concentrations using the calibration curves calculated for solvent and C18-cleaned mussel extracts. Figure 5 shows the median, the percentile 25% and 75%, minimum and maximum of each toxin concentrations found in the mussel samples after calibration curves prepared with solvent and mussel extract. Except for dcGTX2+3 no significant differences (p<0.05) were found for all the quantified compounds. C1+2 and B1 were the most abundant toxins registered in the mussel samples, their concentrations being substantially higher than levels of dcGTX2+3, dcSTX, GTX2+3, STX and dcNEO. The observed abundance of N-sulfocarbamoyl (B1, C1+2) in mussel extracts is in agreement with the *Gymnodinium catenatum* profile described for Portuguese waters (Negri et al. 2007). Mussel metabolic processes may have enhanced the levels of decarbamoyl compounds reported for the algae (e.g., dcGTX2+3 and dcSTX) (Artigas et al. 2007; Oshima 1995). Values of dcNEO may also be related to either its presence in Gymnodinium catenatum (Costa et al. 2009), or resulted from metabolic products of assimilated toxins in mussels.

The broad range found for C1+2 and B1 concentrations, and in a less extent for other minor toxins, may have resulted from the repeated blooms of *Gymnodinium catenatum* exhibiting different toxin profiles. Indeed, a study of toxin profiles of this dinoflagellate in the Gulf of California pointed to differences among strains in different blooms (Band-Schmidt et al. 2005).

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Impact of matrix effect on individual concentration and toxicity

The matrix effect was assessed by the differences of toxin concentrations (ΔC_i , ng g⁻¹) calculated for each compound *i* by the following expression:

$$\Delta C_i = C_{i-\text{solvent}} - C_{i-\text{matrix}} \tag{1}$$

where $C_{i-solvent}$ and $C_{i-matrix}$ are the concentrations of the compound *i* calculated by the calibration curves in solvent and mussel extract or fraction, respectively.

Using the Oshima toxicity equivalence factors (TEF_{*i*},) and conversion factor for units (CF_{*i*}, μ g STX equivalents ng⁻¹) (Quilliam 2007), the calculated Δ C_{*i*} were converted into differences of individual toxicities (Δ T_{*i*}, μ g STX equivalents kg⁻¹) by the expression:

$$\Delta \mathbf{T}_i = \Delta \mathbf{C}_i \, \mathbf{x} \, \mathrm{TEF}_i \, \mathbf{x} \, \mathrm{CF}_i \tag{2}$$

In the case of isomeric pairs (GTX1+4, GTX2+3, C1+2 and dcGTX2+3), the highest toxicity factor was used for each pair, and the toxicity factor of dcSTX was applied for dcNEO.

Figure 6 gives the median, the percentile 25% and 75%, minimum and maximum of ΔCi and ΔTi , for each quantified compound in the mussel samples. The elevated ΔCi obtained for C1+2 (median=421 ng g⁻¹) reflects the considerable difference of calibration equation parameters in solvent and matrix for the same chromatographic peak areas. The other dominant compound of the toxin profile is B1, although showing a small ΔCi (median=46 ng g⁻¹). The similarity between the two calibration curves resulted in a negligible matrix effect for B1. All the other compounds presented also small ΔCi (medians between 0.09 and 58 ng g⁻¹). By converting ΔCi into ΔTi , the differences between C1+2 and the other toxins are less pronounced. The ΔT_{C1+2} and ΔT_{deNEO} were not significantly (*p*<0.05) different. The high TEF_{deNEO} (0.51) in comparison to TEF_{C1+2} (0.10) compensates the differences between $\Delta C_{C1+2} \Delta C_{deNEO}$. In

the contaminated mussels used in this study the two compounds became thus the major contributors to the differences on total toxicity.

Impact on total toxicity

For each sample, the difference on the total toxicity (Δ T, µg STX equivalents kg⁻¹) was calculated by summing Δ T_i for all quantified toxins. The Δ T calculated for the ten mussel samples varied between +53 and +218 µg STX equivalents kg⁻¹. The positive values indicate that the toxicity estimation using solvent calibration curves exceeds the values taking into account the matrix. The use of calibration curves in solvent leads thus to an overestimation of the total toxicity in mussels. Figure 7 presents the Δ T values against the total toxicity estimated by the mussel calibration curves. The values increased with the toxicity of the mussel sample. Considering the toxicity interval between 200 and 800 µg STX equivalents kg⁻¹ (regulatory level for PSTs), the obtained Δ T varied between 88 to 223 µg STX equivalents kg⁻¹, which corresponds to 44% and 28% of the toxicity level, respectively. These results point to a considerable overestimation of toxicity in mussels exposed to *Gymnodinium catenatum* that contain high levels of C1, C2 and B1. Further studies should be performed in order to assess whether matrix effect has an additional impact on toxicity calculation for a more diverse toxin profile.

Acknowledgments

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Table 1. Equations of the calibration <u>curves in solvent and C18-cleaned</u>

Deleted: lines

mussel extract or fractions for PSTs; toxin concentration ranges and

correlation coefficients.

Toxin	Concentration range (ng g ⁻¹)	Matrix	Equation	r
dcGTX2+3	101-1023	Solvent	Y=0.25x-7.6	0.996
		Mussel extract	Y=0.13x+19	0.985
C1+2	274-2814	Solvent	Y=0.16x-23	0.995
		Mussel extract	Y=0.21x+17	0.988
dcSTX	40-406	Solvent	Y=1.1x-18	0.999
		Mussel extract	Y=1.1x+0.058	0.997
GTX2+3	120-1234	Solvent	Y=0.49x-14	0.997
		Mussel extract	Y=0.24x+14	0.993
B1	97-980	Solvent	Y=0.25x-9.1	0.999
		Mussel extract	Y=0.26x-1.2	0.999
STX	48-479	Solvent	Y=0.39x-9.7	0.997
		Mussel extract	Y=0.40x+0.68	0.997
dcNEO	146-1199	Solvent	Y=0.12x-0.57	0.994
		Mussel extract	Y=0.15x+4.6	0.996
GTX1+4	312-1870	Solvent	Y=0.18x+1.2	0.995
		Mussel fraction	Y=0.16x+15	0.997
NEO	272-1925	Solvent	Y=0.04x+2.6	0.988
		Mussel fraction	Y=0.05x-3.6	0.995
	0			











Figure 5.







Figure 7.



oxicity (µg S1x σ.

Figure captions

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Figure 1. PSTs chemical structure and the Oshima toxicity equivalence factors (Quilliam, 2007) (nk = not known). STX = Saxitoxin, Neo = Neosaxitoxin, GTX = Gonyautoxins.

Figure 2. Flow diagram with the sequence of oxidation reactions (1 = peroxide oxidation of C18 extract; 2 = periodate oxidation of C18 extract; 3 = periodate oxidation of fractions 1 to 3).

Figure 3. Calibration plots of GTX2+3 (a), C1+2 (b) and B1 (c) concentrations against detector response for standards prepared in mussel extract after C18 cleanup (shaded boxes) and in solvent (open triangles), over the working calibration range Figure 4. Chromatograms obtained for a composite sample of mussels exposed to blooms of *Gymnodinium catenatum* in Aveiro lagoon. (a) quantification of dcGTX2+3, C1+2, dcSTX, GTX2+3, B1 and STX was achieved after peroxide oxidation of the C18-cleaned extract; (b) dcNEO was quantified after periodate oxidation of the same extract.

Figure 5. Median, percentile 25% and 75%, minimum and maximum of dcGTX2+3, C1+2, dcSTX, GTX2+3, B1 and STX concentrations (ng g⁻¹) in mussel extract and solvent; n=10.

Figure 6. Median, percentile 25% and 75%, minimum and maximum of the differences between toxin concentrations (ΔC_i , ng g⁻¹) (a) and between individual toxicities (ΔT_i , μg STX equivalents kg⁻¹) (b); ΔC_i was calculated by the calibration curves in solvent and mussel extract; ΔT_i was calculated by ΔC_i and the corresponding toxicity factors and conversion unit factors; n=10.

Figure 7. Differences between total toxicities (μg STX equivalents kg⁻¹), as sum of individual toxicities based on concentrations calculated by the calibration curves in solvent and mussel extract, against total toxicity estimated by the mussel calibration lines; n=10.