Application of a screening method for cyanobacterial toxins in natural samples

S. Hiller¹, B. Krock², A. Cembella², B. Luckas¹



¹ Friedrich Schiller University, Institute of Nutrition, D-07743 Jena, Germany

² Alfred Wegener Institute for Polar and Marine Research, Dpt. Ecological Chemistry, D-27570 Bremerhaven, Germany

bernd.luckas@uni-jena.de

MS parameters

MRM mode

NEO

5000 V

550 °C

50 L h

701 h

25 L h

30 eV

40 eV

MS parameters

Precursor Ion mode

[M+H]*

350-450 am

5200 V

550 °C

501 h⁻¹

70 L h-1

25 L h⁻¹

50 eV

80 eV

high level

high leve

[M+H]*/[M+H - H2O]



Introduction

Cyanobacterial toxins as microcystins (MCs), nodularins (NODs), Paralytic Shellfish Poisoning (PSP) toxins, anatoxins (ANAs), and cylindrospermopsins (CYNs) with over 100 known varieties, occur worldwide associated with human and animal lethal poisoning.

In contrast to all analytical methods for toxin determination are based on LC/MS-MS measurements with Multiple Reaction Monitoring (MRM) the application of Precursor Ion mode allows the coverage of all these structural variants. Although in MRM mode enables a higher sensitivity, a lot of information regarding structural changes is missed. The new generation of Q-TRAPs combines the advantages of quadrupoles having a high selectivity with the high sensitivity of ion-trap systems

Here we published results, showing the suitability of Precursor Ion mode for detection of cyanobacterial toxins extracted from phytoplankton.

Table 1: Retention times, MRMs, precursor ions and LOD of cyanobacterial toxins

min)	mass transition	LOD								
	(m/z)	(pg)	Toxin	t _R (min)	Precursor ion (m/z)	LOD (pg)	Toxin	t _R (min)	Precursor ion (m/z)	LOD (pg)
.4	316 > 298	1.0	ANA	5.2	91.0	700	MC-RR	12.3	135.0	20
.4	257 > 239	9.0	CYN	5.4	194.0	9	MC-YR	14.9	135.0	15
.4	300 > 282	10.0	doCYN	5.5	194.0	no standa rd	MC-LR	15.5	135.0	15
.5	380 > 300	3.0					MC-LA	19.7	135.0	18
1.6	353 > 273	25.0					MC-LW	21.0	135.0	100
.6	396 > 316	12.0					MC-LF	22.0	135.0	100
.7	412 > 332	6.0	1.0	1.00	21. C.		NOD	14.6	135.0	6
	.4 .4 .5 .6 .7	4 316 > 298 4 257 > 239 4 300 > 282 5 380 > 300 6 353 > 273 6 396 > 316 7 412 > 332	$\begin{array}{cccccc} 4 & 316 > 298 & 1.0 \\ 4 & 257 > 239 & 9.0 \\ 4 & 300 > 282 & 10.0 \\ 5 & 380 > 300 & 3.0 \\ .6 & 353 > 273 & 25.0 \\ .6 & 396 > 316 & 12.0 \\ .7 & 412 > 332 & 6.0 \end{array}$	4 316 > 298 1.0 ANA 4 267 > 239 9.0 CYN 4 300 > 282 10.0 doCYN 5 380 > 300 3.0 doCYN .6 353 > 273 25.0 .6 .6 395 > 316 12.0 .7 .7 412 > 332 6.0 .0	4 316 > 298 1.0 ANA 5.2 4 267 > 239 9.0 CYN 5.4 4 300 > 282 10.0 doCYN 5.5 5 380 > 300 3.0 doCYN 5.5 6 363 > 273 25.0	4 316 > 298 1.0 ANA 5.2 91.0 4 267 > 239 9.0 CYN 5.4 194.0 4 300 > 282 10.0 GCYN 5.4 194.0 5 380 > 300 3.0 doCYN 5.5 194.0 6 363 > 273 25.0 6 369 > 316 12.0 .7 412 > 332 6.0 5 5 194.0	4 316 > 298 1.0 ANA 5.2 91.0 700 4 267 > 239 9.0 CYN 5.4 194.0 9 4 300 > 282 10.0 no no no namada 5 380 > 300 3.0 .5 194.0 grad nd .6 363 > 273 25.0 .6 369 > 316 12.0 rd .7 412 > 332 6.0 5 5 194.0 104.0 <td< td=""><td>4 316 > 298 1.0 ANA 5.2 91.0 700 MC-RR 4 267 > 239 9.0 CYN 5.4 194.0 9 MC-YR 4 300 > 282 10.0 ocryn 5.5 194.0 9 MC-LR 5 380 > 300 3.0 ocryn 5.5 194.0 rd MC-LR 6 363 > 273 25.0 . MC-LW MC-LW .6 396 > 316 12.0 MC-LW MC-LW .7 412 > 332 6.0 NOD NOD</td><td>4 316 > 298 1.0 ANA 5.2 91.0 700 MC-RR 12.3 4 257 > 239 9.0 CYN 5.4 194.0 9 MC-YR 14.9 4 300 > 282 10.0 ocYN 5.5 194.0 9 MC-LR 15.5 5 380 > 300 3.0 ocYN 5.5 194.0 rd MC-LA 19.7 6 363 > 273 25.0 . MC-LW 21.0 MC-LW 21.0 .6 396 > 316 12.0 MC-LE 20.0 MC-LE 20.0 .7 412 > 332 6.0 NOD 14.6 NOD 14.6</td><td>4 316 > 298 1.0 ANA 5.2 91.0 700 MC-RR 12.3 135.0 4 267 > 239 9.0 CYN 5.4 194.0 9 MC-YR 14.9 135.0 4 300 > 282 10.0 5.5 194.0 9 MC-LR 15.5 135.0 5 380 > 300 3.0 doCYN 5.5 194.0 9 MC-LR 15.5 135.0 6. 353 > 273 25.0 6 MC-LK 19.7 135.0 7. 412 > 332 6.0 MC-LK 135.0 MC-LK 12.5</td></td<>	4 316 > 298 1.0 ANA 5.2 91.0 700 MC-RR 4 267 > 239 9.0 CYN 5.4 194.0 9 MC-YR 4 300 > 282 10.0 ocryn 5.5 194.0 9 MC-LR 5 380 > 300 3.0 ocryn 5.5 194.0 rd MC-LR 6 363 > 273 25.0 . MC-LW MC-LW .6 396 > 316 12.0 MC-LW MC-LW .7 412 > 332 6.0 NOD NOD	4 316 > 298 1.0 ANA 5.2 91.0 700 MC-RR 12.3 4 257 > 239 9.0 CYN 5.4 194.0 9 MC-YR 14.9 4 300 > 282 10.0 ocYN 5.5 194.0 9 MC-LR 15.5 5 380 > 300 3.0 ocYN 5.5 194.0 rd MC-LA 19.7 6 363 > 273 25.0 . MC-LW 21.0 MC-LW 21.0 .6 396 > 316 12.0 MC-LE 20.0 MC-LE 20.0 .7 412 > 332 6.0 NOD 14.6 NOD 14.6	4 316 > 298 1.0 ANA 5.2 91.0 700 MC-RR 12.3 135.0 4 267 > 239 9.0 CYN 5.4 194.0 9 MC-YR 14.9 135.0 4 300 > 282 10.0 5.5 194.0 9 MC-LR 15.5 135.0 5 380 > 300 3.0 doCYN 5.5 194.0 9 MC-LR 15.5 135.0 6. 353 > 273 25.0 6 MC-LK 19.7 135.0 7. 412 > 332 6.0 MC-LK 135.0 MC-LK 12.5

t_e Retention time; LOD: S/N = 3



Fig 1: MRM chromatogram of STX and NEO at te 1.43 min from Aphanizomenon flos-aquae extract



Precursor Ion spectrum of total run (a); of time period 2 (b) containing CYN at te 5.40 min and Fig 2: doCYN at t_R 5.55 min; Precursor Ion chromatogram of doCYN (c) and CYN (d) from Lyngbya wollei extract

Material and Methods

Lyophilised phytoplankton samples of Aphanizomenon flos-aquae [Fig 1], Lyngbya wollei [Fig 2], Nodularia spumigena [Fig 3] and Microcystis aeruginosa [Fig 4] were extracted with a methanol - 0.1 M acetic acid (1:1) solution using ultrasonic bath and ultrasonic stick. An HPLC system equipped with Agilent 1100 series components was applied for the separation. LC/MS-MS experiments were performed using a 4000 Q Trap (ABI Sciex, Darmstadt, Germany) equipped with a turbo ion-spray source. The chromatographic separation was carried out with a Luna column (3 µm, 150 mm x 3.0 mm; Phenomenex, USA) using two eluents containing 50 mM formic acid and 2 mM ammonia formate in water (eluent A) or methanol / water (95/5, eluent B) and gradient elution.

Based on the retention times [Table 1], three time periods with different detection modes and parameters [Table 2-5] were generated for the different toxin classes. Only PSP toxins were detected in MRM mode, due to no known daughter ion usable in Precursor Ion mode. For ANAs, CYNs, MCs and NODs a fragment characteristic for each toxin group was utilized to analyse the compounds in Precursor Ion mode [Table 1].





Precursor Ion spectrum of total run (a); of time period 3 with experiment for MCs containing dmMC-Fig 4: LR at t_R 14.79 min and MC-YR at t_R 15.56 min (b); Precursor lon chromatogram of dmMC-LR (c) and MC-YR (d) from Microcystis aeruginosa extract

Conclusions

It could be shown, that a qualitative screening method using Precursor Ion mode is well suited for detection cyanobacterial toxin variants, which allows a very rapid screening of putatively toxic cyanobacterial samples of uncertain taxonomic composition and unknown toxin profile.