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Pharmaceuticals and endocrine disrupting compounds modulate adverse effects of climate change on resource quality in freshwater food webs

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Abstract:	Freshwater biodiversity, ecosystem functions and services are changing at an unprecedented rate due to the impacts of vast number of stressors overlapping in time and space. Our study aimed at characterizing individual and combined impacts of pollution with pharmaceuticals (PhACs) and endocrine disrupting compounds (EDCs) and increased water temperature (as a proxy for climate change) on primary producers and first level consumers in freshwaters. We conducted a microcosm experiment with a simplified freshwater food web containing moss (<i>Bryophyta</i>) and shredding caddisfly larvae of <i>Micropterna nycterobia</i> (<i>Trichoptera</i>). The experiment was conducted with four treatments; control (C), increased water temperature +4 °C (T2), emerging contaminants' mix (EC = 15 PhACs & 5 EDCs), and multiple stressor treatment (MS = EC + T2). Moss exhibited an overall mild response to selected stressors and their combination. Higher water temperature negatively affected development of <i>M. nycterobia</i> through causing earlier emergence of adults and changes in their lipidome profiles. Pollution with PhACs and EDCs had higher impact on metabolism of all life stages of <i>M. nycterobia</i> than warming. Multiple stressor effect was recorded in <i>M. nycterobia</i> adults in metabolic response, lipidome profiles and as a decrease in total lipid content. Sex specific response to stressor effects was observed in adults, with impacts on metabolome generally more pronounced in females, and on lipidome in males. Thus, our study highlights the variability of both single and multiple stressor impacts on different traits, different life stages and sexes of a single insect species. Furthermore, our research suggests that the combined impacts of warming, linked to climate change, and contamination with PhACs and EDCs could have adverse consequences on the population dynamics of aquatic insects. Additionally, these findings point to a potential decrease in the quality of resources available for both aquatic and potentially terrestrial food webs.
Response to Reviewers:	

Revision

MS ref. STOTEN-D-23-17284

Title: Pharmaceuticals and endocrine disrupting compounds modulate adverse effects of climate change on resource quality in freshwater food webs

Authors: Iva Kokotović, Marina Veseli, Filip Ložek, Zrinka Karačić, Marko Rožman, Ana Previšić
Science of the Total Environment

Dear Prof. Sabater,

Thank you for the constructive comments that help to improve the manuscript. I would also like to thank the reviewer for time and effort invested in the second round, we really appreciate the constructive comments. We have integrated all the comments and suggestions and corrected the manuscript accordingly. More specifically, we have reanalysed parts of the data as suggested and subsequently rewritten parts of the manuscript.

We appreciate yours as well as the reviewer's feedback, which prompted us to revise and clarify our sampling strategy description. Hence, we have included a paragraph explaining the background of our sampling approach into the Methods section.

As instructed, we have added detailed clarifications to all comments, thus, please find attached the file with a point-by-point response on the queries provided to our submission.

Thank you for giving us the opportunity to revise our work and I am looking forward to receiving your reply.

Kind regards,



Ana Previšić on behalf of the authors

Response letter

MS ref. STOTEN-D-23-17284R1

Title: Pharmaceuticals and endocrine disrupting compounds modulate adverse effects of climate change on resource quality in freshwater food webs

Authors: Iva Kokotović, Marina Veseli, Filip Ložek, Zrinka Karačić, Marko Rožman, Ana Previšić

Following the suggestions of the reviewer, we have corrected the manuscript to improve the quality. All changes we made are listed and explained in detail following the reviewers' comments below (**reply in green colour**). Page and line numbers correspond to the revised (clean) manuscript, hence they may differ in the file with track changes (due to changes in the document).

Reviewer #1:

General comments:

The authors have made substantial modifications, according to the reviewers' comments, which greatly improve the manuscript's quality.

However, I have a significant concern regarding the differentiation between technical and biological replicates in the methodology employed in this study. To detect the effects of the treatments on the caddisfly population accurately, biological replicates are essential. While I understand that in some cases, pooling individuals may be necessary to obtain sufficient tissue for analysis, it is crucial to emphasize that biological replicates are vital for extrapolating observed effects on the samples to the entire population. Technical replicates, on the other hand, primarily assess the reliability of the analytical method. Pooling individuals to reduce variability, as mentioned in the paper, is an unconventional approach. Individual variation within biological replicates is essential for making meaningful extrapolations to the broader population. Unless the authors can provide robust justification for this method, with references to established practices or prior studies, it is challenging to validate such an approach.

Upon investigation, I found that in Previšić, et al. 2020, the authors employed 'at least two replicate samples' per treatment, which aligns with common biological replicate practices. However, in Previšić, et al. 2021, a departure from this approach is evident as samples were pooled also to reduce variability. This discrepancy raises concerns about the consistency and reliability of the methodology employed in this study.

To maintain the rigor and validity of the research, it is advisable to reconsider the approach to replicates and justify its use, especially when it deviates from widely accepted scientific practices. For further clarification on this topic, I recommend reviewing the following sources:

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3321166/>

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4825082/#:~:text=Broadly%20speaking%2C%20biological%20replicates%20are,the%20measuring%20equipment%20and%20protocols.>

<https://onlinelibrary.wiley.com/doi/pdf/10.1002/ejlt.201200260>

Reply: We are grateful to the reviewer for highlighting areas in need of improvement. The initial description of our sampling strategy was acknowledged as inappropriate, and we have rephrased it in response to the reviewer's valuable feedback. The phrase "pooling biological replicates" has been reworked, recognizing its intuitive illogicality. We aimed to avoid overemphasizing potential extreme effects of individual microcosms. Thus, we have added a paragraph explaining the background of our approach (P7-8; L195-207) and two relevant references (Kraufvelin, 1998 and Sanderson 2002).

In the context of working with micro and mesocosms, the conventional use of biological replicates for generalization, widely accepted in ecology, faces challenges. As pointed out by (Kraufvelin, 1998), the high variability in these

systems often makes it difficult or impossible to find statistically significant deviations from the controls, even with rigorous replication and large effect sizes. A review on replicability in pesticide studies found that 88% of test biological variables showed no statistical significance, despite a theoretically adequate number of replicates (Sanderson, 2002). Similar trends were observed across different systems and taxa groups (e.g. Knauer et al., 2005; Pandey et al., 2017), leading to the recognition of these challenges in guidance on aquatic ecotoxicology assessment (European Food Safety Authority, 2013). Moreover, the increasing complexity and duration of such test systems reveal problems like "aquarium individuality," where initially identical replicates diverge from one another due to random factors or chance events, even when no experimental errors are made (Kraufvelin, 1998).

In our current experiment, as well as in the experiment presented in Previšić et al. 2021 (ES&T), we incorporated simplified food webs, exposing parts of natural systems to treatments over 2 months and spanning different life stages. Despite efforts to achieve uniformity among individual microcosms, random effects leading to differences in the final stages cannot be fully excluded. However, we ensured replication by employing three replicates for each treatment, although we opted to pool tissue samples to address potential extreme effects. Additionally, the weight reduction of adult aquatic insects during metamorphosis posed a challenge, resulting in high tissue demand. The applied approach aims to strike a balance between providing ecologically meaningful results with non-model organisms and minimizing methodological constraints.

European Food Safety Authority, 2013. Guidance on tiered risk assessment for plant protection products for aquatic organisms in edge-of-field surface waters. EFSA J. 11. <https://doi.org/10.2903/j.efsa.2013.3290>

Knauer, K., Maise, S., Thoma, G., Hommen, U., Gonzalez-Valero, J., 2005. Long-term variability of zooplankton populations in aquatic mesocosms. Environ. Toxicol. Chem. 24, 1182–1189. <https://doi.org/10.1897/04-010R.1>

Kraufvelin, P., 1998. Model ecosystem replicability challenged by the "soft" reality of a hard bottom mesocosm. J. Exp. Mar. Bio. Ecol. 222, 247–267. [https://doi.org/10.1016/S0022-0981\(97\)00143-3](https://doi.org/10.1016/S0022-0981(97)00143-3)

Pandey, L.K., Bergey, E.A., Lyu, J., Park, J., Choi, S., Lee, H., Depuydt, S., Oh, Y.T., Lee, S.M., Han, T., 2017. The use of diatoms in ecotoxicology and bioassessment: Insights, advances and challenges. Water Res. 118, 39–58. <https://doi.org/10.1016/j.watres.2017.01.062>

Sanderson, H., 2002. Pesticide studies: Replicability of micro/mesocosms. Environ. Sci. Pollut. Res. 9, 429–435. <https://doi.org/10.1007/BF02987597>

Other comments:

In reference to my previous comments on the use of PCA and PRC, I would like to clarify that I did not object to the application of PRC to your data. Instead, my concern was the absence of the y-axis in the PRC representation.

Reply: We thank the reviewer for these remarks. As we did not focus on a few particular metabolites/lipids the y axis would be filled with a lot of values representing m/z values as there are hundreds of metabolites/lipids extracted from the data and that would not give any additional information to the reader (as an example on appearance we added a raw figure with the y axis; Fig.1). Moreover, we were only able to identify some metabolites/lipids and those were putatively annotated. However, putative annotation does not provide definitive identification of a metabolite/lipid, and further verification is needed to confirm its identity using methods such as targeted metabolomics/lipidomics which is beyond the scope of our study. Thus, we have chosen to omit the y axis when presenting the current results.

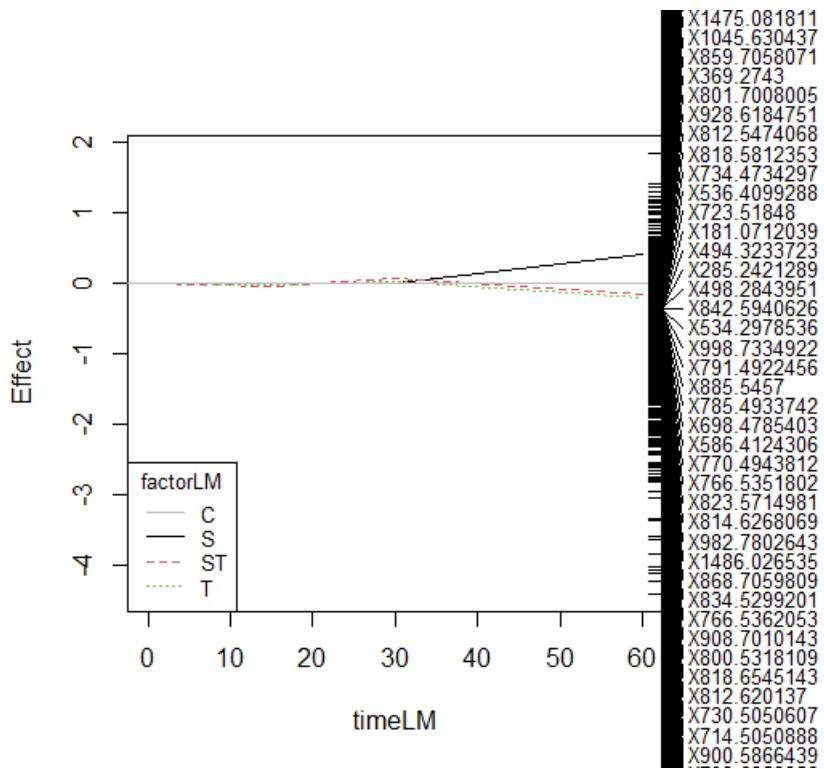


Fig.1. Lipidome profiles of the caddisfly *Micropterna nycterobia*; PRC of changes in the lipidome profiles of caddisfly life stages and female adults exposed to treatments in relation to control (please note that the figure is generated in R without any editing so color of lines and treatment abbreviations differ from those in the manuscript).

Additionally, I suggested to consider running RDA as an alternative to PCA for two reasons: 1) PCA is primarily a visual tool and not a formal statistical analysis; 2) given the notable time effect in your data, RDA would enable you to include time as a covariate, enhancing the analysis.

We agree with the reviewer that PCA is primarily a visualization tool and we used it primarily as a method of visualisation, moreover, formal statistical analysis was provided by the PRC (tables with statistics provided in supporting information). However, due to the missing data for metabolome and lipidome of moss at day 30 (treatment with ECs, as explained in the section 2.4.2. at P12) we did not run the PRC for that dataset. Therefore, in order to compensate for this oversight and include a formal statistical analysis for this dataset, we added the RDA analysis for moss metabolome and lipidome changes. Accordingly, parts of the text in materials and methods (P12 paragraph 2.4.2. Lines 295-299) as well as results (P13 Lines 328-331) and discussion (section 4.1. P21-22) were rewritten. In addition, new figures were created and integrated into the supporting information (Fig. S2).

However, as we wanted to emphasize the effect of time i.e. plant development and growth rather than the effects of treatment in moss, as the latter was not evident in HSP response or total lipid content changes, we decided to keep the previous PCA figures in the paper.

Introduction:

Line 112: a full stop is missing.

Line 117: shouldn't you say global warming then?

Line 127: aquatic organisms (plural)

Reply: Corrected as suggested.

Line 136: How do you want to address that? Or do you mean assess instead of address?

Reply: The sentence was rewritten as suggested (P4-5, Lines 115-118).

In your hypothesis, it is not explicitly stated that you also intend to test the response across the different stages. This omission was the basis of my earlier comment that comparing data between different dates and life stages seems incongruent with the study's objectives. It would be beneficial to explicitly include this in your hypothesis.

Reply: We thank the reviewer for pointing this out. We have added the information that changes in non-model organisms were evaluated across their life cycles into the hypothesis section (P6, Lines 146-149).

Materials and methods:

Please provide clarification in the description of the Generalized Linear Models (GzLM) regarding which data you analyzed using a normal distribution and which ones you analyzed using a gamma distribution.

Reply: Added as suggested, P11, Lines 277-279: "Normal distribution linear scale response was used for all data except for body weight of adults where gamma scale response with log link was used as the data did not achieve normal distribution."

Discussion:

The discussion is clear and very well-written.

1 **Pharmaceuticals and endocrine disrupting compounds modulate adverse effects of climate
2 change on resource quality in freshwater food webs**

3

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24 **Abstract**

25 Freshwater biodiversity, ecosystem functions and services are changing at an unprecedented rate due to
26 the impacts of vast number of stressors overlapping in time and space. Our study aimed at characterizing
27 individual and combined impacts of pollution with pharmaceuticals (PhACs) and endocrine disrupting
28 compounds (EDCs) and increased water temperature (as a proxy for climate change) on primary producers
29 and first level consumers in freshwaters. We conducted a microcosm experiment with a simplified
30 freshwater food web containing moss (*Bryophyta*) and shredding caddisfly larvae of *Micropterna*
31 *nycterobia* (Trichoptera). The experiment was conducted with four treatments; control (C), increased
32 water temperature +4 °C (T2), emerging contaminants' mix (EC = 15 PhACs & 5 EDCs), and multiple
33 stressor treatment (MS = EC + T2). Moss exhibited an overall mild response to selected stressors and their
34 combination. Higher water temperature negatively affected development of *M. nycterobia* through
35 causing earlier emergence of adults and changes in their lipidome profiles. Pollution with PhACs and EDCs
36 had higher impact on metabolism of all life stages of *M. nycterobia* than warming. Multiple stressor effect
37 was recorded in *M. nycterobia* adults in metabolic response, lipidome profiles and as a decrease in total
38 lipid content. Sex specific response to stressor effects was observed in adults, with impacts on
39 metabolome generally more pronounced in females, and on lipidome in males. Thus, our study highlights
40 the variability of both single and multiple stressor impacts on different traits, different life stages and
41 sexes of a single insect species. Furthermore, our research suggests that the combined impacts of
42 warming, linked to climate change, and contamination with PhACs and EDCs could have adverse
43 consequences on the population dynamics of aquatic insects. Additionally, these findings point to a
44 potential decrease in the quality of resources available for both aquatic and potentially terrestrial food
45 webs.

46

47 **Keywords:**

48 climate change, pollution, caddisflies, sex specific stress response, aquatic-terrestrial subsidies, ecosystem
49 subsidies

50 **Highlights:**

51 • warming was a dominant stressor for development-related traits of the caddisfly
52 • negative effects of warming on lipids were increased by presence of PhACs&EDCs
53 • pollution with PhACs & EDCs has higher impact on caddisfly metabolism than warming
54 • trait-, sex- and life stage-specific responses to multiple stressors were observed
55 • impacts of warming and PhACs & EDCs cross the aquatic-terrestrial interface

56

57

58

59 **1. INTRODUCTION**

60 Freshwater ecosystems are susceptible to various anthropogenic stressors (e.g. chemical
61 pollution, climate change, habitat loss, invasive species) which mostly coincide. Pharmaceuticals
62 (PhACs) and endocrine disrupting compounds (EDCs) are a diverse group of pollutants designed
63 to be biologically active at low doses, targeting specific metabolic and molecular pathways in
64 humans and animals, thus posing risk for aquatic organisms even at low environmental
65 concentrations (Ebele et al., 2017; Tijani et al., 2013; Wilkinson et al., 2017). Moreover, EDCs
66 encompass a wide range of chemicals (e.g. personal care products, cleaning products, food
67 preservatives, etc.) that interfere with normal function(s) of the endocrine system (Ebele et al.,
68 2017). PhACs and EDCs were shown to affect aquatic insects in many ways, causing changes in
69 growth and development (Jarvis et al., 2014), biomass (López-Doval et al., 2012), enzymatic
70 activity (Pestana et al., 2014), metabolome composition (Grgić et al., 2023; Previšić et al., 2020;
71 Späth et al., 2022), behavior (Jarvis et al., 2014; Späth et al., 2022) and survival rate (López-Doval
72 et al., 2012; Maenpaa and Kukkonen, 2006). Furthermore, PhACs and EDCs have the potential to
73 bioaccumulate in aquatic insects (Grabicova et al., 2015; Lagesson et al., 2016; Previšić et al.,
74 2021; Veseli et al., 2022) and to cross ecosystem boundaries through emerging aquatic insects
75 and thus contaminate terrestrial habitats (Previšić et al., 2021; Veseli et al., 2022). Moreover, in
76 freshwater ecosystems these compounds rarely occur one at a time but rather in complex
77 mixtures of several different emerging contaminants, thus making it harder to investigate their
78 effects (Wilkinson et al., 2017).

79 Climate change, with its long-term shifts in global weather patterns, poses significant challenges
80 to freshwater ecosystems. Within freshwater ecosystems, aquatic insect groups, such as
81 caddisflies, mayflies, and stoneflies, play a crucial role as inter-habitat linkages between aquatic
82 and terrestrial ecosystems, facilitating the flow of energy and nutrients (Huryn and Wallace,
83 2000). Additionally, they serve as valuable bioindicators for assessing the health of freshwater
84 environments (Water Framework Directive (WFD) 2000/60/EC). Their vulnerability to climate
85 change is influenced by their specific biological traits and ecological preferences, with a
86 considerable proportion of them belonging to cold-adapted taxa (Conti et al., 2014; Hershkovitz

87 et al., 2015). The impact of climate change, characterized by rising temperatures and changes in
88 precipitation levels (Webb et al., 2008), is particularly profound on these cold-adapted taxa in
89 higher altitudes, making them highly vulnerable to warming (Krajick, 2004; Macadam et al.,
90 2022). As a consequence of climate change, temperature increase affects various aspects of
91 aquatic insects' lives. It directly impacts their growth, development, and body size (Cogo et al.,
92 2020), as well as their emergence patterns (Finn et al., 2022). The anticipated rise in the
93 frequency and extent of intermittent rivers and streams, which periodically cease flow or even
94 completely dry, is a direct consequence of global climate change and the increasing human
95 demand for freshwater resources (Blackman et al., 2021). This trend holds significant implications
96 for aquatic insect communities, as considerably altered environmental conditions not only
97 impact their geographic distribution (Cogo et al., 2020 and references therein), but also their
98 population dynamics (Nukazawa et al., 2018), and community structure (Dorić et al., 2023).

99 Global warmingClimate change is likely to exacerbate impact of other anthropogenic stressors
100 (Wrona et al., 2006). For instance, as temperature rises, the solubility and mobility of PhACs and
101 EDCs in water can increase, leading to higher concentrations and potentially greater toxicity
102 (Kazmi et al., 2022; Noyes et al., 2009). Temperature change may also alter degradation rates of
103 some chemical contaminants, with increasing temperature usually shortening their half-life and
104 reducing the overall risk (Bhangare et al., 2022; Noyes et al., 2009). While accelerated
105 decomposition reduces the concentration of the parent compound, it increases the
106 concentration of the degradation products, which in some cases could be even more toxic for
107 aquatic organisms (Noyes et al., 2009). Warmer water usually increases the metabolic rate of
108 aquatic organisms, thus leading to potentially increased uptake of these chemicals (Kazmi et al.,
109 2022). In addition to increasing uptake, warming can also affect behaviour and physiology of
110 aquatic organisms making them more susceptible to stressors (Polazzo et al., 2022). Toxicity of
111 chemicals in water can depend on variety of abiotic (e.g. photolysis, hydrolysis, etc.) and biotic
112 processes (e.g. biotransformation, biodegradation, etc.) (von Schiller et al., 2017). Moreover, the
113 impact of warming on the toxicity of PhACs and EDCs in water is complex and can depend on a
114 variety of factors, including the type of the chemical (Serra-Compte et al., 2018), aquatic species
115 (Duchet et al., 2023, preprint), and life-stage tested (DeCourten and Brander, 2017). Due to the

116 increase in temperature caused by climate change, the temperature-dependent toxicity of PhACs
117 and EDCs in water will become a matter of growing significance that warrants assessment an
118 ~~increasingly important issue that needs to be addressed~~.

119 It is generally very challenging to gain empirical understanding of the effects of climate change
120 in comparison with other stressors (Halsch et al., 2021), as well as their combined effects (Dinh
121 et al., 2022). Consequently, there have been only a handful of studies investigating single and
122 combined effects of increased water temperature and PhACs and EDCs in aquatic invertebrates
123 (e.g. Barbosa et al., 2017; Cruzeiro et al., 2019; Heye et al., 2019). More specifically,
124 carbamazepine and higher temperatures increased *Chironomus riparius* mortality (Heye et al.,
125 2019); fluoxetine combined with higher temperature reduced reproductive success and
126 population growth in *Daphnia magna* (Barbosa et al., 2017), whereas levonorgestrel and
127 increased temperature did not cause DNA damage in *Gammarus locusta* cells (Cruzeiro et al.,
128 2019). To address this knowledge gap, we conducted a study aimed at characterizing effects of
129 increased water temperature and exposure to PhACs and EDCs on primary producers (non-
130 vascular macrophytes; moss) and first level consumers (shredding aquatic insects) in freshwaters.
131 Considering the importance of aquatic insects as fundamental links between aquatic and
132 terrestrial food webs and reliable bioindicators to pollution (Erasmus et al., 2021; Muñoz et al.,
133 2015) we chose caddisflies as our model organisms. Caddisflies are a species-rich and ecologically
134 diverse insect order, that is well-suited to reflect effects of various stressors on aquatic
135 ecosystems (Hering et al., 2009). Despite of the high ecological plasticity and thermal tolerance
136 of intermittent rivers specialists (Stubbington et al., 2017) we hypothesized that the individual
137 and combined stressor effects of both, increased water temperature and PhACs and EDCs, will
138 trigger a stress response in an intermittent river caddisfly, *Micropterna nycterobia* (McLachlan,
139 1875). Chronic *in situ* exposure to pollution with ECs results in measurable changes of metabolite
140 levels in relatively pollution-tolerant caddisfly larvae (Previšić et al., 2020), whereas increased
141 temperature results in depletion of lipids and reduces developmental period of mayfly larvae
142 (Chou et al., 2018). Moreover, variable impacts on emergence and survival were observed in
143 dragonflies and an aquatic heteropteran exposed to increased water temperature, PhACs and
144 their combination (Duchet et al., 2023, preprint). Hence, we conducted a 78-day microcosm

145 experiment composed of a simplified freshwater food web exposed to a mixture of PhACs and
146 EDCs and increased water temperature as a proxy for climate change using the randomized
147 factorial design. We analyzed the physiological changes in caddisflies and moss via non-targeted
148 metabolomics and lipidomics, i.e. by evaluating alterations in the metabolite and lipid profiles of
149 non-model organisms across their life cycles, as well as changes in emergence patterns, body
150 weight and total lipid content.

151

152 **2. MATERIALS AND METHODS**

153 2.1 Microcosm Experiment: Experimental Design and Sample Collection

154 We conducted the microcosm experiment with a simplified freshwater food web containing
155 nonvascular macrophytes (Bryophyta), hereafter moss and caddisfly larvae *Micropterna*
156 *nycterobia* (McLachlan, 1875) (Limnephilidae, Trichoptera) feeding mainly as shredders.
157 Trichoptera larvae, moss (*Cinclidotus aquaticus* (Hedw.) Bruch & Schimp and *Rhynchosstegium*
158 *riparioides* (Hedw.) Cardot), water, sand and stones collected from the pristine Krčić River
159 (N44.027321 E16.318936), minimally impacted by anthropogenic activity, were used for the
160 experiment. Microcosm setup followed Previšić et al., 2021 with modifications in number of
161 microcosms, temperature regime and mixture of moss species. Upon collection, 12 microcosms
162 (aquaria 30 × 20 × 15 cm) were installed with 3 L of water, 10 tablespoons of sand, 3 large stones
163 (> 10 cm), 10 small stones (2–5 cm), 3 tufts of moss (6–8 cm in diameter and plants up to 15 cm
164 in length) and 5th instar *M. nycterobia* larvae (ca. 30 larvae per aquarium). Constant oxygen levels
165 were kept using aquaria air pumps, and to minimize evaporation, each microcosm was covered
166 with a glass cover. Natural light and day-night regime was supplemented with the artificial light
167 (with sunlight's spectrum) in the regime of 12 hours of light followed by 12 hours without light.
168 All microcosms were acclimatized for 10 days at 10 °C under aforementioned conditions
169 preceding the start of the experiment. The experiment was conducted in the randomized
170 factorial design, with treatments as follows: Control (C), Increased temperature (T2), ECs mix
171 (EC), multiple stressor treatment = ECs mix + increased temperature (EC + T2 = MS), with three
172 replicates of each. Subsequently, 6 of them were exposed to a mixture of 20 ECs over a 78-days

173 period. The composition of the ECs mixture was selected based on occurrence of particular
174 compounds in freshwaters in Europe (Mandaric et al., 2015), and included 15 PhACs; azaperol,
175 acetaminophen, thiabendazole, levamisol hydrochloride, dexamethasone, ketoprofen,
176 naproxen, ranitidine hydrochloride, soltalol hydrochloride, valsartan, diphenhydramine,
177 clopidogrel hydrogen sulfate, hydrochlorothiazide, sertraline hydrochloride, cimetidine and 5
178 EDCs; benylparaben, ethylparaben, propylparaben, estriol, estradiol- β . The volume of water was
179 kept constant by adding fresh dechlorinated tap water (ca. 100 mL every week), and the
180 concentration of each compound was kept at a pseudo-constant concentration of 500 ng L⁻¹.
181 Taking into consideration knowledge gained from our previous experiments (Cetinić et al., 2022;
182 Grgić et al., 2023; Previšić et al., 2021), three stock solutions were prepared and 100 μ L of the
183 solution was added each day, every three days or once a month, depending on the compound.
184 In this way, abiotic attenuation (sorption and/or (photo)degradation) was taken in consideration
185 and the nominal concentration of each compound was maintained, more details provided in
186 Supporting information (SI 1). As different temperature regimes needed to be followed, aquaria
187 were placed in two different incubators (POL-EKO APARATURA, Poland). "Natural" temperature
188 regime (T1) mimicked the regime of the Krčić spring reach before the drying phase (10 °C) and
189 temperature was successively increased 0.5 °C every 15 days. Increased temperature regime (T2)
190 followed the same pattern but with temperature increased by 4 °C, in accordance with patterns
191 of reduced flow observed in the selected river coupled with projections of temperature increase
192 due to climate change in the Mediterranean montane regions (Bravo et al., 2008).

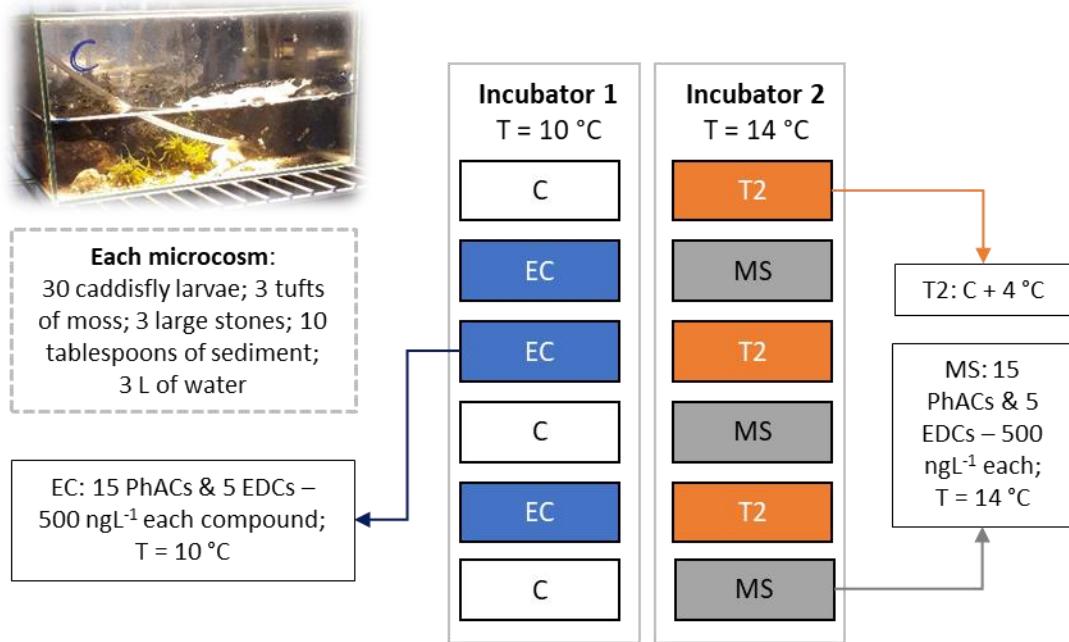
193 Biota sampling included initial (after the acclimatization period - day 0 (D0)) and several
194 consecutive collections (ca. day 15 (D15), day 30 (D30) and day 60 (D60) of exposure) including
195 different life stages (larvae, pupae and adult stage), in accordance with the life cycle of
196 holometabolous caddisflies. At each sampling date, we collected replicate samples from each
197 microcosm, consisting of 2 g of moss and 3–5 Trichoptera larvae/pupae. However, these samples
198 were pooled per treatment to mitigate the potential extreme effects of individual microcosms
199 (Kraufvelin, 1998). The complexity and extended duration of micro and mesocosm test systems
200 exacerbate issues like "aquarium individuality," where initially identical replicates diverge due to
201 random effects, introducing significant variability and complicating the identification of

202 statistically significant deviations (Kraufvelin, 1998; Sanderson, 2002). Additionally, the weight
203 reduction of adult aquatic insects during metamorphosis (Huryn and Wallace, 2000) poses a
204 challenge, leading to high tissue demand. Consequently, analytical replicates for each treatment
205 per sampling date were created after homogenizing the pooled samples (details under 2.2, Biota
206 Sample Processing). The chosen approach aims to strike a balance between providing ecologically
207 meaningful results with non-model organisms and minimizing methodological constraints.

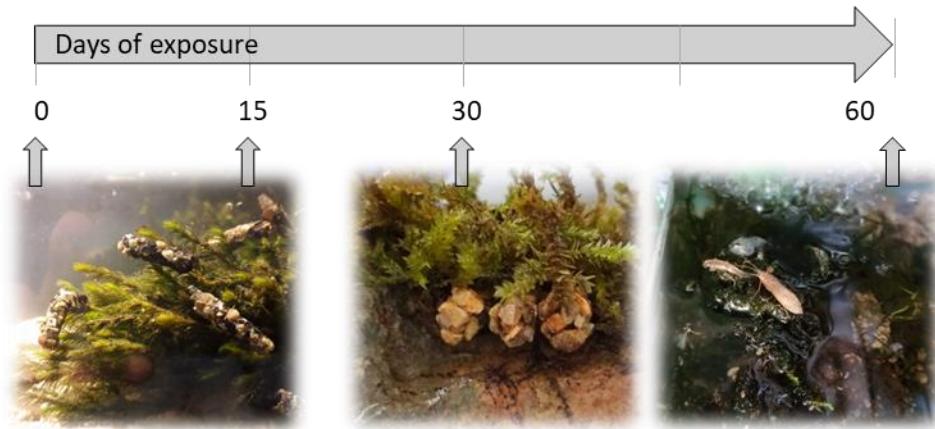
208 Trichoptera larvae were kept in clean aquaria for 24 h to allow for gut clearance prior to collection
209 (Van Geest et al., 2010). Additionally, emerging adult *M. nycterobia* were collected as they
210 emerged (daily), and sex of each individual was determined. These samples were pooled
211 depending on sex for subsequent analyses due to tissue requirements and to match the overall
212 sampling scheme, according to temperature treatments. Emergence following the „natural”
213 temperature regime (T1) started ca. 2 weeks later than in T2, thus samples were pooled for dates
214 45-60 and 60-75 days of exposure. Samples in elevated temperature regime (T2) were pooled for
215 dates: 30-37 and 38-47 days of exposure. We combined adult *M. nycterobia* from 45-60 days of
216 exposure in T1 and 38-47 days of exposure in T2 to one time point (day 60 of exposure) in order
217 to have approximately the same time period of exposure to selected stressors. All samples were
218 freeze-dried upon collection and stored at -80 °C until further processing.

219 Oxygen concentration (mg L⁻¹), oxygen saturation (%), pH and electrical conductivity (mS cm⁻¹)
220 were measured in every microcosm at the beginning of the experiment (D0) and subsequently
221 every two weeks (D15, D30, D45 and D60) using Hach HQ40D portable multi-parameter probe
222 (Hach, Germany).

a)



b) Sampling



223

224 Figure 1. A) Experiment design with the following treatments: C - Control (T1 = 10 °C), T2 -
225 Increased temperature (14 °C), EC - ECs mix, MS - multiple stressor treatment (EC + T2) and b)
226 sampling scheme with caddisfly larvae, pupae and adults sampled at various days of exposure.

227 2.2. Biota sample processing: extractions of metabolites and lipids

228 Within this study, the term “metabolome” refers to the complete set of low molecular weight
229 molecules or metabolites present within an organism, while “lipidome” is used to describe the
230 complete lipid profile within an organism (i.e. all lipids).

231 Biota samples processing, metabolite and protein extraction and metabolite profiling analyses
232 followed (Grgić et al., 2023). In order to detect Hsp70 proteins, we performed Western blot
233 analysis of protein samples, the details are provided in Supporting Information (SI 2). As there
234 was no detection of the aforementioned proteins no results are shown.

235 The Folch lipid extraction method (Folch et al., 1957) was used and performed following the
236 protocol of (Sarafian et al., 2014) with modifications. Briefly, for lipidome profiling and
237 determination of the total lipid content (TLC), each sample (30 mg) was dissolved in 600 µL CHCl₃
238 : MeOH (2:1 v:v). Samples were vortexed at medium speed (IKA® Vortex Genius 3, Germany) for
239 5 min. After 10 min of incubation at room temperature, samples were cooled at -20 °C for 10 min
240 and additional lysis was done via ultrasonic probe (Sonoplus HD4050, Bandelin electronic GmbH,
241 Germany) for 1 min at 50% of intensity. Samples were stored overnight at -20 °C to improve
242 protein precipitation and then centrifuged at 14 000g for 20 min (Tehtnica-Centric 200R,
243 Slovenia). The supernatant was collected (600 µL) in a previously weighed tube, filtered through
244 a PVDF filer (MILLEX® - GV Syringe Filter 0.22 µm Hydrophilic PVDF, 13 mm, Sterile) and
245 evaporated to dryness. The tube was weighed to determine the TLC. TLC was determined using
246 the following equation; TLC = weight of "full" tube – empty tube. Samples were dissolved in 200µL
247 IPA : ACN : H₂O (2:1:1, v:v:v) for subsequent LCMSMS non-target analysis.

248 For both metabolome and lipidome analysis, set of quality control samples was prepared by
249 taking small aliquot of the each sample solution from the entire set and pooling them together.
250 Subaliquots of this pooled sample are regarded as set of quality control samples.

251

252 2.3 Non-target metabolome and lipidome analysis

253 Non-target analyses of the metabolome and lipidome samples were performed using a high-
254 resolution mass spectrometry system; LTQ-Orbitrap VelosTM (Thermo Fisher Scientific, USA)
255 coupled with an ultra-performance liquid chromatography (UPLC) system (Ultimate 3000
256 RSLC nano system, Dionex, Amsterdam, Netherlands). Instrument parameters and UPLC gradients
257 are provided in Supporting Information (SI). Data extraction, chromatographic deconvolution and
258 final alignment were done using the MZmine program (Katajamaa et al., 2006). Steps and settings

259 used in the MZmine program are provided in Supporting information (SI 3). The exported .csv
260 files were further filtered and sorted using modified parts of Bqunat script written in
261 Mathematica (Wolfram Research Inc., Campaign, IL, USA) (Rožman et al., 2018). Data were
262 cleaned by removing of all blank-related features. Feature was considered as blank related if an
263 intensity ratio sample:blank was < 10. Quality acceptance criteria for each metabolite were:
264 detection rate > 70%, relative standard deviation < 30% and dispersion ratio < 40%. Based on the
265 exact mass match, metabolite and lipid identification was performed in
266 <http://ceumass.eps.uspceu.es/> and by searching Metlin, Kegg, LipidMaps, PubChem, and HMDB
267 databases. It is worth noting that the metabolites and lipids reported here are only the
268 metabolites that were putatively annotated.

269

270 2.4 Statistical Analysis

271 2.4.1 Body weight changes & total lipid content of *Micropterna nycterobia* and non-vascular
272 macrophytes, and physico-chemical water parameters

273 The effects of experimental treatments on body weight (evaluated individually in *M. nycterobia*
274 specimens; N = 12 per treatment per collecting date) and total lipid content (TLC; evaluated in
275 composite samples of *M. nycterobia* pooled per life stage and treatment; N = 3 per treatment
276 per collection date) of different life stages of *M. nycterobia* were analysed using Generalized
277 Linear Models (GZLMs) constructed in IBM SPSS Statistics 27.0 (IBM Corporation). Additionally,
278 for adults the differences between the sexes were determined. Normal distribution linear scale
279 response was used for all data except for body weight of adults where gamma scale response
280 with log link was used as the data did not achieve normal distribution. Maximum likelihood
281 estimate was used for parameter estimation. Pairwise contrasts of estimated means were
282 performed using Wald's statistics.

283 The changes in total lipid content in moss, as well as changes in the physico-chemical water
284 properties, between different treatments over time were tested using repeated measures
285 ANOVA using the IBM SPSS Statistics 27.0 (IBM Corporation). Pairwise comparisons were

286 conducted with Bonferroni adjustment for multiple comparisons. Obtained data were analyzed
287 and visualized using Principal Component Analysis (PCA) in Primer 7.

288

289 2.4.2. Data analysis of non-target metabolomic and lipidomic profiles of *Micropterna nycterobia*
290 and non-vascular macrophytes

291 Obtained metabolomic and lipidomic data matrices were forth root transformed and was
292 analyzed using Principal Component Analysis (PCA) and Principal Response Curves (PRC) in
293 package vegan (version 2.5-7) RStudio version 4.1.2 (Oksanen et al., 2020). PRC analysis was
294 performed using forth root transformed data. Additionally, significance of the results was tested
295 using the Monte Carlo test in the 'permute' package, with 99 permutations, more specifically
296 significance of the 1st canonical axis of the PRC and significance of sampling date/insect stage
297 was tested. Due to the missing moss sample D30 EC, Redundancy Analysis (RDA) was performed
298 instead of PRC for moss metabolome and lipidome data using CANOCO software (version
299 5.11ter Braak and Šmilauer, 2012). We used treatment as the categorical explanatory variable,
300 metabolites and lipids as response, respectively and time as a covariate. The RDA significances
301 were tested using Monte Carlo test with 999 permutations. Values of MZ masses of the
302 metabolome dataset were normalized and processed by Principal Component Analysis (PCA) in
303 Rstudio. The PCA was visualized in Primer 7 (Clarke and Gorley, 2015). The first 100 variables (MZ
304 masses) that contribute most to separation along certain PCs were selected for identification of
305 metabolites.

306 **3. RESULTS**

307 3.1. Physico-chemical properties of water during microcosm experiment

308 Oxygen concentration (mg L⁻¹) and oxygen saturation (%) throughout the experiment did not
309 differ significantly among treatments, they were impacted only by the day of measurement
310 (repeated measures ANOVA, Table S1, S2; and PCA analysis, the total variance accounted by the
311 two components shown was ~69 %; variance from [PC1, PC2]≈[46.4 %, 22.6 %]; Fig. S1). Day of
312 measurement and interactive effects; temperature x ECs, temperature x time and ECs x time

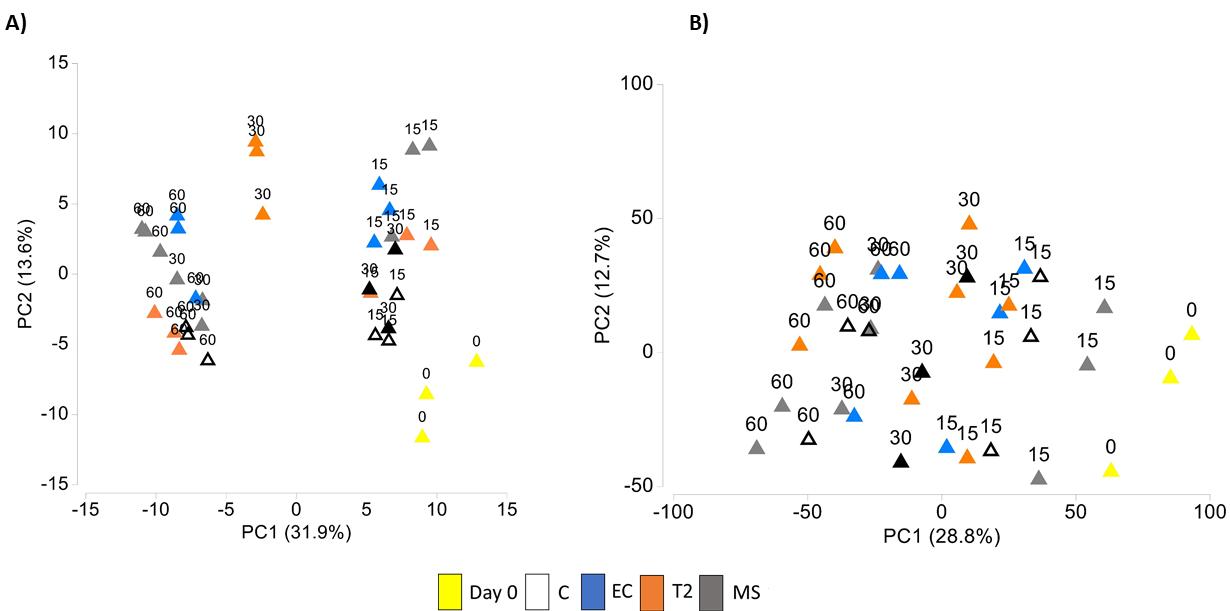
313 caused changes in pH levels (repeated measures ANOVA, Table S3). Specifically, pH was higher
314 on D15 and D60 in treatments with ECs mixture (EC and MS). Additionally, on D30 and D45 in
315 treatments with elevated water temperature (T2 and MS) pH was higher and lower, respectively
316 (repeated measures ANOVA, Table S3). Electrical conductivity differed between treatments, i.e.
317 treatments with increased water temperature (T2 and MS) had higher conductivity compared to
318 the “natural” temperature regime (C and ECs) (repeated measures ANOVA, Table S4). Moreover,
319 electrical conductivity was generally rising throughout the whole experiment in all treatments,
320 thus it was also impacted by the day of exposure (repeated measures ANOVA, Table S4).

321

322 3.2. Total lipid content, metabolome and lipidome profiles of non-vascular macrophytes

323 Principal component analysis (PCA) based on non-target metabolic profiles and lipidome profile
324 of moss revealed clustering primarily based on the duration of the experiment rather than
325 treatment (Fig. 2A&B). In the analysis of the metabolome and lipidome, the total variance
326 accounted by the first two components was ~45.5 % (variance from [PC1, PC2]≈[31.9 %, 13.6 %])
327 and ~41,5 % (variance from [PC1, PC2]≈[28.8 %, 12.7 %]), respectively. In both analyses, the first
328 principal component (PC) axis separated the profiles between D0 and D15 from D60, with D30
329 lacking a consistent grouping patterns (Fig. 2A&B; note however, that D30 EC samples are
330 missing, as they were lost during the processing). In addition, RDA analyses shows that
331 metabolome and lipidome profiles differed significantly among treatments (RDA: pseudo-F = 3.0,
332 p = 0.002, explained variability = 12.1 %; Fig. S2A and RDA: pseudo-F = 2.2, p = 0.004, explained
333 variability = 7.7 %; Fig. S2B, respectively). Majority of metabolite groups (17 in total) showing the
334 most significant changes in abundance to stressor treatments were terpenoids, terpenes class
335 (50%) followed by lipids and fatty acids (29%), amino acids, peptides and proteins (11%), carbonyl
336 compounds (5%), organic acids, carboxylic acids and monocarboxylic acids (5%) (Fig. S3, Table
337 S5). Within the lipidome, most significant changes in abundance of 51 lipids to stressor
338 treatments were noticed in glycerophospholipids (51%) followed by glycerolipids (20%), sterol
339 lipids (12%), sphingolipids (8%), prenol lipids (8%) and fatty acyls (2%) (Fig. S4, Table S6). The
340 lowest total lipid content in all treatments was measured on D 15, however, no significant

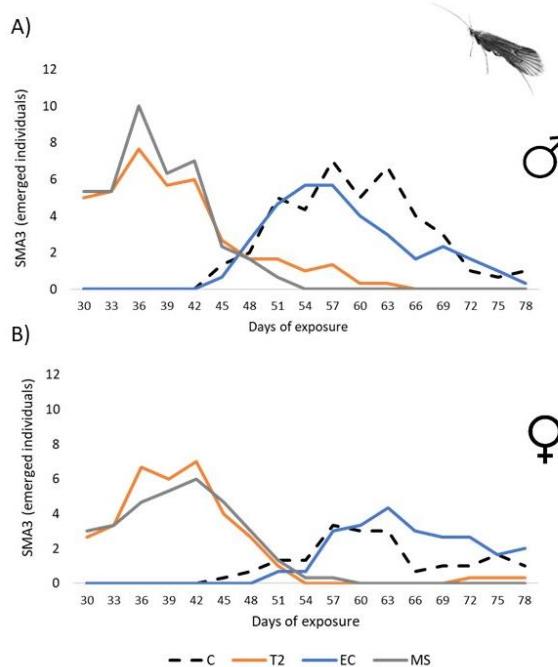
341 changes in TLC was observed related to days of exposure or treatments (Fig. S5, repeated
342 measures ANOVA, Table S7).



343
344 Figure 2. PCA plot showing separation based on A) metabolome and B) lipidome of moss in
345 different treatments. Abbreviations of treatments are as follows: C – Control ($T = 10\text{ }^{\circ}\text{C}$), T2 –
346 Increased temperature ($14\text{ }^{\circ}\text{C}$), EC - ECs mix, MS - multiple stressor treatment (T2 + EC); Day 0 –
347 pre-exposure sample.

348
349 3.3. Phenology (emergence patterns) of the caddisfly *Micropterna nycterobia*
350 Increased water temperature caused earlier emergence of both males and females, resulting in
351 approximately three-week shift in peak emergence between the normal (C and EC) and elevated
352 temperature (T2 and MS) treatments (Fig. 3). Overall, more males emerged throughout the
353 experiment, however, the majority of pupae that did not emerge by the end of experiment were
354 females. Only minor differences between emergence patterns of males and females were
355 observed within treatments (Fig. 3).

356



357

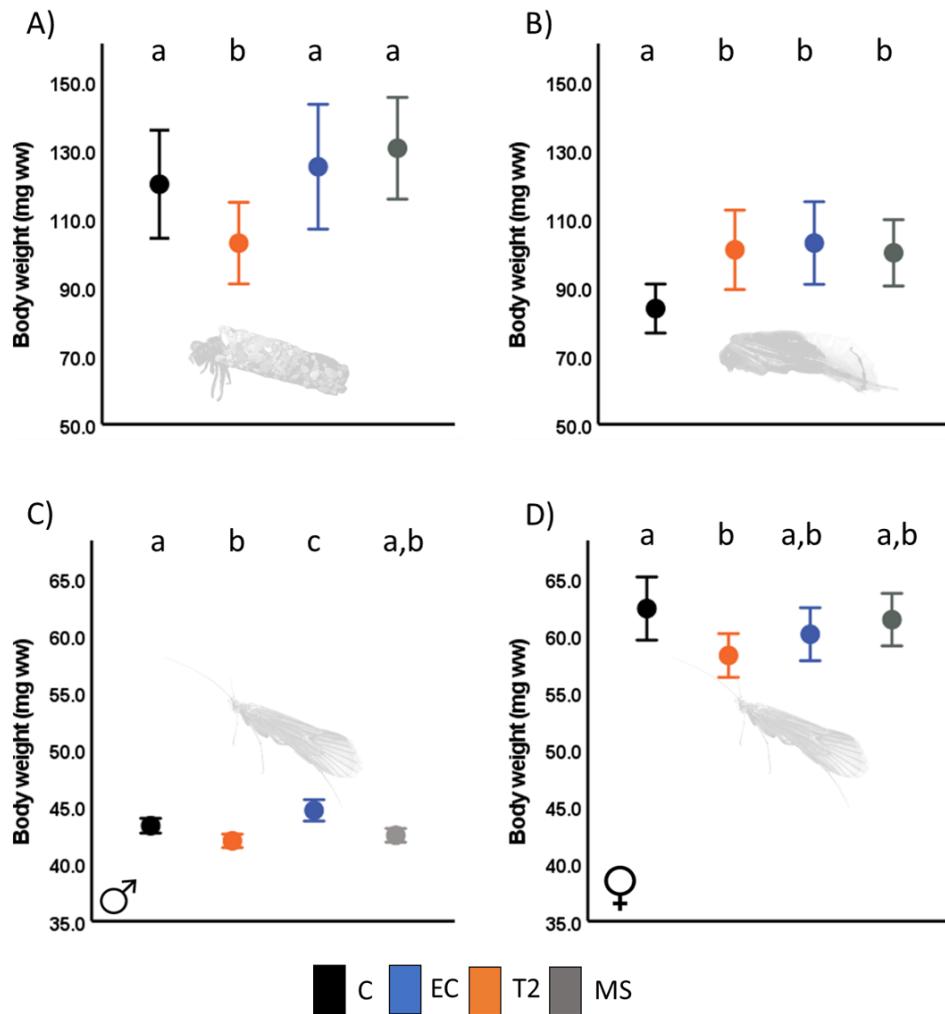
358 Figure 3. Three-day simple moving average (SMA3) of emerged A) male and B) female adults of
 359 *Micropterna nycterobia* across treatments. Abbreviations of treatments are as follows: C - Control
 360 (T = 10 °C), T2 - Increased temperature (14 °C), EC - ECs mix, MS - multiple stressor treatment (T2
 361 + EC).

362

363

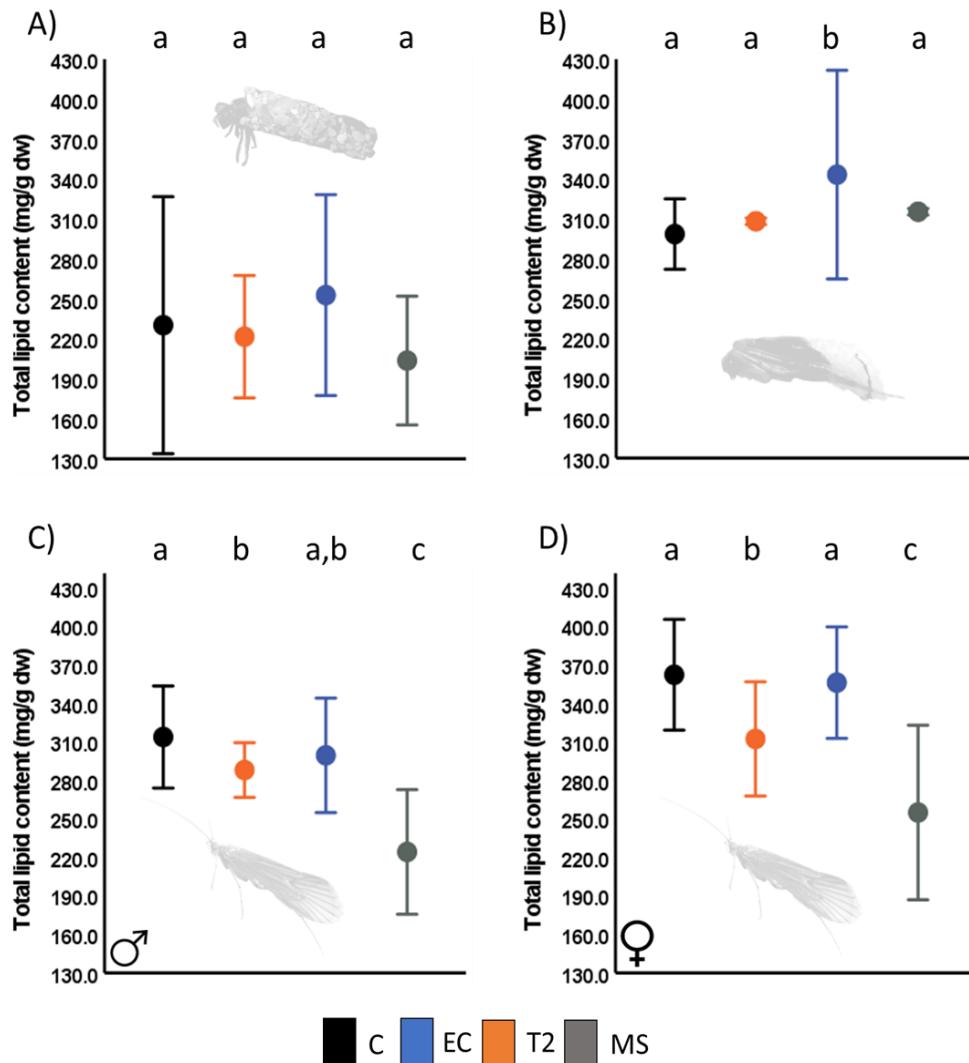
364 3.4. Body weight and total lipid content changes of the caddisfly *Micropterna nycterobia*

365 Overall, a loss in body mass was recorded in *M. nycterobia* throughout the life cycle, with larvae
 366 having the highest body weight and adults the lowest (Fig. 4A-D). A statistically significant drop
 367 in body weight was observed in larvae in T2 compared to control (4A, Table S8). All experimental
 368 treatments increased the body weight of pupae compared to control (Fig. 4B, Table S9). Adult
 369 females had significantly higher body weight compared to males (Fig. 4C & 4D, Table S10),
 370 however, in adults of both sexes a statistically significant drop in body weight was observed in T2
 371 compared to control (Fig. 4C & 4D, Table S11 and S12).



372

373 Figure 4. Model predictions illustrating the effect of treatment on body weight of A) larvae B)
 374 pupae C) adult males and D) adult females of *M. nycterobia*. Mean values of twelve replicates are
 375 presented with 95% confidence intervals. Different letters indicate significant differences among
 376 treatments ($p < 0.05$). Abbreviations of treatments are as follows: C – Control ($T = 10$ °C), T2 –
 377 Increased temperature (14 °C), EC – ECs mix, MS – multiple stressor treatment (T2 + EC).



378

379 Figure 5. Model predictions illustrating the effect of treatment on total lipid content of A) larvae
 380 B) pupae C) adult males and D) adult females of *M. nycterobia*. Mean values of three replicates
 381 are presented with 95% confidence intervals. Different letters indicate significant differences
 382 among treatments ($p < 0.05$). Abbreviations of treatments are as follows: C – Control ($T = 10$ °C),
 383 T2 - Increased temperature (14 °C), EC - ECs mix, MS - multiple stressor treatment (T2 + EC).

384

385 Changes in the TLC were more pronounced post-metamorphoses (Fig. 5A-D). Experimental
 386 treatments had no effect on TLC on larvae (Fig. 5A, Table S13), while pupae exhibited an increase
 387 in the EC treatment compared to control (Fig. 5B, Table S14). Total lipid content of adults was

388 lower compared to control in treatments with increased temperature (T2 and MS) (Fig. 5C & 5D,
389 Table S15 & S16). Moreover, the greatest drop in TLC of adults was observed in the MS treatment
390 ((Fig. 5C & 5D, Table S15 & S16), corresponding with the negative synergistic effect according to
391 (Piggott et al., 2015). Females had significantly higher total lipid content compared to males
392 (Figure 5C & 5D, Table S17).

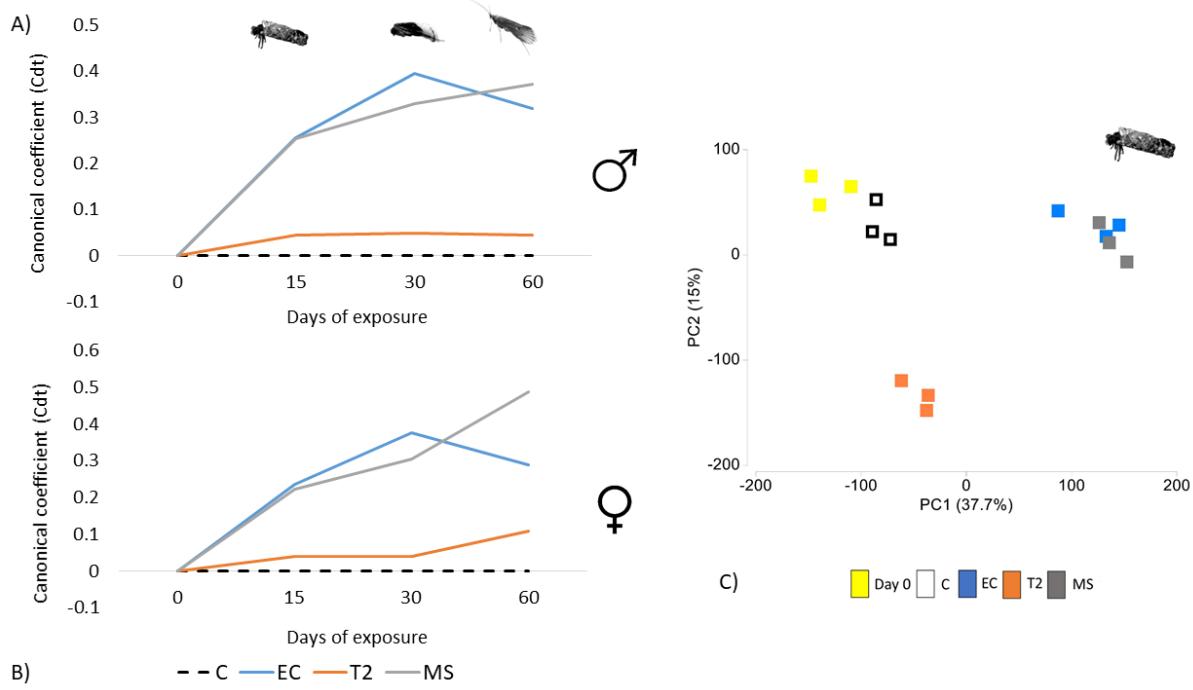
393

394 3.5. Metabolome profiles of the caddisfly *Micropterna nycterobia*

395 Principal Response Curves (PRC) of non-target metabolome profile of larvae, pupae and adult
396 caddisflies show that the metabolome of all caddisfly life stages was mostly affected by the ECs
397 mixture (EC and MS), as evident by the highest deviation from the control (Fig. 5A & B). Deviations
398 were observed in larvae at D15 already, and further increased in pupae and adults. The MS
399 treatment showed highest impact on metabolome of both male and female adult caddisflies (Fig.
400 5A & B). Additionally, 62.6 % of total variance in males and 59.5 % in females could be attributed
401 to time, whereas 22.1 % in males and 25.8 % in females could be attributed to the treatment
402 (including its interaction with time, Table S18). The first PRC axis was significant (males – $F (1, 32)$
403 = 18.714 $p < 0.05$, females – $F (1, 32) = 28.172, p < 0.05$) and based on the Monte Carlo tests per
404 sampling date, the treatment regime had a significant influence on all sampling dates.

405 Principal component (PCA) analysis based on non-target metabolic profiles of all life stages of *M.*
406 *nycterobia* revealed clear separation of pre-metamorphosis larvae and post-metamorphosis
407 pupae and adult imagines (Fig. S6, PC1). However, when particular life stages were analyzed
408 separately, the PCA also revealed separation into distinct groups based on treatments. In larvae,
409 for instance, PC1 axis separating larvae in ECs and MS treatments from D0, C and T2 treatments
410 accounted for 37.7 % of variability (Fig. 4C; variance from [PC1, PC2]≈[37.7 %, 15 %]).

411 Majority of metabolite groups (18 in total) showing the most significant changes in abundance to
412 stressor treatments in *M. nycterobia* were lipids and fatty acids (39%) followed by amino acids
413 (22%), quinones (6%), acylcholine (6%), adrenergic agents (6%), lactones (6%), alcohols (5%),
414 pyridines (5%), alkaloids (5%) (Fig. S7, Table S19).



415

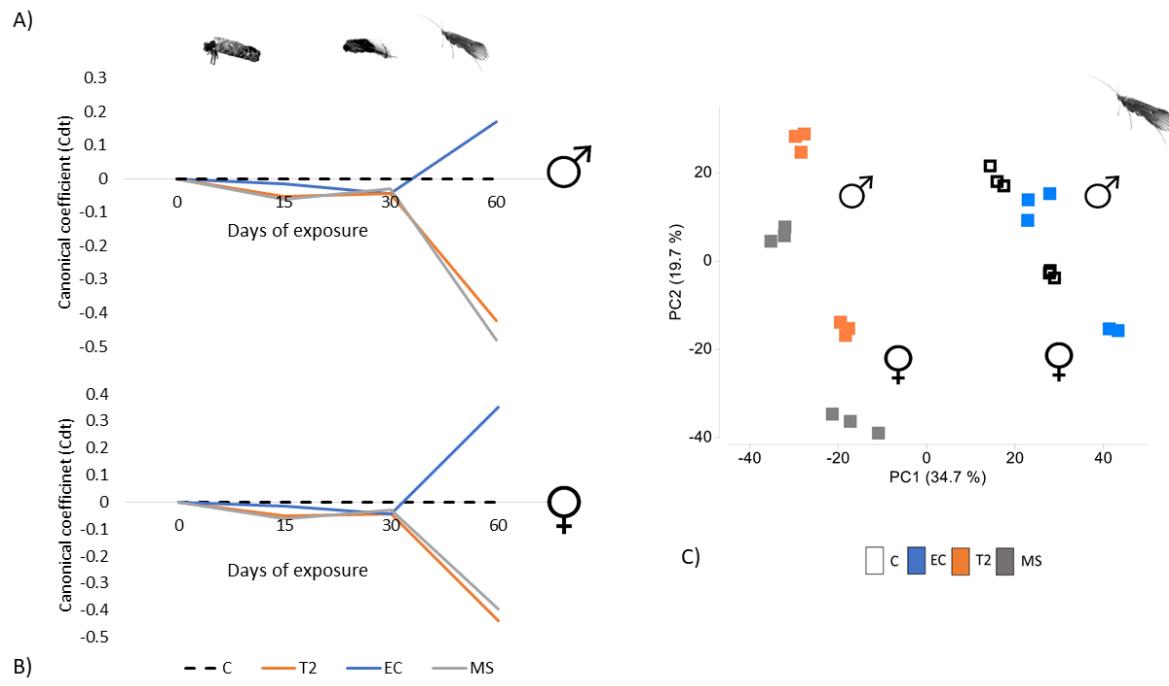
416 Figure 5. Metabolome profiles of the caddisfly *Micropterna nycterobia*; PRC of changes in the
 417 metabolic profiles along the caddisfly life cycle in A) male and B) female adults exposed to
 418 treatments in relation to control. Numbers on x-axis denote days of exposure. C) PCA plot
 419 showing separation based on metabolome of *M. nycterobia* larvae in different treatments at 15
 420 days of exposure. Abbreviations of treatments are as follows: C – Control ($T = 10\text{ }^{\circ}\text{C}$), T2 -
 421 Increased temperature ($14\text{ }^{\circ}\text{C}$), EC - ECs mix, MS - multiple stressor treatment (T2 + EC); Day 0 –
 422 pre-exposure sample.

423

424 3.5. Lipidome profiles of the caddisfly *Micropterna nycterobia*

425 Principal Response Curves (PRC) of non-target lipidome profile of larvae, pupae and adult
 426 caddisflies shows the highest deviation from the control in male and female adults, with an
 427 opposing individual stressor effect (EC vs T2; Fig. 6A & B). In MS treatments, increased
 428 temperature was the dominant stressor for both sexes, however, there were differences
 429 between sexes, as male caddisflies lipidome was more affected in T2 and MS treatments,
 430 whereas female caddisflies lipidome was more affected in the EC (Fig. 6A & 5B). Moreover, table
 431 S20 shows that 79.8 % of total variance in male and 68.4 % in female caddisflies can be attributed

432 to time, whereas 13.3 % in male and 17.3% in female can be attributed to the treatment
 433 (including its interaction with time). The first PRC axis was significant (males - $F (1, 32) = 17.475$
 434 $p < 0.05$, females – $F (1, 32) = 14.583, p < 0.05$) and based on the Monte Carlo tests per sampling
 435 date, the treatment regime had a significant influence on all sampling dates.



436

437 Figure 6. Lipidome profiles of the caddisfly *Micropterna nycterobia*; PRC of changes in the
 438 lipidome profiles of caddisfly life stages and A) male and B) female adults exposed to treatments
 439 in relation to control. Numbers on x-axis denote days of exposure. C) PCA plot showing separation
 440 adult *M. nycterobia* separated by sex in different treatments. Abbreviations of treatments are as
 441 follows: C – Control ($T = 10$ °C), T2 - Increased temperature (14 °C), EC - ECs mix, MS - multiple
 442 stressor treatment (T2 + EC); Day 0 –pre-exposure sample.

443 Principal component (PCA) analysis based on non-target lipidome profiles of all life stages of *M.*
 444 *nycterobia* showed clear separation of three major life stages, larvae, pupae and adults (Fig. S8).
 445 The total variance accounted by the three clusters was ~68.8 % (variance from [PC1, PC2,
 446 PC3]≈[47.7 %, 14.8 %, 6.3 %]). Clustering of particular treatments was particularly evident in
 447 separate analyses of each life stage. The highest degree of clustering based on treatments was
 448 inferred for adults, with the first principle component axis (PC1 = 34.7 %) separating adults based

449 on increased water temperature (T2 and MS treatments), whereas the second axis separated
450 males from females (PC2 = 19.7 %, Fig. 6C).

451 Within the lipidome, most significant changes in abundance to stressor treatments were noticed
452 in glycerophospholipids (67%) followed by fatty acyls (12%), sphingolipids (12%), glycerolipids
453 (5%), prenol lipids (2%) and sterol lipids (1%) (Fig. S9, Table S21).

454

455 **4. DISCUSSION**

456 Water pollution has far-reaching consequences for the ecosystem health and functioning, and it
457 is important to understand these impacts, especially in a context of climate change. Here we used
458 simplified freshwater food web exposed to a mixture of PhACs and EDCs and increased water
459 temperature to broaden our understanding of the impacts of climate change and pollution on
460 freshwater ecosystems.

461 4.1. Warming and pollution with PhACs & EDCs triggered a mild response in moss

462 A mild response of the moss to both individual stressors (increased water temperature and
463 contamination with ECs) and their combination suggests mosses' resilience. It has been shown
464 that plants have specific temperature and pollution thresholds that trigger or inhibit certain
465 physiological processes, allowing them to respond to stressful conditions (Firmansyah and
466 Argosubekti, 2020; Gorovits et al., 2020; Sun et al., 2018; Zezulka et al., 2013). One of the most
467 common physiological responses includes production of heat shock proteins (HSPs), and lack of
468 observable change in regulation of HSPs may suggest that the thermal and pollution threshold
469 necessary to trigger stress response in the moss was not reached. This observation is in
470 agreement with established thermal threshold of plants of minimum 5 °C (Firmansyah and
471 Argosubekti, 2020). Even though changes in metabolomic and lipidomic profiles among
472 treatments were significant, one should keep in mind that changes in metabolite and lipid
473 composition can be related to stress response but also developmental stages (Lu et al., 2019;
474 Mikami and Hartmann, 2004). In addition, the biotic stress induced by the feeding of *M.*
475 *nycterobia* larvae on the moss might have masked the impact of the pollution and increased

476 temperature. Plants can prioritize their responses to address individual stressors when exposed
477 to multiple abiotic and/or biotic stressors (Rejeb et al., 2014; Suzuki et al., 2014). We argue that
478 the moss in the current experiment might have prioritized biotic stress over abiotic stressors and
479 activated different defence mechanisms to mitigate larval feeding. However, we could not test
480 for the latter, since feeding of *M. nycterobia* larvae on the moss was also present in control
481 treatments. Moreover, research has shown that different stress combinations activate different
482 pathways and signals thus making it harder to predict multiple stressor effects (Rejeb et al., 2014;
483 Suzuki et al., 2014; Vescio et al., 2022).

484

485 4.2. Single stressor impacts: effects of warming and pollution with PhACs and EDCs on *M.*
486 *nycterobia*

487 In the current experiment, we recorded a body mass loss in *M. nycterobia* that is in line with the
488 usual life cycle patterns of the holometabolous caddisflies, with larvae having the highest body
489 weight and adults the lowest (Huryn and Wallace, 2000). Increased temperature during insect
490 development typically leads to reduced adult body size, negatively influencing fecundity and
491 longevity (Mirth and Riddiford, 2007), this effect was however, not observed in the current study.
492 Our observations are in line with data on chronic exposure to pesticides in the caddisfly
493 *Limnephilus lunatus*, where reduced body weight of adults was observed only if younger instar
494 larvae were exposed, and not the fifth-instars (Liess and Schulz, 1996; Schulz and Liess, 2001,
495 1995).

496 *M. nycterobia* inhabits clean crenal and rhithral sections and is therefore expected to be sensitive
497 to presence of contaminants (Graf et al., 2023). Indeed, sensitivity is displayed through intense
498 change in regulation of both metabolites and lipids in respect to control, however, the
499 contaminants seem to have a more significant impact on metabolome than temperature. More
500 precisely, the most pronounced metabolome response was post-metamorphosis, yet changes in
501 metabolite regulation are already notable in larvae at D15. Notably, the sampled caddisflies'
502 metabolome contained the biogenic amine octopamine, a significant neurotransmitter,
503 neuromodulator, and neurohormone influencing various physiological functions, behaviour and

504 endocrine activity (Farooqui, 2012) Changes in octopamine levels due to PhACs and EDCs during
505 metamorphosis could affect not only the subsequent life stage but potentially extend across
506 multiple generations.

507 Observed difference in dynamics of regulation of metabolites vs lipids can be related to
508 physiological roles of metabolites and lipids which response tends to differ depending on the
509 type of stress and the metabolic pathways involved (Kainz and Fisk, 2009; Snart et al., 2015).
510 Generally, lipids serve as a long-term energy source and are stored in lipid droplets, which can
511 be mobilized to provide energy during times of starvation, embryogenesis, prolonged periods of
512 flight and stress (Arrese and Soulages, 2010; Kainz and Fisk, 2009). Here, metabolites were more
513 regulated than lipids in response to stress probably in order to maintain cellular homeostasis and
514 ensure energy reserves (lipids) for the emerging adults (Arrese and Soulages, 2010). Glycerolipids
515 such as triglycerides are stored in the core of the lipid droplets surrounded by
516 glycerophospholipids (Arrese and Soulages, 2010). As glycerophospholipids were mostly affected
517 by experimental treatments, this further supports the fact that lipid reserves were preserved for
518 adults. However, changes in glycerophospholipids of insects can also be related to development
519 and metamorphosis (Bashan et al., 2002; Cargill et al., 1985; Duarte, 2019) as well as food source
520 (Hanson et al., 1985; Torres-Ruiz et al., 2010).

521 The lack of strong effects of increased water temperature on metabolite regulation, as well as
522 absence of heat shock protein HSP70 expression, is most likely due to adaptation of *M. nycterobia*
523 to thermal stress regularly occurring in intermittent streams (Qin et al., 2003). This finding
524 suggests that *M. nycterobia* and possibly other intermittent habitats indicators may have
525 metabolic flexibility to cope with thermal stress, allowing them to survive extreme climatic events
526 characterised by fluctuating temperature regimes. In addition, the regulation of lipidome of *M.*
527 *nycterobia* aquatic stages exhibited intriguing resilience to both increased water temperature
528 and pollution with PhACs and EDCs. The limited impact on lipid regulation suggests that the stress
529 response threshold triggering significant lipid mobilisation may not have been surpassed.
530 Instead, the priority for the aquatic stages was directed towards lipid accumulation rather than
531 mobilization in response to stress challenges (Arrese and Soulages, 2010; Hoppeler et al., 2018).
532 Emphasis on lipid accumulation was evident through the observed increase in total lipid content

533 from larval to pupal stages, serving as a crucial energy source to sustain adult insects during non-
534 feeding periods and fuel their flights (Arrese and Soulages, 2010; Hoppeler et al., 2018). While
535 the anticipation of intense lipidome activity in adult insects is well-founded, it is surprising that
536 so distinct regulatory mechanisms are operating in response to different stressors. However,
537 lipidomic profiles of multiple stressor treatment were in both males and females congruent with
538 those of increased temperature, implying the dominant impact of increased water temperature
539 on regulation of lipids in aquatic insects.

540 Increased water temperature accelerated development of *M. nycterobia*, resulting in earlier
541 adult emergence and lower total lipid content of all life stages in treatments with increased
542 temperature. Similarly, the mayfly larvae chronically exposed to increased temperature used
543 lipids and amino acids as alternative energy sources to support their growth and maintenance
544 costs, ultimately resulting in reduced total lipid content (Chou et al., 2018). Furthermore,
545 sensitivity of the temporal emergence patterns of aquatic insects was already discussed as
546 toxicological endpoint for exposure to pesticides (Schulz and Liess, 2001), as timing of aquatic
547 insect emergence plays a crucial role for riparian predators (review in Bundschuh et al., 2020).
548 More precisely, insectivorous birds almost exclusively obtain the omega-3 long-chain
549 polyunsaturated fatty acids from emerging aquatic insects, thus shifts in the relative availability
550 and phenology of aquatic insects in response to a changing climate are likely to have major fitness
551 consequences for their breeding success (Shipley et al., 2022). Hence, such shifts can have
552 cascading effects on cross-ecosystem energy flow. This is of particular importance in intermittent
553 water bodies, like those inhabited by *M. nycterobia*, where mass emergence during short periods
554 is typical and riparian food webs are highly dependent on the aquatic subsidies (McIntosh et al.,
555 2017).

556

557 4.3. Multiple stressor impacts of warming and PhACs and EDCs on aquatic insects

558 A synergistic interactive effect was observed, leading to a decrease in total lipid content and
559 significant variation in lipid profiles in adults of both sexes under the MS treatment. *Micropterna*
560 *nycterobia*, a specialist in intermittent rivers, exhibits a behaviour where adults leave the water

561 bodies upon emergence and migrate to cooler mountainous regions or nearby caves for a few
562 months until their gonads develop (Waringer and Graf, 2011). In autumn, after copulation, they
563 lay eggs in re-established surface flow. Therefore, the observed decrease in lipid reserves in
564 adults (8.9% and 10.7% decrease in total lipid content in males and females, respectively) could
565 have a major impact on their reproduction and population dynamics. Lipids serve as crucial
566 energy reserves for insects, especially during non-feeding life stages and long-distance flights
567 (Arrese and Soulages, 2010; Downer and Matthews, 1976). Maintaining metapopulation
568 dynamics is particularly important for inhabitants of intermittent water bodies (Datry et al.,
569 2017). Various pollutants, such as fungicides and copper, can decrease the lipid content of
570 limnephilid caddisflies (Konschak et al., 2019). However, this effect was not observed in the
571 current study as PhACs and EDCs did not influence the lipid content of *M. nycterobia*.
572 Furthermore, the negative effects of pollutants on lipids can be exacerbated by elevated water
573 temperatures (Yoon et al., 2022). However, in our study, increased water temperature primarily
574 influenced the lipids of caddisflies, and its adverse effects were amplified by pollution with PhACs
575 and EDCs. Additionally, warming indirectly contributed to the further deterioration of
576 environmental conditions in the T2 and MS treatments, as evidenced by increased conductivity
577 within these two treatments.

578 In terms of the timing of the strongest stress response, our results differ from a previous
579 experiment involving the same caddisfly species, where the effects of ECs and microplastic
580 particles were most pronounced in the first 15 days of exposure, both in single and combined
581 stressor treatments (Grgić et al., 2023). Apart from the dominant impact of increased
582 temperature, these differences may also be attributed to variations in the mixture of ECs used,
583 as different compounds can have varying effects on biota (Muñoz et al., 2015; Nilsen et al., 2019).
584 Nevertheless, our study indicates that the adverse synergistic effects of warming events and
585 freshwater contamination with ECs could intensify throughout the life cycle of aquatic insects,
586 potentially leading to developmental impairments and disturbances in population dynamics
587 (Kazmi et al., 2022). However, in most environmental health assessment and monitoring
588 programs, only the aquatic stages of aquatic insects are considered (Water Framework Directive
589 (WFD) 2000/60/EC). Furthermore, the multiple stressor effects observed in the current study not

590 only resulted in reduced resource quality for aquatic food webs but also affected the quality of
591 emergence, thus impacting the riparian food webs at the aquatic-terrestrial interface (Bundschuh
592 et al., 2020).

593

594 4.5. Differential response to stressor impacts of male and female caddisflies

595 Our study reveals sex-specific responses to both single and multiple stressors, with females
596 exhibiting more pronounced impacts on the metabolome while males show greater effects on
597 the lipidome. In the majority of insects, there is sexual dimorphism in lipid content due to distinct
598 roles played by lipids, such as egg production in females and flight behaviour in males (Lease and
599 Wolf, 2011). Certain aquatic insect species, characterized by specific male flight behaviour (Lease
600 and Wolf, 2011) or swarming (Sartori et al., 1992), experience negative impacts on population
601 fitness when males have decreased lipid content. Furthermore, this study identifies 4-
602 hydroxyestradiol, an endogenous metabolite of 17 β -estradiol, from *M. nycterobia*, which has
603 been shown to have significant lipid-modulating effects in rats (Wang and Zhu, 2017).
604 Additionally, in *Drosophila*, sexual dimorphism has been observed in metabolic genes and
605 mechanisms involved in triglyceride homeostasis (Wat et al., 2020).

606 Likewise, the findings of this study highlight sex-dependent variation in metabolites induced by
607 stress, consistent with a previous study involving *M. nycterobia* exposed to microplastic particles
608 and a mixture of personal care products (Grgić et al., 2023). Moreover, female insects generally
609 exhibit a stronger stress response across different taxa and under various stress conditions,
610 including parasite infections, predation, food quality, chemical stress, and the impacts of climate
611 change (Lindsey and Altizer, 2009; Slos et al., 2009; Stillwell and Davidowitz, 2010). This is likely
612 due to the different evolutionary roles of male and female insects, which have led to the
613 development of distinct stress-defence mechanisms. The fitness of females is closely linked to
614 their life expectancy and the number of offspring they produce.

615 Therefore, our study emphasizes the variability in the impacts of both single and multiple
616 stressors on various traits, different life stages, and sexes within a single species. Consequently,
617 it underscores the importance of developing a more comprehensive understanding of the

618 sensitivity of freshwater organisms to the adverse effects of single and multiple stressors,
619 particularly when addressing the management of freshwater ecosystems in the context of global
620 change (Schäfer and Piggott, 2018).

621

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630

631 **LITERATURE**

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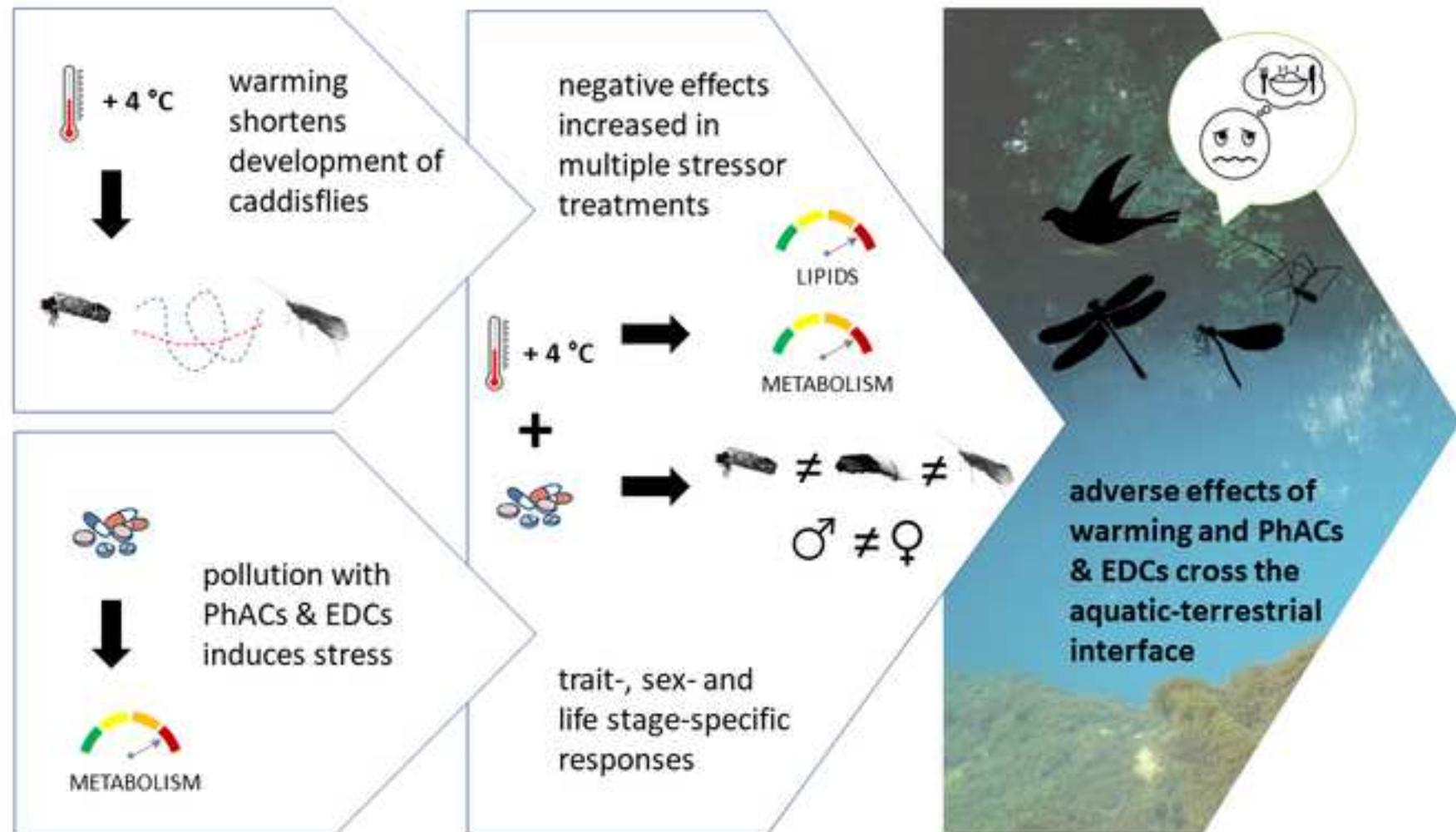
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Highlights

1. Warming was a dominant stressor for development-related traits of the caddisfly
2. Negative effects of warming on lipids were increased by presence of PhACs&EDCs
3. Pollution with PhACs & EDCs has higher impact on caddisfly metabolism than warming
4. Trait-, sex- and life stage-specific responses to multiple stressors were observed
5. Impacts of warming and PhACs & EDCs cross the aquatic-terrestrial interface

1 **Pharmaceuticals and endocrine disrupting compounds modulate adverse effects of climate
2 change on resource quality in freshwater food webs**

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24 **Abstract**

25 Freshwater biodiversity, ecosystem functions and services are changing at an unprecedented rate due to
26 the impacts of vast number of stressors overlapping in time and space. Our study aimed at characterizing
27 individual and combined impacts of pollution with pharmaceuticals (PhACs) and endocrine disrupting
28 compounds (EDCs) and increased water temperature (as a proxy for climate change) on primary producers
29 and first level consumers in freshwaters. We conducted a microcosm experiment with a simplified
30 freshwater food web containing moss (*Bryophyta*) and shredding caddisfly larvae of *Micropterna*
31 *nycterobia* (Trichoptera). The experiment was conducted with four treatments; control (C), increased
32 water temperature +4 °C (T2), emerging contaminants' mix (EC = 15 PhACs & 5 EDCs), and multiple
33 stressor treatment (MS = EC + T2). Moss exhibited an overall mild response to selected stressors and their
34 combination. Higher water temperature negatively affected development of *M. nycterobia* through
35 causing earlier emergence of adults and changes in their lipidome profiles. Pollution with PhACs and EDCs
36 had higher impact on metabolism of all life stages of *M. nycterobia* than warming. Multiple stressor effect
37 was recorded in *M. nycterobia* adults in metabolic response, lipidome profiles and as a decrease in total
38 lipid content. Sex specific response to stressor effects was observed in adults, with impacts on
39 metabolome generally more pronounced in females, and on lipidome in males. Thus, our study highlights
40 the variability of both single and multiple stressor impacts on different traits, different life stages and
41 sexes of a single insect species. Furthermore, our research suggests that the combined impacts of
42 warming, linked to climate change, and contamination with PhACs and EDCs could have adverse
43 consequences on the population dynamics of aquatic insects. Additionally, these findings point to a
44 potential decrease in the quality of resources available for both aquatic and potentially terrestrial food
45 webs.

46

47 **Keywords:**

48 climate change, pollution, caddisflies, sex specific stress response, aquatic-terrestrial subsidies, ecosystem
49 subsidies

50 **Highlights:**

51 • warming was a dominant stressor for development-related traits of the caddisfly
52 • negative effects of warming on lipids were increased by presence of PhACs&EDCs
53 • pollution with PhACs & EDCs has higher impact on caddisfly metabolism than warming
54 • trait-, sex- and life stage-specific responses to multiple stressors were observed
55 • impacts of warming and PhACs & EDCs cross the aquatic-terrestrial interface

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59 **1. INTRODUCTION**

60 Freshwater ecosystems are susceptible to various anthropogenic stressors (e.g. chemical
61 pollution, climate change, habitat loss, invasive species) which mostly coincide. Pharmaceuticals
62 (PhACs) and endocrine disrupting compounds (EDCs) are a diverse group of pollutants designed
63 to be biologically active at low doses, targeting specific metabolic and molecular pathways in
64 humans and animals, thus posing risk for aquatic organisms even at low environmental
65 concentrations (Ebele et al., 2017; Tijani et al., 2013; Wilkinson et al., 2017). Moreover, EDCs
66 encompass a wide range of chemicals (e.g. personal care products, cleaning products, food
67 preservatives, etc.) that interfere with normal function(s) of the endocrine system (Ebele et al.,
68 2017). PhACs and EDCs were shown to affect aquatic insects in many ways, causing changes in
69 growth and development (Jarvis et al., 2014), biomass (López-Doval et al., 2012), enzymatic
70 activity (Pestana et al., 2014), metabolome composition (Grgić et al., 2023; Previšić et al., 2020;
71 Späth et al., 2022), behavior (Jarvis et al., 2014; Späth et al., 2022) and survival rate (López-Doval
72 et al., 2012; Maenpaa and Kukkonen, 2006). Furthermore, PhACs and EDCs have the potential to
73 bioaccumulate in aquatic insects (Grabicova et al., 2015; Lagesson et al., 2016; Previšić et al.,
74 2021; Veseli et al., 2022) and to cross ecosystem boundaries through emerging aquatic insects
75 and thus contaminate terrestrial habitats (Previšić et al., 2021; Veseli et al., 2022). Moreover, in
76 freshwater ecosystems these compounds rarely occur one at a time but rather in complex
77 mixtures of several different emerging contaminants, thus making it harder to investigate their
78 effects (Wilkinson et al., 2017).

79 Climate change, with its long-term shifts in global weather patterns, poses significant challenges
80 to freshwater ecosystems. Within freshwater ecosystems, aquatic insect groups, such as
81 caddisflies, mayflies, and stoneflies, play a crucial role as inter-habitat linkages between aquatic
82 and terrestrial ecosystems, facilitating the flow of energy and nutrients (Huryn and Wallace,
83 2000). Additionally, they serve as valuable bioindicators for assessing the health of freshwater
84 environments (Water Framework Directive (WFD) 2000/60/EC). Their vulnerability to climate
85 change is influenced by their specific biological traits and ecological preferences, with a
86 considerable proportion of them belonging to cold-adapted taxa (Conti et al., 2014; Hershkovitz

87 et al., 2015). The impact of climate change, characterized by rising temperatures and changes in
88 precipitation levels (Webb et al., 2008), is particularly profound on these cold-adapted taxa in
89 higher altitudes, making them highly vulnerable to warming (Krajick, 2004; Macadam et al.,
90 2022). As a consequence of climate change, temperature increase affects various aspects of
91 aquatic insects' lives. It directly impacts their growth, development, and body size (Cogo et al.,
92 2020), as well as their emergence patterns (Finn et al., 2022). The anticipated rise in the
93 frequency and extent of intermittent rivers and streams, which periodically cease flow or even
94 completely dry, is a direct consequence of global climate change and the increasing human
95 demand for freshwater resources (Blackman et al., 2021). This trend holds significant implications
96 for aquatic insect communities, as considerably altered environmental conditions not only
97 impact their geographic distribution (Cogo et al., 2020 and references therein), but also their
98 population dynamics (Nukazawa et al., 2018), and community structure (Dorić et al., 2023).

99 Global warming is likely to exacerbate impact of other anthropogenic stressors (Wrona et al.,
100 2006). For instance, as temperature rises, the solubility and mobility of PhACs and EDCs in water
101 can increase, leading to higher concentrations and potentially greater toxicity (Kazmi et al., 2022;
102 Noyes et al., 2009). Temperature change may also alter degradation rates of some chemical
103 contaminants, with increasing temperature usually shortening their half-life and reducing the
104 overall risk (Bhangare et al., 2022; Noyes et al., 2009). While accelerated decomposition reduces
105 the concentration of the parent compound, it increases the concentration of the degradation
106 products, which in some cases could be even more toxic for aquatic organisms (Noyes et al.,
107 2009). Warmer water usually increases the metabolic rate of aquatic organisms, thus leading to
108 potentially increased uptake of these chemicals (Kazmi et al., 2022). In addition to increasing
109 uptake, warming can also affect behaviour and physiology of aquatic organisms making them
110 more susceptible to stressors (Polazzo et al., 2022). Toxicity of chemicals in water can depend on
111 variety of abiotic (e.g. photolysis, hydrolysis, etc.) and biotic processes (e.g. biotransformation,
112 biodegradation, etc.) (von Schiller et al., 2017). Moreover, the impact of warming on the toxicity
113 of PhACs and EDCs in water is complex and can depend on a variety of factors, including the type
114 of the chemical (Serra-Compte et al., 2018), aquatic species (Duchet et al., 2023, preprint), and
115 life-stage tested (DeCourten and Brander, 2017). Due to the increase in temperature caused by

116 climate change, the temperature-dependent toxicity of PhACs and EDCs in water will become a
117 matter of growing significance that warrants assessment.

118 It is generally very challenging to gain empirical understanding of the effects of climate change
119 in comparison with other stressors (Halsch et al., 2021), as well as their combined effects (Dinh
120 et al., 2022). Consequently, there have been only a handful of studies investigating single and
121 combined effects of increased water temperature and PhACs and EDCs in aquatic invertebrates
122 (e.g. Barbosa et al., 2017; Cruzeiro et al., 2019; Heye et al., 2019). More specifically,
123 carbamazepine and higher temperatures increased *Chironomus riparius* mortality (Heye et al.,
124 2019); fluoxetine combined with higher temperature reduced reproductive success and
125 population growth in *Daphnia magna* (Barbosa et al., 2017), whereas levonorgestrel and
126 increased temperature did not cause DNA damage in *Gammarus locusta* cells (Cruzeiro et al.,
127 2019). To address this knowledge gap, we conducted a study aimed at characterizing effects of
128 increased water temperature and exposure to PhACs and EDCs on primary producers (non-
129 vascular macrophytes; moss) and first level consumers (shredding aquatic insects) in freshwaters.
130 Considering the importance of aquatic insects as fundamental links between aquatic and
131 terrestrial food webs and reliable bioindicators to pollution (Erasmus et al., 2021; Muñoz et al.,
132 2015) we chose caddisflies as our model organisms. Caddisflies are a species-rich and ecologically
133 diverse insect order, that is well-suited to reflect effects of various stressors on aquatic
134 ecosystems (Hering et al., 2009). Despite of the high ecological plasticity and thermal tolerance
135 of intermittent rivers specialists (Stubbington et al., 2017) we hypothesized that the individual
136 and combined stressor effects of both, increased water temperature and PhACs and EDCs, will
137 trigger a stress response in an intermittent river caddisfly, *Micropterna nycterobia* (McLachlan,
138 1875). Chronic *in situ* exposure to pollution with ECs results in measurable changes of metabolite
139 levels in relatively pollution-tolerant caddisfly larvae (Previšić et al., 2020), whereas increased
140 temperature results in depletion of lipids and reduces developmental period of mayfly larvae
141 (Chou et al., 2018). Moreover, variable impacts on emergence and survival were observed in
142 dragonflies and an aquatic heteropteran exposed to increased water temperature, PhACs and
143 their combination (Duchet et al., 2023, preprint). Hence, we conducted a 78-day microcosm
144 experiment composed of a simplified freshwater food web exposed to a mixture of PhACs and

145 EDCs and increased water temperature as a proxy for climate change using the randomized
146 factorial design. We analyzed the physiological changes in caddisflies and moss via non-targeted
147 metabolomics and lipidomics, i.e. by evaluating alterations in the metabolite and lipid profiles of
148 non-model organisms across their life cycles, as well as changes in emergence patterns, body
149 weight and total lipid content.

150

151 **2. MATERIALS AND METHODS**

152 2.1 Microcosm Experiment: Experimental Design and Sample Collection

153 We conducted the microcosm experiment with a simplified freshwater food web containing
154 nonvascular macrophytes (Bryophyta), hereafter moss and caddisfly larvae *Micropterna*
155 *nycterobia* (McLachlan, 1875) (Limnephilidae, Trichoptera) feeding mainly as shredders.
156 Trichoptera larvae, moss (*Cinclidotus aquaticus* (Hedw.) Bruch & Schimp and *Rhynchosstegium*
157 *riparioides* (Hedw.) Cardot), water, sand and stones collected from the pristine Krčić River
158 (N44.027321 E16.318936), minimally impacted by anthropogenic activity, were used for the
159 experiment. Microcosm setup followed Previšić et al., 2021 with modifications in number of
160 microcosms, temperature regime and mixture of moss species. Upon collection, 12 microcosms
161 (aquaria 30 × 20 × 15 cm) were installed with 3 L of water, 10 tablespoons of sand, 3 large stones
162 (> 10 cm), 10 small stones (2–5 cm), 3 tufts of moss (6–8 cm in diameter and plants up to 15 cm
163 in length) and 5th instar *M. nycterobia* larvae (ca. 30 larvae per aquarium). Constant oxygen levels
164 were kept using aquaria air pumps, and to minimize evaporation, each microcosm was covered
165 with a glass cover. Natural light and day-night regime was supplemented with the artificial light
166 (with sunlight's spectrum) in the regime of 12 hours of light followed by 12 hours without light.
167 All microcosms were acclimatized for 10 days at 10 °C under aforementioned conditions
168 preceding the start of the experiment. The experiment was conducted in the randomized
169 factorial design, with treatments as follows: Control (C), Increased temperature (T2), ECs mix
170 (EC), multiple stressor treatment = ECs mix + increased temperature (EC + T2 = MS), with three
171 replicates of each. Subsequently, 6 of them were exposed to a mixture of 20 ECs over a 78-days
172 period. The composition of the ECs mixture was selected based on occurrence of particular

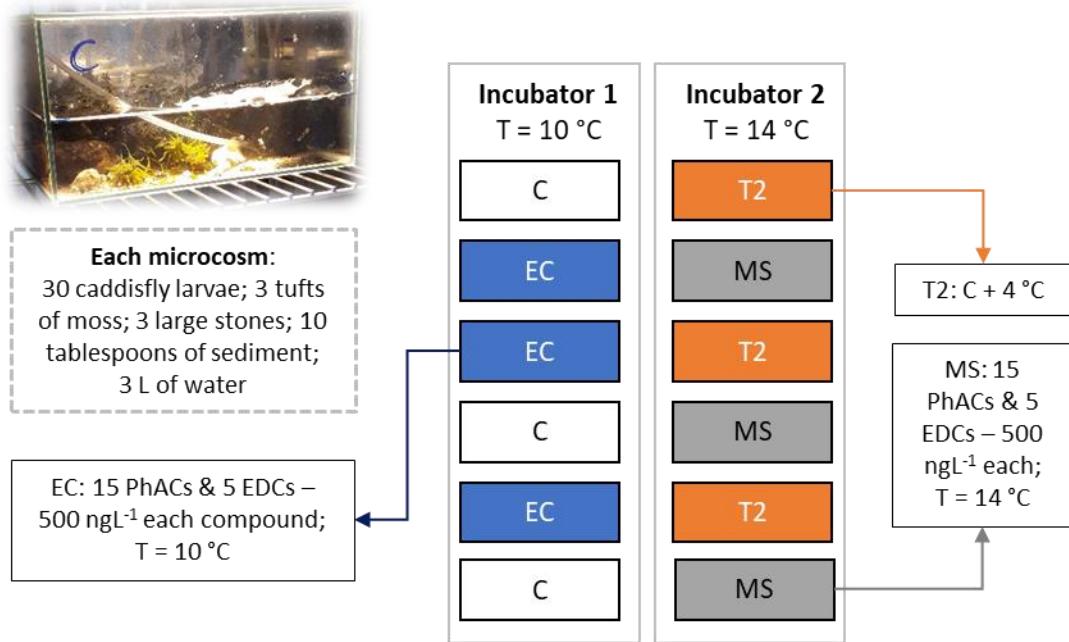
173 compounds in freshwaters in Europe (Mandaric et al., 2015), and included 15 PhACs; azaperol,
174 acetaminophen, thiabendazole, levamisol hydrochloride, dexamethasone, ketoprofen,
175 naproxen, ranitidine hydrochloride, soltalol hydrochloride, valsartan, diphenhydramine,
176 clopidogrel hydrogen sulfate, hydrochlorothiazide, sertraline hydrochloride, cimetidine and 5
177 EDCs; benylparaben, ethylparaben, propylparaben, estriol, estradiol- β . The volume of water was
178 kept constant by adding fresh dechlorinated tap water (ca. 100 mL every week), and the
179 concentration of each compound was kept at a pseudo-constant concentration of 500 ng L⁻¹.
180 Taking into consideration knowledge gained from our previous experiments (Cetinić et al., 2022;
181 Grgić et al., 2023; Previšić et al., 2021), three stock solutions were prepared and 100 μ L of the
182 solution was added each day, every three days or once a month, depending on the compound.
183 In this way, abiotic attenuation (sorption and/or (photo)degradation) was taken in consideration
184 and the nominal concentration of each compound was maintained, more details provided in
185 Supporting information (SI 1). As different temperature regimes needed to be followed, aquaria
186 were placed in two different incubators (POL-EKO APARATURA, Poland). "Natural" temperature
187 regime (T1) mimicked the regime of the Krčić spring reach before the drying phase (10 °C) and
188 temperature was successively increased 0.5 °C every 15 days. Increased temperature regime (T2)
189 followed the same pattern but with temperature increased by 4 °C, in accordance with patterns
190 of reduced flow observed in the selected river coupled with projections of temperature increase
191 due to climate change in the Mediterranean montane regions (Bravo et al., 2008).

192 Biota sampling included initial (after the acclimatization period - day 0 (D0)) and several
193 consecutive collections (ca. day 15 (D15), day 30 (D30) and day 60 (D60) of exposure) including
194 different life stages (larvae, pupae and adult stage), in accordance with the life cycle of
195 holometabolous caddisflies. At each sampling date, we collected replicate samples from each
196 microcosm, consisting of 2 g of moss and 3–5 Trichoptera larvae/pupae. However, these samples
197 were pooled per treatment to mitigate the potential extreme effects of individual microcosms
198 (Kraufvelin, 1998). The complexity and extended duration of micro and mesocosm test systems
199 exacerbate issues like "aquarium individuality," where initially identical replicates diverge due to
200 random effects, introducing significant variability and complicating the identification of
201 statistically significant deviations (Kraufvelin, 1998; Sanderson, 2002). Additionally, the weight

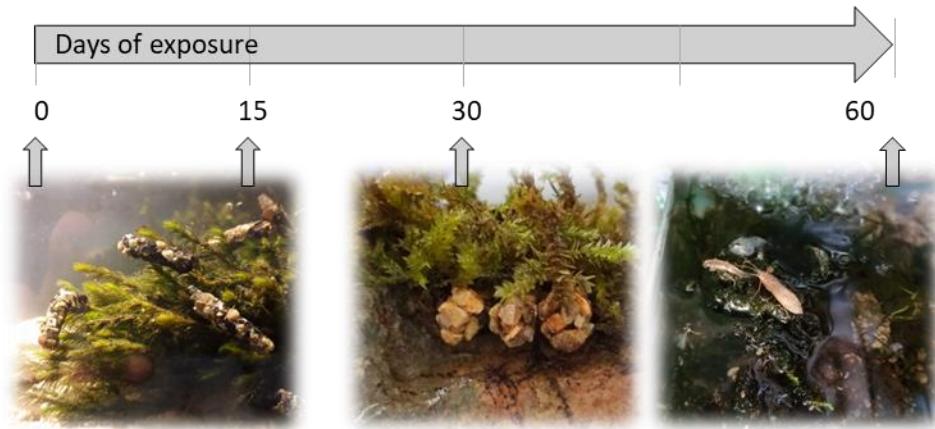
202 reduction of adult aquatic insects during metamorphosis (Huryn and Wallace, 2000) poses a
203 challenge, leading to high tissue demand. Consequently, analytical replicates for each treatment
204 per sampling date were created after homogenizing the pooled samples (details under 2.2, Biota
205 Sample Processing). The chosen approach aims to strike a balance between providing ecologically
206 meaningful results with non-model organisms and minimizing methodological constraints.
207 Trichoptera larvae were kept in clean aquaria for 24 h to allow for gut clearance prior to collection
208 (Van Geest et al., 2010). Additionally, emerging adult *M. nycterobia* were collected as they
209 emerged (daily), and sex of each individual was determined. These samples were pooled
210 depending on sex for subsequent analyses due to tissue requirements and to match the overall
211 sampling scheme, according to temperature treatments. Emergence following the „natural”
212 temperature regime (T1) started ca. 2 weeks later than in T2, thus samples were pooled for dates
213 45-60 and 60-75 days of exposure. Samples in elevated temperature regime (T2) were pooled for
214 dates: 30-37 and 38-47 days of exposure. We combined adult *M. nycterobia* from 45-60 days of
215 exposure in T1 and 38-47 days of exposure in T2 to one time point (day 60 of exposure) in order
216 to have approximately the same time period of exposure to selected stressors. All samples were
217 freeze-dried upon collection and stored at -80 °C until further processing.

218 Oxygen concentration (mg L⁻¹), oxygen saturation (%), pH and electrical conductivity (mS cm⁻¹)
219 were measured in every microcosm at the beginning of the experiment (D0) and subsequently
220 every two weeks (D15, D30, D45 and D60) using Hach HQ40D portable multi-parameter probe
221 (Hach, Germany).

a)



b) Sampling



222

223 Figure 1. A) Experiment design with the following treatments: C - Control (T1 = 10 °C), T2 -
224 Increased temperature (14 °C), EC - ECs mix, MS - multiple stressor treatment (EC + T2) and b)
225 sampling scheme with caddisfly larvae, pupae and adults sampled at various days of exposure.

226 2.2. Biota sample processing: extractions of metabolites and lipids

227 Within this study, the term “metabolome” refers to the complete set of low molecular weight
228 molecules or metabolites present within an organism, while “lipidome” is used to describe the
229 complete lipid profile within an organism (i.e. all lipids).

230 Biota samples processing, metabolite and protein extraction and metabolite profiling analyses
231 followed (Grgić et al., 2023). In order to detect Hsp70 proteins, we performed Western blot
232 analysis of protein samples, the details are provided in Supporting Information (SI 2). As there
233 was no detection of the aforementioned proteins no results are shown.

234 The Folch lipid extraction method (Folch et al., 1957) was used and performed following the
235 protocol of (Sarafian et al., 2014) with modifications. Briefly, for lipidome profiling and
236 determination of the total lipid content (TLC), each sample (30 mg) was dissolved in 600 µL CHCl₃
237 : MeOH (2:1 v:v). Samples were vortexed at medium speed (IKA® Vortex Genius 3, Germany) for
238 5 min. After 10 min of incubation at room temperature, samples were cooled at -20 °C for 10 min
239 and additional lysis was done via ultrasonic probe (Sonoplus HD4050, Bandelin electronic GmbH,
240 Germany) for 1 min at 50% of intensity. Samples were stored overnight at -20 °C to improve
241 protein precipitation and then centrifuged at 14 000g for 20 min (Tehtnica-Centric 200R,
242 Slovenia). The supernatant was collected (600 µL) in a previously weighed tube, filtered through
243 a PVDF filer (MILLEX® - GV Syringe Filter 0.22 µm Hydrophilic PVDF, 13 mm, Sterile) and
244 evaporated to dryness. The tube was weighed to determine the TLC. TLC was determined using
245 the following equation; TLC = weight of "full" tube – empty tube. Samples were dissolved in 200µL
246 IPA : ACN : H₂O (2:1:1, v:v:v) for subsequent LCMSMS non-target analysis.

247 For both metabolome and lipidome analysis, set of quality control samples was prepared by
248 taking small aliquot of the each sample solution from the entire set and pooling them together.
249 Subaliquots of this pooled sample are regarded as set of quality control samples.

250

251 2.3 Non-target metabolome and lipidome analysis

252 Non-target analyses of the metabolome and lipidome samples were performed using a high-
253 resolution mass spectrometry system; LTQ-Orbitrap VelosTM (Thermo Fisher Scientific, USA)
254 coupled with an ultra-performance liquid chromatography (UPLC) system (Ultimate 3000
255 RSLC nano system, Dionex, Amsterdam, Netherlands). Instrument parameters and UPLC gradients
256 are provided in Supporting Information (SI). Data extraction, chromatographic deconvolution and
257 final alignment were done using the MZmine program (Katajamaa et al., 2006). Steps and settings

258 used in the MZmine program are provided in Supporting information (SI 3). The exported .csv
259 files were further filtered and sorted using modified parts of Bqunat script written in
260 Mathematica (Wolfram Research Inc., Campaign, IL, USA) (Rožman et al., 2018). Data were
261 cleaned by removing of all blank-related features. Feature was considered as blank related if an
262 intensity ratio sample:blank was < 10. Quality acceptance criteria for each metabolite were:
263 detection rate > 70%, relative standard deviation < 30% and dispersion ratio < 40%. Based on the
264 exact mass match, metabolite and lipid identification was performed in
265 <http://ceumass.eps.uspceu.es/> and by searching Metlin, Kegg, LipidMaps, PubChem, and HMDB
266 databases. It is worth noting that the metabolites and lipids reported here are only the
267 metabolites that were putatively annotated.

268

269 2.4 Statistical Analysis

270 2.4.1 Body weight changes & total lipid content of *Micropterna nycterobia* and non-vascular
271 macrophytes, and physico-chemical water parameters

272 The effects of experimental treatments on body weight (evaluated individually in *M. nycterobia*
273 specimens; N = 12 per treatment per collecting date) and total lipid content (TLC; evaluated in
274 composite samples of *M. nycterobia* pooled per life stage and treatment; N = 3 per treatment
275 per collection date) of different life stages of *M. nycterobia* were analysed using Generalized
276 Linear Models (GZLMs) constructed in IBM SPSS Statistics 27.0 (IBM Corporation). Additionally,
277 for adults the differences between the sexes were determined. Normal distribution linear scale
278 response was used for all data except for body weight of adults where gamma scale response
279 with log link was used as the data did not achieve normal distribution. Maximum likelihood
280 estimate was used for parameter estimation. Pairwise contrasts of estimated means were
281 performed using Wald's statistics.

282 The changes in total lipid content in moss, as well as changes in the physico-chemical water
283 properties, between different treatments over time were tested using repeated measures
284 ANOVA using the IBM SPSS Statistics 27.0 (IBM Corporation). Pairwise comparisons were

285 conducted with Bonferroni adjustment for multiple comparisons. Obtained data were analyzed
286 and visualized using Principal Component Analysis (PCA) in Primer 7.

287

288 2.4.2. Data analysis of non-target metabolomic and lipidomic profiles of *Micropterna nycterobia*
289 and non-vascular macrophytes

290 Obtained metabolomic and lipidomic data matrices were forth root transformed and analyzed
291 using Principal Component Analysis (PCA) and Principal Response Curves (PRC) in package vegan
292 (version 2.5-7) RStudio version 4.1.2 (Oksanen et al., 2020). Additionally, significance of the
293 results was tested using the Monte Carlo test in the 'permute' package, with 99 permutations,
294 more specifically significance of the 1st canonical axis of the PRC and significance of sampling
295 date/insect stage was tested. Due to the missing moss sample D30 EC, Redundancy Analysis
296 (RDA) was performed instead of PRC for moss metabolome and lipidome data using CANOCO
297 software (version 5.11,ter Braak and Šmilauer, 2012). We used treatment as the categorical
298 explanatory variable, metabolites and lipids as response, respectively and time as a covariate.
299 The RDA significances were tested using Monte Carlo test with 999 permutations. Values of MZ
300 masses of the metabolome dataset were normalized and processed by Principal Component
301 Analysis (PCA) in Rstudio. The PCA was visualized in Primer 7 (Clarke and Gorley, 2015). The first
302 100 variables (MZ masses) that contribute most to separation along certain PCs were selected
303 for identification of metabolites.

304 **3. RESULTS**

305 3.1. Physico-chemical properties of water during microcosm experiment

306 Oxygen concentration (mg L⁻¹) and oxygen saturation (%) throughout the experiment did not
307 differ significantly among treatments, they were impacted only by the day of measurement
308 (repeated measures ANOVA, Table S1, S2; and PCA analysis, the total variance accounted by the
309 two components shown was ~69 %; variance from [PC1, PC2]≈[46.4 %, 22.6 %]; Fig. S1). Day of
310 measurement and interactive effects; temperature x ECs, temperature x time and ECs x time
311 caused changes in pH levels (repeated measures ANOVA, Table S3). Specifically, pH was higher

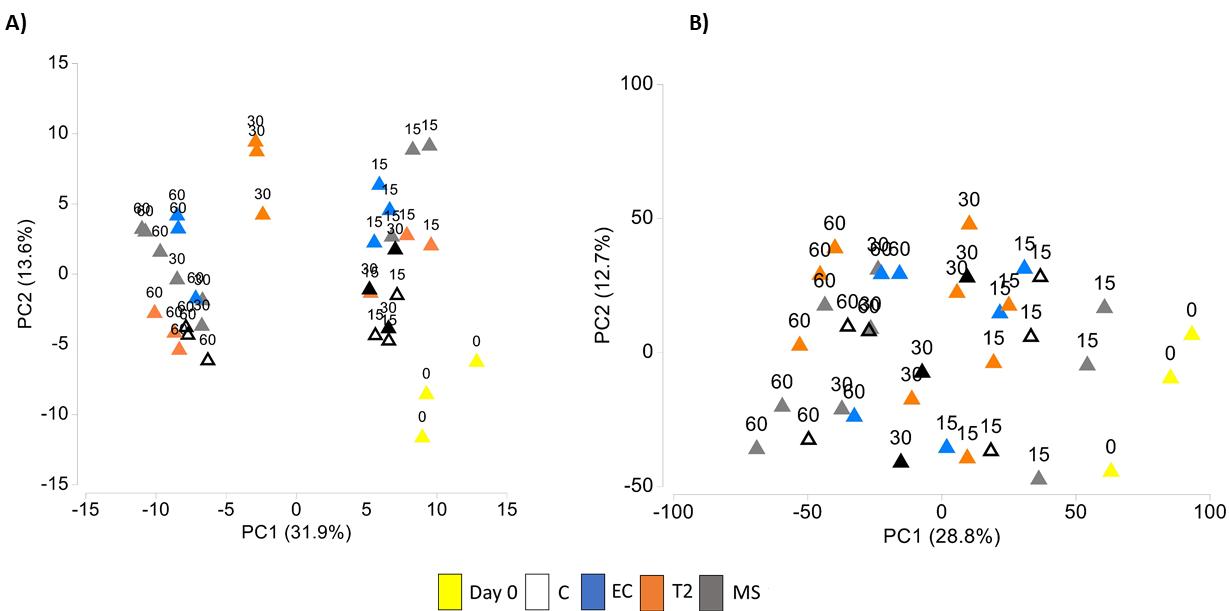
312 on D15 and D60 in treatments with ECs mixture (EC and MS). Additionally, on D30 and D45 in
313 treatments with elevated water temperature (T2 and MS) pH was higher and lower, respectively
314 (repeated measures ANOVA, Table S3). Electrical conductivity differed between treatments, i.e.
315 treatments with increased water temperature (T2 and MS) had higher conductivity compared to
316 the “natural” temperature regime (C and ECs) (repeated measures ANOVA, Table S4). Moreover,
317 electrical conductivity was generally rising throughout the whole experiment in all treatments,
318 thus it was also impacted by the day of exposure (repeated measures ANOVA, Table S4).

319

320 3.2. Total lipid content, metabolome and lipidome profiles of non-vascular macrophytes

321 Principal component analysis (PCA) based on non-target metabolic profiles and lipidome profile
322 of moss revealed clustering primarily based on the duration of the experiment rather than
323 treatment (Fig. 2A&B). In the analysis of the metabolome and lipidome, the total variance
324 accounted by the first two components was ~45.5 % (variance from [PC1, PC2]≈[31.9 %, 13.6 %])
325 and ~41,5 % (variance from [PC1, PC2]≈[28.8 %, 12.7 %]), respectively. In both analyses, the first
326 principal component (PC) axis separated the profiles between D0 and D15 from D60, with D30
327 lacking a consistent grouping patterns (Fig. 2A&B; note however, that D30 EC samples are
328 missing, as they were lost during the processing). In addition, RDA analyses shows that
329 metabolome and lipidome profiles differed significantly among treatments (RDA: pseudo-F = 3.0,
330 $p = 0.002$, explained variability = 12.1 %; Fig. S2A and RDA: pseudo-F = 2.2, $p = 0.004$, explained
331 variability = 7.7 %; Fig. S2B, respectively). Majority of metabolite groups (17 in total) showing the
332 most significant changes in abundance to stressor treatments were terpenoids, terpenes class
333 (50%) followed by lipids and fatty acids (29%), amino acids, peptides and proteins (11%), carbonyl
334 compounds (5%), organic acids, carboxylic acids and monocarboxylic acids (5%) (Fig. S3, Table
335 S5). Within the lipidome, most significant changes in abundance of 51 lipids to stressor
336 treatments were noticed in glycerophospholipids (51%) followed by glycerolipids (20%), sterol
337 lipids (12%), sphingolipids (8%), prenol lipids (8%) and fatty acyls (2%) (Fig. S4, Table S6). The
338 lowest total lipid content in all treatments was measured on D 15, however, no significant

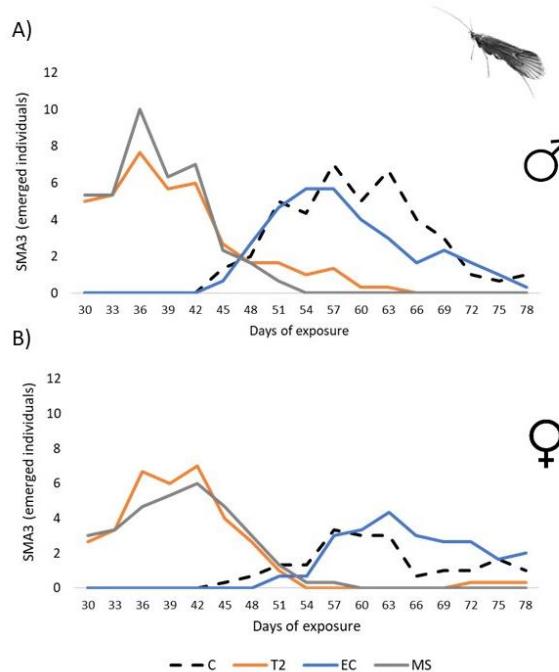
339 changes in TLC was observed related to days of exposure or treatments (Fig. S5, repeated
340 measures ANOVA, Table S7).



341
342 Figure 2. PCA plot showing separation based on A) metabolome and B) lipidome of moss in
343 different treatments. Abbreviations of treatments are as follows: C – Control ($T = 10\text{ }^{\circ}\text{C}$), T2 -
344 Increased temperature ($14\text{ }^{\circ}\text{C}$), EC - ECs mix, MS - multiple stressor treatment (T2 + EC); Day 0 –
345 pre-exposure sample.

346
347 3.3. Phenology (emergence patterns) of the caddisfly *Micropterna nycterobia*
348 Increased water temperature caused earlier emergence of both males and females, resulting in
349 approximately three-week shift in peak emergence between the normal (C and EC) and elevated
350 temperature (T2 and MS) treatments (Fig. 3). Overall, more males emerged throughout the
351 experiment, however, the majority of pupae that did not emerge by the end of experiment were
352 females. Only minor differences between emergence patterns of males and females were
353 observed within treatments (Fig. 3).

354



355

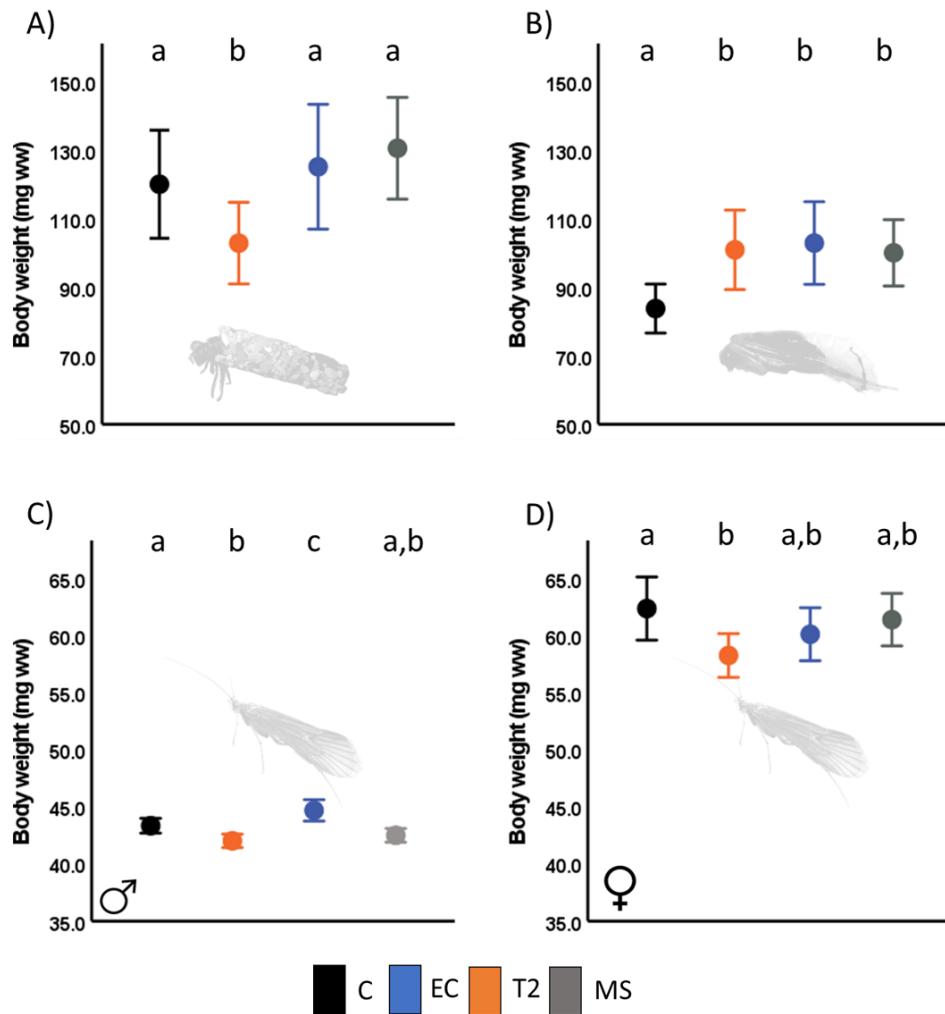
356 Figure 3. Three-day simple moving average (SMA3) of emerged A) male and B) female adults of
 357 *Micropterna nycterobia* across treatments. Abbreviations of treatments are as follows: C - Control
 358 (T = 10 °C), T2 - Increased temperature (14 °C), EC - ECs mix, MS - multiple stressor treatment (T2
 359 + EC).

360

361

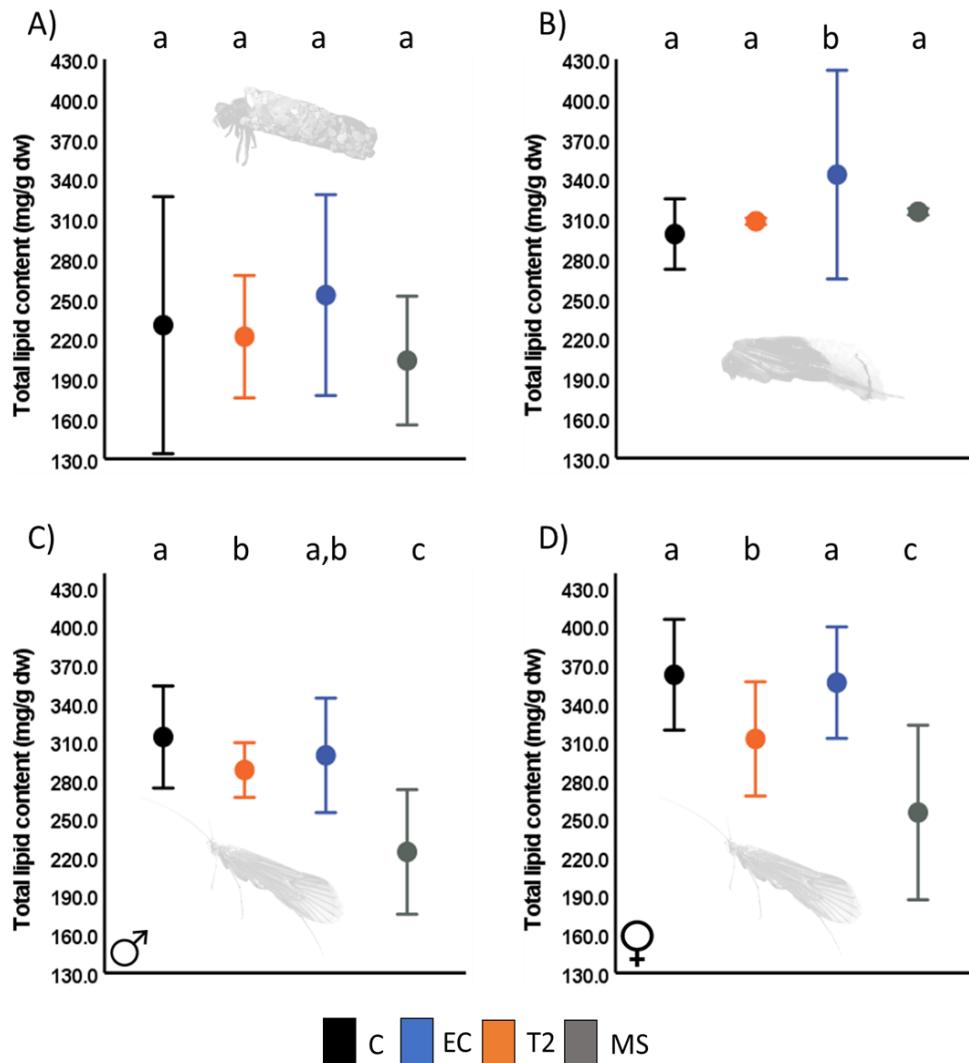
362 3.4. Body weight and total lipid content changes of the caddisfly *Micropterna nycterobia*

363 Overall, a loss in body mass was recorded in *M. nycterobia* throughout the life cycle, with larvae
 364 having the highest body weight and adults the lowest (Fig. 4A-D). A statistically significant drop
 365 in body weight was observed in larvae in T2 compared to control (4A, Table S8). All experimental
 366 treatments increased the body weight of pupae compared to control (Fig. 4B, Table S9). Adult
 367 females had significantly higher body weight compared to males (Fig. 4C & 4D, Table S10),
 368 however, in adults of both sexes a statistically significant drop in body weight was observed in T2
 369 compared to control (Fig. 4C & 4D, Table S11 and S12).



370

371 Figure 4. Model predictions illustrating the effect of treatment on body weight of A) larvae B)
 372 pupae C) adult males and D) adult females of *M. nycterobia*. Mean values of twelve replicates are
 373 presented with 95% confidence intervals. Different letters indicate significant differences among
 374 treatments ($p < 0.05$). Abbreviations of treatments are as follows: C – Control ($T = 10$ °C), T2 –
 375 Increased temperature (14 °C), EC – ECs mix, MS – multiple stressor treatment (T2 + EC).



376

377 Figure 5. Model predictions illustrating the effect of treatment on total lipid content of A) larvae
 378 B) pupae C) adult males and D) adult females of *M. nycterobia*. Mean values of three replicates
 379 are presented with 95% confidence intervals. Different letters indicate significant differences
 380 among treatments ($p < 0.05$). Abbreviations of treatments are as follows: C – Control ($T = 10$ °C),
 381 T2 - Increased temperature (14 °C), EC - ECs mix, MS - multiple stressor treatment (T2 + EC).

382

383 Changes in the TLC were more pronounced post-metamorphoses (Fig. 5A-D). Experimental
 384 treatments had no effect on TLC on larvae (Fig. 5A, Table S13), while pupae exhibited an increase
 385 in the EC treatment compared to control (Fig. 5B, Table S14). Total lipid content of adults was

386 lower compared to control in treatments with increased temperature (T2 and MS) (Fig. 5C & 5D,
387 Table S15 & S16). Moreover, the greatest drop in TLC of adults was observed in the MS treatment
388 ((Fig. 5C & 5D, Table S15 & S16), corresponding with the negative synergistic effect according to
389 (Piggott et al., 2015). Females had significantly higher total lipid content compared to males
390 (Figure 5C & 5D, Table S17).

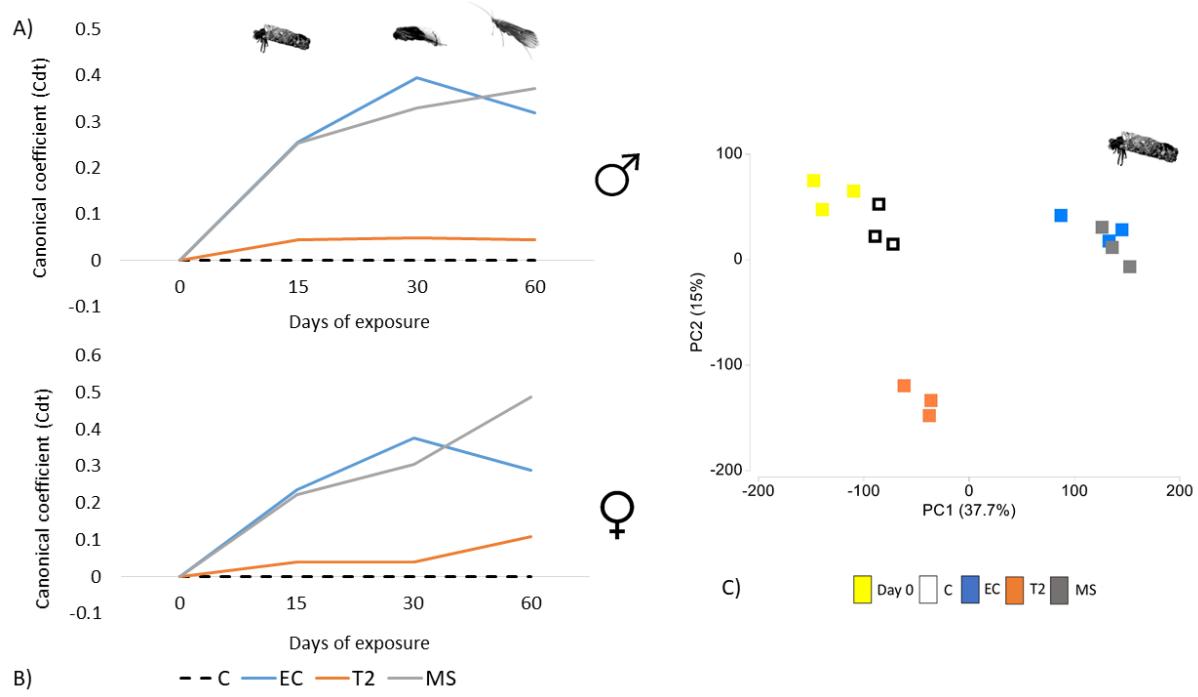
391

392 3.5. Metabolome profiles of the caddisfly *Micropterna nycterobia*

393 Principal Response Curves (PRC) of non-target metabolome profile of larvae, pupae and adult
394 caddisflies show that the metabolome of all caddisfly life stages was mostly affected by the ECs
395 mixture (EC and MS), as evident by the highest deviation from the control (Fig. 5A & B). Deviations
396 were observed in larvae at D15 already, and further increased in pupae and adults. The MS
397 treatment showed highest impact on metabolome of both male and female adult caddisflies (Fig.
398 5A & B). Additionally, 62.6 % of total variance in males and 59.5 % in females could be attributed
399 to time, whereas 22.1 % in males and 25.8 % in females could be attributed to the treatment
400 (including its interaction with time, Table S18). The first PRC axis was significant (males – $F (1, 32)$
401 = 18.714 $p < 0.05$, females – $F (1, 32) = 28.172, p < 0.05$) and based on the Monte Carlo tests per
402 sampling date, the treatment regime had a significant influence on all sampling dates.

403 Principal component (PCA) analysis based on non-target metabolic profiles of all life stages of *M.*
404 *nycterobia* revealed clear separation of pre-metamorphosis larvae and post-metamorphosis
405 pupae and adult imagines (Fig. S6, PC1). However, when particular life stages were analyzed
406 separately, the PCA also revealed separation into distinct groups based on treatments. In larvae,
407 for instance, PC1 axis separating larvae in ECs and MS treatments from D0, C and T2 treatments
408 accounted for 37.7 % of variability (Fig. 4C; variance from [PC1, PC2]≈[37.7 %, 15 %]).

409 Majority of metabolite groups (18 in total) showing the most significant changes in abundance to
410 stressor treatments in *M. nycterobia* were lipids and fatty acids (39%) followed by amino acids
411 (22%), quinones (6%), acylcholine (6%), adrenergic agents (6%), lactones (6%), alcohols (5%),
412 pyridines (5%), alkaloids (5%) (Fig. S7, Table S19).



413

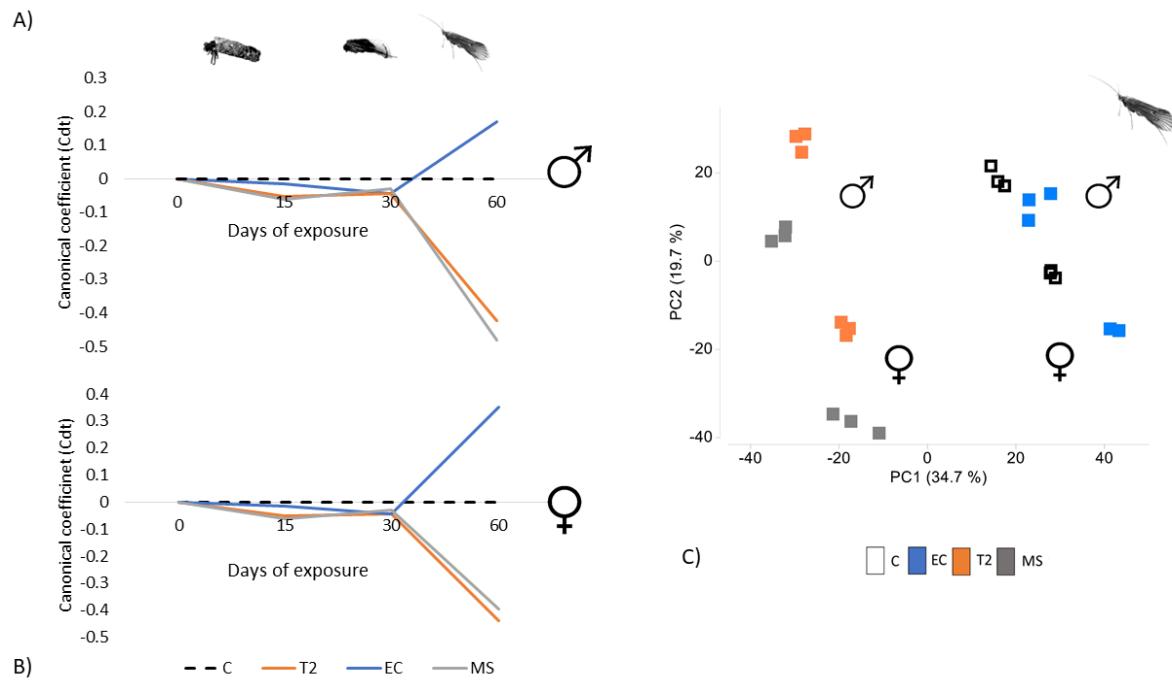
414 Figure 5. Metabolome profiles of the caddisfly *Micropterna nycterobia*; PRC of changes in the
 415 metabolic profiles along the caddisfly life cycle in A) male and B) female adults exposed to
 416 treatments in relation to control. Numbers on x-axis denote days of exposure. C) PCA plot
 417 showing separation based on metabolome of *M. nycterobia* larvae in different treatments at 15
 418 days of exposure. Abbreviations of treatments are as follows: C – Control ($T = 10\text{ }^{\circ}\text{C}$), T2 -
 419 Increased temperature ($14\text{ }^{\circ}\text{C}$), EC - ECs mix, MS - multiple stressor treatment (T2 + EC); Day 0 –
 420 pre-exposure sample.

421

422 3.5. Lipidome profiles of the caddisfly *Micropterna nycterobia*

423 Principal Response Curves (PRC) of non-target lipidome profile of larvae, pupae and adult
 424 caddisflies shows the highest deviation from the control in male and female adults, with an
 425 opposing individual stressor effect (EC vs T2; Fig. 6A & B). In MS treatments, increased
 426 temperature was the dominant stressor for both sexes, however, there were differences
 427 between sexes, as male caddisflies lipidome was more affected in T2 and MS treatments,
 428 whereas female caddisflies lipidome was more affected in the EC (Fig. 6A & 5B). Moreover, table
 429 S20 shows that 79.8 % of total variance in male and 68.4 % in female caddisflies can be attributed

430 to time, whereas 13.3 % in male and 17.3% in female can be attributed to the treatment
 431 (including its interaction with time). The first PRC axis was significant (males - $F (1, 32) = 17.475$
 432 $p < 0.05$, females – $F (1, 32) = 14.583, p < 0.05$) and based on the Monte Carlo tests per sampling
 433 date, the treatment regime had a significant influence on all sampling dates.



434

435 Figure 6. Lipidome profiles of the caddisfly *Micropterna nycterobia*; PRC of changes in the
 436 lipidome profiles of caddisfly life stages and A) male and B) female adults exposed to treatments
 437 in relation to control. Numbers on x-axis denote days of exposure. C) PCA plot showing separation
 438 adult *M. nycterobia* separated by sex in different treatments. Abbreviations of treatments are as
 439 follows: C – Control ($T = 10$ °C), T2 - Increased temperature (14 °C), EC - ECs mix, MS - multiple
 440 stressor treatment (T2 + EC); Day 0 –pre-exposure sample.

441 Principal component (PCA) analysis based on non-target lipidome profiles of all life stages of *M.*
 442 *nycterobia* showed clear separation of three major life stages, larvae, pupae and adults (Fig. S8).
 443 The total variance accounted by the three clusters was ~68.8 % (variance from [PC1, PC2,
 444 PC3]≈[47.7 %, 14.8 %, 6.3 %]). Clustering of particular treatments was particularly evident in
 445 separate analyses of each life stage. The highest degree of clustering based on treatments was
 446 inferred for adults, with the first principle component axis (PC1 = 34.7 %) separating adults based

447 on increased water temperature (T2 and MS treatments), whereas the second axis separated
448 males from females (PC2 = 19.7 %, Fig. 6C).

449 Within the lipidome, most significant changes in abundance to stressor treatments were noticed
450 in glycerophospholipids (67%) followed by fatty acyls (12%), sphingolipids (12%), glycerolipids
451 (5%), prenol lipids (2%) and sterol lipids (1%) (Fig. S9, Table S21).

452

453 **4. DISCUSSION**

454 Water pollution has far-reaching consequences for the ecosystem health and functioning, and it
455 is important to understand these impacts, especially in a context of climate change. Here we used
456 simplified freshwater food web exposed to a mixture of PhACs and EDCs and increased water
457 temperature to broaden our understanding of the impacts of climate change and pollution on
458 freshwater ecosystems.

459 4.1. Warming and pollution with PhACs & EDCs triggered a mild response in moss

460 A mild response of the moss to both individual stressors (increased water temperature and
461 contamination with ECs) and their combination suggests mosses' resilience. It has been shown
462 that plants have specific temperature and pollution thresholds that trigger or inhibit certain
463 physiological processes, allowing them to respond to stressful conditions (Firmansyah and
464 Argosubekti, 2020; Gorovits et al., 2020; Sun et al., 2018; Zezulka et al., 2013). One of the most
465 common physiological responses includes production of heat shock proteins (HSPs), and lack of
466 observable change in regulation of HSPs may suggest that the thermal and pollution threshold
467 necessary to trigger stress response in the moss was not reached. This observation is in
468 agreement with established thermal threshold of plants of minimum 5 °C (Firmansyah and
469 Argosubekti, 2020). Even though changes in metabolomic and lipidomic profiles among
470 treatments were significant, one should keep in mind that changes in metabolite and lipid
471 composition can be related to stress response but also developmental stages (Lu et al., 2019;
472 Mikami and Hartmann, 2004). In addition, the biotic stress induced by the feeding of *M.*
473 *nycterobia* larvae on the moss might have masked the impact of the pollution and increased

474 temperature. Plants can prioritize their responses to address individual stressors when exposed
475 to multiple abiotic and/or biotic stressors (Rejeb et al., 2014; Suzuki et al., 2014). We argue that
476 the moss in the current experiment might have prioritized biotic stress over abiotic stressors and
477 activated different defence mechanisms to mitigate larval feeding. However, we could not test
478 for the latter, since feeding of *M. nycterobia* larvae on the moss was also present in control
479 treatments. Moreover, research has shown that different stress combinations activate different
480 pathways and signals thus making it harder to predict multiple stressor effects (Rejeb et al., 2014;
481 Suzuki et al., 2014; Vescio et al., 2022).

482

483 4.2. Single stressor impacts: effects of warming and pollution with PhACs and EDCs on *M.*
484 *nycterobia*

485 In the current experiment, we recorded a body mass loss in *M. nycterobia* that is in line with the
486 usual life cycle patterns of the holometabolous caddisflies, with larvae having the highest body
487 weight and adults the lowest (Huryn and Wallace, 2000). Increased temperature during insect
488 development typically leads to reduced adult body size, negatively influencing fecundity and
489 longevity (Mirth and Riddiford, 2007), this effect was however, not observed in the current study.
490 Our observations are in line with data on chronic exposure to pesticides in the caddisfly
491 *Limnephilus lunatus*, where reduced body weight of adults was observed only if younger instar
492 larvae were exposed, and not the fifth-instars (Liess and Schulz, 1996; Schulz and Liess, 2001,
493 1995).

494 *M. nycterobia* inhabits clean crenal and rhithral sections and is therefore expected to be sensitive
495 to presence of contaminants (Graf et al., 2023). Indeed, sensitivity is displayed through intense
496 change in regulation of both metabolites and lipids in respect to control, however, the
497 contaminants seem to have a more significant impact on metabolome than temperature. More
498 precisely, the most pronounced metabolome response was post-metamorphosis, yet changes in
499 metabolite regulation are already notable in larvae at D15. Notably, the sampled caddisflies'
500 metabolome contained the biogenic amine octopamine, a significant neurotransmitter,
501 neuromodulator, and neurohormone influencing various physiological functions, behaviour and

502 endocrine activity (Farooqui, 2012) Changes in octopamine levels due to PhACs and EDCs during
503 metamorphosis could affect not only the subsequent life stage but potentially extend across
504 multiple generations.

505 Observed difference in dynamics of regulation of metabolites vs lipids can be related to
506 physiological roles of metabolites and lipids which response tends to differ depending on the
507 type of stress and the metabolic pathways involved (Kainz and Fisk, 2009; Snart et al., 2015).
508 Generally, lipids serve as a long-term energy source and are stored in lipid droplets, which can
509 be mobilized to provide energy during times of starvation, embryogenesis, prolonged periods of
510 flight and stress (Arrese and Soulages, 2010; Kainz and Fisk, 2009). Here, metabolites were more
511 regulated than lipids in response to stress probably in order to maintain cellular homeostasis and
512 ensure energy reserves (lipids) for the emerging adults (Arrese and Soulages, 2010). Glycerolipids
513 such as triglycerides are stored in the core of the lipid droplets surrounded by
514 glycerophospholipids (Arrese and Soulages, 2010). As glycerophospholipids were mostly affected
515 by experimental treatments, this further supports the fact that lipid reserves were preserved for
516 adults. However, changes in glycerophospholipids of insects can also be related to development
517 and metamorphosis (Bashan et al., 2002; Cargill et al., 1985; Duarte, 2019) as well as food source
518 (Hanson et al., 1985; Torres-Ruiz et al., 2010).

519 The lack of strong effects of increased water temperature on metabolite regulation, as well as
520 absence of heat shock protein HSP70 expression, is most likely due to adaptation of *M. nycterobia*
521 to thermal stress regularly occurring in intermittent streams (Qin et al., 2003). This finding
522 suggests that *M. nycterobia* and possibly other intermittent habitats indicators may have
523 metabolic flexibility to cope with thermal stress, allowing them to survive extreme climatic events
524 characterised by fluctuating temperature regimes. In addition, the regulation of lipidome of *M.*
525 *nycterobia* aquatic stages exhibited intriguing resilience to both increased water temperature
526 and pollution with PhACs and EDCs. The limited impact on lipid regulation suggests that the stress
527 response threshold triggering significant lipid mobilisation may not have been surpassed.
528 Instead, the priority for the aquatic stages was directed towards lipid accumulation rather than
529 mobilization in response to stress challenges (Arrese and Soulages, 2010; Hoppeler et al., 2018).
530 Emphasis on lipid accumulation was evident through the observed increase in total lipid content

531 from larval to pupal stages, serving as a crucial energy source to sustain adult insects during non-
532 feeding periods and fuel their flights (Arrese and Soulages, 2010; Hoppeler et al., 2018). While
533 the anticipation of intense lipidome activity in adult insects is well-founded, it is surprising that
534 so distinct regulatory mechanisms are operating in response to different stressors. However,
535 lipidomic profiles of multiple stressor treatment were in both males and females congruent with
536 those of increased temperature, implying the dominant impact of increased water temperature
537 on regulation of lipids in aquatic insects.

538 Increased water temperature accelerated development of *M. nycterobia*, resulting in earlier
539 adult emergence and lower total lipid content of all life stages in treatments with increased
540 temperature. Similarly, the mayfly larvae chronically exposed to increased temperature used
541 lipids and amino acids as alternative energy sources to support their growth and maintenance
542 costs, ultimately resulting in reduced total lipid content (Chou et al., 2018). Furthermore,
543 sensitivity of the temporal emergence patterns of aquatic insects was already discussed as
544 toxicological endpoint for exposure to pesticides (Schulz and Liess, 2001), as timing of aquatic
545 insect emergence plays a crucial role for riparian predators (review in Bundschuh et al., 2020).
546 More precisely, insectivorous birds almost exclusively obtain the omega-3 long-chain
547 polyunsaturated fatty acids from emerging aquatic insects, thus shifts in the relative availability
548 and phenology of aquatic insects in response to a changing climate are likely to have major fitness
549 consequences for their breeding success (Shipley et al., 2022). Hence, such shifts can have
550 cascading effects on cross-ecosystem energy flow. This is of particular importance in intermittent
551 water bodies, like those inhabited by *M. nycterobia*, where mass emergence during short periods
552 is typical and riparian food webs are highly dependent on the aquatic subsidies (McIntosh et al.,
553 2017).

554

555 4.3. Multiple stressor impacts of warming and PhACs and EDCs on aquatic insects

556 A synergistic interactive effect was observed, leading to a decrease in total lipid content and
557 significant variation in lipid profiles in adults of both sexes under the MS treatment. *Micropterna*
558 *nycterobia*, a specialist in intermittent rivers, exhibits a behaviour where adults leave the water

559 bodies upon emergence and migrate to cooler mountainous regions or nearby caves for a few
560 months until their gonads develop (Waringer and Graf, 2011). In autumn, after copulation, they
561 lay eggs in re-established surface flow. Therefore, the observed decrease in lipid reserves in
562 adults (8.9% and 10.7% decrease in total lipid content in males and females, respectively) could
563 have a major impact on their reproduction and population dynamics. Lipids serve as crucial
564 energy reserves for insects, especially during non-feeding life stages and long-distance flights
565 (Arrese and Soulages, 2010; Downer and Matthews, 1976). Maintaining metapopulation
566 dynamics is particularly important for inhabitants of intermittent water bodies (Datry et al.,
567 2017). Various pollutants, such as fungicides and copper, can decrease the lipid content of
568 limnephilid caddisflies (Konschak et al., 2019). However, this effect was not observed in the
569 current study as PhACs and EDCs did not influence the lipid content of *M. nycterobia*.
570 Furthermore, the negative effects of pollutants on lipids can be exacerbated by elevated water
571 temperatures (Yoon et al., 2022). However, in our study, increased water temperature primarily
572 influenced the lipids of caddisflies, and its adverse effects were amplified by pollution with PhACs
573 and EDCs. Additionally, warming indirectly contributed to the further deterioration of
574 environmental conditions in the T2 and MS treatments, as evidenced by increased conductivity
575 within these two treatments.

576 In terms of the timing of the strongest stress response, our results differ from a previous
577 experiment involving the same caddisfly species, where the effects of ECs and microplastic
578 particles were most pronounced in the first 15 days of exposure, both in single and combined
579 stressor treatments (Grgić et al., 2023). Apart from the dominant impact of increased
580 temperature, these differences may also be attributed to variations in the mixture of ECs used,
581 as different compounds can have varying effects on biota (Muñoz et al., 2015; Nilsen et al., 2019).
582 Nevertheless, our study indicates that the adverse synergistic effects of warming events and
583 freshwater contamination with ECs could intensify throughout the life cycle of aquatic insects,
584 potentially leading to developmental impairments and disturbances in population dynamics
585 (Kazmi et al., 2022). However, in most environmental health assessment and monitoring
586 programs, only the aquatic stages of aquatic insects are considered (Water Framework Directive
587 (WFD) 2000/60/EC). Furthermore, the multiple stressor effects observed in the current study not

588 only resulted in reduced resource quality for aquatic food webs but also affected the quality of
589 emergence, thus impacting the riparian food webs at the aquatic-terrestrial interface (Bundschuh
590 et al., 2020).

591

592 4.5. Differential response to stressor impacts of male and female caddisflies

593 Our study reveals sex-specific responses to both single and multiple stressors, with females
594 exhibiting more pronounced impacts on the metabolome while males show greater effects on
595 the lipidome. In the majority of insects, there is sexual dimorphism in lipid content due to distinct
596 roles played by lipids, such as egg production in females and flight behaviour in males (Lease and
597 Wolf, 2011). Certain aquatic insect species, characterized by specific male flight behaviour (Lease
598 and Wolf, 2011) or swarming (Sartori et al., 1992), experience negative impacts on population
599 fitness when males have decreased lipid content. Furthermore, this study identifies 4-
600 hydroxyestradiol, an endogenous metabolite of 17 β -estradiol, from *M. nycterobia*, which has
601 been shown to have significant lipid-modulating effects in rats (Wang and Zhu, 2017).
602 Additionally, in *Drosophila*, sexual dimorphism has been observed in metabolic genes and
603 mechanisms involved in triglyceride homeostasis (Wat et al., 2020).

604 Likewise, the findings of this study highlight sex-dependent variation in metabolites induced by
605 stress, consistent with a previous study involving *M. nycterobia* exposed to microplastic particles
606 and a mixture of personal care products (Grgić et al., 2023). Moreover, female insects generally
607 exhibit a stronger stress response across different taxa and under various stress conditions,
608 including parasite infections, predation, food quality, chemical stress, and the impacts of climate
609 change (Lindsey and Altizer, 2009; Slos et al., 2009; Stillwell and Davidowitz, 2010). This is likely
610 due to the different evolutionary roles of male and female insects, which have led to the
611 development of distinct stress-defence mechanisms. The fitness of females is closely linked to
612 their life expectancy and the number of offspring they produce.

613 Therefore, our study emphasizes the variability in the impacts of both single and multiple
614 stressors on various traits, different life stages, and sexes within a single species. Consequently,
615 it underscores the importance of developing a more comprehensive understanding of the

616 sensitivity of freshwater organisms to the adverse effects of single and multiple stressors,
617 particularly when addressing the management of freshwater ecosystems in the context of global
618 change (Schäfer and Piggott, 2018).

619

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629 **LITERATURE**

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Supplementary Material

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

CRediT authorship contribution statement

Iva Kokotović: Data curation, Investigation, Methodology, Visualization, Writing - original draft, Writing - review & editing. **Marina Veseli:** Investigation, Methodology. **Filip Ložek:** Investigation, Methodology, Visualization, Writing - original draft. **Zrinka Karačić:** Investigation, Methodology. **Marko Rožman:** Conceptualization, Investigation, Methodology, Writing - original draft, Writing - review & editing. **Ana Previšić:** Conceptualization, Investigation, Methodology, Funding acquisition, Writing - original draft, Writing - review & editing.