**Table S1** : BLAST alignment results from LSU partial sequence.

| Strains | BLAST results | | Accession number |
|---|---|---|---|
| | Description | Percentage identity | |
| G6-7, IFR-ACA-15, B9-1, C11-4, F5-4, G2-1, C2-4, H8-4, IFR-ACA-17 | *A. pacificum* strain CCMP-1493 large subunit ribosomal RNA gene, partial sequence | 100% | MK566192.1 |

**Table S2:** STX analogues analysed in by HPLC-FLD with limits of detection (LOD) and quantification (LOQ) for each analogue (expressed as µmol $L^{-1}$).

| **STX and analogues** | **LOD (µmol $L^{-1}$)** | **LOQ (µmol $L^{-1}$)** |
|---|---|---|
| GTX4 | 0.030 | 0,090 |
| GTX1 | 0.035 | 0.105 |
| GTX3 | 0.010 | 0.030 |
| GTX2 | 0.015 | 0.045 |
| dcGTX3 | 0.003 | 0.009 |
| dcGTX2 | 0.012 | 0.036 |
| GTX5 | 0.040 | 0.120 |
| NeoSTX | 0.030 | 0.090 |
| dcSTX | 0.018 | 0.054 |
| STX | 0.020 | 0.060 |
| C1 | 0.033 | 0.099 |
| C2 | 0.018 | 0.054 |

**Table S3:** Primers used in this study.

| Gene | Primer name | Forward and reverse primers 5' -> 3' | Product size (pb) | Application | References |
|---|---|---|---|---|---|
| *sxtA4* | sxt007 | ATG CTC AAC ATG GGA GTC ATC C | 715 | Genomic amplification | Stüken et al., 2011 |
| | sxt008 | GGG TCC AGT AGA TGT TGA CGA TG | | | Stüken et al., 2011 |
| | sxt072-MinuPaci | GAC TTG CCC TCC ATA TGT GC | 184 | Quantitative PCR target | This publication |
| | sxt073 | GCC CGG CGT AGA TGA TGT TG | | | Stüken et al., 2015 |

**Table S4:** Sequence and accession numbers, including several clones of the strains RCC2645 (Genbank Accession No MW546902.1/MW546903.1/MW546904.1), IFR-ACA-15 (Genbank Accession No MW546905.1/MW546906.1) and B9-1 (Genbank Accession No MW546907.1/MW546908.1) used for molecular analyses.

| Species | Gene | Accession number |
|---|---|---|
| *Alexandrium fundyense* | *sxtA* domain A4 | KJ879208.1 |
| | | KJ879196.1 |
| *Alexandrium minutum* | *sxtA* domain A4 | JF343314.1 |
| | | JF343312.1 |
| | | KM438017.1 |
| | | KM438018.1 |
| | | JF343348.1 |
| | | JF343316.1 |
| | | MW546902.1 |
| | | MW546903.1 |
| | | MW546904.1 |
| *Alexandrium pacificum* | *sxtA* | JF343329.1 |
| | | JF343259.1 |
| | *sxtA* domain A4 | KM100455.1 |
| | | KM100453.1 |
| | | MW546905.1 |
| | | MW546906.1 |
| | | MW546907.1 |
| | | MW546908.1 |

**Table S5:** Protocol of sample preparation for genome size analysis (from Marie et al., 2000 with minor modifications)

| |
|---|
| For each strain, 20 µL Pluronic F68 (Sigma P1300) was added to 2 mL of exponentially-growing culture and centrifuged for 15 min at 3,000 g. The supernatant was discarded, and the cells were resuspended in 50 µL 0.2 µm-filtered seawater. Then 2 mL 80% ethanol was added and the samples were stored at -20°C. Prior to the analysis, the samples were centrifuged for 15 min at 3,000 g and resuspended in 500 µL of PBS (1X) supplemented with 5 µL of RNAse A (10%) and then incubated at 37°C for 30 min. Human blood cells (HBC, 2C=6.8 Gbp) were used as an internal standard. A blood input volume of 50 µL was injected into 1 mL of nuclei isolation buffer medium (30 mM MgCl2, 20 mM sodium citrate, 120 mM Sorbitol, 55 mM Hepes, 5 mM EDTA, pH 8.0) diluted twice with MilliQ water. Twenty µL of the blood cell suspension was added to each sample before introducing Propidium iodide at 30 µg/mL (final concentration). |