Supporting Information File

Microcystis, *Raphidiopsis raciborskii* and *Dolichospermum smithii*, toxin-producing and non-toxigenic cyanobacteria in Yezin Dam, Myanmar

Thida Swe[1,2,3], Christopher O. Miles[4], Leonardo Cerasino[5], Marit Mjelde[1], Synne Kleiven[3], Andreas Ballot[1,*]

[1] Norwegian Institute for Water Research, Gaustadalléen 21, N-0349 Oslo, Norway

[2] Forest Research Institute, 15013 Yezin, Myanmar

[3] Department of Natural Sciences and Environmental Health, University of South- Eastern Norway, Campus Bø, N-3833 Bø, Norway

[4] Biotoxin Metrology, National Research Council Canada, 1411 Oxford Street, Halifax, NS, B3H 3Z1, Canada

[5] Department of Sustainable Agro-ecosystem and Bioresources, Research and Innovation Centre, Fondazione Edmund Mach, Via E. Mach 1, 38010 San Michele all'Adige, Italy

* Corresponding author. Email-address: andreas.ballot@niva.no

Contents*

Figure S1	ML tree based on 16S rRNA gene of *Dolichospermum* spp	S2
Figure S2	ML tree based on 16S rRNA gene of *Raphidiopsis raciborskii*	S3
Figure S3	ML tree based on 16S rRNA gene of *Microcystis*	S4
Figure S4	Thiol subtraction LC–HRMS chromatograms	S5
Figure S5	LC–HRMS/MS of MC-LR (**10**) and [Mser^7]MC-LR (**6**) in AB2017/08	S6
Figure S6	LC–HRMS/MS of MC-LR (**10**) and [Asp^3]MC-LR (**8**) in AB2017/08	S7
Figure S7	LC–HRMS/MS of MC-LR (**10**) and MC-HilR (**12**) in AB2017/08	S8

*Table S1 is a full listing of the properties of microcystins identified in *M. aeruginosa* AB2017/08, and is available as a separate file.

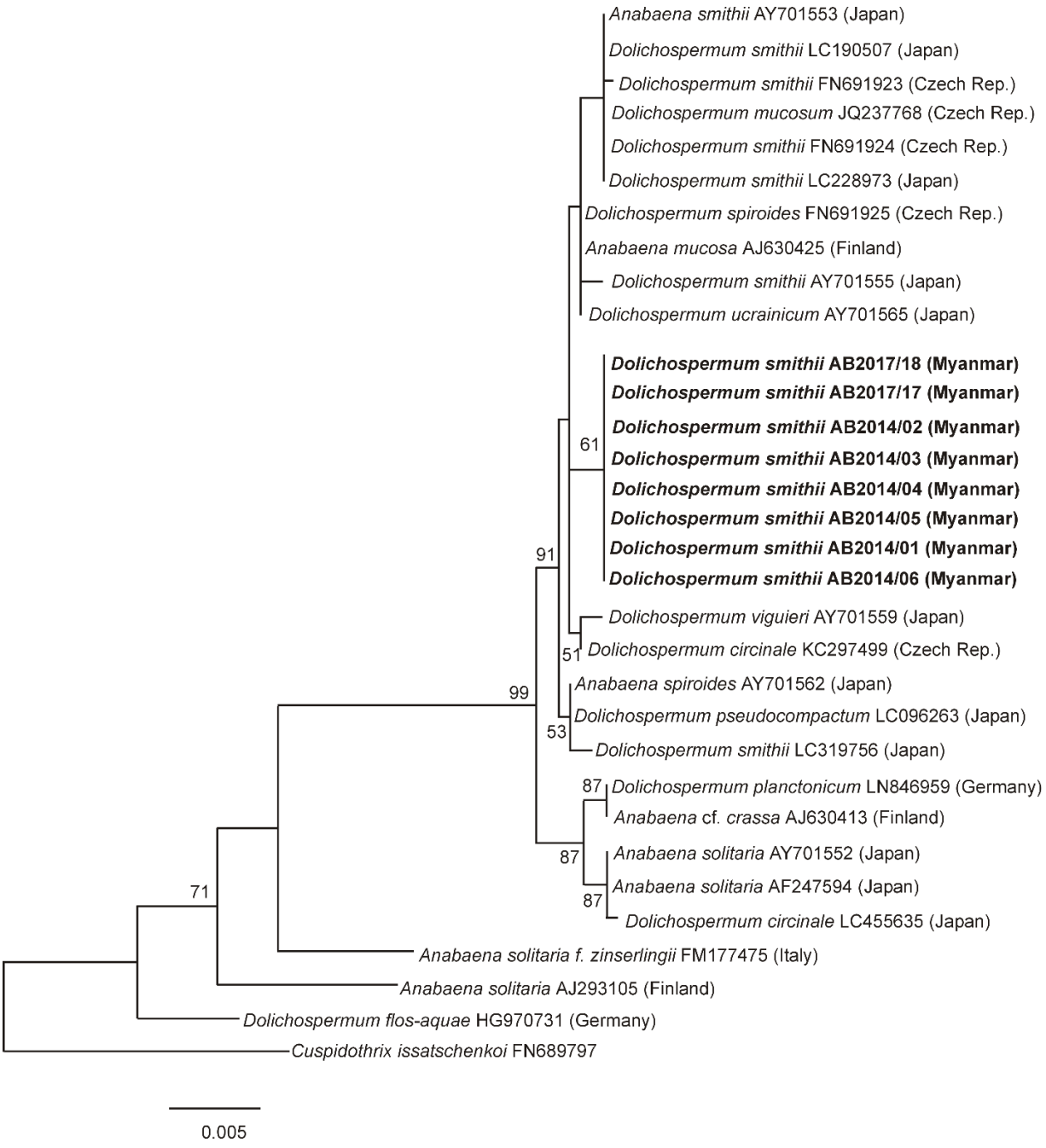

Fig. S1. Maximum likelihood tree determined on the basis of partial 16S rRNA gene sequences of 31 *Anabaena*/*Dolichospermum* strains. Outgroup = *C. issatschenkoi* (FN689797). Strains from Yezin Dam are in bold text. Bootstrap values above 50 are included. The scale bar represents 0.5% sequence difference.

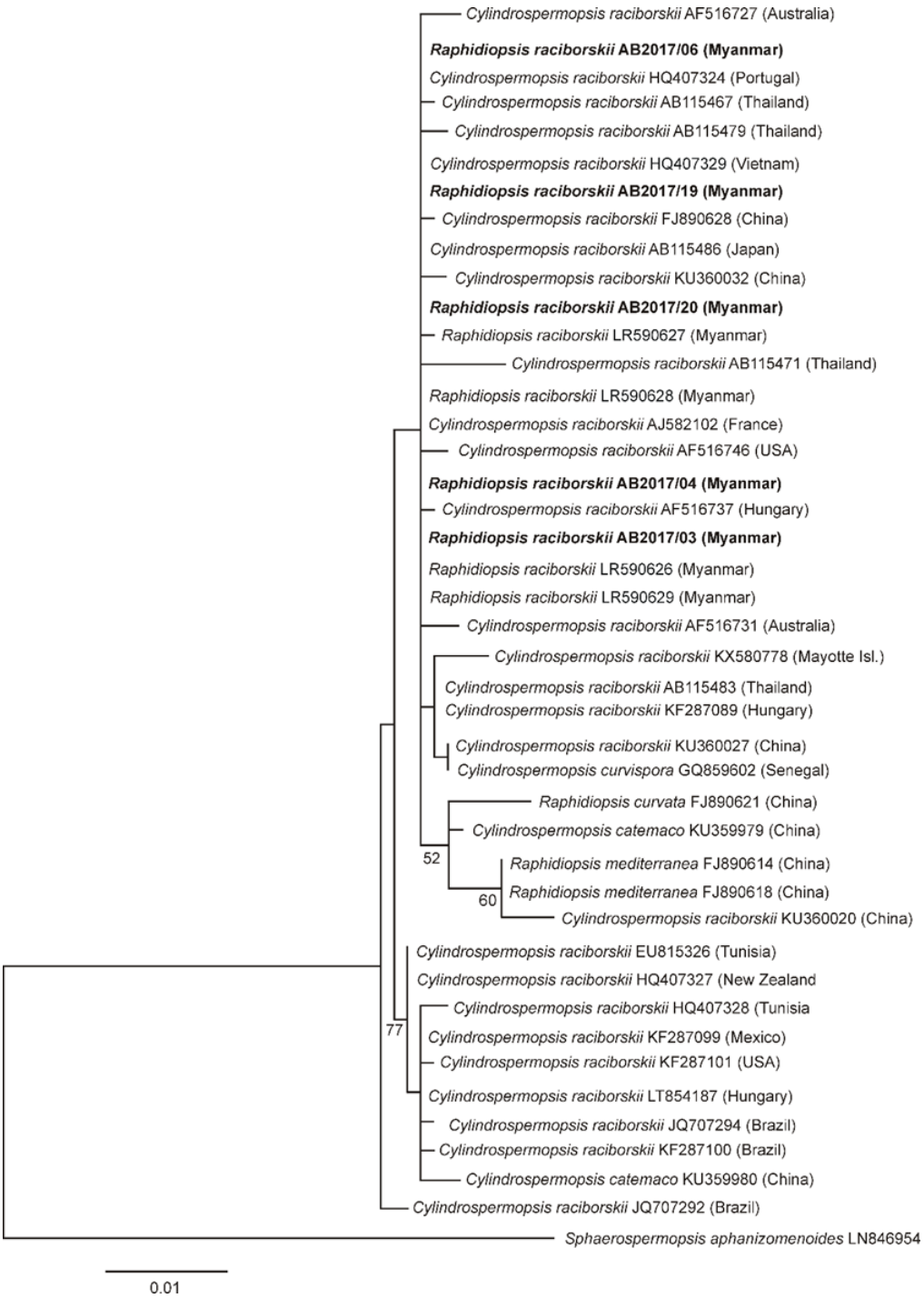

Fig. S2. Maximum likelihood tree determined based on partial 16S rRNA gene sequences of 42 *Raphidiopsis*/*Cylindrospermopsis* strains. Outgroup = *S. aphanizomenoides* (LN846954). Strains from Yezin Dam are in bold text. Bootstrap values above 50 are included. The scale bar represents 1% sequence difference.

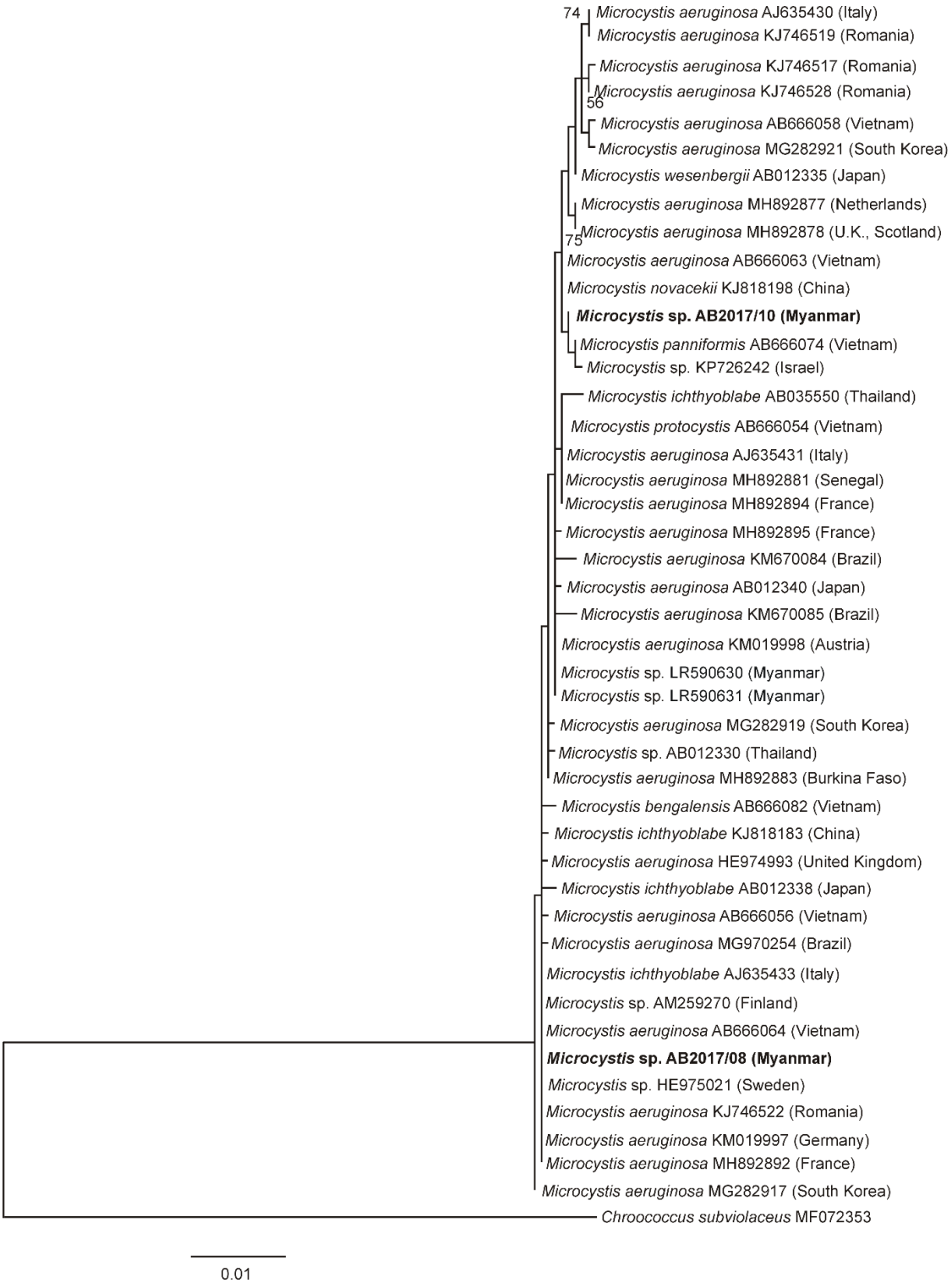

Fig. S3. Maximum likelihood tree determined on the basis of partial 16S rRNA gene sequences of 44 *Microcystis* strains. Outgroup = *C. subviolaceus* (LN846954). Strains from Yezin Dam are in bold text. Bootstrap values above 50 are included. The scale bar represents 1 % sequence difference.

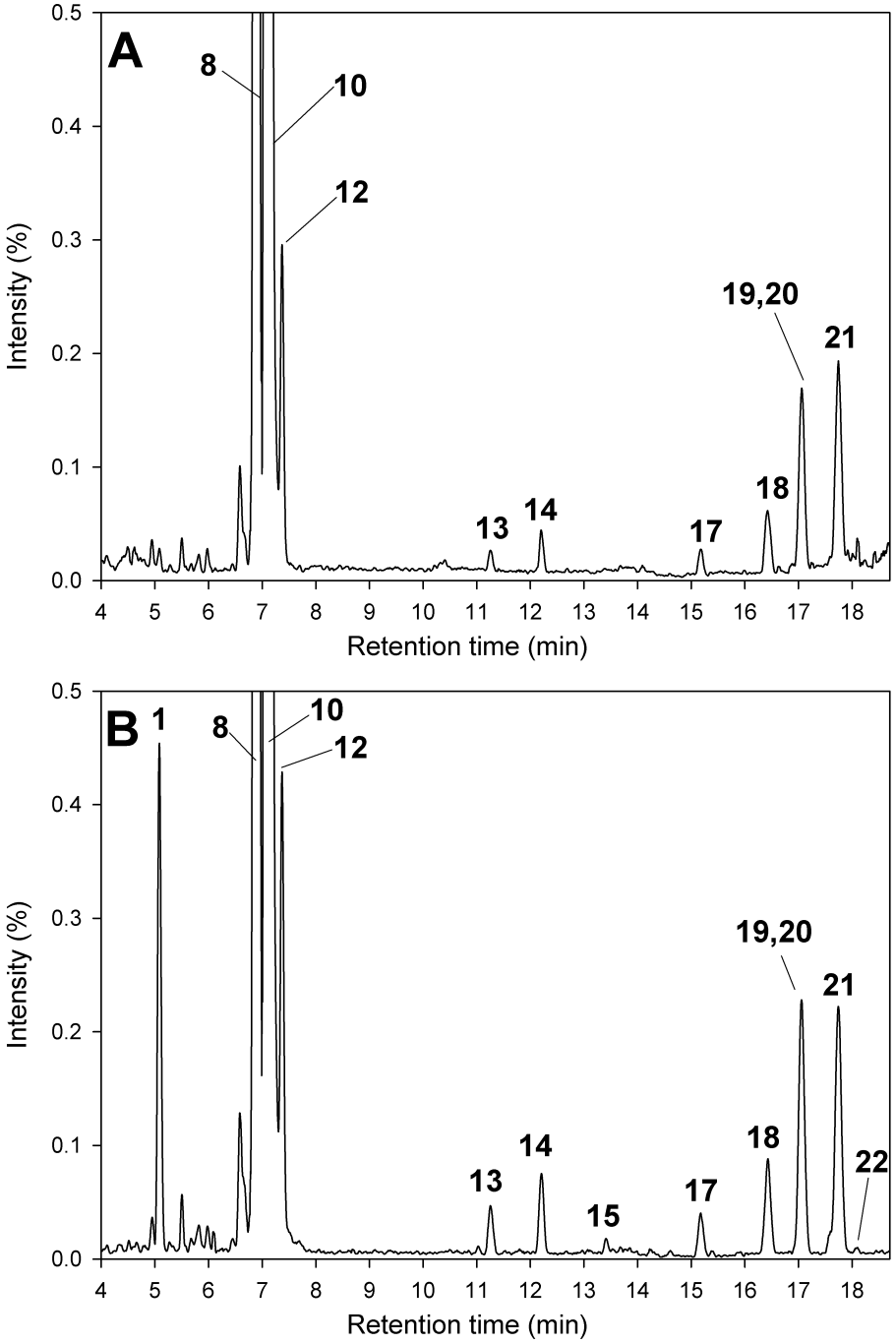

Figure S4. A, positive ionization mode, and; B, negative ionization mode subtraction chromatograms (thiol-derivatized chromatogram subtracted from the control chromatogram, *m*/*z* 900–1120) of extracts of *M. aeruginosa* AB2017/08 after derivatization with mercaptoethanol, with a 200-fold vertical expansion (MC-LR (**10**) at 100%) to show minor thiol-reactive components. Bold numbers correspond to compound (entry) numbers in Tables 4 and S1. Compounds that do not react with thiols (i.e. **2**–**7**) do not appear in such thiol-derivatization subtraction chromatograms.

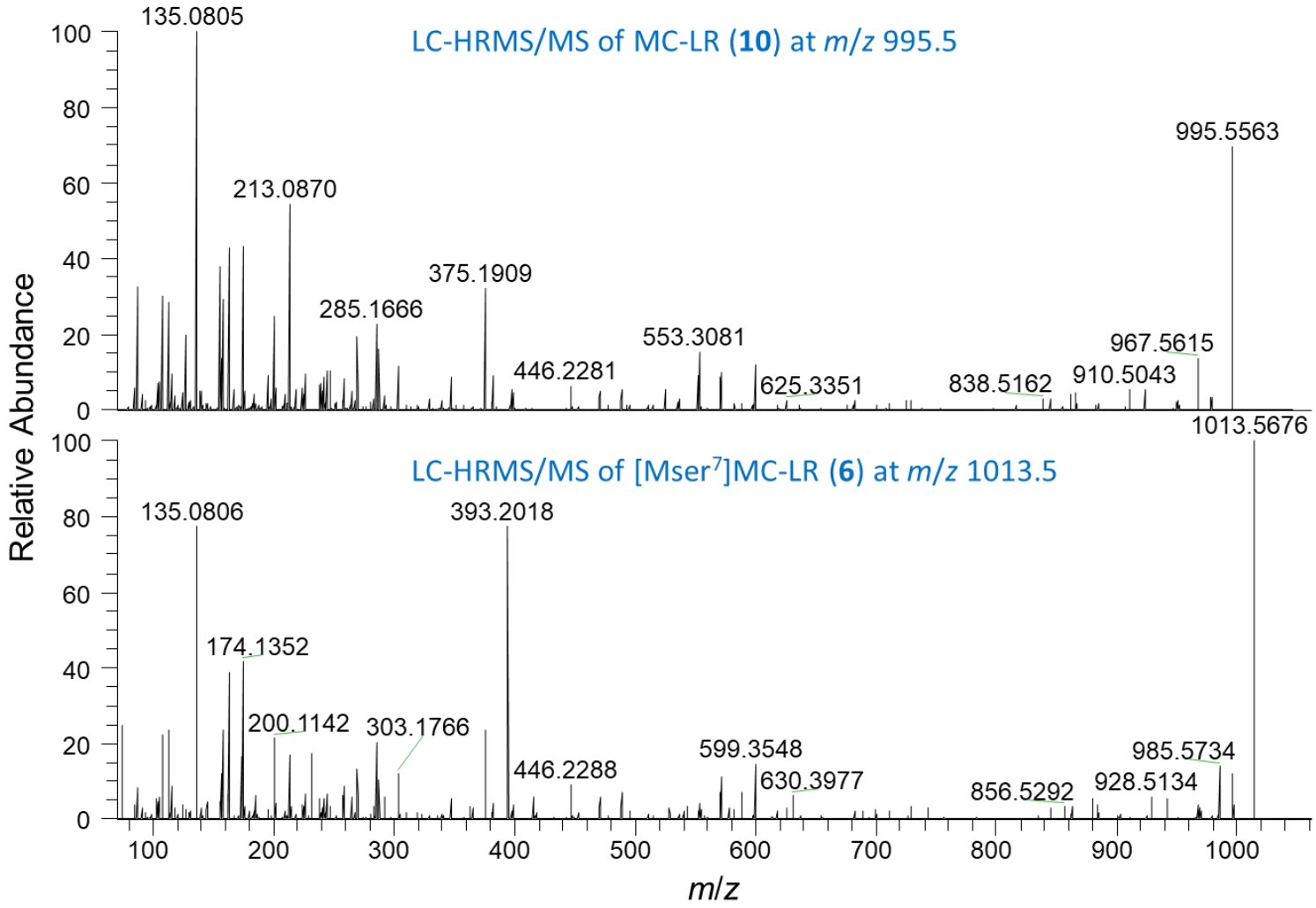

Figure S5. LC–HRMS/MS chromatograms of MC-LR (**10**) and [Mser^7]MC-LR (**6**) in *M. aeruginosa* AB2017/08. Note the presence of the product ion at *m*/*z* 393.2020 ($C_{20}H_{29}O_6N_2^+$) in the spectrum of **6**, which is characteristic of microcystins containing *N*-methylserine at position-7.

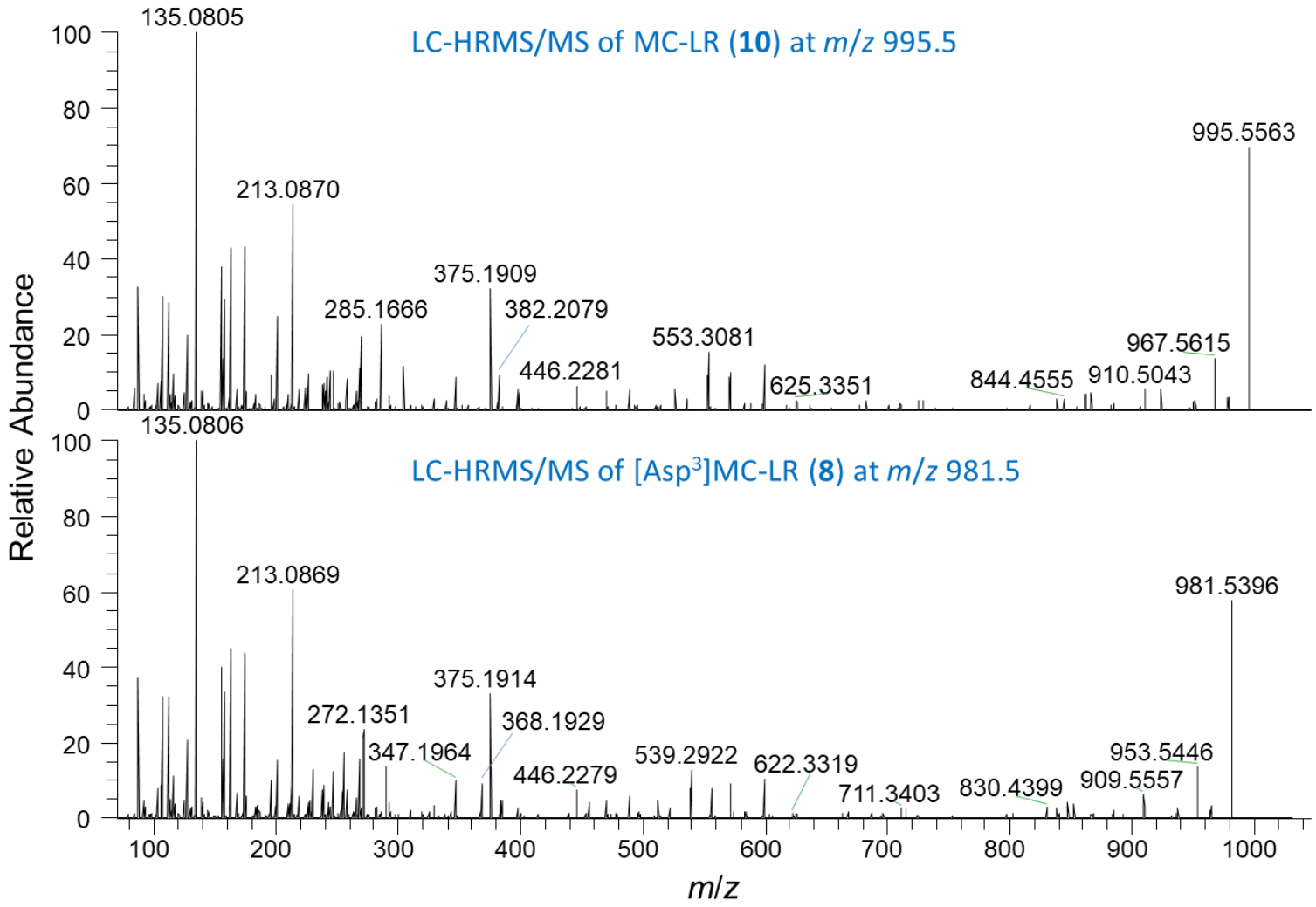

Figure S6. LC–HRMS/MS chromatograms of MC-LR (**10**) and [Asp^3]MC-LR (**8**) in *M. aeruginosa* AB2017/08. Note the presence of the product ion at *m/z* 368.1928 ($C_{16}H_{26}O_5N_5^+$) and 375.1914 ($C_{20}H_{27}O_5N_2^+$) in the spectrum of **8**, which is consistent with a microcystins containing aspartic acid at position-3.

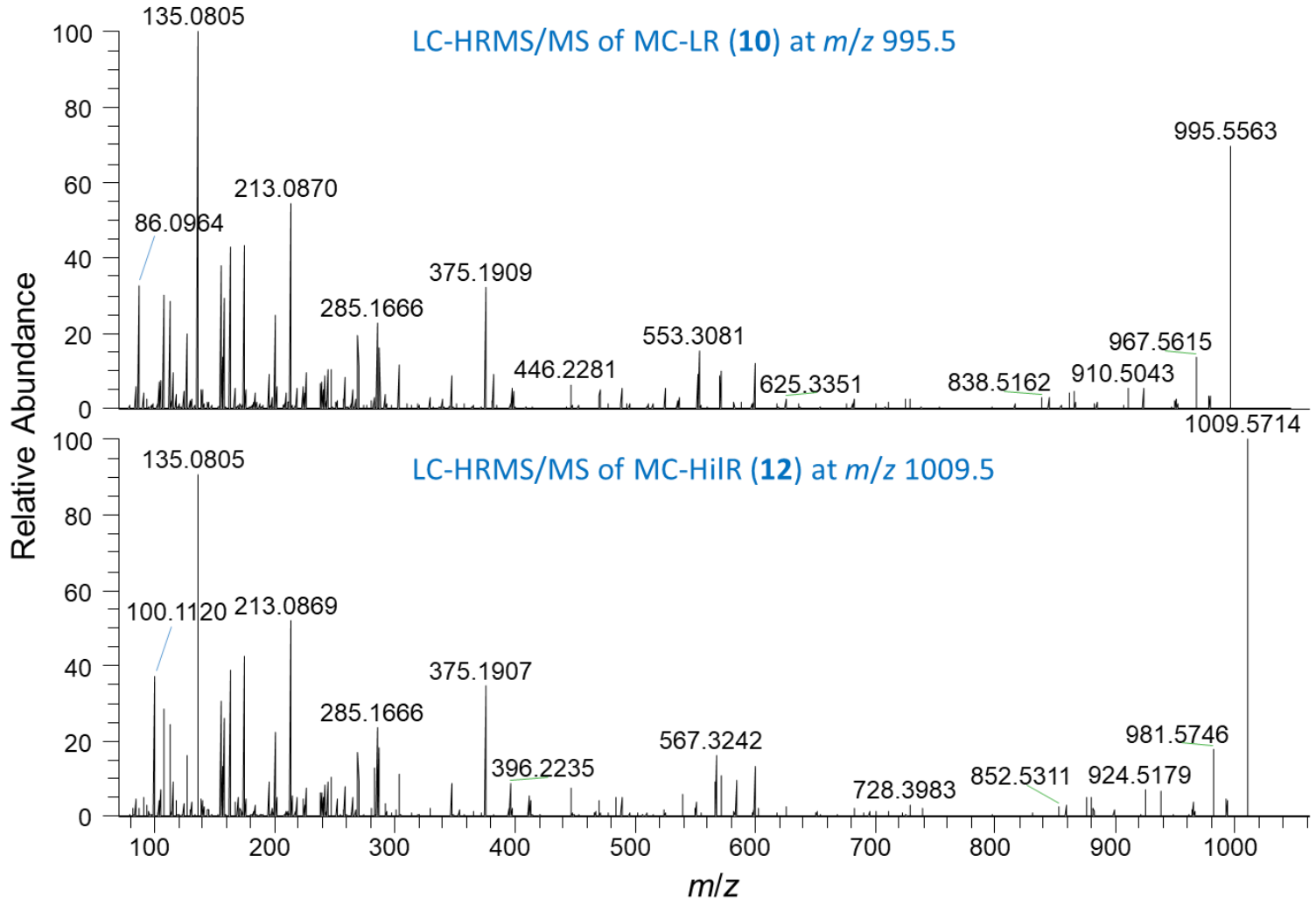

Figure S7. LC–HRMS/MS chromatograms of MC-LR (**10**) and MC-HilR (**12**) in *M. aeruginosa* AB2017/08. Note the presence of the product ion at *m/z* 100.1120 ($C_6H_{14}N^+$) in the spectrum of **12**, which is consistent with a microcystin containing homoisoleucine at position-2.