- 1 Night fish avoidance of *Microcystis* bloom revealed by simultaneous hydroacoustic
- 2 measurements of both organisms
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# 17 Abstract

- 18 Simultaneous observations of fish and cyanobacteria were conducted in the shallow Sulejów
- 19 Reservoir (Poland) during the occurrence of *Microcystis* bloom. A Simrad EY60 split beam
- 20 echosounder with a 200 kHz transducer beaming horizontally was applied to assess fish and
- 21 cyanobacteria spatial distribution. Additionally, fish size distribution and species composition
- 22 were evaluated with gillnets, and cyanobacterial biomass was determined by using an online
- 23 phycocyanin fluorescence probe. Physico-chemical parameters and water samples for
- 24 biological analyses were collected at 14 fixed stations situated along the acoustic transects.
- 25 We found cyanobacteria represented by the genus *Microcystis*, with their toxigenic genotypes
- 26 in all analyzed samples. The hydroacoustic results provided direct evidence for fish night
- 27 avoidance of the bloom. The biomass of fish and cyanobacteria demonstrated opposing trends
- and their peak values spatially mismatched. The number of fish caught in gillnets within the
- 29 bloom area was about half that caught outside the bloom area. In spite of the presence of

intracellular microcystins (hepatotoxin) at all stations, no extracellular microcystins were
identified in water samples and in fish tissues.

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Key words: hydroacoustics; fish spatial distribution; microcystins; toxic bloom; eutrophic
 reservoir

#### 35 **1. Introduction**

Deterioration of water quality is a world-wide problem. In the past decades, increasing 36 eutrophication has led to frequent outbreaks of cyanobacterial blooms in many lakes around 37 the world (Anderson et al., 2002; Briand et al., 2003; Chorus, 2005; Gkelis et al., 2006; 38 39 Kobus et al., 2013; Meriluoto et al., 2017; Tarczyńska et al., 2001). In addition, recent climate 40 change observations and scenarios suggest that the probability of the occurrence of cyanobacterial blooms will be even higher in the near future (Jöhnk et al., 2008; Paerl and 41 Huisman, 2008; Wagner and Adrian, 2009). Cyanobacterial dominance in water systems can 42 have serious economic and societal consequences, as it limits the range and value of important 43 44 ecosystem services of inland waters, including recreational use, aquaculture and drinking water usage (Carmichael, 1992; Huisman et al., 2005; Ibelings et al., 2014; Paerl and 45 Huisman, 2009; Paerl et al., 2001). Microcystis, one of the major components of 46 cyanobacterial blooms, produces metabolites such as microcystins (MCs). These can be toxic 47 to many aquatic organisms, including zooplankton and fish (Babica et al., 2007; Hansson et 48 al., 2007; Sotton et al., 2014, 2012a, 2012b; Sun et al., 2012, 2011; Tellenbach et al., 2016; 49 Trinchet et al., 2013). MCs are mainly retained within producer-cells during cyanobacterial 50 bloom development and might be released into water after lysis of cyanobacterial cells during 51 bloom collapse. The released toxins can then affect a wide range of aquatic organisms and 52 have deleterious effects on them, including accumulation in animal tissues (Papadimitriou et 53 al., 2009; Sierosławska et al., 2012; Sotton et al., 2012a, 2012b; Xie et al., 2007b, 2005). 54

Cyanobacteria have gas vesicles responsible for the adjustment of cell position in the water 55 56 column to get optimal position for photosynthesis and growth. Usually the shape of the gas vesicles is spherical, but *Microcystis aeruginosa* have a form of a hollow cylindrical tube with 57 a diameter of 60–70 nm and maximum length of ca. 600 nm (Dunton and Walsby, 2005). 58 Additionally, M. aeruginosa forms large colonies ranging from 100 µm to even 2 cm in size 59 60 (Kaczkowski et al., 2017). These properties make cyanobacteria effective sound scatterers. 61 Usually, signals from cyanobacteria recorded by an echosounder are treated as unwanted noise and removed during analysis of hydroacoustic survey data. We did, however, measure 62 fish and cyanobacteria spatial distribution simultaneously, which enabled us to observe them 63 64 with the same resolution in space and time. 65 In spite of the extensive literature concerning the negative effects of cyanobacteria on fish, 66 there are only a few studies related to natural ecosystems, which deal with the spatial distribution of fish during toxic cyanobacterial bloom events (Ernst, 2008; Godlewska et al., 67 68 2016; Kaczkowski et al., 2017; Potter et al., 1983; Sotton et al., 2011; Wojtalik et al., 2006). In all published studies so far, fish spatial distribution has been measured continuously with 69 an echosounder, while cyanobacteria have been measured at fixed locations along the 70 71 transects. The distributions of both fish and bloom are highly variable and change continuously in time and space (Izydorczyk et al., 2005), hence, non-point rapid measurement 72 methods are required to enable a deeper understanding of the complex relationships between 73 them. However, to our knowledge, no research presenting simultaneous and continuous 74 spatial measurement of cyanobacteria and fish occurrence with an echosounder has yet been 75 published. 76

The study is a part of the project "Do fish adapt to cyanobacterial blooms" financed by the
Polish National Science Centre (http://www.erce.unesco.lodz.pl/story/national-projects), and
this fraction aims at an assessment of fish spatial distribution in the Sulejów Reservoir in

relation to cyanobacterial bloom and its toxicity. We hypothesize that fish avoid those areas
covered by cyanobacterial blooms, and in this way decrease their exposure to toxic MCs, and
avoid or substantially limit their negative impact.

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## 2. Materials and methods

84 2.1. Study area

Measurements were performed in the Sulejów Reservoir (51°22'-51° 28' N, 19°51'-20°01' E), 85 central Poland, on two consecutive nights (September 2 and 3, 2015) during the occurrence of 86 87 a cyanobacterial bloom. The Sulejów Reservoir is a typical lowland shallow reservoir, with an area of approximately 2,700 ha and an average depth of 3.3 m, in which cyanobacterial 88 89 blooms are observed regularly at the end of the vegetation season (Izydorczyk et al., 2008a, 90 2008b; Tarczyńska et al., 2001). The dominant species of bloom-forming cyanobacteria is usually *M. aeruginosa*, which produces the microcystins MC-LR, MC-YR and MC-RR 91 (Gagała et al., 2013; Jurczak et al., 2004; Kaczkowski et al., 2017; Mankiewicz-Boczek, 92 2006). The dominant fish species of the reservoir assemblage include roach (*Rutilus rutilus*), 93 bream (Abramis brama), ruffe (Gymnocephalus cernua), white bream (Blicca bjoerkna), 94 perch (Perca fluviatilis), pikeperch (Sander lucioperca) and pike (Esox lucius). The average 95 sizes of the most common cyprinids are 20-30 cm total length, but larger specimens of bream 96 and piscivorous fish, up to more than 50 cm, are quite common (Frankiewicz and 97 98 Świerzowski, 2004; Kaczkowski et al., 2017).

99 2.2 Hydroacoustic measurements

100 Hydroacoustic measurements were performed from a boat sailing at a constant speed of

approximately 1.5 m s<sup>-1</sup> along 10 pre-determined parallel transects (Tr1–Tr10, Fig. 1). The

transects were separated by a distance of approximately 500 m. Data were collected on

103 September 2 and 3, 2015, starting one hour after sunset, when fish are dispersed in the open

water, and were completed at least one hour before sunrise. A Simrad EY60, 200 kHz split 104 beam echosounder, equipped with an ES200-7x7 (opening at -3 dB) composite transducer 105 beaming horizontally was used to record the data. The transducer was mounted to the side of 106 the boat at a depth of 0.5 m, tilted down by  $3.5^{\circ}$  and panning  $90^{\circ}$  to the boat's along-ship axis. 107 The pulse duration was 0.128 ms, and the repetition rate was 10 pings per second. The 108 echosounder was calibrated beaming vertically in the deepest part of the lake at the beginning 109 110 of the study, following the standard calibration procedure (Foote et al., 1987). Data were stored on a computer and later processed by the Sonar5-Pro (S5) software (Balk and Lindem, 111 2014). 112

113 Fish and cyanobacteria were separated using the Cross-Filter Detector (CFD) module in S5, set up for target-noise separation. The CFD method and module were originally developed to 114 overcome tracking problems in noisy environments, where missing single echo detections 115 from fish and false detections from noise tend to fool ordinary trackers. The CFD uses filters 116 to obtain an adaptive threshold of the echogram. The regions found by the adaptive 117 thresholder are tested with respect to features such as echo-length and track-length to ensure 118 119 that only single fish tracks are detected. A classical single echo detector is applied to the detected tracks to obtain correct target strength, range and beam position. 120 When fish targets have been detected, these detections can either be removed from the 121 echogram as noise or kept while removing everything else. We could have set up the CFD to 122 directly do the fish tracking and cyanobacteria estimation on the original echograms, but in 123 order to verify the detection process we let the CFD produce a set of echogram-files with fish-124 tracks and another set of echogram-files with cyanobacteria and with the detected fish-tracks 125 removed. Studying these two different echogram-sets before carrying out the final processing 126

127 provided us with a good way of verifying that the CFD had separated fish and cyanobacteria

128 well.

129	The same CFD detector parameters were applied to produce the two echogram-file sets,
130	except for a growing operation applied for the production of the cyanobacteria echograms.
131	The growing operator has a similar function as the margin has for the bottom detection. It
132	reduces the risk the cyanobacteria data being infested by higher intensity fish echoes. For
133	detecting the fish echogram set, the CFD's adaptive thresholder was set up with foreground
134	filter [1, 3], background filter [55, 1], and offset=7dB. The notation [x, y] indicates the
135	number of samples in the range domain followed by the number of samples in the ping
136	domain. The CFD's evaluator was set up to remove targets smaller than 5 samples and longer
137	than 125 samples in the ping domain. No other features appeared to be needed for correct
138	detection. TS for individual echoes in detected fish tracks were found using the CFD's built in
139	classical single echo detector setup with Echo length=[0.7 1.3], Multiple peak
140	suppression=medium, Max gain comp=3 (one way), and Max Phase dev=0.8. Threshold for
141	the SED was set to -45 dB in order to match the applied -51dB echogram threshold with
142	respect to the split beams off-axis compensation (6 dB for 2-ways).
143	For detecting the cyanobacteria echogram-file set, the CFD was set up in the same way except
144	for an additional growing operator applied after the track length evaluator. The operator was
145	set to add 5 samples before and after the track detections in the ping domain and to add 3
146	samples above and below in the range domain. The regions covered by these grown detections
147	of fish were then removed from the echograms resulting in cyanobacteria echograms without
148	fish tracks.
149	The final analysis was then performed on the two echogram sets using the same positioned
150	analysis cells and the same threshold (-51dB). The applied threshold models where 40LogR

151 for the fish-echograms and 20logR for the cyanobacteria echograms.

152 The areal sound backscattering coefficient Sa  $(m^2ha^{-1})$  (MacLennan et al., 2002) was

153 considered as a proxy for fish and cyanobacterial biomass (Simmonds and MacLennan,

154 2005).

Maps of fish and cyanobacteria spatial distributions were based on an Elementary Sampling
Distance Unit (ESDU) of 100 m and were produced using the kriging interpolation method in
Surfer 8 software. The t-test for unequal sample sizes was used for comparison of the acoustic
measurements, with cyanobacterial biomass as the discriminating factor.

159 2.3 Fish gillnet catches

Fish sampling was performed with multi-mesh gillnets during the night on September 2, 160 161 2015. Gillnets were used only as an additional tool to obtain information on species composition and size distribution. The gillnet effort had to be limited to adopt our fishing 162 effort to the annual gillnet yield level used by the fishery manager at the reservoir, i.e. 500 kg 163 per year. One set of the gillnets was 77 m long and 3 m deep with 11 different mesh-sizes, 164 ranging from 11 mm to 80 mm knot to knot. Fishing gear was described in detail in 165 Kaczkowski et al. (2017). Based on information on historical cyanobacterial bloom 166 distributions in the Sulejów Reservoir and daytime visual screening, one set of nets was 167 located in the area of Tr2 (downstream part of the reservoir), and a second one was located in 168 the area of Tr9 (upstream part of the reservoir) (Fig. 1). Each gillnet was set perpendicular to 169 170 the shoreline and was exposed at the same time as the hydroacoustic survey, i.e. from 9 PM to 12 PM (sunrise was at 6:40 AM and sunset at 6:46 PM local time). There was a 45-minute 171 difference between the setting and collecting of the two gillnets, i.e. the gillnet that was set 172 173 first was also collected first to ensure equal fishing effort. After sampling, catch data were recorded, including the determination of the taxonomic classification of fish, and the total 174 length and weight for each specimen. None of the activities in this study involved endangered 175

or protected species. Sampling *via* gillnetting was performed in accordance with the Inland
Fishery Act with the permission of the Lodz Voivodeship Marshal (No. RŚI.7143.3.2015.PP).

178 2.4 Phycocyanin fluorescence

The measurements of phycocyanin fluorescence were synchronized in time with the 179 hydroacoustic measurements. They were recorded in situ applying a Turner 10-AU-005 180 fluorometer using the Phycocyanin Optical Kit (P/N: 10–305). The fluorometer was operated 181 in continuous flow mode, pumping the water from a depth of about 0.5 m, and letting it flow 182 through a 25 mm cell. During the flow, measurements were taken at 2 s intervals and recorded 183 by a data logger. To calibrate the measurements for the phycocyanin fluorescence and 184 185 cyanobacterial biomass, subsamples of surface water were collected from the pump during the 186 continuous fluorescence measurements (for details, see Godlewska et al., 2016). Based on all records from 2 September, a regression was produced between cyanobacterial biomass 187 assessed by fluorometer (in mgL<sup>-1</sup>) and cyanobacterial biomass assessed by an echosounder 188 (in  $m^2 ha^{-1}$ ). The relationship was used to express hydroacoustic data in the same units as 189 those from the fluorometer i.e.  $mgL^{-1}$ . 190

191 The cyanobacteria biomass derived from the fluorescence measurements and acoustic survey192 was compared with the t-test analysis.

193

194 2.5 Physico-chemical parameters of water

On September 3, 2015 physico-chemical parameters at 14 stations situated along the acoustic transects were measured simultaneously with the hydroacoustic survey, i.e. during night time (Table 2), including temperature and oxygen profiles. The temperature profile was applied as input to the S5 ray tracer to verify how the acoustic beam behaved and determine if it covered the whole water column.

At the same time, integrated water samples were collected using a 5-liter sampler from each meter of the entire water column. These samples were used for biological analyses: microscopic identification of cyanobacteria, chlorophyll *a* and cyanobacterial chlorophyll *a* concentration, the number of 16S rRNA and the *mcy*A gene copies, and microcystins concentrations.

205 2.6 Genetic assessment of *Microcystis* 

206 DNA assays were prepared according to Mankiewicz-Boczek et al. (2006). Always 100 mL of

207 water was used for filtering. Next, filter with cyanobacterial material (0.45 μm, Millipore,

USA) were put into lysis buffer (40 mM EDTA, 400 mMNaCl, 0.75 M sucrose, and 50 mM

209 TRIS-HCl, pH 8.3) and kept at -20°C until further analysis. Genetic material was extracted

from the filter according to Giovannoni et al. (1990) with some modifications: for the

211 centrifugation, a speed of  $13,000 \times g$  was used; for the enzymatic lysis step, a final

concentration of proteinase K of 275  $\mu$ g mL<sup>-1</sup> was used; and during the phenol/chloroform

step, a volume of chloroform/isoamyl alcohol (24:1) equal to the volume of supernatant was

214 applied.

Extracted DNA was used as the template for quantitative (qRT-PCR, quantitative real-time

PCR) determination of: 16S rRNA (250 bp) gene fragment specific for the genus *Microcystis* 

and mcyA (395 bp) gene fragment specific for toxigenic Microcystis genotypes. The analysis

of qRT-PCR was made by using Maxima<sup>™</sup> SYBR Green/ROX qPCR Master Mix (MBI

219 Fermentas) and a real-time PCR system (7900HT, Applied Biosystems).

220 The qRT-PCR analyses for 16S rRNA and *mcyA* were prepared according to Gagała et al.

221 (2010). In order to prepare the calibration standards for 16S rRNA/mcyA, the genomic DNA

of *M. aeruginosa* strain PCC7820 was used as a template for PCR amplification of reference

sequences.

224 2.7 Microcystins in cyanobacteria, water and fish tissue

Water samples for determination of microcystin concentrations were collected from 14 225 stations in a volume of 1 L and were filtered immediately after sampling with GF/C 226 Whatmann filters (0.45 µm) for separation of cyanobacteria from water. Extracellular 227 228 microcystins were extracted by solid phase extraction according to the method described by Kaczkowski et al., (2017). Filters with cyanobacterial wet biomass were sonicated (sonicator 229 model XL 2020, Misonix Inc. USA) in 75% of aqueous methanol for extraction of 230 231 microcystins into solvent. In turn, biological material (organs isolated separately from A. brama and R. rutilus) collected 232 233 from the Sulejów Reservoir was frozen and then lyophilized using an Eppendorf lyophilizer. 234 A total of 1–2 g of lyophilized material (livers and kidneys) was extracted according to a

modified method described by Xie and Park (2007a), using 75% aqueous methanol and a
sonication process for extraction MCs from tissue. Crude extracts were filtered using GHP
Acrodisc minispike filters and these were then analyzed using the HPLC method with diode
array detection at 238 nm according to Jurczak et al. (2005).

## **3. Results**

240 3.1 Hydroacoustic survey

The area occupied by cyanobacterial bloom was limited in space and had a clear boundary between bloom-occupied and bloom-free areas. Hydroacoustic transects passed several times through the border of the cyanobacterial bloom. An example of a strong bloom edge is presented in Fig. 2. The echogram shows, in a spectacular way, great numbers of fish crowded just at the bloom edge, while very few fish were present within the bloom. Detailed investigation of transects passing through the bloom border with the selected ESDU resolution of 100 m indicated clearly that cyanobacterial and fish biomass adopted opposite

trends in their spatial distribution (Fig. 3). The most dramatic slope was observed at the edge 248 249 of the bloom. The abundance of fish was the highest just next to the border and decreased further with increasing distance from the edge of the bloom. A map of fish spatial distribution 250 251 (Fig.4) shows maximum fish concentrations in the middle part of the study area where bloom was present. Indeed, in two out of three transects with high concentrations of cyanobacteria, 252 253 peak values of cyanobacteria and fish were observed along the same transects (7 and 8). However, analyses at a scale of 100 m showed that these maxima mismatched in space. 254 255 Analyses of fish areal abundance, fish biomass (expressed as a sound scattering coefficient, Sa in m<sup>2</sup>ha<sup>-1</sup>, which is often used as a proxy for fish biomass), average fish size TS in dB, and 256 the number of single echo detections (SED) along the gradient of cyanobacterial biomass 257 show that all these parameters change their characteristics at the same border line of about 7 258 mgL<sup>-1</sup> of cyanobacteria biomass (Fig. 5a,b,c,d). Therefore, based on Fig. 5 we assumed that 7 259 mgL<sup>-1</sup> was the threshold in cyanobacterial biomass causing fish avoidance in the Sulejów 260 Reservoir in September 2015. Statistical analyses confirmed that all fish parameters, i.e. fish 261 abundance, fish biomass, number of SED and average fish size differed significantly above 262 and below 7 mgL<sup>-1</sup> of cyanobacterial biomass (Table 1). 263

## 264 3.2 Gillnet catches

Based on cyanobacteria distribution (Fig. 4), Tr2 in our study was in the area without bloom, while Tr9 was inside the bloom (at its periphery). The total number of fish caught at Tr2 was more than twice as high as at Tr9 (Fig. 6). Near Tr2, we captured 8 species with an average length and weight of  $21.2 \pm 8.5$  cm,  $174 \pm 197$  g. Near Tr9, 5 species were captured, with an average size of  $24.9 \pm 9.7$  cm,  $292 \pm 338$  g.

270 At both sites, one species made up over 60% of the catch. *B. bjoerkna* was the dominant fish

species at the downstream site (Tr2), while it was *R. rutilus* at the upstream gillnetting site

272 (Tr9). Both species were also the second most abundant taxa, B. bjoerkna and R. rutilus near

- 273 Tr9 and Tr2, respectively, and formed equally 20% of the catch (Table 2). Other fish species
- observed at both sites were *P. fluviatilis* and *G. cernua*. *A. brama*, *A. alburnus* and *S.*

*lucioperca* were only near Tr2, and Wels catfish *S. glanis* only near Tr9.

- 276 3.3 Cyanobacteria distribution
- There was a strong correlation between cyanobacterial biomass recorded by an echosounderand by fluorometer, with the following regression line:
- cyanobacterial biomass (mgL<sup>-1</sup>)=0.69 x cyanobacterial biomass (m<sup>2</sup>ha<sup>-1</sup>) 6.25, R<sup>2</sup>=0.895.
- 280 Maps of the cyanobacterial biomass distribution, based on phycocyanin fluorescence

measurements and hydroacoustics received on September 2, 2015 (the day with most

favorable measurement conditions), are presented in Fig. 4 along with the fish spatial

distribution. During measurements, the cyanobacterial bloom was concentrated in the central

- part of the study area between Tr5 and Tr7, and the highest cyanobacterial biomass reached
  33.8 mgL<sup>-1</sup>.
- Comparison of cyanobacterial biomass results based on phycocyanin fluorescence (mean value =  $4.08 \text{ mgL}^{-1}$ , SD = 3.39) and acoustics (mean value =  $4.10 \text{ mgL}^{-1}$ , SD =3.19) shows no statistical differentiation (t = 0.97, df = 207, p > 0.05).
- 289 3.4 Physico-chemical parameters

Physico-chemical parameters for 14 sampling stations are summarized in Table 3. Water temperature was about 20°C and this was stable both between the sampling stations and with depth (max difference between surface and the bottom was 1.7°C). Thus, the water had a fairly homogenous temperature profile, which did not cause any significant refraction and misshaping of the acoustic beam. Also, pH was practically constant, with an average value equal to 8.57±0.18. The whole water column was characterized by relatively good oxygen conditions. Only at 4 stations did the oxygen concentration drop below 4 mgL<sup>-1</sup> at the very
bottom. At all other stations and depth levels, concentrations were close to or above 6 mgL<sup>-1</sup>.

298 3.5 Toxigenic *Microcystis* 

Cyanobacteria of the genus Microcystis occurred at all 14 stations (Fig. 7). The greatest 299 number of copies of 16S rRNA  $(1.94 \times 10^5)$  were observed at station7 (Tr5). The average 300 amount of *Microcystis* (calculated from 14 stations) was equal to  $1.09 \times 10^5$  gene copy 301 number. In turn, the highest amount of toxigenic genotypes of *Microcystis*  $(8.49 \times 10^4$  gene 302 copy number based on mcyA) was observed at station 11 (Tr8). The average amount of 303 toxigenic genotypes was equal to  $2.8 \times 10^4$ . An increase was observed from the dam to the 304 305 center of the reservoir in terms of the amount of toxigenic genotypes (mcyA gene) with the 306 potential for microcystins production, relative to the whole population of Microcystis (16S rRNA gene) (Fig. 7). 307

308 3.6 Toxins in cyanobacteria, water and fish tissue

At all analyzed stations three microcystins (MC-RR, MC-YR and MC-LR) were identified in cyanobacterial biomass, but only intracellular variants. The average concentration of total microcystins was  $1.71 \ \mu g L^{-1}$ , with a maximum of  $4.34 \ \mu g L^{-1}$ . The highest concentrations of MCs were found at stations 10, 11, 12, 13, and 14 (Fig. 8). No extracellular MCs were found in any water or fish-tissue samples.

314 **4. Discussion** 

The present study provides the results of *in situ* investigations of the relationship between spatial distributions of fish and cyanobacterial bloom dominated by *Microcystis* in a lowland eutrophic reservoir. Only few studies exist on fish distribution during phytoplankton bloom events in natural environments. As early as in the1980s evidence was presented, which indicated that dense blooms of blue-green algae *Nodularia spumigena* had affected fish and

crab populations in a large estuarine system of south western Australia (Potter et al., 1983). 320 The numbers of fish were very low at sites where chlorophyll *a* levels were>100  $\mu$ gL<sup>-1</sup>, while 321 more active species moved into regions where N. spumigena was virtually absent. Two of the 322 323 field studies (Ernst, 2008; Sotton et al., 2011) were related to peri-alpine oligotrophic lakes, where coregonids are among the dominant species of the ichthyofauna with a dominance of 324 325 whitefish (Coregonus lavaretus) and simultaneous presence of Planktothrix rubescens, which 326 belongs to the most ubiquitous cyanobacterial species. Their results, however, were 327 contradictory. Thus, Sotton detected a spatial match between P. rubescens and whitefish in the mesotrophic Lake Bourget (France), while Ernst observed a spatial mismatch between the 328 two taxa in the oligotrophic Lake Ammersee (Germany). 329

Thus, none of the previous papers referred to fish behavior relative to *Microcystis* bloom. Our paper (Godlewska et al., 2016), which studied such relationships in the Sulejów Reservoir in 2013, did not provide direct evidence for fish avoidance. However, in 2013 the *Microcystis* bloom was observed only in the downstream part of the reservoir, and moreover, it was distributed in parallel to acoustic transects, so that the boat never passed the border of the bloom.

The results of the present study thus provide the first published direct evidence for night fish 336 337 avoidance of *Microcystis* bloom. The horizontal recordings from the boat passing in and out of the bloom clearly showed aggregation of fish at the edge outside the bloom. The fish 338 abundance was low inside the bloom, it increased dramatically after crossing the border of the 339 bloom and it declined again with increasing distance away from the bloom edge. There may 340 be different reasons for the higher concentration just outside the bloom. Either the 341 aggregations of fish had not yet had time to diffuse further into the non-infested waters or the 342 343 fish found some attraction near the bloom and thereby preferred to stay there. Of course, avoidance is only possible if the bloom does not cover the entire water body and fish are able 344

to detect "the edge". The fact that fish were crowded just outside the bloom border and then 345 slowly dispersed suggests that the factor causing fish avoidance was present only within the 346 bloom and disappeared as soon as fish passed the border. The present paper does not provide 347 348 the answer to the question of what exactly the factor is that causes fish avoidance. Avoidance behavior could be due to the clogging of the gills (Engström-Őst et al., 2006) or lowered 349 vision caused by turbidity (Gray et al., 2014; Utne-Palm, 2002). The latter is difficult to 350 resolve in our case because of the darkness during the data collection. Mayr (2002) also 351 352 reported spatial mismatch between whitefish abundance and turbidity, caused by high flows of the main tributary. Generally, turbidity may have many detrimental effects on fish, 353 including problems with feeding success (Mayr, 2002), social behavior (Borner et al., 2015), 354 etc. Cyanobacteria-induced turbidity may also interfere with foraging (Keshavanath et al., 355 1994), predator avoidance (Lehtiniemi et al., 2005), and refuge use of fish (Maes et al., 1998). 356 357 Recently, Vejřík et al. (2016) found that a high abundance of YOY perch was associated with low oxygen concentrations, suggesting that juvenile perch are using the hypoxic layer as a 358 359 refuge from large predators. We do not know if this hypoxia was associated with Microcystis 360 bloom, which often occurs in the studied lake. Nevertheless, juvenile perch may survive in oxygen concentrations of ca.  $1 \text{ mgL}^{-1}$  (Suthers and Gee, 1986), while for example adult perch, 361 one of the main predators of juvenile perch, avoid oxygen concentrations below  $6.7 \text{ mgL}^{-1}$ 362 (Alabaster and Robertson, 1961). Therefore, the use of the hypoxic pelagic zone as a refuge 363 by YOY fish is highly probable. Engström-Őst et al. (2006) have shown in a laboratory 364 experiment that cyanobacteria bloom may function as an important refuge for small fish 365 366 during predation pressure in pelagic algal blooms. According to our acoustic results, average size of fish within a bloom was statistically significantly smaller than that outside of the 367 368 bloom, which supports the above literature findings. However, the gillnet catches have brought about the opposite pattern resulting with mean TL = 24.9 cm and 21.2 cm in high and 369

low cyanobacteria densities, respectively (Fig. 7). One of the possible explanations is that the 370 371 gillnet catches can give biased results, especially when low fish number is caught (CEN, 2005; Šmejkal et al., 2015). Lower number of fish caught in the area with higher 372 373 cyanobacteria density gives lower reliability in statistical sense. The gillnets were situated only at two positions in the reservoir and they can reflect characteristics of the site and not the 374 375 presence or absence of the bloom. So, due to the low fishing effort, the gillnet data may not be 376 treated as representative for the whole reservoir and their value is limited to the species 377 discrimination. Additionally, one must be aware that acoustic sizing of fish when beaming horizontally is also problematic. We do not know the orientation of the fish relative to the 378 379 transducer, so normally it is assumed that fish are oriented randomly, which means that each aspect is equally probable. To account for this the deconvolution method is used (Kubečka et 380 al., 1996). Our measurements were performed only in the lacustrine part of the reservoir, 381 382 where such assumption seems to be reasonable (Tušer et al., 2009). However, if this assumption is not fulfilled, and majority of fish are swimming along the main axis of the 383 reservoir, while hydroacoustic transects are perpendicular to this axis, than the fish will be 384 mainly seen from their head or tail aspect, and they will look smaller than they really are. 385 Another possibility for bias in the acoustically obtained fish size distribution is the processing 386 387 of the data. Tracking targets with a method like the CFD, where the threshold adaptively follows the cyanobacteria layer, do raise the question whether some detections regarded as 388 fish, simply contained cyanobacteria echoes. A large number of such detections could shift 389 390 the average fish size down. There are, however, three arguments against this hypothesis. Firstly, larger fish echoes contribute essentially more to the average target size than smaller 391 targets, due to the logarithmic character of the data. One would need an essential number of 392 false detections to shift the average size noticeably down. Secondly, since the CFD only apply 393 phase stable single echo detections with strict criteria for echo length and positions, the 394

chance of falsely included cyanobacteria echoes is low. Thirdly and finally, visual studies of
the fish echogram set did not reveal tracks looking as if they originate from blobs in the
cyanobacteria. Even if a few erroneous tracks could have slipped our attention, it is unlikely
that the number of false detections of plankton needed to shift the average target strength
down, would have been easily spotted.

Apart from lowered visibility, other factors, such as diurnal instability of oxygen 400 concentrations or pH values following the bloom physiological activity (Gągała et al., 2013; 401 402 Rashidan and Bird, 2001), could also affect fish behavior. In areas of dense bloom, night time oxygen depletion and low pH can be expected. In our case, however, the values of oxygen and 403 pH did not exceed the values that could fall outside the tolerance range for cyprinids 404 (Alabaster and Lloyd, 1982). Unfortunately we do not know how these values changed 405 through the night, as each station was sampled only once. We can only judge from the 3 hours 406 407 difference between the first and the last station, that these changes were not noticeable. 408 According to Tom (1998), the oxygen requirements of roach and bream are 1.51 and 1.41, 409 respectively, comparing to the oxygen requirement of common carp Cyprinus carpio, which can perform well at oxygen levels of  $3-5 \text{ mgL}^{-1}$  (critical value  $2 \text{ mgL}^{-1}$ ) (Bryliński, 2000). 410 During our studies, oxygen dropped below 4 mgL<sup>-1</sup> only at 4 stations and only at the narrow 411 layer near the bottom; at all other stations and depths it was above 6 mgL<sup>-1</sup>, which is sufficient 412 even for large fish, especially for cyprinid dominants, i.e. common bream and roach. The pH 413 values were fairly homogenous across the study area and did not noticeably differ between the 414 stations situated within and outside the bloom (mean pH = 8.56; SD = 0.18). So, in our case 415 416 environmental parameters were unlikely to be responsible for fish avoidance. The threshold in cyanobacterial biomass causing fish avoidance in the Sulejów Reservoir was estimated in this 417 study at 7 mgL<sup>-1</sup>. This was higher than the threshold  $(3 \text{ mgL}^{-1})$  estimated in the Sulejów 418 Reservoir in July 2013 (Godlewska et al., 2016). The threshold might depend on the toxicity 419

of cyanobacteria. The number of intracellular microcystins recorded in 2013 was much higher
than that in 2015 (Kaczkowski et al., 2017), which may suggest that toxicity is one of the
factors responsible for fish avoidance.

Cyanobacteria distribution obtained with phycocyanin fluorescence and hydroacoustic 423 methods differed only slightly (Fig. 4) and without statistical significance. There are several 424 reasons, which could cause such discrepancy. Firstly, fluorescence measurements were 425 collected at a depth of 0.5 m, i.e. practically only in the surface layer, while hydroacoustics 426 427 surveyed the total water column. Secondly, one must be aware that cyanobacterial biomass estimated acoustically may incidentally include biomass of small fish, whose TS is so small 428 that they are buried in signals from cyanobacteria, as well as zooplankton. Zooplankton 429 430 without gas bubbles is a much weaker scatterer than objects possessing gas bubbles in their 431 bodies. Usually it is below the threshold, but when it occurs in high densities, it can be recorded by a high frequency echosounder (Guillard et al., 2014). These additional scatterers 432 433 could cause acoustic estimates of cyanobacteria biomass to become higher. However, it is unlikely that this was the case in our studies. Fig.5d shows that we observed even smaller fish 434 within the bloom than outside the bloom, which indicates that filter did effectively separate 435 436 cyanobacteria and small fish. Also zooplankton biomass during our studies in 2015, but also in 2013 (Kaczkowski et al., 2017), was higher outside the bloom than within the bloom. Since 437 with our threshold of -45 dB we did not see any zooplankton in areas free of bloom, we 438 assume it was not present within the bloom either. 439

Cyanobacterial and fish biomass showed opposite trends in their spatial distribution, with the most dramatic slopes at the edge of the bloom. It is particularly evident from small scale analyses (100 m) that both fish and cyanobacteria maximum concentrations do not overlap in space, but they are rather situated next to each other. Therefore, the reason why Sotton et al. (2011) concluded that *P. rubescens* distribution did not seem to affect the vertical or

horizontal distribution of whitefish could be the too low spatial resolution of their 445 446 measurements. They estimated fish biomass at intervals of 250 m (ESDU), while cyanobacteria were measured at 3 single points about 1,000 m apart, so the comparison was 447 based on the assumption that the concentrations of P. rubescens were constant within this 448 range, which might not have been true. While their conclusion was well supported by the 449 450 vertical data, we wonder if the ESDU and spatial resolution of cyanobacteria measurements 451 were small enough to account for the heterogeneous distributions of fish and P. rubescens in the horizontal dimension. 452

Fish avoidance behavior was also confirmed by gillnet catches, with over twice less fish 453 caught in the net situated on the periphery of the bloom than in the net situated outside of the 454 bloom. Clearly lower fish numbers and bream dominance in gillnets placed in the bloom area 455 456 were observed in the Sulejów Reservoir in 2013 (Godlewska et al., 2016; Kaczkowski et al., 2017). In 2015, the dominant fish in the bloom area was roach (over 60% of all caught fish 457 458 specimens), but there were only large specimens of this species (over 27 cm in total length). There are at least two possible explanations for our observation. At the size of 27 cm or more, 459 roach prey mostly on zebra mussel Dreissena polymorpha, which becomes an available food 460 source for fish longer than 16 cm (Kobak et al., 2010; Nagelkerke and Sibbing, 1996; Prejs et 461 al., 1990). Utilization of this food source might prevail over any disadvantage related to 462 463 bloom presence. Alternatively, fish utilizing almost entirely this benthic food source are partly avoiding bloom by occupying the deepest layers of the water, where autotrophic algae density 464 is lower. In comparison, breams are able to utilize zebra mussels when they reach lengths over 465 37 cm and even then they are only able to consume much smaller mussels (mainly 6–8 mm 466 long and a maximum of 13 mm) than roach (mainly 6–18 mm long and a maximum 19 mm), 467 and thus are not able to compete effectively with the latter species. Bream prefer other food 468 sources such as zooplankton and chironomids, similar to smaller roach specimens, of average 469

length 18 cm, present in gillnets situated outside of the bloom (Kakareko, 2001; Lammens,
1989; Martyniak et al., 1987; Nagelkerke and Sibbing, 1996; Persson and Hansson, 1999;
Prus, 2009; van den Berg, 1993).

Applied quantitative genetic analyzes confirmed the presence of cyanobacteria of the genus 473 Microcystis (based on 16S rRNA gene analysis) and their toxigenic genotypes (based on 474 mcyA gene analysis) at all 14 stations. The fact that MCs were not found in the fish tissue 475 may indicate that the avoidance occurred fairly fast, preventing accumulation of microcystins 476 by fish, or that they were present in fish bodies only in small concentrations, making 477 impossible their identification by chromatographic methods using diode array detection. 478 Moreover, the absence of microcystins in the water could explain lack of presence of 479 480 identified toxins in the organs of fishes, although they are known to be well accumulated by 481 fish (Papadimitriou et al., 2012; Xie et al., 2004). Thus, our results confirm the observations of Kamjunke et al. (2002) that microcystins are not dangerous for fish as long as they are 482 closed in the *Microcystis* cells, because they are not digested when passing through fish guts. 483

## 484 **5.** Conclusions

485 Fish avoidance has been clearly documented, indicating that fish can actively react to their exposure to microcystin-producing cyanobacteria and minimize adverse effects, regardless of 486 the nature of such interaction, for example intoxication (Sotton et al., 2012a, 2012b), visual 487 488 deprivation (Gray et al., 2014) or food shortages (Reichwaldt et al., 2013). Both, hydroacoustic measurements and gillnet catches confirmed that maxima of fish and 489 490 cyanobacteria biomass mismatch in space. In spite of toxic bloom occurrence, no microcystins were detected in fish bodies, suggesting that in the Sulejów Reservoir fish 491 avoidance was effective. The paper also demonstrates that a high frequency echosounder 492 493 provides an effective tool for monitoring bloom development and propagation and its results

494 are highly correlated with measurements of cyanobacteria biomass based on fluorescence of495 phycocyanin.

496 Further investigations are needed to fully understand the mechanisms of the effect of

497 Microcystis on fish, and to determine the densities of cyanobacteria which trigger fish

498 avoidance behavior for different densities and species of fish and cyanobacteria. An

499 interesting question is whether avoidance behavior depends on the density of cyanobacteria

500 alone or also on their toxicity.

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819	Figure captions
820	
821	Fig. 1. Localization of hydroacoustic transects (A), point water sampling stations and gillnet
822	location (B) in the Sulejów Reservoir.

- Fig. 2. An example of a horizontal beam echogram with a *Microcystis* bloom border crossed
- during the hydroacoustic survey in the Sulejów Reservoir on September 2, 2015.

826

Fig. 3. Fish and cyanobacterial biomass expressed as an area sound backscattering coefficient 827 Sa total  $(m^2ha^{-1})$  for the horizontal beam echogram of transect 7, at which the bloom edge 828 (segment 8 and partly 9) presented in Fig.2 occurred. 829 830 831 Fig. 4. Spatial distribution of fish abundance estimated acoustically (A), cyanobacterial biomass estimated acoustically (B) and cyanobacterial biomass estimated from fluorescence 832 833 of phycocyanin (C) based on 100 m intervals along 10 transects in the Sulejów Reservoir on September 2, 2015, plotted in Surfer software. Tr2 and Tr9 correspond to the position of the 834 gillnets. 835 836 Fig. 5. Fish abundance (A), fish biomass (B), number of single echo detections (C) and mean 837 838 fish size TS in dB (D) along cyanobacterial biomass gradient for 100 m segments of a survey track in the Sulejów Reservoir on September 2, 2015. 839 840 841 Fig. 6. Diagram of the frequency (number of fish) of length classes of fish caught in multimesh gillnets near transects 2 and 9 at the Sulejów Reservoir. 842 843 844 Fig.7. The dynamics of the genus Microcystis (16S rRNA) and its toxigenic genotypes (mcyA) characterized in molecular analyses in the Sulejów Reservoir at 14 stations on 845 846 September 3, 2015. 847 848 Fig.8. Distribution of intracellular microcystins determined by HPLC in water samples collected from the Sulejów Reservoir on September 3, 2015. 849 850

#### **Tables** 851

Table 1. Results of statistical comparisons (t-test for unequal sample sizes) of the acoustic 852 parameters characterizing fish abundance, biomass and fish sizes below and above the 853

- threshold of cyanobacterial biomass estimated as 7 mgL<sup>-1</sup> in the Sulejów Reservoir on 2 854
- September 2015. 855

856

Table 2. Abundance of fish species (D, %) and fish sizes (total length-TL) in the gillnet catch 857

with respect to cyanobacterial chlorophyll a concentration in the Sulejów Reservoir on 858

859 September 2, 2015. The dominants are in bold.

860

Table 3. Water temperature and dissolved oxygen concentration values at 14 stations in the 861

Sulejów Reservoir, measured from the surface till depth at 1 m intervals on September 2, 862

2015 simultaneously with hydroacoustic measurements. 863

Tab.1 864

	Cyanobacterial biomass												
			< 7 n	ngL⁻¹	> 7 n	ngL⁻¹							
			mean	SD	mean	SD	t-value	df	p-value				
	Fish abundance	fishha <sup>-1</sup> 198.5	14	5.9	54.6	24.4	8.6	101	0.001				
	Sa	m <sup>2</sup> ha <sup>-1</sup> 12.33 13.2		13.26	2.89	2.70	6.06	103	0.001				
	SED		76.21	86.17	5.00	2.73	7.69	87	0.001				
	TS	dB	-29.09	2.87	-33.73	5.37	3.36	3.36 17					
865													
866													
867													
000													
808													
869	Table 2												
	Tree	nggat number			2			0					
	Cyanobactori	nseut number al chlorophylla (u	a I <sup>-1</sup> 1		∠ 5.03			9 27 02	1				
	Cyanobacteria	al chiorophyll <i>a</i>  µ	ig L <sup>*</sup>		5.93		27.92						

Bleak Alburnus alburnus	0.91	10.9		
Common bream Abramis brama	6.36	$40.4 \pm 2.9$		
White bream Blicca bjoerkna	63.64	$21.2 \pm 5.4$	20.00	$18.9 \pm 6.7$
Roach Rutillus rutillus	20.00	$18.0 \pm 5.7$	64.44	$27.2 \pm 5.4$
Eurasian perch Perca fluviatilis	0.91	8.7	6.67	$22.9 \pm 8.1$
Pikeperch Sander lucioperca	1.82	$44.2 \pm 3.2$		
Ruffe Gymnocephalus cernua	6.36	$9.3 \pm 0.3$	6.67	$9.4 \pm 3.0$
Wels catfish Silurus glanis			2.22	65.2
n tot.	110		45	

	depth. m	0	0	1	1	2	2	3	3	4	4	5	5	6	6	7	7
		Temp.	Oxyg.														
Time																	
(h:min)	station	Deg.	mg/L	Deg	mg/L	Deg.	mg/L										
20:51	1	22.5	11.44	22.5	11.34	22.4	10.1	21.4	6.17	21.1	5.45	21,00	5.14	20.9	4.24	20.7	4.24
21:07	2	22.2	9.39	22.1	7.24	21.7	5.19	21.6	5.89								
21:18	3	22.6	11.48	22.6	11.55	22.7	11.55	21.8	6.94	21.2	5.42	20.9	4.76	20.8	4.3	20.5	1.66
21:33	4	22.1	10.51	22.1	10.49	22.1	10.34	21.9	9.59	21.3	7.23						
21:44	5	21.9	10.11	21.9	10,00	21.9	9.89										
21:57	6	22.7	11.64	22.8	11.65	22.9	11.48	22.7	10.4	22,00	6.95	21.4	5.19				
22:12	7	21.8	10.67	22,00	10.61	21.9	10.16	21.7	9.88	21.6	8.34	21.5	7.24				
22:26	8	21.2	9.11	21.3	9.09	21.3	9.05	21.3	9.01	21.3	8.98	21.2	7.12	21.1	6.44		
22:42	9	22.7	12.86	22.9	12.89	22.9	12.9										
22:51	10	21.5	9.29	21.6	9.27	21.6	9.25	21.6	9.23	21.6	9.22	21.6	8.92	20.7	2.9		
23:06	11	22.4	12.23	22.5	12.32	22.5	12.34										
23:21	12	21.4	10.21	21.5	10.15	21.5	9.75	21.2	8.09	21.2	7.66	21.1	6.88				
23:32	13	21.9	11.51	22,00	11.52	22.1	11.4	22.1	11.26	22,00	9.91	21.6	10.28				
23:45	14	22.4	12.4	22.4	12.4	22.4	12.41	22.4	12.42	22.4	12.22	20.9	3.54				

872 Tab.3















884 Fig. 4

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**2-09-2015, all transects** cyanobacterial biomass mgL<sup>-1</sup> 5 10 15

D







888 Fig. 5



891 Fig. 6







895 Fig.8