

1 **Title:** Stress response of *Chironomus riparius* to changes in water temperature and oxygen
2 concentration in a lowland stream

3
4 **Short title:** *Chironomus riparius* stress response

5
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34 warming

35

36 **Abstract**

37 The increasing impairment of lotic ecosystems has promoted a growing effort into assessing their
38 ecological status by means of biological indicators. While community-based approaches have
39 proven valuable to assess ecosystem integrity, they mostly reflect long-term changes and might not
40 be suitable for tracking and monitoring short-term events. Responses to rapid changes in
41 environmental conditions have been rarely studied under natural conditions. Biomarkers offer the
42 benefit of integrating biological responses at different time scales. Here we used a field experiment
43 to test how the synthesis of heat shock protein 70 (HSP70) and Haemoglobin (Hb) in laboratory-
44 reared larvae of *Chironomus riparius* (Diptera, Chironomidae) were influenced by short-term
45 changes to water temperature and oxygen concentration in a lowland stream. Our aim was to
46 determine whether HSP70 mRNA expression and Hb content could be used as an *in situ* “early
47 warning system” for freshwater habitats undergoing environmental change. HSP70 exhibited a clear
48 response to changes in temperature measured over a one-day period, confirming its suitability as an
49 indicator of environmental stress. Hb concentration was related to oxygen concentration, but not to
50 temperature. Our findings support the hypothesis that depletion in oxygen induces Hb synthesis in
51 *C. riparius* larvae. Because tolerance to low oxygen is not only related to total Hb, but also to a
52 more efficient uptake (binding to Hb, e.g. Bohr effect) and release of oxygen to the cell (Root
53 effect), we cannot discern from our data whether increased efficiency played a role. We suggest that
54 *C. riparius* is a suitable model organism for monitoring sub-lethal stress in the field and that the
55 approach could be applied to other species as more genomic data are available for non-model
56 organisms.

57

58 **Introduction**

59

60 Streams and rivers are among the most threatened ecosystems, having been modified globally by
61 catchment land-use changes, water abstraction, channelization, pollution and invasion of alien
62 species (Vörösmarty et al., 2010; Dudgeon et al., 2006). Additionally, climate change is expected to
63 alter hydrology and temperature regimes with severe effects on organisms and ecosystem functions
64 (Ormerod and Durance 2012; Li et al., 2012; Floury et al., 2013). This increasing impairment of
65 lotic ecosystems has promoted a growing effort into assessing their ecological status by means of
66 biological indicators and sentinel species (Friberg, 2014). The classification of the ecological status
67 of rivers is officially based on the assemblage structure of key taxonomic groups (e.g., Hering et al.,
68 2003; Traversetti et al., 2015). While assemblage-based approaches have been proven valuable in
69 the assessment of ecosystem integrity (Bae et al., 2014), they mostly reflect long-term changes,

70 associated with the local extirpation of sensitive taxa and overall changes in community
71 composition. This approach may not be suitable for identifying and monitoring the effects of short-
72 term events such as droughts and floods or other sub-lethal episodic events, whose frequency and
73 magnitude is expected to increase in the near future (Ledger and Milner 2015). Biomarker assays
74 (i.e. non-lethal responses of biological systems) are often used in eco-toxicological studies to assess
75 the effects of pollutants, but their potential for tracking environmental change in the field has
76 received little attention (Traversetti et al., 2017). Ideally, integrating indicators in a hierarchical
77 fashion, from sub-organismal to organismal, population and community levels (Sures et al., 2015)
78 should improve the assessment of ecosystem health over multiple spatio-temporal scales
79 (Cajaraville et al., 2000; Lagadic et al., 2000; Colin et al., 2016).

80
81 A promising approach is to use multiple indicators of stress in organisms (Frank et al., 2013).
82 Multiple biomarkers may produce the benefit of integrating biological responses at different time
83 scales and levels of organisation (Den Besten, 1998; Lagadic et al., 2000; Scalici et al., 2015). Two
84 potential biomarkers for measuring sub-lethal effects in stream macroinvertebrates are heat shock
85 proteins (HSP) and haemoglobin (Hb). HSP70 is a set of chaperon proteins involved in ensuring the
86 correct folding and unfolding of proteins, and its expression is rapidly regulated by changes in
87 physical (i.e. temperature) and chemical conditions (Lencioni et al., 2009; Lee et al., 2006), but it is
88 not affected by handling stress (Sanders, 1993). The expression of HSP70 is therefore considered a
89 short-term “early warning” indicator of environmental changes (Yoshimi et al., 2009; Folgar et al.,
90 2015). For example, Lencioni et al (2013) observed an increase in HSP70 expression after 1h of
91 heat stress at 26 °C in a cold-adapted non-biting midge (Diptera, Chironomidae) larvae.

92
93 Chironomidae larvae can be abundant in degraded freshwater habitats, and are thus considered
94 indicators of poor water quality and early colonizers after large-scale disturbances (Serra et al.
95 2017). Resistance and resilience of chironomids is often attributed to the presence of hemoglobin
96 (Hb), which allows them to tolerate low oxygen concentrations (Moller Pilot, 2009). In
97 *Chironomus riparius*, Choi et al. (2001) observed a 151% increase in total Hb after 24 hours of
98 hypoxia. Chironomidae larvae have been reported to secrete up to 16 different Hb types (Choi and
99 Ha, 2009; Green et al., 1998). Such diversity of Hbs with specific binding properties allows for a
100 fine-tuned loading and unloading of O₂ that regulates its delivery to specific tissues under variable
101 environmental conditions (Choi and Ha, 2009; Ha and Choi, 2008; Weber and Vinogradov, 2001).

102

103 We used a field experiment to test how HSP70 expression and Hb production were influenced by
104 short-term changes to temperature and oxygen concentration in a lowland stream. Laboratory-
105 reared larvae of *Chironomus riparius* (Diptera, Chironomidae), a widespread species considered a
106 model organism in aquatic toxicology (Lee et al., 2006; Lencioni et al., 2009; Morales et al., 2011;
107 Marinkovic et al., 2011), were placed in a stream and sampled over a period of 1 to 8 days, while
108 experiencing rapid variation in temperature and oxygen concentration.

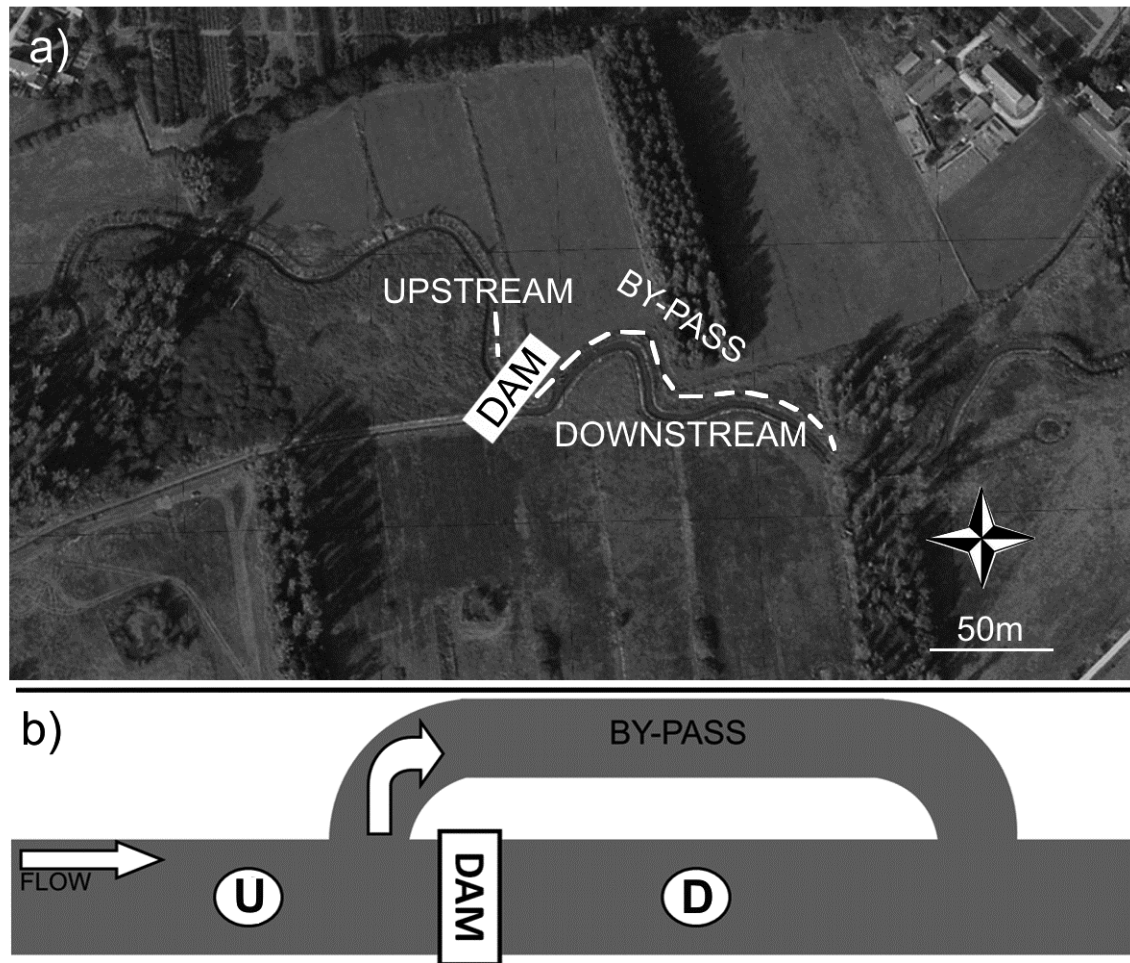
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110 **Methods**

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112 The study was carried out in the lowland stream Groote Molenbeek in Limburg, Netherlands. In
113 June 2010, two experimental reaches (upstream, downstream) were designated along the stream,
114 each *ca.* 50 m in length and separated by *ca.* 200 m. In July 2010 the upstream and downstream
115 reaches were separated by an artificial dam and a by-pass was constructed (Fig. 1a, b). The aim was
116 to simulate summer drought conditions in the downstream reach, e.g., reduced water flow, reduced
117 oxygen concentration, and increased water temperature. Experiments were performed in the
118 upstream reach in June, prior to dam construction, and in both upstream and downstream reaches in
119 August, after dam construction. No experiment was conducted in the downstream reach in June
120 because abiotic conditions were nearly identical to those in the upstream reach. In August, heavy
121 rainfall caused large and rapid variations in oxygen and water temperature in both reaches. While
122 this event disrupted the desired effect of the experimental drought, it provided the opportunity to
123 quantify short-term responses to sub-lethal environmental change in all reaches. Therefore, we did
124 not compare control and experimental reaches, but rather we measured the physiological responses
125 of *C. riparius* to the environmental changes experienced *in situ*. The following environmental
126 variables were measured each day at 08:00 throughout the sampling periods in June and August:
127 Temperature (°C), dissolved oxygen (mg O₂ l⁻¹), conductivity (µS cm⁻¹), and pH (measured with a
128 Multi 340i/SET immersion probe WTW, Weilheim, Germany), water depth (m) and flow velocity
129 (m sec⁻¹) (measured using a 2030 flow-meter; General Oceanics, Miami, USA).

130



131

132 **Figure 1.** Study site. (a) overview of experimental reaches and dam position on the River Grote
133 Molenbeek (51°23'30.79" N 6°2'31.89" E) (Sevenum, NL); (b) schematic view of dam, by-pass,
134 upstream (U) and downstream (D) sites.

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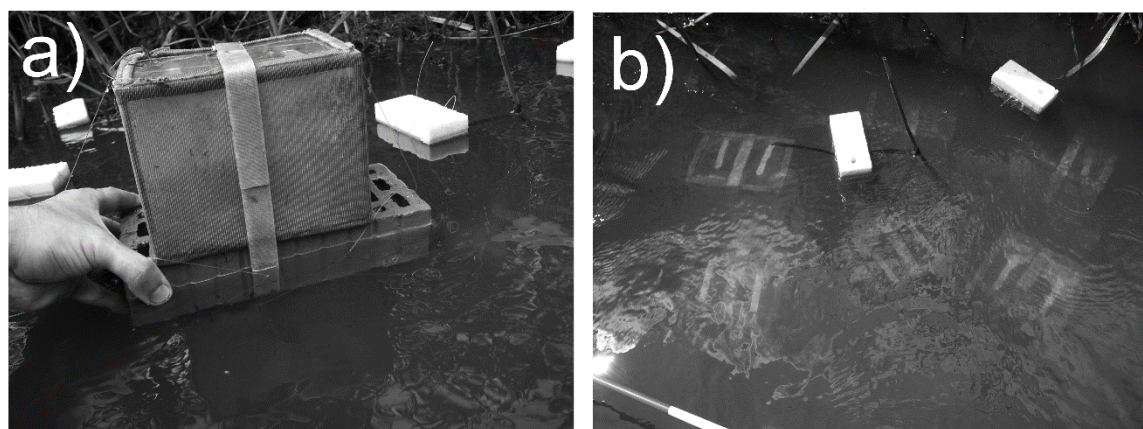
136

137 *Chironomus riparius* individuals were obtained from a permanent laboratory population at the
138 Department of Aquatic Ecotoxicology in Frankfurt am Main, Germany. The single origin
139 presumably minimized the genetic diversity among individuals (Nowak et al., 2012). Eggs were
140 shipped to the IGB in Berlin, and after hatching, larvae were reared in aquaria for 4 months prior to
141 the experiment according to the OECD (2004) guidelines. Laboratory aquaria were filled with fine
142 quartz sand as substrate. Aquaria were constantly aerated and kept in a climate chamber in
143 controlled conditions (20 °C, light:dark 16h:8h). Larvae were fed with commercial TetraMin® fish
144 food (Tetrawerke, Melle, Germany). Mesh cages (16 x 12 x 12 cm; mesh: 0.2 mm; Fig. 2a) were
145 designed ad-hoc from aquarium isolation chambers (Hagen Marina, Montreal, Canada) and used to
146 transfer *C. riparius* larvae from the laboratory to the field and to introduce larvae into the

147 experimental reaches. This procedure enabled rapid sample collection, thus minimising handling
148 stress.

149
150 At the start of experiments, 25 mesh cages, with 100 larvae each (third and fourth instar), were
151 placed on the stream bottom (Fig. 2b) in each reach (upstream in June, upstream and downstream in
152 August). Fourth-instar larvae were used for HSP70 expression analysis (collected after 24, 96 and
153 192 hours of exposure) and Hb analyses (24, 48, 96 and 192 hours of exposure; sample sizes in
154 Appendix 1). Larvae were removed from cages with forceps, placed in cryo vials (Eppendorf),
155 immediately placed in liquid nitrogen and stored at -80°C until analysis.

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159 **Figure 2.** Experimental step in the stream: (a) *Chironomus riparius* experimental cages (16 x 12 x
160 12 cm), and (b) their positioning on the river bed in a 100 x 250 cm area in upstream and
161 downstream sites (see Fig. 1).

162

163 Total RNA was extracted from 7 individuals per time point and reach (n = 63; Appendix 1) using a
164 Rneasy Mini kit (Qiagen, Hilden, Germany) with on-column DNase digestion (Trubiroha et al.
165 2009). RNA concentration was measured using a Nanodrop ND-1000 (Thermo Fisher Scientific,
166 Darmstadt, Germany). Reverse transcription was carried out with Affinity Script transcriptase
167 (Agilent/Stratagene, Waldbronn, Germany). Primers for HSP70 and β -actin (Appendix 2) were
168 designed using data from Park et al. (2010) and Morales et al. (2011) and specificity was confirmed
169 by direct sequencing. Quantitative PCR was carried out with a Mx3005 (Agilent/Stratagene) using
170 hot start polymerase (Phire Taq II, Life Technologies) and SYBR Green in a 20 μ L reaction volume
171 (2 μ L diluted cDNA, 375 nM of each primer, 1x Taq buffer, 2 mM MgCl₂, 0.5 mM each dNTP, 0.5
172 fold diluted SYBR-Green I solution, 1 U polymerase) under the following conditions: 98°C initial

173 denaturation for 4 min, followed by 40 cycles of 98°C denaturation for 20 s, 62°C primer annealing
174 for 15 s, and 72°C extension for 20 s. PCR efficiencies were determined in triplicate with a dilution
175 series of pooled cDNA (β actin 99.6%; HSP70 98.4%). All samples were determined in duplicate.
176 Expression was determined by the comparative $\Delta\Delta C_T$ method (Pfaffl, 2001) with β actin used as a
177 baseline (housekeeping) gene considering a calibrator sample (pooled cDNA) and correction for
178 efficiency. Specificity of amplification was monitored by melting curve analysis.

179

180 Total Hb was measured in nine individuals per time point and reach (n=108; Appendix 1) using the
181 cyanomethemoglobin method with a diagnostic haemoglobin reagent (DiaSys, International,
182 Holzheim, Germany) as described by Wuertz et al. (2013). All samples were measured twice with
183 an Infinite 200 microplate reader (Tecan, Mainz-Kastel, Germany) at 540 nm and concentration was
184 calculated using a standard dilution series (120 mg/L haemoglobin standard, Diaglobal GmbH,
185 Berlin, Germany). Total Hb was normalized to the total protein concentration determined by the
186 Bradford (1976) method (RotiQuant Kit, Germany) as $\mu\text{g Hb}/\mu\text{g total proteins}$.

187

188 Linear mixed-effect (LME) models were used to analyse variation in HSP70 expression and Hb
189 concentration in relation to variation in environmental conditions.

190 After testing for collinearity using a Spearman test (also from among all the measured
191 environmental variables, see Appendix 3) the model for both HSP70 and Hb initially incorporated
192 T, O₂ and changes in temperature (ΔT) and oxygen (ΔO_2) as fixed factors. The latter two variables
193 were calculated as the absolute change (i.e., increase or decrease) in T (°C) or O₂ (mg O₂ L⁻¹) from
194 the previous sampling time (every 24h). Model factors were then backward-selected using
195 likelihood ratio tests against reduced models (without the fixed factor) (Zuur et al. 2009). Final
196 models included fixed factors ΔT , ΔO_2 and T for HSP70 model and O₂ for Hb model. Collection
197 time nested in the reach-season (upstream-June; upstream-August; downstream-August) was
198 considered as a random factor to account for repeated sampling. The variance explained by each
199 model was calculated as marginal (R^2_m) (Nakagawa and Schielzeth, 2013) using the MuMIn
200 package (Barton 2016) for R v3.3.1 (R Core Team, 2015). Residuals were tested for normality
201 with a Wilk-Shapiro test and qq-plots, and scores were log-transformed to remove
202 heteroscedasticity if necessary.

203

204

205 **Results**

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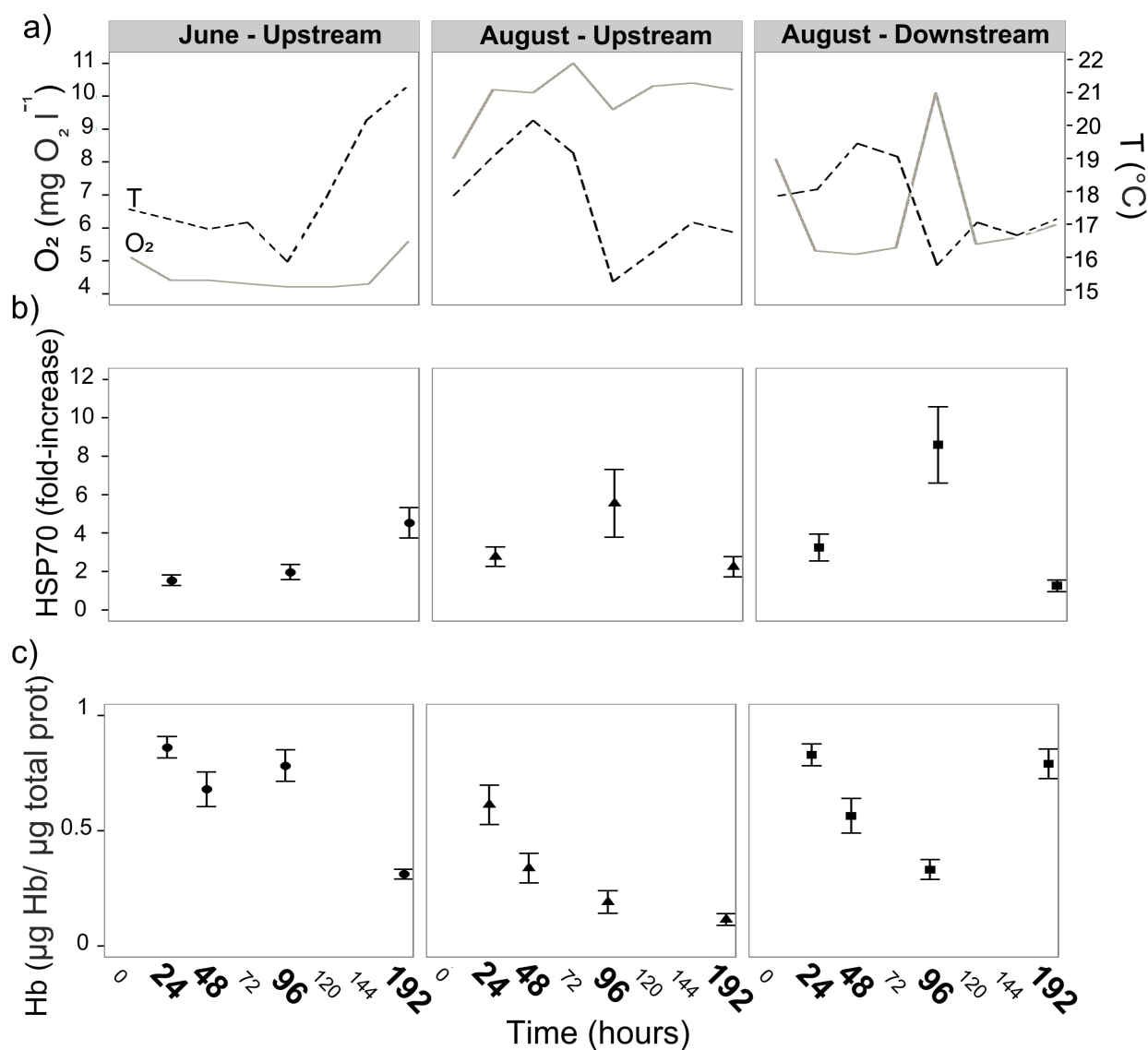
207 Initial environmental conditions in June (Fig. 3) were assumed to be identical between the upstream
 208 and downstream sites in August due to their close proximity and the lack of a dam. In August, mean
 209 water flow, channel depth, dissolved oxygen, and conductivity varied after placement of the dam
 210 and after heavy rain events (Appendix 4b, c, e, f). Flow, depth, and conductivity all decreased in
 211 August and varied between reaches (Appendix 4c, f), whereas oxygen increased substantially in the
 212 upstream reach and less in the downstream reach, compared to June (Fig. 3a, Appendix 4b). HSP70
 213 expression in the upstream reach in June was stable after 24 and 96 hours but increased at 192 hours
 214 in June. Expression peaked at 96 hours in both reaches in August, following a rapid change in T
 215 (Fig. 3b). The mixed effect model combining all data from June and August indicated significant
 216 positive relationships between HSP70 expression and change in temperature (ΔT) and oxygen
 217 (ΔO_2) over the previous 24 hr (Table 1).

218

219 **Table 1.** Results of linear mixed effect (LME) models for the relative heat shock protein 70
 220 (HSP70) expression (standardized to the calibrator) and hemoglobin (Hb) response to
 221 environmental changes, including marginal variance (R^2_m), estimate of the fixed effects (Estim),
 222 standard error (SE), degrees of freedom (dF) and t-statistic (t-value and factor significance). Fixed
 223 factors: change in Oxygen (ΔO_2 , mg O_2 l^{-1}); absolute change in T (ΔT , $^{\circ}C$); Temperature (T, $^{\circ}C$);
 224 oxygen (O_2 , mg O_2 l^{-1}). * = $p < 0.05$, ** = $p < 0.01$, *** = $p < 0.001$.

	Factors	Estim	SE	dF	t-value	p
HSP70 (fold-increase) ($R^2_m = 0.43$)	Intercept	-1.127	0.844	5	-1.33	0.239
	ΔO_2	0.139	0.052	5	2.65	0.045*
	ΔT	0.227	0.071	5	3.17	0.025*
	T	0.111	0.046	5	2.42	0.066*
Hb (μg Hb/ μg total prot) ($R^2_m = 0.34$)	Intercept	0.716	0.089	18	8.01	<0.001***
	O_2	-0.044	0.012	20	-3.73	0.001***

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Figure 3. Environmental variables and physiological responses of *Chironomus riparius* larvae: (a) changes in oxygen concentration (solid line) and temperature (broken line) as measured at 08:00 each day during the experiments in June and August and at 1 hour before sample collection (hours indicated in bold on the y-axis); (b) mean (\pm SE) relative heat shock protein 70 (HSP70) expression standardized to the calibrator at 24, 96, and 192 hours; (c) mean (\pm SE) haemoglobin (Hb) concentration at 24, 48, 96 and 192 hours.

249 Hb concentrations in the upstream reach remained similar after 24, 48, and 96 hours and were
250 lowest after 192 hours in June, after a mild increase in dissolved O₂. (Fig. 3c). In August, Hb
251 declined steadily over 24, 28, and 96 hours in both reaches. In the upstream reach, Hb continued to
252 decline after 192 hours during relatively stable O₂ levels, but increased markedly in the
253 downstream reach following a peak and subsequent rapid decline in O₂ after in 192 hours (Fig. 3c).
254 The mixed effect model indicated that Hb content increased with decreasing oxygen concentration
255 (O₂) (Table 1).

256

257 **Discussion**

258 We applied an eco-toxicological stress-response approach to a field experiment in order to examine
259 how changes in water temperature and dissolved oxygen concentration influenced two
260 physiological biomarkers in a model organism. Our markers were chosen to reflect short-term
261 (HSP70 mRNA expression) and medium-term (blood Hb content) responses to environmental
262 changes. Contrary to conventional bio-assessment programmes, where the presence or abundance of
263 different aquatic organisms are used as indicator of environmental change or degradation, our aim
264 was to determine whether physiological biomarkers in a model organism could be used *in situ* as an
265 “early warning system” for freshwater habitats undergoing environmental change. Assemblage-
266 level responses may manifest only at a later stage of environmental degradation, thus hindering
267 prompt mitigation actions. Many studies of stress response are conducted in the laboratory and
268 often under conditions unlikely to represent those of natural habitats (see Sures et al. 2015). Our
269 intent was to extend this approach to realistic field conditions. In addition, we used a model
270 organism group (Chironomidae) that is almost ubiquitous in aquatic habitats and is among the first
271 colonizers after disturbance events such as droughts or floods (Calle-Martinez and Casas, 2006;
272 Langton and Casas, 1998; Marziali et al., 2010; Puntì et al., 2007). HSP70 exhibited a clear
273 response to changes in temperature (and partially in oxygen) measured over a one-day period prior
274 to sampling. The expression of HSP70 is known to be related to acute cellular stresses (Morimoto
275 and Santoro 1998), and Feder and Hofmann (1999) observed the presence of HSP-inducing
276 microhabitats (e.g. shallow or stagnant water systems) where mild environmental variations (e.g.
277 temperature) induced variations in HSP expression. HSP70s have also been reported reliable means
278 of detecting such stress (Lencioni et al., 2009, Foster et al., 2015). This may be due to the fact that
279 in dynamic systems such as small waterbodies, environmental parameters like temperature and
280 oxygen vary slightly but continuously, causing an increase of the long-term memory formation as
281 an adaptive response of the organisms (Foster et al., 2015). Memory formation increases synaptic
282 efficacy and improves the adaptive responses to stress conditions including the basal mRNA

283 transcriptional system (Stork and Welzl, 1999, Monari et al., 2011) in which HSP70 are also
284 included. This further supports the suitability of the HSP70 as multi-stressors indicator.

285

286 In this study, haemoglobin concentration was related to oxygen concentration, but not to water
287 temperature. Results from other studies indicate that the tolerance of *C. riparius* larvae to low levels
288 of dissolved oxygen is associated with increased haemoglobin in their hemolymph (Weber, 1980;
289 Choi et al., 2000), which allows sustaining aerobic and anaerobic metabolism (alcoholic
290 fermentation) at the same time for short periods (Frank, 1983). Under hypoxic conditions, Hb
291 synthesis is stimulated and used for aerobic metabolism (Choi et al., 2000; Lee et al., 2006; Rossaro
292 et al., 2007). This process likely occurred in our experiment where the observed depletion in
293 oxygen concentration induced synthesis of Hb in *C. riparius* larvae. Nonetheless, tolerance to low
294 oxygen is not only related to total Hb, but also to a more efficient uptake (binding to Hb; Bohr
295 effect) and release of oxygen to the cell (Root effect). However, we cannot discern from our data
296 whether increased efficiency played a role. The synthesis of HSP70 and Hb are likely linked,
297 because temperature and oxygen concentration are closely interconnected. Our results suggest that
298 the responses of HSP70 and Hb to environmental change represent an integrated process in which
299 HSP70 increased as a direct consequence of increased temperature. Subsequently, increased
300 temperatures likely led to a decline in Oxygen concentration that promoted additional synthesis of
301 Hb.

302

303 In conclusion, we suggest that the sub-lethal stress response at multiple markers make *C. riparius* a
304 suitable biological tool for the assessment of short-term, sub-lethal effects of environmental change
305 in the field. The different temporal scales involved in the response of the two markers indicate that
306 a variety of impacts could be assessed prior to local extinction. Because the frequency of extreme
307 hydrological events is likely to increase in the future owing to global climate change, 'early-
308 warning' indicators could allow the rapid assessment of environmental degradation. As more
309 genomic data are made available, our approach could be extended to other taxonomic groups with
310 different environmental requirements and additional genetic markers.

311

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320

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492 **Supplementary material**

493

494 **Appendix 1.** Sample sizes (number of individual *C. riparius*) for each analysis in the study given
495 for each time point of collection in hours (h), with HSP70 = heat shock protein 70 mRNA
496 expression; Hb = haemoglobin concentration.

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Reach	Marker	Number of samples (<i>n</i>)				
		24h	48h	96h	192h	total
June – upstream	HSP70	7		7	7	21
	Hb	9	9	9	9	36
August – upstream	HSP70	7		7	7	21
	Hb	9	9	9	9	36
August – downstream	HSP70	7		7	7	21
	Hb	9	9	9	9	36

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504 **Appendix 2.** Newly designed forward (F) and reverse (R) primer sequences used for the RT- PCR
505 for heat shock protein 70 (HSP70) and β actin gene expression in *C. riparius*.
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Primer	Sequence
HSP70 F	5'-CATGTGAACGAGCCAAGAGA-3'
HSP70 R	5'-TCGAGTTGATCCACCAACAA-3'
β actin F	5'-GATGAAGATCCTCACCGAAC-3'
β actin R	5'-CCTTACGGATATCAACGTCG-3'

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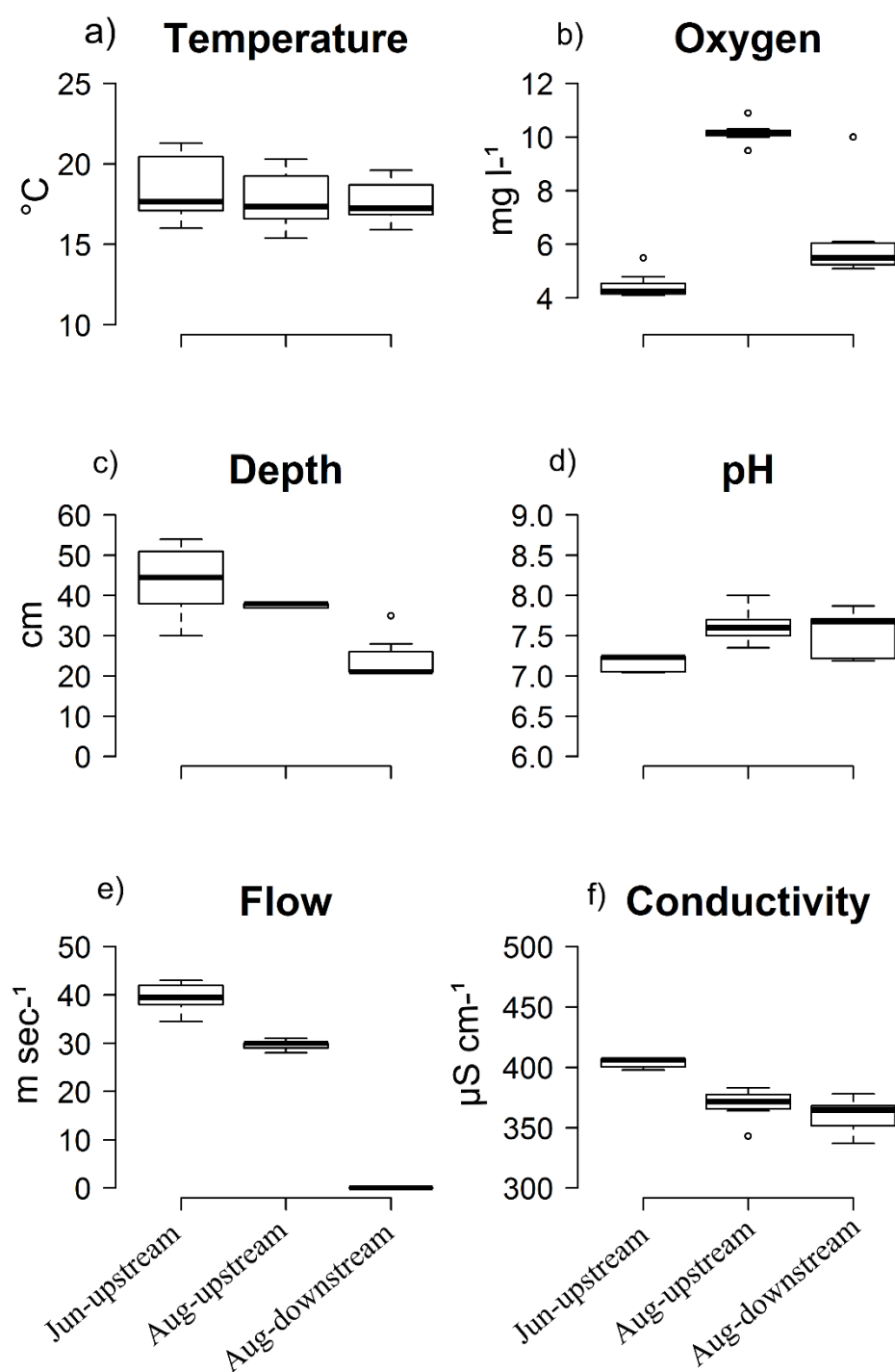
509 **Appendix 3.** Statistics from Spearman correlation test (scores under diagonal) and p-values (over
510 diagonal) for correlated environmental variables: oxygen (O_2 , $\text{mg O}_2 \text{ l}^{-1}$); temperature (T, $^\circ\text{C}$);
511 conductivity (Cond, $\mu\text{S cm}^{-1}$); pH; water flow (Flow, m s^{-1}); change in Oxygen (ΔO_2 , $\text{mg O}_2 \text{ l}^{-1}$);
512 changes in T (ΔT , $^\circ\text{C}$).

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	O_2	T	Cond	pH	Flow	ΔO	ΔT
O_2			*	***	*		
T							**
Cond	-0.489			**	***		
pH	0.664		-0.597		**		
Flow	-0.447		0.750	-0.530			
ΔO							
ΔT		0.565					

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519 **Appendix 4.** Environmental variables (panels a to f) (median, first and third quartile, minimum and
520 maximum) from data collected every 24 hours at 08:00 from 24h to 192 h of the experiments) in the
521 two reaches in June and August.
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