## **Supporting Information**

## Jonasson et al. 10.1073/pnas.0914417107

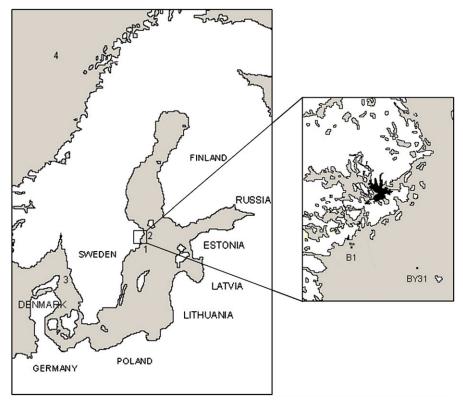


Fig. S1. The semi-enclosed brackish water Baltic Sea provides services but also is affected by activities of the nine surrounding countries. The insert shows the sites in mid-Sweden used for the collection of cyanobacteria: B1, a coastal site close to the Askö Marine Biology Research Station, and BY31, an open-water site in the Baltic Sea.

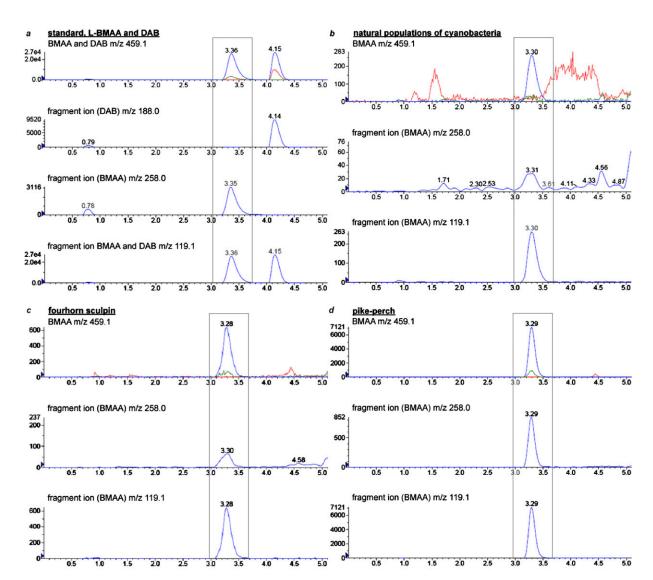


Fig. S2. (Continued)

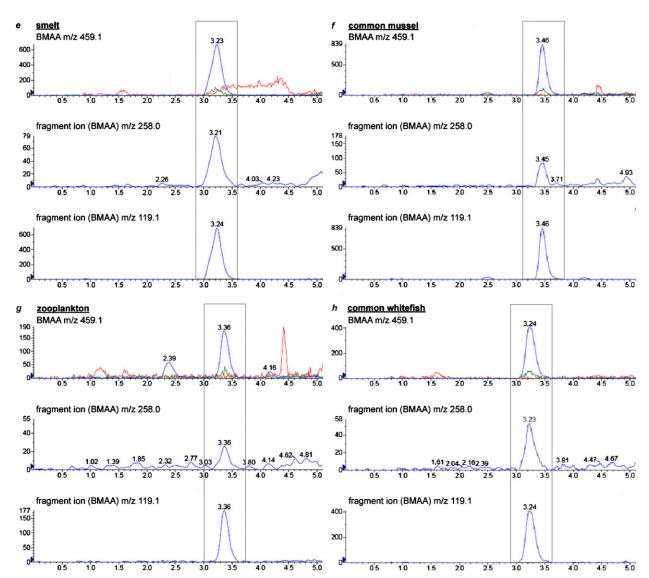


Fig. S2. Selected mass spectra from the species examined: a BMAA/DAB standard (A), a sample of natural populations of cyanobacteria (*N. spumigena* and *Aphanizomenon* spp.) (*B*), fourhorn sculpin (*C*), pike-perch (*D*), smelt (*E*), common mussel (*F*), zooplankton (*G*), and common whitefish (*H*). (*A*) Injections of BMAA and DAB standards. (*Top*) The peaks *m/z* 119.1, *m/z* 188.0, and *m/z* 258.0. The separation of BMAA [retention time (RT), 3.36 min] and DAB (RT 4.15 min) in time is clearly visible with regard to the *m/z* 119.1 peak. (*Middle Upper*) The diagnostic fragment belonging to DAB (*m/z* 188.0), which is clearly absent under the RT (3.36 min) of BMAA. (*Middle Lower*) The diagnostic fragment of BMAA (*m/z* 258.0), which is absent under the RT (4.15 min) of DAB. (*Bottom*) The *m/z* 119.1 fragment, which is a product of both double-derivatized BMAA (RT 3.36 min) and double-derivatized DAB (RT 4.15 min). (*B–H*) The fragment *m/z* 258.0 (*Middle*) is present at the RT corresponding to the fragment *m/z* 119.1 (*Bottom*). This ensures that BMAA is present in the sample and is not confused with DAB, because they are separated in both time and space. More details on the method and fragmentation pattern have been provided by Spacil et al. (1).

<sup>1.</sup> Spacil Z, et al. (2010) Analytical protocol for identification of BMAA and DAB in biological samples. Analyst (Lond) 135:127–132.

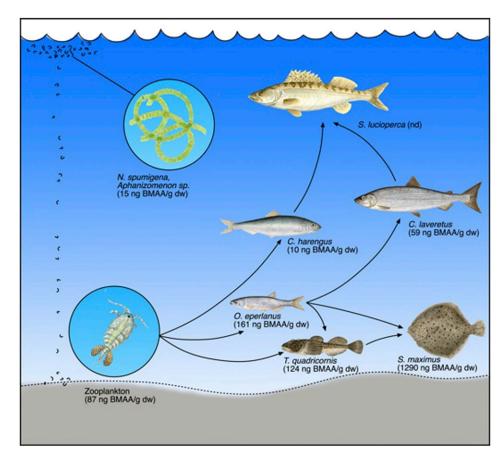


Fig. S3. Schematic sketch illustrating the food web interactions among species used in the Baltic Sea study. Numbers within parentheses indicate the highest BMAA level found in each species, expressed as μg BMAA/g dry weight. Of note, BMAA levels indicated for *T. quadricornis*, *S. maximus*, and *O. eperlanus* were found in brain tissue, whereas those indicated for *C. harengus* and *C. lavaretus* were found in muscle tissue. ND, not detectable.