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1 **Title: Seasonal monitoring of cellular energy metabolism in a sentinel species, *Dreissena***  
2 ***polymorpha* (Bivalve): effect of global change?**

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9 **Keywords:** energy, ATP, *Dreissena polymorpha*, biomarkers

10 **Highlights:**

- 11 • Energy metabolism disturbances were observed from April to June 2019
- 12 • Asynchronous spawning between male and female organisms was noticed in 2019
- 13 • Markers are potentially proposed in a biomonitoring perspective

14 **Abstract:** Aquatic organisms such as bivalves are particularly sensitive to seasonal fluctuations  
15 associated with climate changes. Energy metabolism management is also closely related to  
16 environmental fluctuations. Changes in both biotic and abiotic conditions, such as the reproduction  
17 status and temperature respectively, may affect the organism energy status. A bivalve sentinel species,  
18 *Dreissena polymorpha* was sampled along its one-year reproduction cycle *in situ* (2018-2019) to study  
19 natural modulations on several markers of energy metabolism regarding seasonal variations *in situ*. A  
20 panel of different processes involved in energy metabolism was monitored through different functions  
21 such as energy balance regulation, mitochondrial density, and aerobic/anaerobic metabolism. The  
22 typical schema expected was observed in a major part of measured responses. However, the monitored  
23 population of *D. polymorpha* showed signs of metabolism disturbances caused by an external stressor  
24 from April 2019. Targeting a major part of energy metabolism functions, a global analysis of  
25 responses suggested a putative impact on the mitochondrial respiratory chain due to potential

26 pollution. This study highlighted also the particular relevance of *in situ* monitoring to investigate the  
27 impacts of environmental change on sentinel species.

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## 30 1. Introduction

31            Depending on scenarios, a 0.3 to 0.7°C increase is predicted in the mean Earth surface  
32 temperature by 2019 to 2035 (IPCC, 2014). The global climate change also includes the appearance of  
33 “exceptional” climatic events. These occurrences also bring important floods or droughts and may  
34 have an impact on aquatic populations. Since cellular energy production is dependent on multiple  
35 factors such as temperature, food availability or oxygen content (Sokolova et al., 2012), these events  
36 could significantly affect the metabolism management of organisms. Indeed, all biochemical and  
37 physiological processes are closely related to the amount of energy available within organisms  
38 (Frieder et al., 2017; Somero, 2010). Energy metabolism management is also closely related to natural  
39 environmental fluctuations. Seasonal temperature variations may lead to the establishment of  
40 adaptation and acclimation processes such as metabolic restructuring. Indeed, the aerobic metabolism  
41 can be favoured in order to improve the energy available for fitness-related functions including growth  
42 and reproduction (Hochaka and Somero, 2002; Salin et al., 2015; Sokolova and Pörtner, 2001;  
43 Sokolova et al., 2012). Environmental factors directly modulate cellular and mitochondrial energy  
44 management and the energy allocation to vital functions such as maintenance, growth, reproduction  
45 and reserves storage (Amiard and Amiard-Triquet, 2008; Hong et al., 2020; Verslycke et al., 2004). In  
46 invasive species, reproduction represents a large part of energy allocation (Louis et al., 2019).  
47 Seasonal modulations of water physicochemical parameters influence the gonadal maturation and  
48 spawning regulation. Fluctuations in energy investment priorities between vital functions have already  
49 been observed during the spawning in marine bivalves (Cheung, 1993; Louis et al., 2019; Petes et al.,  
50 2008). In this way, natural fluctuations monitoring could be a potential lead to understand energy  
51 metabolism management and ATP production in the model species, *Dreissena polymorpha*, along one  
52 reproduction cycle.

53            Mitochondria are the key organelles involved in multiple essential cellular processes (Lane,  
54 2005; Sokolov et al., 2019). They provide more than 90% of cellular ATP and serve as a cellular  
55 centre connecting energy metabolism, stress response, signalling and cell survival (Lane, 2007;  
56 Monlun et al., 2017; Naquet et al., 2016). Studies on different model species have demonstrated that

57 mitochondria are particularly sensitive to environmental stressors (Kurochkin et al., 2011; Sokolov et  
58 al., 2019; Sokolova et al., 2012). In such context, mitochondria are considered as a stress target and/or  
59 the coordinating centre of the adaptive cellular response (Eisner et al., 2018; Sokolova and Lannig,  
60 2008). Positive thermal stress is known to reduce ATP production leading thus to an increase of  
61 oxidative phosphorylation (OXPHOS) activity and of reactive oxygen species (ROS) production  
62 associated with oxidative damage in bivalve species (Cherkasov et al., 2010; Hraoui et al., 2020;  
63 Sokolova et al., 2005). The environmental temperature increase has been associated with a higher  
64 respiration rate, leading to a strong proton leak and a gradual mitochondria dissociation in *Crassostrea*  
65 *virginica* (Sokolova and Pörtner, 2001; Sokolova et al., 2005). An increase of mitochondrial damage  
66 could also engage the pathway of apoptosis in order to eliminate damage and ensure survival  
67 (Vakifahmetoglu-Norberg et al., 2017).

68 For freshwater risk assessment, integrative biomarkers are required in an active biomonitoring  
69 perspective. As the energy metabolism is crucial for all physiological reactions, several studies were  
70 realised to develop new energy markers in different model species. The energy cost of metabolism  
71 management against environmental disturbances have been discussed in several reviews (Calow,  
72 1991; Calow and Forbes, 1998; Sokolova et al., 2012). The scope for growth and/or the cellular energy  
73 charge was investigated in *Dreissena polymorpha* along a pollution gradient (Smolders et al., 2004) or  
74 after a metal stress (Louis et al., 2019). These studies pointed out a decrease of the energy allocation to  
75 growth and reproduction in presence of stress. Furthermore, the measurement of energy reserves is a  
76 useful tool to provide information about the global organism's energy available for maintenance,  
77 growth and reproduction (Palais et al., 2011; Sprung, 1995). The adenylate energy charge (AEC) is  
78 used as a biomarker of the global health status of the organisms (Le Gal et al., 1997, Smolders et al.,  
79 2004). After a chemical contamination, Sokolova et al. (2000, 2005) highlighted the decrease of the  
80 AEC in the oyster (*Crassostrea virginica*) and in the White Sea periwinkles (*Littorina spp*).

81 The zebra mussel, *Dreissena polymorpha* is an invasive filter feeder bivalve widespread in  
82 European freshwaters. Due to several biological characteristics such as its abundance, wide  
83 geographical distribution and high filtration activity, *D. polymorpha* has been used as a model species

84 for freshwater biomonitoring for several years (de Lafontaine et al., 2000; Faria et al., 2011, 2009;  
85 Kerambrun et al., 2016; Pain and Parant, 2007; Palais et al., 2011). At the cellular level, mitochondria  
86 activities are usually reflected by the electron transport system (ETS). Potet et al., (2016) have  
87 observed an increase of ETS activity under a metal stress and a decrease after a thermal or dietary  
88 stress in *D. polymorpha*. At the molecular level, some units of the OXPHOS were followed (ATP  
89 synthase and cytochrome c oxidase). It was shown that the relative gene expression level of ATP  
90 synthase increased in summer (Kerambrun et al., 2016).

91 In this study, cellular energy production (ATP) and management were monitored during one  
92 reproduction cycle *in situ*. The whole energy metabolism was targeted through different functions such  
93 as energy balance regulation, mitochondrial density and aerobic/anaerobic metabolism. Digestive  
94 gland was principally targeted for gene expression and enzymatic activities. Indeed, this organ,  
95 similarly to vertebrate liver, play a key role in detoxification mechanisms and has already been noticed  
96 as a target for bioaccumulation and biomarker analysis in mollusks (Faggio et al., 2018; Rodrigo and  
97 Costa, 2017). Furthermore, most of literature focused on digestive glands concerning biomarker  
98 analyses analysis (Faria et al. 2014; Potet et al. 2016, 2018; Louis et al., 2019). In parallel, energy  
99 reserves, condition index and the gonadal stage were analysed. As the respiratory chain may be a  
100 major source of ROS production, lipid peroxidation content was also measured. Our approach allows a  
101 better understanding of the physiology of *Dreissena polymorpha*, under changing natural fluctuations.  
102 Energy metabolism studies in *Dreissena polymorpha* are still too few and are only taking in account  
103 one or 2 parameters concerning energy management (Louis et al., 2019; Weber et al., 2020). A  
104 previous study of our laboratory aimed to characterise the reproduction cycle of the same population  
105 of dreissenids. Indeed, Palais et al. (2011) studied *D. polymorpha* gonadal development stage as well  
106 as reserves storage for one year. Since this sentinel species is commonly used for *in situ* monitoring, it  
107 is essential (1) to characterise the response pattern of monitored markers along the years and (2) to  
108 develop new and complemental markers of energy metabolism.

## 109 2. Material and Methods

### 110 2.1 Organisms collection

111 Specimens were hand-collected in the Meuse channel (Euville, France, E05°37'28'',  
112 N48°44'59'') for one reproduction cycle from May 2018 to June 2019 with a monthly or bimonthly  
113 frequency. This site was chosen since data about physiology responses were available on this  
114 population of *D. polymorpha* as well as the reproduction cycle characterisation along one year (Palais  
115 et al., 2011). Organisms with a length between 15 and 25mm were selected in a depth of 1.5m  
116 maximum. Organisms were measured and weighted in order to determine the condition index using  
117 the following formula: CI= fresh weight / volume (length x height x width). For gene expression and  
118 enzymatic activity analysis ( $n=12$  for each sampling time), digestive glands were dissected and snap  
119 frozen. For reserve contents measurement ( $n=12$ ), the whole organism was dissected and snap frozen.  
120 Whole body mussels were frozen for energy nucleotide contents analysis ( $n=10$ ). All of these  
121 procedures were done in the field, except for organisms intended to the gonadal development analysis  
122 that were quickly transported to the laboratory in field water ( $n=12$ ). All marker measurements were  
123 realized without taking into account organisms' gender. Dissections and freezing were performed at  
124 the sampling site in order to avoid mRNA and protein degradation and to limit marker measurements  
125 bias.

### 126 2.2 Environmental parameters

127 At each sampling time, physicochemical parameters were recorded. Water samples (10 L)  
128 were carried to the laboratory and processed for analysis in black container. Ammonium ( $\text{NH}_4$ ),  
129 nitrates ( $\text{NO}_2$ ), nitrites ( $\text{NO}_3$ ) and chlorophyll a (chl a) contents were measured by spectrophotometric  
130 analyses. Chemical oxygen demand and suspended matter were measured by electrochemical and  
131 gravimetric methods, respectively. The temperature was recorded every 10min from June 2018 to June  
132 2019 using two probes (TidbiT v2 Temp) installed on the site. The average temperature was calculated  
133 for each month.

### 134 **2.3 Gene expression**

135 Total RNA was extracted from digestive gland using TriReagent (Euromedex) following  
136 manufacturer's protocol. RNA integrity was estimated by UV revelation after electrophoresis on 1%  
137 agarose gel in TBE (Tris Borate EDTA 0.5%) buffer. RNA purity was estimated by the measurement  
138 of the ratio of absorbance at 260 and 280nm. Reverse transcription was performed on 400ng of total  
139 RNA using Verso cDNA Synthesis Kit (Thermo Scientific) according to manufacturer's instructions.  
140 The reaction was conducted at 42°C for 30min using a PCR Mastercycle (Eppendorf).

141 Gene expression levels were carried out by real-time quantitative PCR using Absolute Blue  
142 qPCR SYBR Green ROX Mix (Thermo Scientific) according to the manufacturer's protocol. Specific  
143 primers are given in Table 1. Energy balance regulation was studied through *ampk* (AMP-activated  
144 protein kinase) and *ampd* (AMP deaminase) gene expressions. Concerning the OXPHOS, three genes  
145 were selected: beta subunit ATP synthase (*atp*), cytochrome b (*cytb*), cytochrome c oxidase (*cox*) and  
146 succinate dehydrogenase (*sdh*). Another unit of the respiratory chain, the alternative oxidase (*aox*) was  
147 recorded. Gene expression levels were also measured for citrate synthase (*cs*) and lactate  
148 dehydrogenase (*ldh*), an anaerobic metabolism enzyme. The optimal primer quantity was evaluated  
149 across a range of concentrations between 150 and 600nM. Dilutions of the cDNA mixture between  
150 1:10 and 1:1000 were tested to calculate the PCR efficiency. The PCR steps consisted in 15 min initial  
151 denaturation at 95°C followed by 40 cycles of heat denaturation at 95°C for 10sec, annealing at 60°C  
152 for 60sec and were carried out in a CFX Manager (BioRad) on 1/10<sup>e</sup> of ADNc. The relative gene  
153 expression level was calculated using the Pfaffl method (Pfaffl, 2001) taking into account the PCR  
154 efficiency and normalized by the geometric mean of the two housekeeping genes (actine and  
155 ribosomal protein S3) according to Navarro et al. (2011).

### 156 **2.4 Enzymatic activities**

157 The set of enzymatic activities was individually measured in each mussel. The digestive  
158 glands were weighted and crushed in 50mM phosphate buffer containing protease inhibitors (pH 7.6,  
159 supplemented with 1mM phenylmethylsulfonyl fluoride and 1mM L-serineborate) at 8:1 (v/w) ratio.



160 Samples were then centrifuged (3000g, 10min, 4°C). The supernatant was collected for the enzymatic  
161 activity measurement. Assays were performed with an automated spectrophotometer (Galery,  
162 ThermoScientific) and with a spectrofluorimeter (SAFAS, Xenius). ETS, lactate dehydrogenase  
163 (LDH) as well as proteins content and lipid peroxidation were measured according to Garaud et al.  
164 (2016) and Potet et al. (2016). Caspase-3 activity was measured according to Garaud et al. (2016) in  
165 cytosolic extract.

166 For cytochrome c oxidase (COX) activity, supernatant was diluted to 1:45 in 100mM Tris  
167 buffer (pH 8.1). Reduced cytochrome c at 1mM (Merck) supplemented with 16% of ascorbate (Merck)  
168 was added to the previous dilution. Cytochrome c oxidation was then monitored for 3min at 550nm.  
169 For citrate synthase (CS) activity, supernatant was diluted to 1:55 in 0.1M Tris buffer (pH 8.1)  
170 supplemented with 0.15mM DTNB (Merck) and 0.2mM acetyl co enzyme A (Merck). The activity  
171 was first monitored 3min at 420nm. A second measure was performed after the addition of 4mM  
172 oxaloacetate (Merck). Enzymatic activity was expressed in  $U \cdot g^{-1}$  proteins (molar extinction coefficient  
173 ( $\epsilon$ ) reduced cytochrome c =  $7040M^{-1} \cdot cm^{-1}$ ,  $\epsilon$  oxaloacetate =  $14140M^{-1} \cdot cm^{-1}$ ).

## 174 **2.5 Energy reserve contents**

175 Organisms were weighted and crushed in 50mM phosphate buffer (pH 8) at 5:1 (v/w) ratio.  
176 Protein, lipid and glycogen contents were measured on the homogenate. Protein content was  
177 determined by the Bradford's method. Lipid and glycogen contents were measured according to the  
178 method of Van Handel (1985) and adapted by Plaistow et al. (2001). Results were expressed in  $mg \cdot g^{-1}$   
179 of fresh weight (FW).

## 180 **2.6 Energy nucleotide contents**

181 Nucleotides extraction was realised as described by Sokolova et al. (2005). Briefly, frozen  
182 mussels were quickly dissected and lyophilized for 48h. Samples were then crushed in 0.6M  
183 perchloric acid (Merck) solution, centrifuged (3000g, 10min, 4°C) and the supernatant was collected.  
184 The pH of each extract was adjusted to 5 - 6.5 with 5mM potassium hydroxide and 1M bicine solution.  
185 Precipitated potassium perchlorate was removed by a second centrifugation. Extracts were then

186 filtered (0.45µM) and stored at -80°C. Concentrations of ATP, ADP, AMP and IMP were measured  
187 with an HPLC system and Nucleosic C18 column (Nucleosil) according Sokolova et al. (2005). The  
188 separation was performed at a flow rate of 0.8ml.min<sup>-1</sup> using a mobile phase of 1M phosphate buffer  
189 with 5% methanol (pH 6) for 15min. Nucleotide contents were monitored at 254nm and nucleotide  
190 quantifications were calculated using ATP, ADP, AMP and IMP standards (Sigma) of 20, 10, 2 and  
191 10µM, respectively.

192 Adenylate energy charge (AEC) was calculated from the tissue concentrations of adenylates as  
193 follows:

$$194 \text{ AEC} = \frac{[\text{ATP}] + 0.5 \times [\text{ADP}]}{[\text{ATP}] + [\text{ADP}] + [\text{AMP}]}$$

## 195 **2.7 Gonadal development analysis**

196 Dissected organisms (without byssus and shell) were fixed in Bouin's aqueous solution for  
197 24h followed by successive alcohol dehydration baths from 50° to 100°. After deshydration, sampled  
198 were placed in a butanol solution in order to permeate all tissues. Samples were then paraffin-  
199 embedded and 7µM sections were prepared from the foot to gonads of organisms. Sections were  
200 stained with picro indigo carmin and solid nuclear red and observed with a microscope to sex the  
201 gonads and to assign them to a development stage (Gist et al., 1997; Palais et al., 2011). This method  
202 was based on the size and the number of present oocytes as well as spermatogenesis steps.

## 203 **2.8 Statistical analysis**

204 Marker responses were analysed by a one-way ANOVA to assess time effect. Parametric  
205 (Tukey) or non-parametric (Kruskal-Wallis) post-hoc tests were processed on markers and obtained *p*-  
206 values were adjusted for multiple comparisons by a correction method (Benjamini and Hochberg).  
207 Normality and homoscedasticity of the data were tested with Shapiro and Bartlett tests respectively.  
208 Correlations were performed on the total data set. A clustered map was built on a complete linkage  
209 using Euclidean distance measures between different variables. The obtained values can be seen as a  
210 robust approximation of the Pearson correlation. A global analysis of biomarker results was also  
211 performed with a Partial Least Square Discriminant Analysis (PLS-DA) to identify the overall

212 capacity of biomarkers to discriminate the months and to define the most relevant markers among the  
213 battery. Relevance of marker responses was based on the individual role of each marker in the overall  
214 model, estimated by the VIP (Variable Importance in the Projection). Only markers with a  $VIP > 1$   
215 were considered significant in the model (PLS-DA). Since only four organisms could be sampled in  
216 February (used for gene expression) and 16 in March 2019 (4 for gene expression, 4 for enzymatic  
217 activity, 4 for nucleotide contents and 4 for histology), the results obtained for these months are  
218 presented in the different figures but the data were excluded for statistical analysis. A threshold of  $p <$   
219  $0.05$  was considered significant. Statistical analyses were performed using R software (R Development  
220 Core Team, 3.5.0).

## 221 **3. Results**

### 222 **3.1. Environmental parameters**

223 Water physicochemical features are reported in Table 2 and Fig. 1. Water temperature varied  
224 seasonally, the lowest values were recorded in fall (November) and the highest values were recorded  
225 in summer (August). Strong daily temperature variations were observed in August ( $5^{\circ}\text{C}$  min -  $30^{\circ}\text{C}$   
226 max) and November ( $-2^{\circ}\text{C}$  min –  $20^{\circ}\text{C}$  max). In 2019, suspended matter values were higher than in  
227 2018 as well as the mean of nitrates contents. May and June 2019 chl a levels were not detected. All  
228 physicochemical parameters measured along the study complied with the framework directive on  
229 water (2000/60/CE, 2000).

### 230 **3.2. Reproduction cycle**

231 Gonadal development stages are presented in Fig. 2. Since only one male was observed in  
232 November 2018 in histological analysis, the male gonadal index could not be determined. In 2018,  
233 males spawned their gametes between July and September (Fig. 2A) and females between May and  
234 August (Fig. 2B). The spawning events were synchronous for both sexes in 2018. Females' gonadal  
235 development seemed to be more premature than males' development in 2019. A shift was observed  
236 between males and females' gonadal stage between April and June 2019. Indeed, the spawning of

237 oocytes began in April when males were halfway between maturation and pre-spawn stage. In  
238 addition, in June 2019, all the females had spawned their gametes whereas no male had spawned  
239 theirs. It is also necessary to take into account the sampling randomness resulting in a sex ratio rarely  
240 equals to 1:1.

### 241 **3.3. Global health status**

242 Condition index (CI) (Fig. 3A), lipid and protein contents (Fig. 3C-D) showed globally the  
243 same response variations. CI values decreased just after the spawning (July and August 2018) and then  
244 gradually increased until the next reproduction period (from September 2018 to April 2019). Lipid  
245 contents also decreased in reproduction period (from August to November 2018) and increased from  
246 April 2019. Although protein content variations were less marked, it decreased during the gametes  
247 spawning and then increased again. Concerning glycogen reserves (Fig. 3B), a significant decrease  
248 was observed in August 2018 followed by a significant increase until November 2018 (5-10mg.gFW<sup>-1</sup>  
249 <sup>1</sup>). From April 2019, glycogen content reached the same level as in August 2018 (< 2mg.gFW<sup>-1</sup>).

### 250 **3.4. Mitochondria efficiency**

251 Mitochondria efficiency was assessed in our study by the OXPHOS and the citrate synthase  
252 activity and transcriptional level. CS activity increased during the pre-reproduction and reproduction  
253 periods while trend to decrease during post reproduction and rest (Fig. 4A). Concerning COX activity,  
254 a significant decrease since April 2019 was observed (Fig. 4B). The ETS activity showed a 2-fold  
255 increase in June 2018 and came back to lower level in July and August (Fig. 4C). A gradually increase  
256 was then observed from September 2018 to June 2019. Globally, relative gene expression levels  
257 exhibit two distinct patterns. OXPHOS subunits genes (*cox*, *atp* and *cytb*) reach their highest levels  
258 during the pre-reproduction and reproduction periods while they exhibited a marked decrease during  
259 post reproduction and rest periods (Fig. 5A-B-C). On the contrary, citrate synthase gene expression  
260 (*cs*) level was significantly higher during the rest period (Fig. 5D). No difference of *sdh* relative gene  
261 expression level could be noticed along the year (Fig. S1).

### 262 3.5. Energy balance

263 Energy balance regulation was studied through *ampk* and *ampd* gene expressions (Fig. 6). The  
264 transcript levels of *ampk* (Fig. 6A) gradually increased from May 2018 to November 2018 and  
265 decreased significantly in April 2019. Levels stayed low until June 2019. Although no significant  
266 difference could be observed, the expression of *ampd* gene (Fig. 6B) showed the same pattern of  
267 variation. ATP and ADP contents presented a similar progression over the year than *ampk* and *ampd*  
268 gene expression levels (Fig. 7, part I: A-B). Energy nucleotides concentration was stable from May  
269 2018 to September 2018. A strong increase was observed in November 2018 followed by an important  
270 reduction of ATP and ADP contents in April 2019. The pattern of AMP and IMP contents were  
271 similar but they slightly differed from the previous markers (Fig. 7, part I: C-D). Indeed, the  
272 concentration of these nucleotides were stable from May 2018 to August 2018 and gradually increased  
273 until April 2019 where they reached a steady state ( $p < 0.05$ ). A correlation was observed between  
274 ATP content and the expression of *ampd* involved in energy balance regulation but also with *cs* gene  
275 expression, glycogen and lipid contents (Table S1). The AEC remained stable from May 2018 to  
276 November 2018 (0.5-0.7). Nevertheless, a significant decrease was observed in April 2019 (0.13-0.32)  
277 (Fig. 7, part II).

### 278 3.6. Stress markers

279 Anaerobic metabolism was assessed through *ldh* gene expression and LDH activity, both  
280 presenting a similar pattern of responses (Fig. 8 A-B). Values were higher in pre-reproduction and  
281 reproduction periods than during post-reproduction and rest periods. A gradual increase of *aox* relative  
282 gene expression was observed from May 2018 to August 2018 and it decreased until June 2019 (Fig.  
283 8C). On the contrary, lipid peroxidation (LOOH) content was stable from May 2018 to November  
284 2018, while it displayed a significant increase from April 2019 compared to July and August 2018  
285 (Fig. 8D). LOOH concentration was negatively correlated with condition index, energy reserves  
286 (lipids and glycogen). Positive correlations were also observed between LOOH and LDH activity and  
287 AMP/IMP contents (Table 3). Caspase-3 (CSP3) activity was measured only on 7 sampling times

288 (May, June, July, August and November 2018 and May and June 2019). Its activity increased  
289 significantly from November 2018 to June 2019 (Fig. 8E). Negative correlation between CSP3 activity  
290 and *cytb* gene expression was noticed while positive correlation with stress markers like LOOH  
291 measurements ( $r^2 = 0.57$ ,  $p < 0.05$ ) and IMP/AMP contents were observed (Table 3).

### 292 **3.7. Global analysis**

293 A PLS-DA model was built and explained 68.2% of between-month variance with the two  
294 first axis. The first three VIP markers were *atp*, *cs* and *ldh* gene expressions (Table S2). Caspase-3  
295 activity was excluded of the total data set.

296 The PLS model built explained 70.6% of between physico-chemical parameters variance with  
297 the two first axis. PLS allowed us to identify the importance of each parameter on biological  
298 responses. A clustered map was then built. The rows and columns were reordered according to  
299 hierarchical clustering method to identify interesting patterns. According to the cluster results (Fig. 9),  
300 stress markers as LOOH and IMP content, condition index and LDH activity were strongly positively  
301 correlated with suspended matter, nitrate and oxygen contents and negatively correlated with  
302 temperature and the content of ammonium. Conversely, *aox* gene expression was negatively correlated  
303 with suspended matter and oxygen content and positively correlated with temperature and the content  
304 of ammonium. Furthermore, cluster results highlighted that environmental parameters such as nitrites  
305 and chl a content had no effect on biological responses along the reproductive cycle. Some biological  
306 responses as *sdh*, *cox*, *cs*, *ampd*, *atp* relative gene expression and ATP content were not influenced by  
307 measured environmental parameters.

### 308 **4. Discussion**

309 The aim of this study was to understand the effect of natural fluctuations and intrinsic  
310 variations on global energy metabolism in the model species *Dreissena polymorpha in situ*.

#### 311 4.1. Global status

312 According to our observations, *D. polymorpha* exhibited a typical annual reproductive cycle  
313 with a gonad development phase during fall, a maturation and spawning phase in spring–summer and,  
314 if present, a resting phase at the end of the summer (males). These observations are consistent with the  
315 reproductive patterns previously described in *D. polymorpha* populations (Binelli et al., 2004; Juhel et  
316 al., 2006; Mackie and Ontario, 1990; Palais et al., 2011). In 2019, the expected reproductive cycle was  
317 observed but the reproduction period was asynchronous between males and females. No reason was  
318 bringing out to explain this observation. Indeed, natural media are continuously submitted to several  
319 perturbations. This asynchronous spawning could be a consequence of a potential pollution or an  
320 accumulation of different exceptional events like drought or flood periods. Concerning energy  
321 reserves, lipid content followed the reproduction cycle with a significant decrease in August 2018  
322 concurrently with gamete emission, similarly to what is reported by Kwan et al. (2003), Hassan et al.  
323 (2018) and Hong et al. (2020). Since females were mostly represented in our samples for histology  
324 analysis, the high lipid content observed until April 2019 might be explained by the accumulation of  
325 lipid nutrients in the oocytes (Palais et al., 2011). According to our results, glycogen content increased  
326 after spawning of the gametes and decreased in April 2019. Tourari et al. (1988) shown that glycogen  
327 was largely used for the formation of the gametes and the gonadal tissues during gametogenesis and is  
328 especially converted into lipid materials in maturing oocytes in *Dreissena polymorpha*. These  
329 observations were also highlighted in oysters through an increase of glycogen content in pre-  
330 reproduction period followed by a net decrease during the spawning one (Hong et al., 2020). However,  
331 in our study, glycogen storage was significantly lower from April to June in 2019 compared to the  
332 same period in 2018. Reproduction cycle and glycogen content observations did not follow the schema  
333 described for *Dreissena polymorpha* and others bivalves' species (Hong et al., 2020; Palais et al.,  
334 2011; Ram et al., 1996, 1993). Glycogen might have been used simultaneously for the gamete  
335 development and spawning as well as for other cellular energy demands since glycogen is a main  
336 source of energy in organisms (Anacleto et al., 2013; Andrade et al., 2017; Cordeiro et al., 2016,  
337 2017).

## 338 4.2. Energy metabolism

339 Globally, energy metabolism appeared to be more active during the pre-reproduction and the  
340 reproduction periods than during the post-reproduction and rest periods. The respiratory chain units  
341 (i.e. *cox*, *atp*, and *cytb* gene expressions) presented the same pattern of responses as the anaerobic  
342 metabolism markers (*ldh* gene expression and LDH activity). Study of the ETS activity during two  
343 years on *D. polymorpha* showed similar responses with an increase of the activity from May to June of  
344 each year (Fanslow et al., 2001). According to our results of *ampk* relative expression level, a  
345 significant decrease was observed from April 2019 compared to November 2018. An accumulation of  
346 AMP was simultaneously measured in the organisms. As the AMPk is activated by high AMP  
347 concentrations (Chauhan et al., 2020; Fredrich and Balschi, 2002), the decrease of *ampk* relative  
348 expression might be the result of a negative feedback. This negative feedback could also be applied to  
349 the *ampd* relative gene expression modulation as this enzyme is activated by AMP intracellular  
350 concentration too (O'Brien et al., 2017; Składanowski et al., 2005). Higher production of ATP should  
351 be observed consequently to counterbalance AMP accumulation and maintain a positive energy  
352 balance. However, in our study, a significant decrease in ATP content was observed from April 2019  
353 while ETS activity seemed to remain stable. The oxygen consumed in the mitochondria is directly  
354 linked to the flow of electrons and the synthesis of ATP by the ATPsynthase. However, part of this  
355 flow can be shunted by an alternative route which bypasses the respiratory chain before complex III.  
356 Hence, especially in the presence of low levels of COX activity, the electron transport system  
357 contributes less to the driving force of the protons, and from there to the production of ATP. Thus  
358 from March to April 2019, the AOX activity could maintain the ETS level in parallel with a decrease  
359 in the ATP level. All these observations suggesting thus an imbalance of the energy metabolism.

360 The observed increase in IMP and AMP concentrations may activate glycogen phosphorylase  
361 and further enhance glycolysis and the tricarboxylic acid (TCA) cycle when the demand for ATP  
362 production increases (Han et al., 2016). Decreased glycogen content observed could be a consequence  
363 of the accumulation of IMP and AMP in organisms. CS catalyses condensation of the acetyl group of  
364 acetyl-CoA with oxaloacetate forming citrate. It represents the first step of the TCA cycle (Eprintsev



365 et al., 2018). Products provided by TCA cycle are then used by the respiratory chain in order to  
366 produce ATP. In our study, CS activity increased during the pre-reproduction and reproduction  
367 periods as well as *atp*, *cytb* and *cox* relative gene expression levels. These results were already  
368 observed through an *atp* and *cox* relative expression increasing during spring and/or summer  
369 (Kerambrun et al., 2018; Navarro et al., 2011). These results suggest an increase in the respiratory  
370 chain functioning during pre-reproduction and reproduction periods. Although it is difficult to  
371 compare a gene expression with the activity of the corresponding enzyme, a global suppression of the  
372 metabolic rate was observed when all biological responses are considered. Indeed, COX activity and  
373 ATP content decreased significantly while ETS activity and LOOH measurements increased from  
374 April 2019 to June 2019. Meanwhile, the caspase-3 (CSP3), a protease involved in apoptosis, was  
375 significantly more active. In addition, CSP3 activity was also correlated with the expression of  
376 OXPHOS-related genes and IMP concentrations. Caspase activation and apoptosis are associated with  
377 a decline in ATP levels and a production of reactive oxygen species (ROS) (Ricci et al., 2004; Sharma  
378 et al., 2017). The changes in metabolic processes and CSP3 activity suggest an activation of apoptosis  
379 pathway likely resulting from a global stress.

#### 380 **4.3. A global response overview**

381 The multivariate analysis allowed us to consider the modulations of the whole panel of  
382 markers. This method showed that some markers were positively or negatively correlated with  
383 environmental parameters. The contents of IMP and LOOH, and LDH activity are modulated by  
384 stressing conditions (Falfushynska et al., 2014; Lushchak, 2011). LDH activity is a marker of global  
385 stress whereas lipid peroxidation is used as an indicator of oxidative stress. AMP deaminase protein  
386 catalyses the hydrolysis of AMP to form IMP and ammonia. AMPd and AMPk proteins play a role in  
387 the energy balance and its regulation. An intracellular AMP content increase reflects an enhanced use  
388 of ATP. To avoid the accumulation of AMP, the AMPd converts it into IMP thus suggesting that some  
389 stress is challenging the organisms (Lushchak, 2011). In our study, these markers were correlated to  
390 all analysed environmental factors except for chl a and nitrite contents. Moreover, lipid peroxidation  
391 was positively correlated with IMP and lipid concentrations. The global health status of the organisms

392 seemed to be affected *in situ* through the induction of stress markers like IMP and LOOH. According  
393 to our global analysis, suspended matter and nitrate concentrations seemed to be associated with an  
394 impact on energy metabolism of *D. polymorpha*.

#### 395 **4.4. Exceptional events: a long-term impact?**

396         There was a significant increase in the frequency and the intensity of meteorological and  
397 hydrological events (EEA, 2007). In the Meuse department, drought periods were recorded in summer  
398 2018 and 2019. The year 2018 was characterized by an exceptional drought that led to placing the  
399 entire department in a situation of alert that was extended from August to December. This prefectural  
400 decree was renewed in summer 2019 (Decree of the 8<sup>th</sup> August 2019 on the water use). Drought events  
401 may have more effects than flood periods on aquatic organisms due to their duration and large spatial  
402 impacts (Hrdinka et al., 2012). The decrease in the water column height leads to a more drastic  
403 increase in water temperature (van Vliet and Zwolsman, 2008). According to our *in situ* observations  
404 in summer 2018, the temperature stayed above 25°C during three weeks in July and August. *D.*  
405 *polymorpha* is an ectotherm organism with a lethal temperature in acute stress between 35°C and 37°C  
406 (Spidle et al., 1995). Several studies reported optimal temperatures for the reproduction, the  
407 development and the survival of *D. polymorpha* between 10°C and 20°C (bij de Vaate et al., 2002;  
408 Ram et al., 1993; Sprung, 1995). Drought periods observed may also have an impact on the  
409 physiology of organisms. Seasonal acclimation to different temperatures changes the tolerance  
410 window for invertebrates due to a switch in energy metabolism management in order to assure vital  
411 functions related to the fitness (Jost et al., 2015; Lannig et al., 2006; Sokolova et al., 2000). Based on  
412 our results, in 2018, temperature varied up to 20°C (November) and 25°C (August) in one day.  
413 Populations of *D. polymorpha* are usually hand-sampling close to the shore. These populations are  
414 also submitted to the strong variations that may have an impact on physiology of mussels, changing  
415 thus their global status. Temperature is also known to have a synergic effect together with  
416 contaminants (Cherkasov et al., 2010; Lannig et al., 2006; Soon and Zheng, 2019). Energy cost caused  
417 by natural fluctuations and exceptional events repetition might make organisms more vulnerable to  
418 anthropic pollution at long term and impact population dynamics.

#### 419 **4.5. Water physicochemistry and biological responses: a potential pollution?**

420 Physicochemical parameters like pH, temperature and ion concentrations ( $\text{NO}_3^-$ ,  $\text{PO}_4^{3-}$ ) are  
421 known to regulate the distribution of *D. polymorpha* populations (McMahon, 2002; Ramcharan et al.,  
422 1992). The values recorded for pH and temperature in the Meuse channel from May 2018 to June 2019  
423 were consistent with the ecological requirements of the species (Ramcharan et al., 1992). However, a  
424 peak of nitrate and phosphate concentrations ( $31\text{mg.L}^{-1}$  and  $0.126\text{mg.L}^{-1}$  respectively) was noticed in  
425 December 2018 in the Meuse channel 20km from the sampling site. These concentrations remained  
426 stable until February 2019 ( $31\text{-}25.96\text{mg.L}^{-1}$   $\text{NO}_3^-$  and  $0.120\text{-}0.114\text{mg.L}^{-1}$   $\text{PO}_4^{3-}$ ) (French Water Agency  
427 data and Table 2). According to the Water Framework Directive, a maximum concentration of  
428  $50\text{mg.L}^{-1}$  of nitrates is defined as a threshold for a “good” ecological status by the regulation  
429 (2000/60/CE, 2000). However, studies showed that effects on aquatic fishes might be observed at  
430 lower concentrations after 30 days of exposure (Camargo et al., 2005). Alonso and Camargo (2003)  
431 exposed the mollusc *Potamopyrgus antipodarum* to N- $\text{NO}_3^-$  to evaluate the  $\text{LC}_{10}$  at 24, 48, 72 and 96h.  
432 The calculated  $\text{LC}_{10}$  values were divided by 2 between 24h (1128 ppm) and 96h (585 ppm) of  
433 exposure. Similar observations were highlighted after a 14-days chronic exposure with a  $\text{LC}_{50}$  divided  
434 by 10 between 1 and 14 days (Benítez-Mora et al., 2014). Camargo et al. (2005) concluded that LC  
435 measured values may be divided by a factor 18 to 20 between acute and chronic exposures. However,  
436 to our knowledge, no data are available on the effect of nitrates in *D. polymorpha*. Simultaneous  
437 presence of nitrates and orthophosphates is known to reflect a pesticides pollution (Majumdar and  
438 Gupta, 2000). Based on the DCE legislation, the limit of pesticides emission is  $0.5\text{mg.L}^{-1}$  in  
439 freshwaters (2000/60/CE, 2000). In December 2018, total pesticides concentration was  $0.495\text{mg.L}^{-1}$   
440 (French Water Agency data). Several pesticides targeting the mitochondria, and especially the  
441 respiratory chain, are extensively found in freshwaters. Nevertheless, more information would be  
442 necessary to approve the hypothesis of a potential pesticide impact on organism’s mitochondria.

## 443 5. Conclusion

444 This study bring deeper knowledge in the management of energy metabolism in a sentinel  
445 species, *D. polymorpha*, in order to develop new potential biomarkers in a biomonitoring perspective.  
446 According to our results, three genes involved in ATP production could constitute potential  
447 biomarkers. Indeed, *sdh*, *atp* and *cs* genes expression were not influenced by natural seasonal  
448 fluctuations. Complementary studies are necessary to confirm their relevance as potential biomarkers.  
449 Targeting a major part of energy metabolism and globally analysing their responses allowed us to  
450 suggest a putative impairment of mitochondrial respiratory chain, likely resulting from an *in situ*  
451 perturbation. Indeed, the monitored population of *D. polymorpha* seemed to be impacted by an  
452 external stress from April 2019. Natural environments are subjected to multiple stressors and it is  
453 impossible to know the origin of the perturbations. However, flood and drought periods associated  
454 with high temperature variations in only one day or during several days may sensitize the organisms to  
455 potential chemical stress and could affect vital functions. The asynchronous gonadal development  
456 between males and females observed in 2019 as well as the metabolic depletion could be a  
457 consequence of exceptional climatic events associated with the pollution. Beyond the characterisation  
458 of the energy metabolism management in *D. polymorpha* along one reproduction cycle, this study  
459 highlighted the relevance of *in situ* monitoring in particular to investigate the impact of global change  
460 on sentinel species.

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Figure 1. Temperature continuously measured on sampling site. The mean, minimum and maximum temperature are presented.

Figure 2. Gonadal development stage for males (A) and females (B) according to the months. Different development stages are presented in terms of percentage of each stage ( $n=12$ ).

Figure 3. Condition index ( $n=60$ ) (A), glycogen (B), lipids (C) and proteins (D) content ( $n=12$ ) according to the months. Data are presented as median  $\pm$  SD, min, max. Different letters indicate significant differences between months ( $p < 0.05$ ).

Figure 4. CS (A), COX (B) and ETS (C) activities according to the months. Data are presented as median  $\pm$  SD, min, max ( $n=12$ ). Different letters indicate significant differences between months ( $p < 0.05$ ).

Figure 5. *atp* (A), *cox* (B), *cytb* (C) and *cs* (D) relative gene expression levels according to the months. Data are presented as median  $\pm$  SD, min, max ( $n=12$ ). Different letters indicate significant differences between months ( $p < 0.05$ ).

Figure 6. *ampk* (A) and *ampd* (B) relative gene expression levels according to the months. Data are presented as median  $\pm$  SD, min, max ( $n=12$ ). Different letters indicate significant differences between months ( $p < 0.05$ ).

Figure 7. Part I: ATP (A), ADP (B), AMP (C) and IMP (D) contents. Part II: adenylate energy charge (AEC). Results are presented according to the months and data are expressed as median  $\pm$  SD, min, max ( $n=12$ ). Different letters indicate significant differences between months ( $p < 0.05$ ).

Figure 8. *ldh* relative gene expression level (A), LDH activity (B), *aox* relative gene expression level (C), lipid peroxidation (LOOH) (D) and caspase-3 activity (E) according to

the months. Data are expressed as median  $\pm$  SD, min, max ( $n=12$ ). Different letters indicate significant differences between months ( $p < 0.05$ ).

Figure 9. Hierarchical cluster analysis (complete linkage using Euclidean distance measures) applied on the PLS model. The values in the similarity matrix can be seen as a robust approximation of the Pearson correlation. The rows and columns were reordered according to some hierarchical clustering method to identify interesting patterns. SM: suspended matter; COD: chemical oxygen demand.

### **Supplementary data:**

Figure S1. *sdh* gene expression level according to the months. Data are expressed as median  $\pm$  SD, min, max ( $n=12$ ). Different letters indicate significant differences between months ( $p < 0.05$ ).



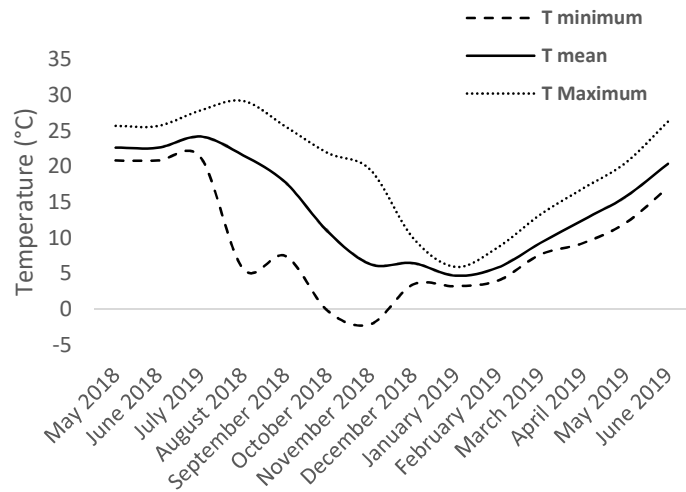


Figure 1.

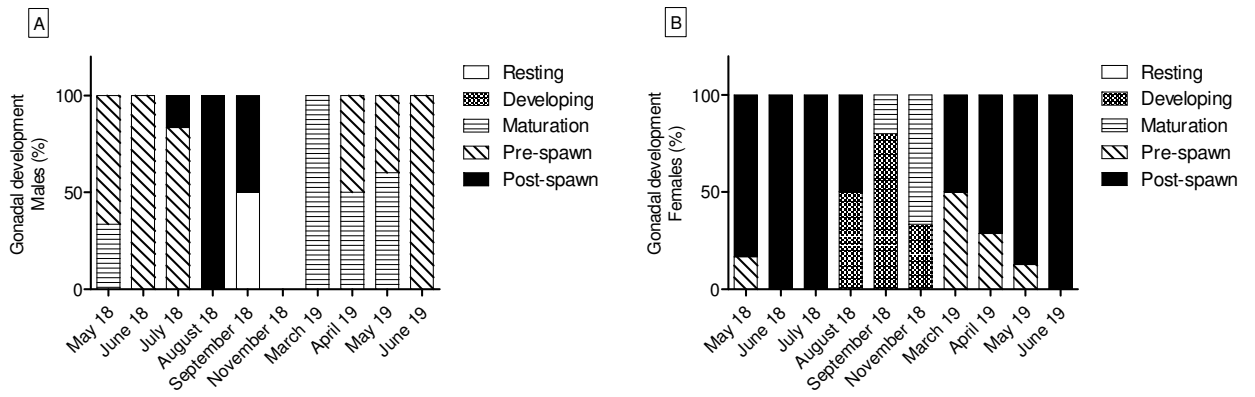


Figure 2.

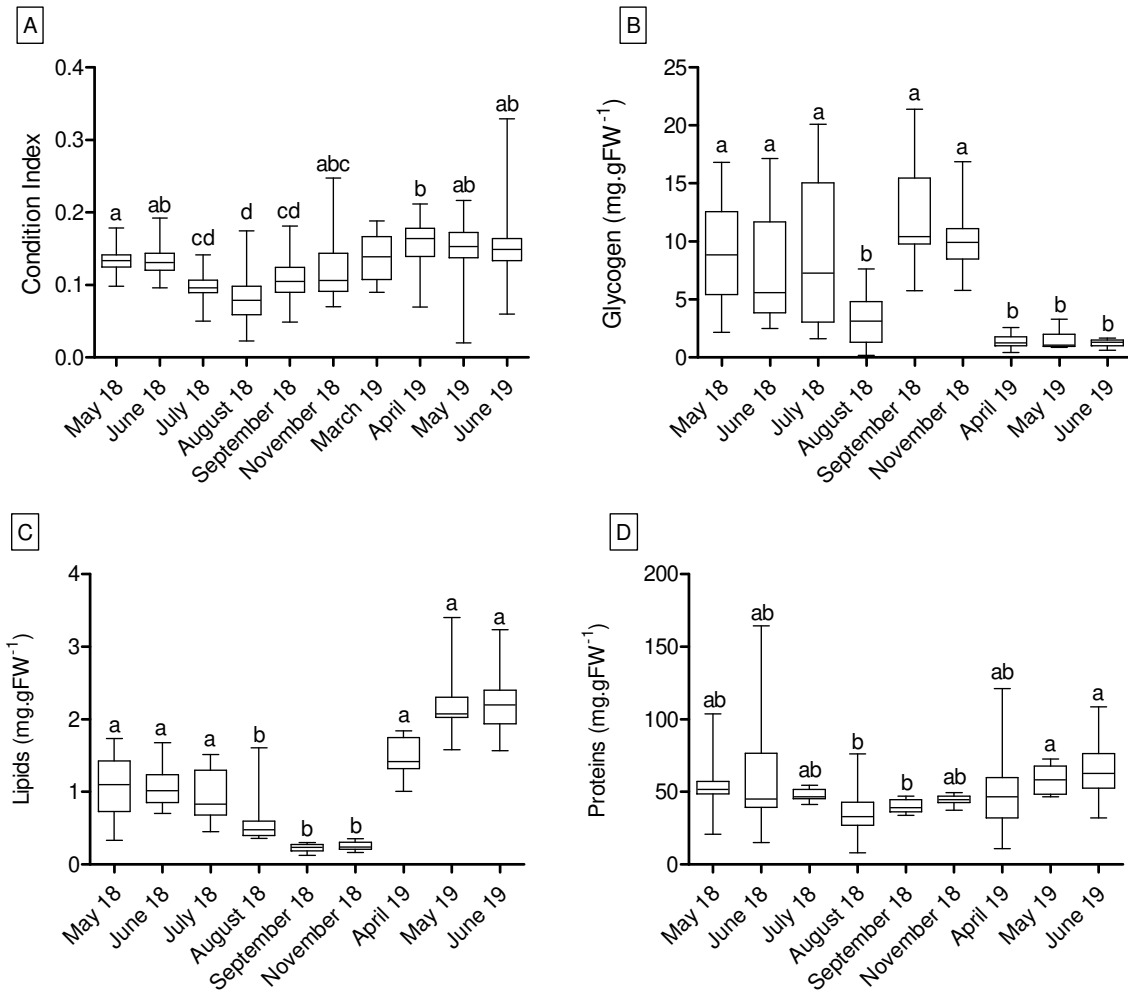


Figure 3.

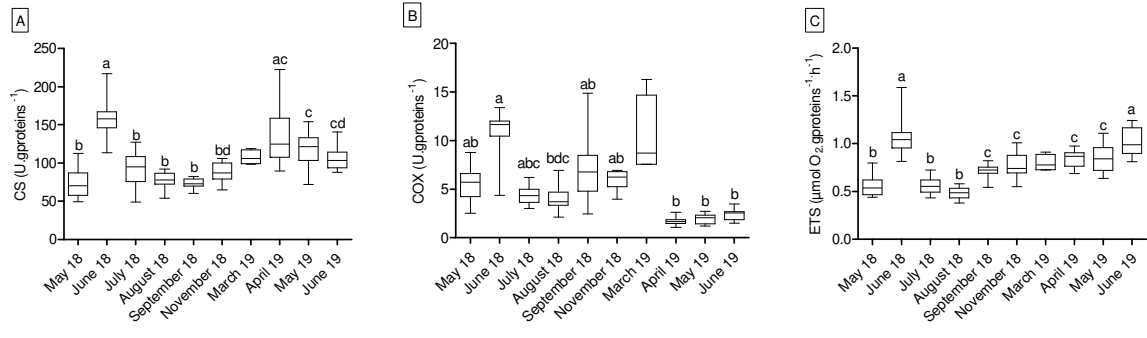


Figure 4.

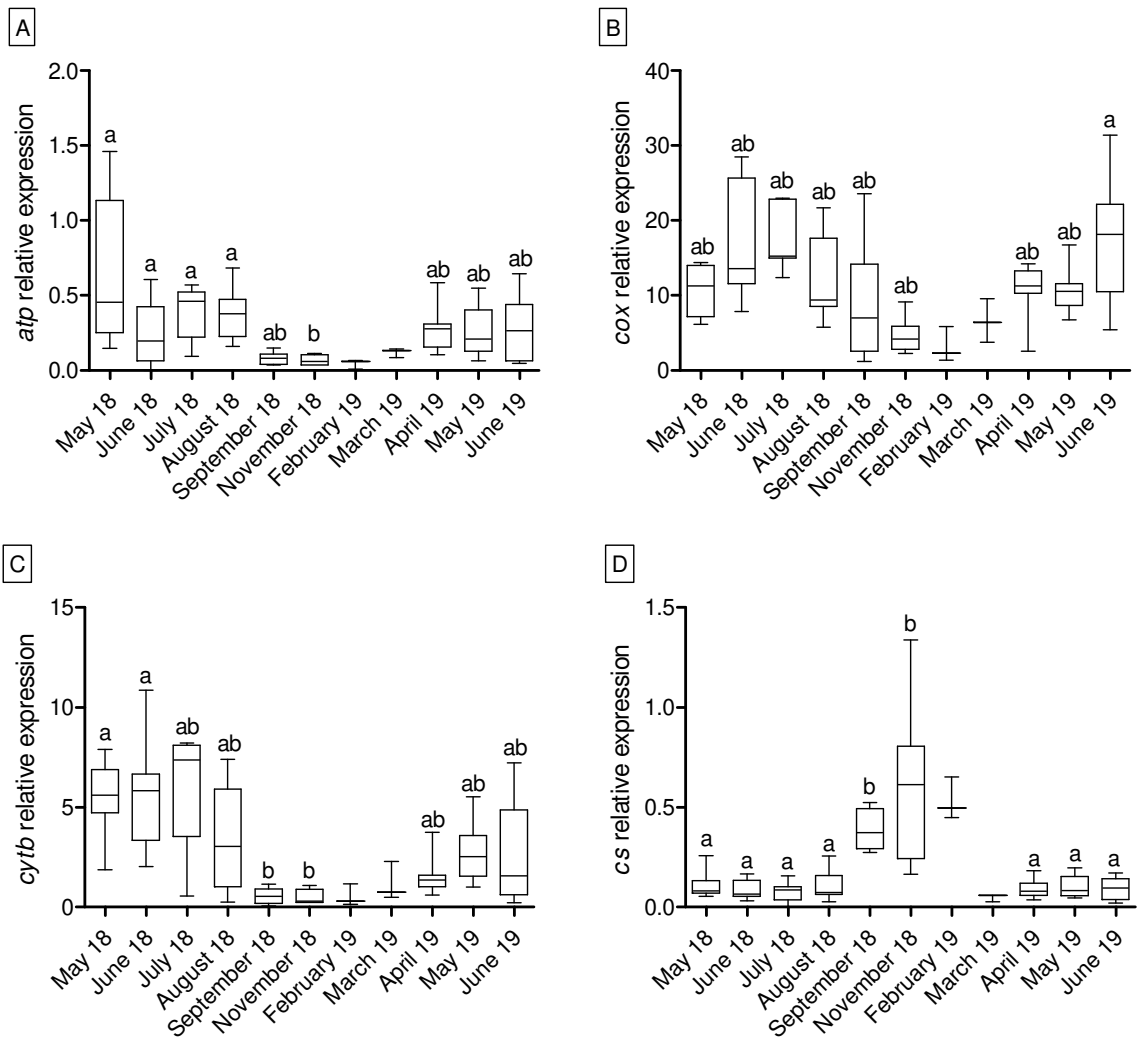


Figure 5.

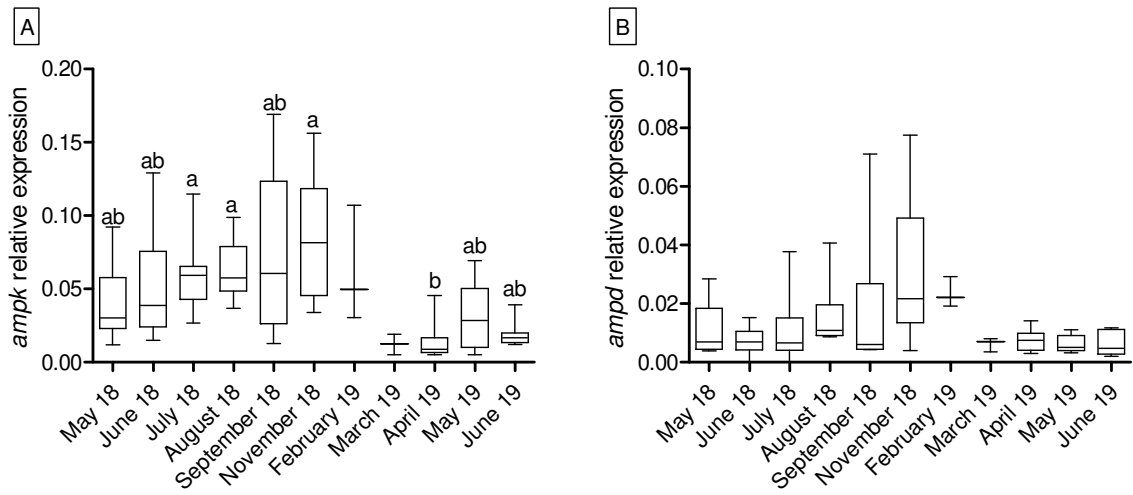


Figure 6.

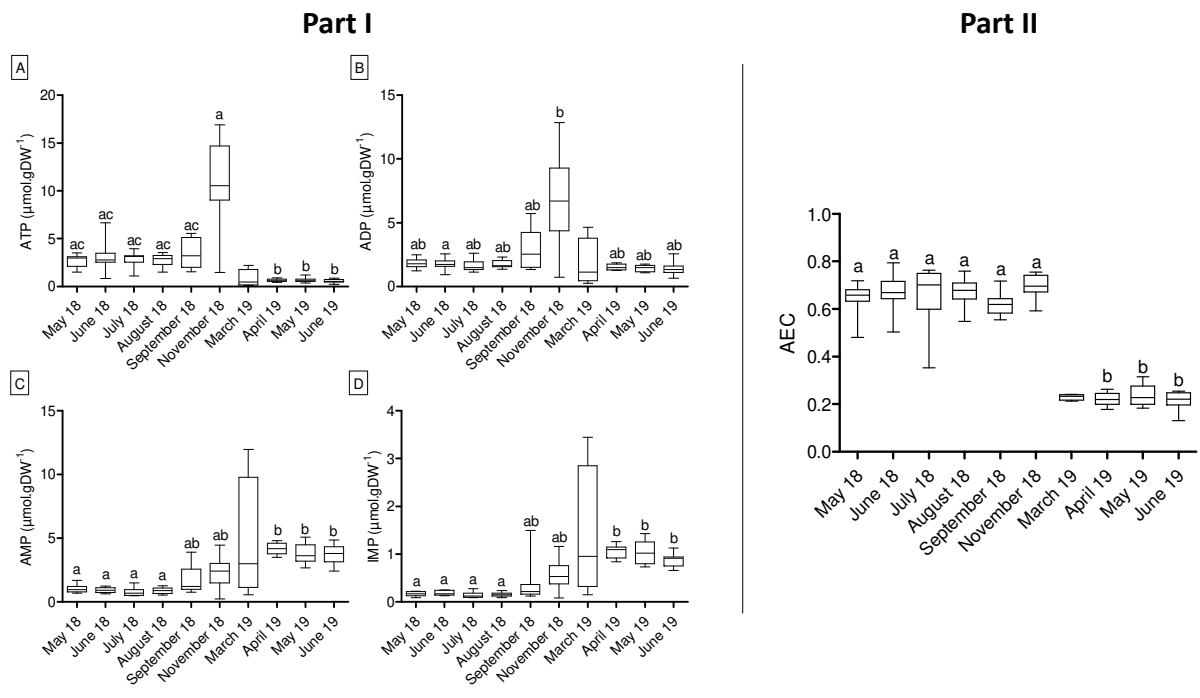


Figure 7.

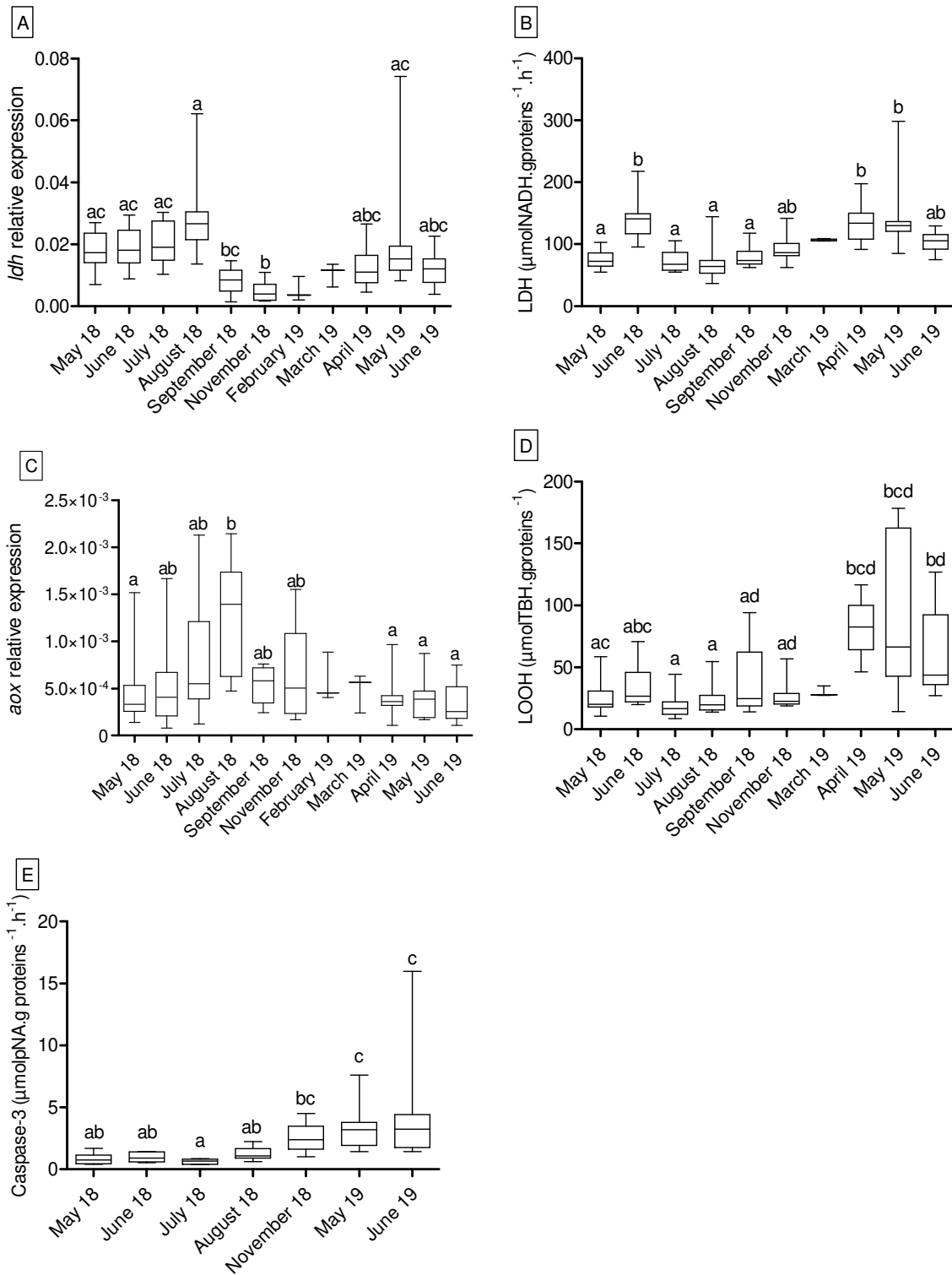


Figure 8.



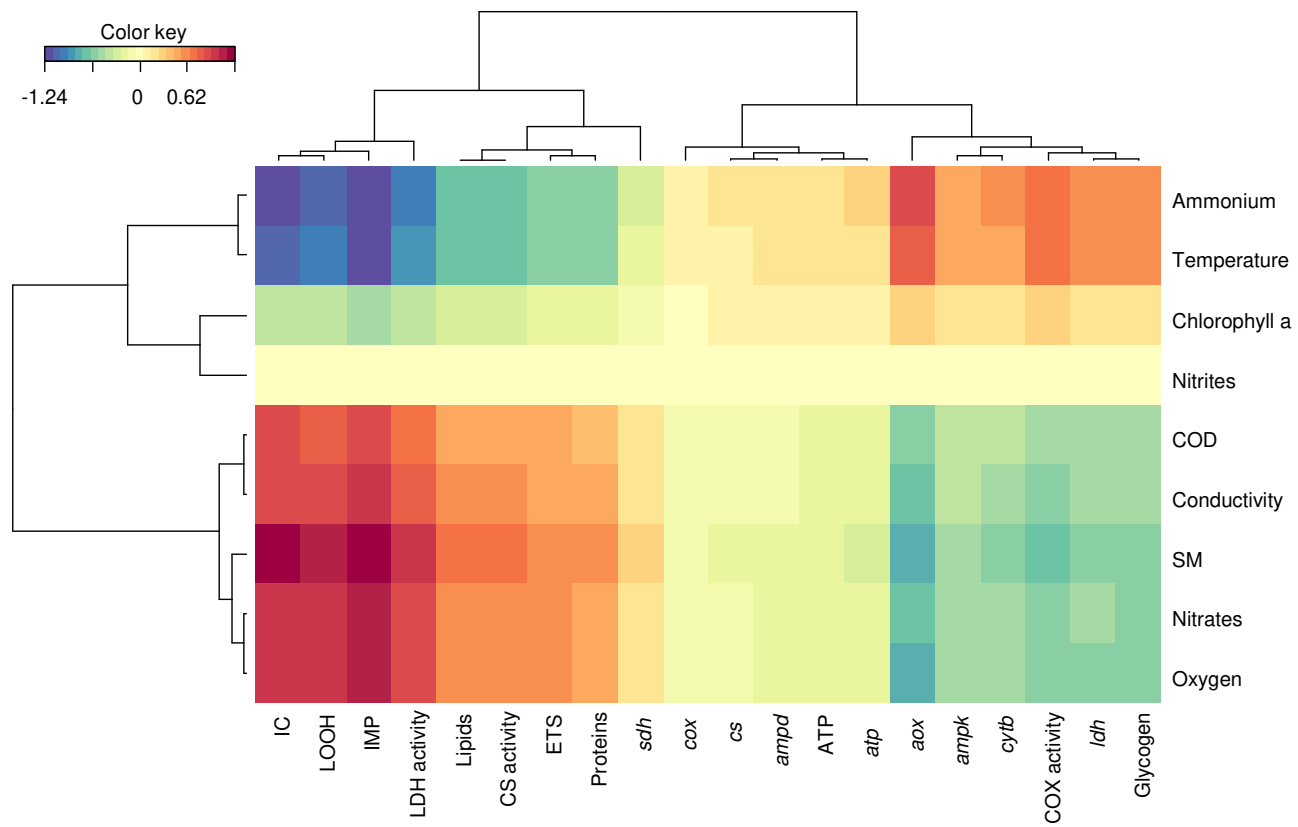


Figure 9.

**Supplementary data :**

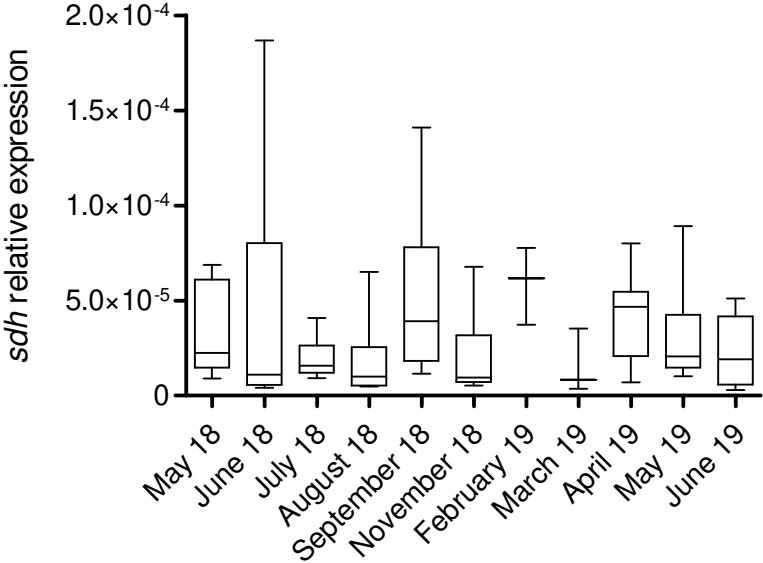


Figure S1.

Table 1. Summary of the primers used for gene expression measurements. Abbreviations, NCBI accession numbers of the original sequences of the target genes in *D. polymorpha*.

Gene	Abbreviation	NCBI	F primers	R primers
Actin	<i>act</i>	AF082863	CCTCACCTCAAGTACCCCAT	TTGGCCTTTGGGTTGAGTG
Alternative oxidase	<i>aox</i>	Q9P959	GTGAACCATAACCTCGCCTC	TGTAGTGA CTGCGGATGGTC
AMP deaminase	<i>ampd</i>	Q9DBT5	ACCCAGCCAGTGTGTTTCA	TTTGCTCGTGGACTCAACGT
AMP kinase $\alpha$ subunit	<i>ampk</i>	Q8BRK8	TGCTAAATGAAAGAGGTGACGC	CATGTGGTGGCATATACGATGT
ATP synthase	<i>atp</i>	JQ781135	GACTCCACCTCCCGTATCCT	TCCTCTGAAAGCTCGTCCAT
Citrate synthase	<i>cs</i>	MN579511	GTGCCCTGTCAGACCCTTAC	CTGTCCTGCCCTTGAGTGTGT
Cytochrome b	<i>cytb</i>	DQ072120.1	CGCCACTTTAAAGCGATTTTT	TGGGTCAGCAAATAGATCTGG
Cytochrome c oxidase	<i>cox</i>	AAL55513	AGGCCCTGCGATAGATTTTT	AAAGGGACCCGGTAAAATTG
Lactate dehydrogenase	<i>ldh</i>	Q7TNG8	TGCCCAA ACTACATTGCCAAAT	ATTGGGATTGGCAAACGGGA
Ribosomal protein S3	<i>s3</i>	AJ517687	CAGTGTGAGTCCCTGAGATACAAG	AACTTCATGGACTTGGCTCTCTG
Succinate dehydrogenase	<i>sdh</i>	Q9YHT2	TAGACCGTCCAGTTTAGCGC	CCTCTGCCACACATGTACGT

Table 2. Environmental parameters recorded *in situ* or in water samples: water physico-chemistry and contamination measurements; dO<sub>2</sub>: dissolved oxygen; SM: suspended matter; COD: chemical oxygen demand; NO<sub>2</sub><sup>-</sup>: nitrites; NO<sub>3</sub><sup>-</sup>: nitrates; NH<sub>4</sub><sup>+</sup>: ammonium; Chl a: chlorophyll a; ND: not detected.

Month	Temperature (°C)	Conductivity (µS.cm <sup>-1</sup> )	dO <sub>2</sub> (mg.L <sup>-1</sup> )	SM (mg.L <sup>-1</sup> )	COD (mg.L <sup>-1</sup> )	NO <sub>2</sub> <sup>-</sup> (mg.L <sup>-1</sup> )	NO <sub>3</sub> <sup>-</sup> (mg.L <sup>-1</sup> )	NH <sub>4</sub> <sup>+</sup> (mg.L <sup>-1</sup> )	Chl a (µg.L <sup>-1</sup> )	Hydrocarbon (mg.L <sup>-1</sup> )
May-18	22.7	497	9.1	ND	15.5	0.14	18	0.14	0.2	ND
June-18	22.9	485	9.8	ND	17.4	0.08	15	0.10	0.4	ND
July-18	24.2	505	9.4	4	18.9	0.13	12	0.10	0.6	0.002
August-18	21.6	410	7.1	5	14.2	0.11	8	0.09	6.7	ND
September-18	17.8	410	9	8	14.2	0.13	7	0.07	2.7	ND
November-18	6.3	740	13	5	8.88	0.08	11	0.01	4.1	0.001
February-19	5.8	521	13.2	20	16.2	0.09	26	0.09	9.8	ND
March-19	9.3	491	10.7	24	16.5	0.12	19	0.19	1.9	ND
April-19	12.5	520	10.4	20	40.5	0.09	21	0.02	1.5	ND
May-19	15.8	547	9.7	25	11.7	0.19	14	0.04	ND	ND
June-19	20.4	527	9.6	20	13.8	0.1	13	0.09	ND	ND

Table 3. Pearson's correlations between the lipid peroxidation and the caspase-3 activity with the target markers for the total dataset. Only significant correlations for LOOH content and/or caspase activity are presented.

	Lipid peroxidation	Caspase-3 activity
	$r^2$	
Lipids	0.59	n.s
Glycogen	0.4	n.s
[AMP]	0.71	0.91
[IMP]	0.68	0.88
Condition Index (CI)	0.57	n.s
LDH activity	0.55	n.s
<i>cytb</i> gene expression	n.s	0.51

### Supplementary data:

Table S1. Correlations of temperature and ATP content according to target markers of the total data set using multiple linear regression. Only significant correlations were presented.

	Temperature		[ATP]	
	<i>p</i> value	r <sup>2</sup>	<i>p</i> value	r <sup>2</sup>
<i>cox</i> gene expression	0.0159	0.43		
<i>atp</i> gene expression	0.0148	0.44		
<i>cytb</i> gene expression	0.001	0.66		
<i>ldh</i> gene expression	0.004	0.56		
<i>cs</i> gene expression	0.036	0.34	0.013	0.50
<i>ampd</i> gene expression			0.015	0.48
Lipids			0.019	0.50
Glycogen			0.025	0.47

Table S2. VIP values of PLS DA model built on biology responses. Only values  $\geq 0.9$  were presented.

Variable	VIP value
<i>atp</i>	1.23
<i>ldh</i>	1.19
<i>cs</i>	1.17
IC	1.12
<i>cytb</i>	1.05
ATP	1.03
LDH	1.02
IMP	1.02
ETS	1.02
LOOH	1.02
Lipids	0.99
<i>ampd</i>	0.99
<i>aox</i>	0.97
Proteins	0.92
<i>ampk</i>	0.91
<i>cox</i>	0.90

Environmental stress

