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ZipChip

A novel integrated strategy for the detection and quantification of the neurotoxin β-N-methylamino-l-alanine in environmental samples

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ABSTRACT: We describe a set of new tools for the detection and quantification of β-N-methylamino-L-alanine (BMAA) which includes a novel stable isotope-labeled BMAA standard ($^{13}C3,^{15}N_2$) and a chip-based capillary electrophoresis mass spectrometry platform for separation and detection. Baseline resolution of BMAA from its potentially confounding structural isomers *N*-2-aminoethylglycine (AEG) and 2,4-diaminobutyric acid (2,4- DAB) is achieved using the chip-based CE-MS system in less than 1 min. Detection and linearity of response are demonstrated across > 3.5 orders of dynamic range using parallel reaction monitoring (PRM). The lower limit of detection and quantification were calculated for BMAA detection at 40 nM (4.8 ng/mL) and 400 nM (48 ng/mL), respectively. Finally, the strategy was applied to detect BMAA in seafood samples purchased at a local market in Raleigh, NC where their harvest location was known. BMAA was detected in a sea scallop sample. Because the BMAA/stable isotope-labeled $^{13}C3,^{15}N_2$-BMAA (SIL-BMAA) ratio in the scallop sample was below the limit of quantification, a semiquantitative analysis of BMAA content was carried out, and BMAA content was estimated to be approximately 820 ng BMAA/1 g of wet scallop tissue. Identification was verified by high mass measurement accuracy of precursor (< 5 ppm) and product ions (< 10 ppm), comigration with SIL-BMAA spike-in standard, and conservation of ion abundance ratios for product ions between BMAA and SIL-BMAA. Interestingly, BMAA was not identified in the free protein fraction but only detected after protein hydrolysis which suggests that BMAA is tightly bound by and/or incorporated into proteins.