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# Section 1. Mesocosm experiments

## Male and female founder characteristics

Table S1: Male and female characteristics at the beginning and end of experiments.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Experiment | ∆t (d) | Ni female | Ni male | Nf female | Nf male | Li female | | Li male | | Lf female | | Lf male | |
| Mean (mm) | Sd | Mean (mm) | Sd | Mean (mm) | Sd | Mean (mm) | Sd |
| 1 | 210 | 165 | 110 | 83 (106) | 39 (57) | 51.41 | ± 4.21 | 49.25 | ± 2.11 | 62.06 | ± 3.71 | 55.08 | ± 3.11 |
| 2 | 213 | 165 | 110 | 72 (105) | 37 (72) | 42.46 | ± 1.69 | 42.37 | ± 2.38 | 56.14 | ± 3.71 | 49.68 | ± 3.13 |

Ni and Nf are the initial and final number of sticklebacks in the experiments, Nf refers to the founder sticklebacks which still had their tag and Nf between parentheses refers to the total number of sticklebacks for each experiment which were probably founders considering their length compared to the other fish in the mesocosms. Initial and final length (Li and Lf respectively) are only given for the founders which still had their tag at the end of the experiments.

**Population characteristics**

Table S2: Population characteristics.

|  |  |  |  |
| --- | --- | --- | --- |
| Experiment | Number of populations | Number of individuals (per population) | Mean length of fish born in all mesocosms (mm) |
| 1 | 11 | 872 ± 183 | 25.03 ± 7.21 |
| 2 | 11 | 931 ± 136 | 23.32 ± 6.99 |

## Introduction of macroinvertebrates and zooplankton in mesocosms.

Before the introduction of sticklebacks in the mesocosms in each experiment, the mesocosms were set up with macroinvertebrates and zooplankton. In November, zooplankton as well as periphyton were introduced in each mesocosm by sieving 36 litres of water with a mesh of 50 µm. The water was collected from an unpolluted artificial pond located next to the mesocosm platform. *Gammarus pulex* was introduced into each mesocosm (80 g, i.e. about 340 individuals per mesocosm). In December, 200 individuals of *Asellus aquaticus* were introduced into each mesocosm. At the same time, the gastropods P*. antipodorum, P.planorbis* and *R. balthica* were introduced into each mesocosm. (200, 17 and 50 individuals per mesocosm, respectively). Finally, each mesocosm received 8 *Notonecta*, 6 *Glossiphonia complanata* and 4 *Erpobdella octoculata*. These macroinvertebrates came from an unpolluted artificial pond located next to the mesocosm platform or from former unpolluted mesocosms. Other invertebrates, such as *Chironomidae* larvae, naturally colonized the mesocosms.

## Samplings of macroinvertebrates and zooplankton.

Zooplankton was sampled every 4 weeks for each experiment with a Perspex tube of 5 cm in diameter and 0.8 m in height. A water sample was taken every meter with a total of 6 L and 19 L of water respectively in the upstream (upper section) and downstream (lower section) of the mesocosm. The collected water was sifted with a 1 mm and 50 µm mesh one after the other. The 1 mm mesh was used to take out most of the filamentous algae. 70% ethanol was then used in order to preserve the individuals. Samples were treated with a pink dye (Rose Bengal, Sigma Aldrich) in order to tint biological materials thus allowing to optimize species identification. Subsamples of 2 mL were then collected. All individuals were enumerated and identified for the first three subsamples. If necessary, further subsamples were processed in order to have a coefficient of variation corresponding to a sub-sampling error lower than 10 %. No more than eight subsamples were analyzed.

Macroinvertebrates were sampled every 4 weeks using two types of artificial substrates (tubes and tiles). Tube substrates were composed of seven tubes (2 cm wide and 20 cm long). Tiles were 11 cm long, 16 cm wide and 1.5 cm in thickness. Ten tubes and ten tiles were placed horizontally on the bottom of each mesocosm. The tubes were placed at 0.5, 2, 4, 6, 8, 10, 12, 14, 16, and 18 meters from the inlet of the water and the tiles were placed at 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19 meters from the inlet of the water. This arrangement follows a sampling plan alternating sides and middle of each mesocosm in order to sample the largest number of individuals according to their habitat preferences. On each sampling date, the artificial substrates were removed one by one from each mesocosm using a landing net. The upper and lower sections were sampled separately. The substrates were washed and scratched in order to retrieve all the macroinvertebrates. Mesocosm walls were also scrubbed twice on both sides (1 and 13 meters from the inlet of the water for one side of the mesocosms and 7 and 19 meters for the second side) to collect macroinvertebrates which lived there. The samples were then sifted with a 500 µm mesh and kept in water. Identification and enumeration were performed immediately after sampling. Macroinvertebrates were identified to the lowest practical taxonomic level. The abundance of macroinvertebrates was recorded by length classes for several species including *Asellus aquaticus* and *Gammarus pulex*. The macroinvertebrates and the artificial substrates were then put back in each mesocosm at the exact places where they had been sampled.

**Table S3.** Size class for macroinvertebrate species found in the samples

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Macroinvertebrates | Small (mm) | Medium (mm) | | | Large (mm) | |
| *Gammarus pulex* | <5 | | - | 5 < X < 20 | |
| *Asellus aquaticus* | <5 | | - | 5 < X < 15 | |

# Section 2. DEB model

Reserve density: with (1)

Structural length: (2)

Maturity level: (3)

if *<*  else

Cumulative number of eggs: (4)

if  else

With , the maximum structural length

, the maximum reserve density

, the energy investment ratio

, the somatic maintenance rate coefficient

For male sticklebacks, with the specific fraction of energy mobilized from reserve allocated to growth and somatic maintenance and the fraction subtracted from *κ* to obtain *κ* in males after maturity.

Definitions of the parameters are given in the Appendix.

To take into account that physiological processes depend on the environmental temperature, five DEB parameters ( and ) were corrected with a temperature correction function. This temperature function is the same than in Leloutre et al. ([2018](#_ENREF_14)) and was provided for sticklebacks by Hovel et al. ([2015](#_ENREF_10)). The temperature function is given by the following equations:

(5)

(6)

(7)

(8)

## DEB model calibration

The calibration of the DEB model was performed using the software R 3.3.1 with the coda package ([Plummer et al. 2016](#_ENREF_15)) and MCSim, which is designed for Bayesian inference through Markov Chain Monte Carlo (MCMC) ([Bois 2009](#_ENREF_4)).We performed three independent MCMC and the quality of convergence was checked by calculating the Gelman–Rubin index ([Gelman and Rubin 1992](#_ENREF_8)). The likelihood functions and the *a priori* distribution were the same as in Leloutre et al. ([2018](#_ENREF_14)). The data used for the calibration are the same as in Leloutre et al. (2018), except for the re-calibration of the parameter α for males where the data on male length during the experiment 1 were used (Table S1).

Calibration of the inter-individual variability of the DEB model

The inter-individual variability of the energy budget was calibrated considering that the parameters related to the feeding processes (surface-area-specific maximum assimilation rate and the proportionality factor to be fed ad libitum φ) were individual-specific. As the founders were adult and mature during the experiments, the inter-individual variability on the parameters related to the maturity level could not be calibrated.

We made the calibration on the female length data of the experiment 1. Indeed, we used the initial and final lengths of each individual (83 individuals). Each individual was fitted separately, yielding one set of parameters for each. Here, and φ were assumed to be distributed log-normally around a ‘‘population’’ mean with a ‘‘population’’ standard deviation. The standard deviation in logscale was sampled from a truncated normal distribution. The geometric population means themselves were specified with the prior distributions found during the calibration with laboratory experiments (Appendix). Both the ‘‘population’’ mean and geometric variance were estimated together with the individual values. At the end, a set of parameters was obtained for each individual with one set of ‘‘population’’ averages as well as a set of ‘‘population’’ variances.

Markov-chain Monte Carlo (MCMC) simulations were performed using GNU MCSim version 5.5.0 (<http://www.gnu.org/software/mcsim>). Three MCMC chains were run in parallel for 100,000 iterations. Their convergence was checked by calculating the criterion of [Gelman](http://www.sciencedirect.com/science/article/pii/S0378427415000119#bib0090) and Rubin ([Gelman and Rubin 1992](#_ENREF_8)).

# Section 3. Integration of the temperature scenario

## Inter-mesocosm variability of the temperature.

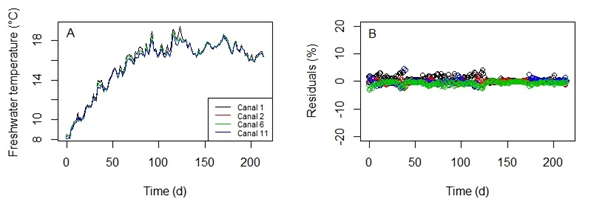
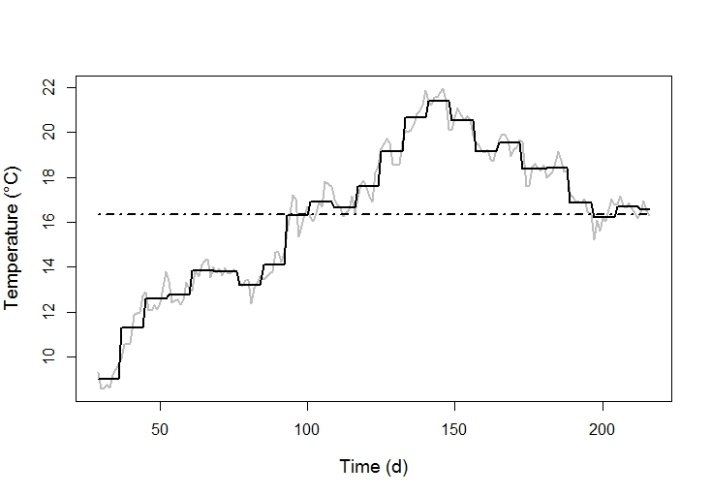


Figure S1. (A) Example of temperatures recorded every 10 minutes by Temp5 in four mesocosms. (B) Temperature differences between each mesocosm and the overall mean temperature recorded every 10 minutes by all Temp5.

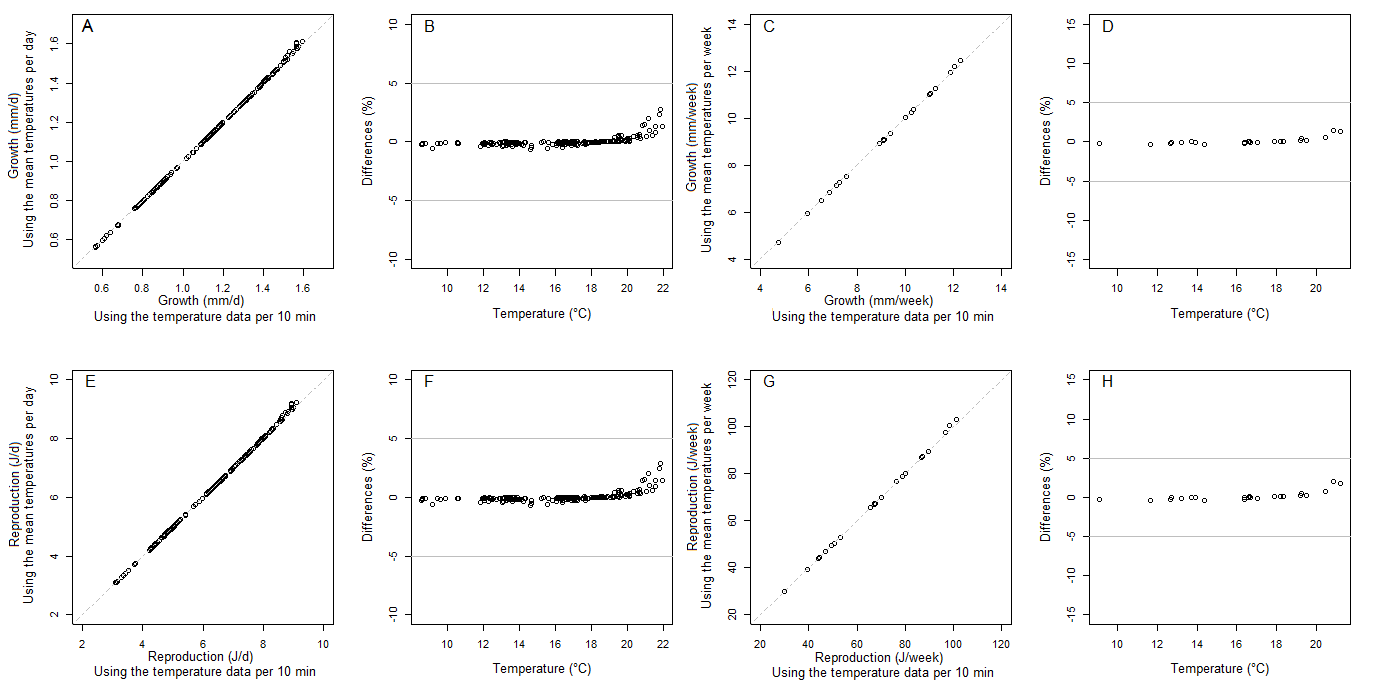
## C:\Users\David\Documents\These\Publication\Article\Temperatuve_var.pngIntra-mesocosm variability of the temperature.

Figure S2. Compared predictions (A, C, E, G) and relative differences (B, D, F, H) of the DEB simulations using the temperature measured by Temp5, Temp15 or the mean temperatures of both sensors. On the upper part, the results are given for the growth and on the lower part, they are given for reproduction. On graph A, B, E, F, the growth and reproduction per day calculated with temperatures from Temp5 or Temp15 are compared to the growth and reproduction calculated with the mean temperatures of both sensors. On graph C, D, G, H, the growth and reproduction per day calculated with the temperatures from Temp5 are compared to the growth and reproduction calculated with the temperatures from Temp15. The calculations were made with the temperatures recorded every 10 minutes but the representation is given per day to be readable.

## Discretization of the semi-continuous temperature scenario.

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**Figure S3.** Example of a scenario ofwater temperature computed for DEB simulation from observed data (recorded every 10 min) with three different time steps: mean temperatures per day (grey line), per week (black full line), and over the entire experiment (black dotted line).

 Figure S4. Compared predictions (A, C, E, G) and relative residuals (B, D, F, H) of the DEB simulations using different discretization of the temperature data. On the upper part, the results are given for growth and on the lower part, they are given for reproduction. On graph A, B, E, F, growth and reproduction per day are compared to growth and reproduction calculated with the mean temperatures recorded every 10 minutes of Temp5 and Temp15. On graph C, D, G, H ,growth and reproduction per week are compared to growth and reproduction calculated with the mean temperatures recorded every 10 minutes of Temp5 and Temp15.

## Temperature scenario characteristics

Table S4: Characteristics of the temperature scenario chosen for both experiments.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Experiment | Temperature °C) | | | |
| Mean | sd | min | max |
| 1 | 15.9 | 3.6 | 7.0 | 21.5 |
| 2 | 15.7 | 2.8 | 7.7 | 19.4 |

# Section 4. Integration of the food scenario

## Uncertainties of the zooplankton samples.

Table S5. Raw data of the 13 water samples performed in the mesocosm upstream

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Location | Water sample location | Rotifera | Cladocera | *Nauplii* | Copepoda |
| 1 m | Center | 527 | 0 | 0 | 1 |
| 1 m | Center | 446 | 0 | 0 | 1 |
| 1 m | Center | 430 | 0 | 0 | 1 |
| 2 m | Center | 143 | 1 | 1 | 1 |
| 2 m | Center | 142 | 0 | 9 | 1 |
| 2 m | Center | 120 | 1 | 3 | 1 |
| 2 m | Side | 20 | 1 | 3 | 1 |
| 2 m | Side | 23 | 0 | 1 | 1 |
| 2 m | Side | 20 | 0 | 0 | 0 |
| 3 m | Center | 78 | 3 | 5 | 1 |
| 3 m | Center | 85 | 1 | 8 | 0 |
| 3 m | Center | 86 | 2 | 5 | 1 |
| 4 m | Center | 83 | 0 | 3 | 2 |
| 4 m | Center | 66 | 0 | 0 | 0 |
| 4 m | Center | 68 | 0 | 4 | 0 |
| 5 m | Center | 43 | 0 | 2 | 1 |
| 5 m | Center | 50 | 1 | 3 | 1 |
| 5 m | Center | 54 | 0 | 3 | 1 |
| 2 m | Side | 16 | 0 | 0 | 0 |
| 2 m | Side | 11 | 1 | 0 | 0 |
| 2 m | Side | 17 | 1 | 1 | 0 |
| 6 m | Center | 137 | 1 | 1 | 0 |
| 6 m | Center | 125 | 1 | 5 | 1 |
| 6 m | Center | 134 | 3 | 5 | 3 |
| 6m | Side | 34 | 0 | 3 | 0 |
| 6m | Side | 26 | 1 | 0 | 1 |
| 6m | Side | 26 | 0 | 2 | 1 |
| 7 m | Center | 36 | 2 | 2 | 1 |
| 7 m | Center | 41 | 2 | 3 | 0 |
| 7 m | Center | 29 | 1 | 4 | 0 |
| 8 m | Center | 45 | 2 | 8 | 2 |
| 8 m | Center | 30 | 4 | 9 | 3 |
| 8 m | Center | 42 | 3 | 5 | 0 |
| 9 m | Center | 44 | 6 | 5 | 1 |
| 9 m | Center | 36 | 6 | 8 | 1 |
| 9 m | Center | 35 | 2 | 4 | 1 |
| 9m | Side | 19 | 4 | 1 | 3 |
| 9m | Side | 13 | 3 | 0 | 1 |
| 9m | Side | 20 | 0 | 2 | 0 |

**Uncertainty of the mesocosm samples.** Data collected from ecosystems contain uncertainty due to the natural dynamics of ecosystems, the technical and economical restraints related to the sampling protocol, and the statistical methods used to analyze the data ([Blukacz et al. 2005](#_ENREF_2)). To test the uncertainty of the zooplankton mesocosm sampling method, exceptionally, 13 water samples performed in the upstream of one mesocosm were analyzed independently for four different taxa (3 laboratory sub-samples were performed). The 13 water samples were used to predict the uncertainty of the methodology which is based on 57 water samples (SI Table S5). To this purpose 10,000 simulated groups of 57 samples were randomly drawn using re-sampling method with replacement.

Table S6. 80% and 95% confidence interval of the ratio between the abundance estimation and prediction using 57 water samples

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Percentile | | | |
|  | 2.5% | 10% | 90% | 97.5% |
| *Rotifera* | 0.69 | 0.78 | 1.23 | 1.37 |
| *Cladocera* | 0.75 | 0.83 | 1.17 | 1.27 |
| *Nauplii* | 0.82 | 0.88 | 1.12 | 1.19 |
| *Copepoda* | 0.87 | 0.92 | 1.08 | 1.12 |

According to these simulations, our mesocosm sampling methodology assesses 80 % of abundances estimated with an error less than 23%, 17%, 12% and 8% for the four taxa. However, this first estimation could under-estimate the real uncertainty, if the 13 real water samples did not represent all possible water samples.

**Uncertainty of the laboratory sub-samples.** Three subsamples were analyzed in laboratory to estimate the abundance of the zooplankton in the entire sample. If necessary, further subsamples were processed in order to have a coefficient of variation corresponding to a sub-sampling error lower than 10 %. Thus, in the uncertainty analysis, we considered that the laboratory error cannot be above 10% by using a truncnormal distribution.

**Global uncertainty on zooplankton.** Global uncertainty was calculated by resampling the two uncertainty distributions and using the following equations:

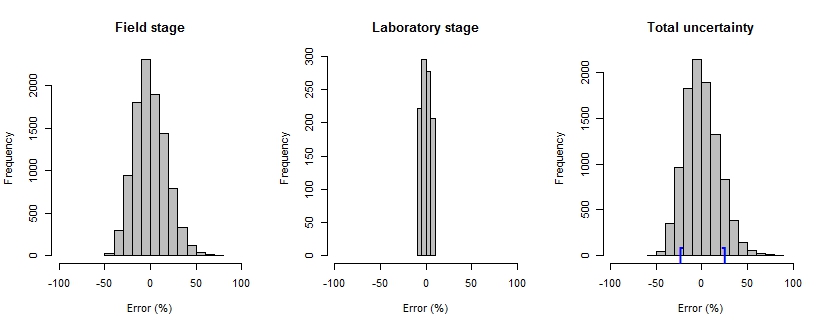
(5)

(6)

(7)

(8)

With *x* the real abundance, *x'* the abundance estimated by the mesocosm sampling stage, *x''* the abundance estimated by the laboratory sub-sampling stage. *Errmeso* and *Errlab*are the relative error (Pred-Obs)/Obs) at the mesocosm and laboratory stage, respectively.

Figure S5. Relative error ((Obs-Pred)/Obs\*100) in mesocosm stage, laboratory stage, and overall for *Rotifera* data. Blue brackets represent 80% of the estimated abundance.

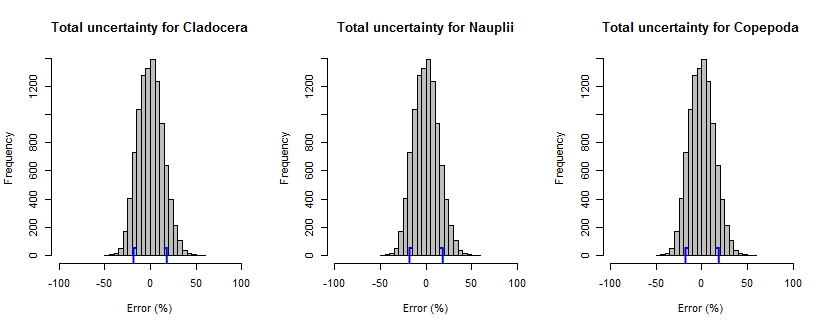


Figure S6. Global uncertainty ((Obs-Pred)/Obs\*100) for *Cladocera, Nauplii* and *Copepoda*. Blue brackets represent 80% of the estimated abundance.

According to these simulations, our mesocosm sampling methodology assesses 80 % of abundances estimated with an error less than 25%, 18%, 15% and 11% for *Rotifera, Cladocera, Nauplii* and *Copepoda* respectively.

## Uncertainties of the macroinvertebrate samples.

To quantify the uncertainty on species abundance estimation of macroinvertebrates, for a limited number of traps (tubes, tiles or scrubbed walls, see SI Section 1), the abundances of macroinvertebrates were measured individually after four weeks of colonization on the sampling devices (before the introduction of sticklebacks in the mesocosms in experiment 2). For each location in each mesocosm (four locations per traps), 5 replicates of samples were made to have a mean abundance per location. Based on this mean data, the uncertainty due to the mesocosm samplings was assessed by a bootstrap with replacement (n=10,000) respecting the proportion of the different sampling devices in each mesocosm, and using data collected on the most abundant species in the mesocosms at the sample date (*Stylaria lacustris*).

Table S7. Mean macroinvertebrate data to estimate the uncertainty of the method (samples were made at the end of march after 4 weeks of colonization on the sampling devices)

 Table S7 continued.

**Table S8.** 80% and 95% confidence interval of the ratio between the abundance estimation and prediction using 24 traps per mesocosms

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Percentile | | | |
|  | 2.5% | 10% | 90% | 97.5% | |
| *Stylaria lacustris* | -0.52 | -0.35 | 0.40 | 0.62 | |

The three sampling devices (tube, tiles or scrubbed walls) were considered independently in the simulations. The global uncertainty of the mesocosm sampling is given in Table S8 for *Stylaria lacustris* which is the most abundant species at the sampling date. This species was chosen to estimate the uncertainty of the sampling because at the sampling date (end of March), the abundance of the macroinvertebrates in the mesocosms were very low. As a consequence, very few macroinvertebrates were caught in the sampling devices. An appropriate uncertainty analysis was thus not possible for *Asellus aquaticus*, *Gammarus pulex* and *Chironomidae.*

According to these simulations, our mesocosm sampling methodology assesses 80 % of abundances estimated with an error less than 40 %.

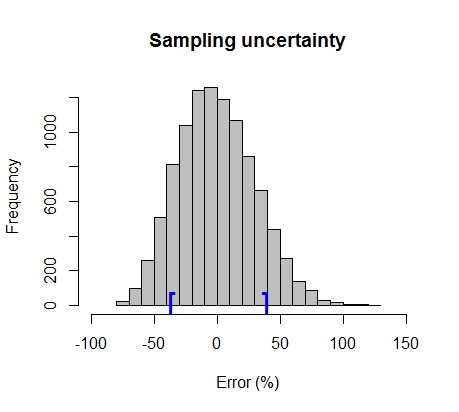


Figure S7 : Relative error ((Obs-Pred)/Obs\*100) during the samplings on macroinvertebrates based on *Stylaria lacustris* data. Blue brackets represent 80% of the abundance estimations.

## Global uncertainties for the food scenario.

Regarding the overall uncertainty for the food availability, we considered that each sampling date and each species abundance were independent and were drawn from a normal distribution with the mean and standard deviation found during the uncertainty analysis of the zooplankton and macroinvertebrate samples and we calculated the global uncertainty of the food scenario by propagation of uncertainty.

## Diet of sticklebacks

 Table S9. Review of the stickleback diet found in literature ([Hynes 1950](#_ENREF_11), [Walkey 1967](#_ENREF_19), [Allen and Wootton 1984](#_ENREF_1))

Table S10 presents the results of gut contents of 80 sticklebacks. These sticklebacks came from a former mesocosm experiment in INERIS (different from experiments 1 and 2). 40 sticklebacks were caught during two different dates (May and September). The diet of four length classes was assessed by dissecting the guts of 10 individuals per length class (26-29 mm; 32-40 mm; 47-53 mm; 60-62 mm).

**Table S10.** Composition of the diet determined by gut contents for sticklebacks in mesocosms during two different periods (May and September).

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | **May** | | | | **September** | | | |
|  | **Length class (mm)** | **26 - 29** | **32 - 40** | **47 - 53** | **60 - 62** | **26 - 29** | **32 - 40** | **47 - 53** | **60 - 62** |
|  | **Number of sticklebacks** | **10** | **10** | **10** | **10** | **10** | **10** | **10** | **10** |
| Nematoda | Nematoda |  | 1.9 | 0.3 |  |  |  |  |  |
| Mollusca | General | 15.8 |  |  |  |  |  | 0.6 | 15.4 |
|  | Lymnaea |  | 13.0 | 70.6 | 55.3 |  |  |  |  |
|  | Physidae |  | 0.1 | 0.3 | 0.2 |  |  |  |  |
| Annelida | Hirudinea |  |  |  | 0.4 |  |  |  | 0.3 |
| Crustacea | Asellus |  |  | 1.4 | 0.7 | 0.1 | 0.3 | 2.0 |  |
|  | Gammarus |  |  |  |  |  |  |  |  |
|  | Crustacean legs |  |  | 0.6 |  |  |  |  |  |
|  | Copepoda | 36.9 | 14.1 | 16.3 | 14.2 | 0.6 | 0.5 | 7.9 | 0.5 |
|  | Ostracoda | 3.9 | 3.7 | 0.9 | 10.3 | 1.7 | 12.0 | 11.4 | 0.5 |
|  | Cladocera | 42.7 | 57.3 | 6.6 | 2.7 | 0.6 | 3.0 | 1.2 |  |
| Adult insects | Ant | 0.2 |  |  |  |  |  |  |  |
|  | Tipulidae |  |  |  |  |  |  |  | 0.3 |
|  | Collembola |  | 6.5 |  |  |  |  |  |  |
|  | Chironomid |  | 0.1 |  |  |  |  |  |  |
|  | Diptera |  |  |  |  | 0.2 | 0.3 | 1.5 |  |
|  | Aphids |  |  |  |  | 5.0 | 0.3 | 0.3 |  |
| Insect larvae | Chironomid |  | 1.2 |  |  | 0.2 | 0.5 | 1.8 | 0.3 |
|  | Tipulidae |  | 1.0 |  | 0.2 |  |  |  |  |
| Insect Nymphs | Chironomid |  | 0.1 |  |  |  | 0.8 |  |  |
| Insect nd | Chironomid | 0.2 |  | 0.3 |  |  |  |  |  |
|  | Cératopogonidae |  |  | 0.3 |  |  | 0.3 |  | 0.3 |
| Arachnida | Hydracarien |  | 0.1 |  |  |  |  |  |  |
| Fish eggs and larvae | Eggs (nd) |  |  | 2.3 |  |  |  |  |  |
|  | Stickleback eggs |  |  |  | 15.1 |  |  |  |  |
| Plant material | Vegetal |  | 0.7 |  | 0.7 |  |  |  |  |
|  | Diatoms |  |  |  |  | 91.6 | 90.9 | 58.5 |  |
|  | Seeds |  |  | 0.3 | 0.2 |  |  |  |  |
| Unidentified |  | 0.2 |  |  |  |  |  |  |  |

According to Tables S9 and S10, the most frequently found preys in the guts of sticklebacks were crustaceans (zooplankton and higher crustacea) and dipterans (mainly *Chironomidae*).

## Conversion of the prey abundance into energy

According to Hynes ([1950](#_ENREF_11)) and Gill and Hart ([1994](#_ENREF_9)), the maximum size for a prey (macroinvertebrate) to be predated by a three-spined stickleback is 10 mm. Thus, we only used the abundance of prey under 10 mm. To do that, we separated the samplings classes into discrete classes (inferior to 10 mm and superior to 10 mm) by considering that the abundance between the different classes are homogeneous. Table S11 and S12 present the conversion factors that we used to estimate the total abundance of zooplankton or macroinvertebrate in mesocosms by taking into account the dimensions of the different sampling devices and the mesocosm.

Table S11. Conversion factors for the calculation of the total abundance for the zooplankton samples

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Vs upstream (m3) | Vs downstream (m3) | Vt upstream (m3) | Vt downstream (m3) |
| Experiment 1 | 4.75 10-3 | 15.75 10-3 | 1.898 | 5.788 |
| Experiment 2 | 5 10-3 | 18 10-3 | 1.898 | 5.788 |

With Vs the volume of the water samplings and Vt the volume of water in the mesocosm

**Table S12.** Conversion factors for the calculation of the total abundance for macroinvertebrate samples

|  |  |  |
| --- | --- | --- |
| Traps | Dimensions (m) | Volume (m3) or Surface (m2) |
| Tubes | 7 cylinders of  0.2 in diameter x 0.20 long | 0.0440 m3 |
| Tiles | 0.11 x 0.16 x 0,013 | 0.0228 m3 |
| Surface sampled in the upstream | 0.25 x 0.21 | 0.2150 m² |
| Surface sampled in the downstream | 0.25 x 0.60 | 0.6000 m² |

The volume of water used for the conversion is given in Table S11. The surface of the mesocosm walls is 3.87 m2 and 10.8 m2 respectively for the upstream and downstream parts.

Tables S13 and S14 present the conversion factors that we used to estimate the total energy from the total abundance of preys per mesocosm. For each experiment, we calculated the food energy from the food throughout time by linearly interpolating the energy between the different sampling dates. The energy used for the simulations is the mean energy for the 11 mesocosms per experiment.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | Family | Species | By g AFDW (Cal) |  | J/individual | Individual weight (µg) | References |
| Copepoda | Artemiidae | Nauplii | 6737 |  | 0.0178 | 4.215 | ([Jørgensen 2002](#_ENREF_13)) |
| Harpacticidae | T. japonicus | 5300 |  | 0.1396 | 41.98 | ([Watanabe 1982](#_ENREF_20)) |
| Harpacticidae | T. Californicus | 5155 |  | 0.1358 | 41.98 | ([Jørgensen 2002](#_ENREF_13)) |
| Calanidae | C. Helgolandicus | 5400 |  | 0.1422 | 41.98 | ([Jørgensen 2002](#_ENREF_13)) |
| Acartiidae | A. Clausi | 4100 |  | 0.1080 | 41.98 | ([Watanabe 1982](#_ENREF_20)) |
|  |  |  | *Mean* | *0.1314* |  |  |
| Cladocera | Leptodoridae | L. Kindtii | 6705 |  | 0.0295 | 7.001 | ([Jørgensen 2002](#_ENREF_13)) |
| Rotifera |  |  | 1.34.10-3 to 2.10-3 per rotifera |  | 0.0070 | 0.628 | ([Støttrup 2003](#_ENREF_18)) |

**Table S13.** Conversion factors for zooplankton

For all zooplankton, the conversion factor used to calculate the energy per individual was 5000 cal/g (DW) ; WW = 50% DW ([Jørgensen 1979](#_ENREF_12)).

**Table S14**. Conversion factors for macroinvertebrates

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Family | Species and size | Calorie per g AFDW | Calorie  per g | Conversion factor | J/individual | Individual weight (mg) | References |
| Higher Crustacea | Gammaridae | G. Fossarum  [2-5 mm] | 5452 | 3738 (DW) | DW = 19.1 % WW ; AFDW = 79.1 % DW | 1.4469 | 0.439 | ([Driver et al. 1974](#_ENREF_5), [Jørgensen 1979](#_ENREF_12), [Ricciardi and Bourget 1998](#_ENREF_16)) |
| G. Fossarum  ]5-9mm] | 5354 | 3896 (DW) | 79.793 | 26 | ([Driver et al. 1974](#_ENREF_5), [Jørgensen 1979](#_ENREF_12), [Ricciardi and Bourget 1998](#_ENREF_16)) |
| G. Fossarum  ]9-13 mm] | 5201 | 3778 (DW) | 77.512 | ([Driver et al. 1974](#_ENREF_5), [Jørgensen 1979](#_ENREF_12), [Ricciardi and Bourget 1998](#_ENREF_16)) |
| Asellidae | A. Aquaticus  [2-5 mm] | 17.6 kJ |  | DW = 20.8 % WW ; AFDW = 68.2 % DW | 3.3874 | 1.04 | ([Rumohr et al. 1987](#_ENREF_17)) |
| A. Aquaticus  ]5-15 mm] | 5521 |  | 90.579 | 27.81 | ([Jørgensen 1979](#_ENREF_12)) |
| Insect | Chironomidae |  |  | 3737 J (WW) | NA | 13.5026 | NA | ([Eggletona and Schramm 2003](#_ENREF_6), [Frouz et al. 2003](#_ENREF_7), [Bogut et al. 2007](#_ENREF_3)) |

For chironomidae, we used : 1g DW = 6g WW = 0.9g AFDW = 5kCal

# Script

**R Script of the DEB model for females (R 3.3.1 software)**

library("deSolve")

library("gplots")

### Function involving the various differential equations and parameters used ###

### With structural variables ###

# Temperature function (Hovel et al.2015):

FT = function( Temp , CTM, CT0, CQ){

tmp = (CTM - Temp)/(CTM-CT0)

V = ifelse(CTM > Temp, tmp, 0)

Z = log(CQ)\*(CTM-CT0)

Y = log(CQ)\*(CTM-CT0+2)

XX = ( Z^2 \* (1 + ( 1 + 40/Y)^(0.5) )^2 ) / 400

res = V^XX \* exp( XX \* (1-V))

return(res)

}

debF = function(t,state,parameters, inputa, inputb){

with( as.list(c(state,parameters)), {

Texp.t = inputa(t)

Tc = FT (Temp = Texp.t , CTM = Tmax, CT0 = Topt, CQ = Cq )

# Correct all parameters depending on time to temperature

v.t = v \* Tc # Energy conductance (mm /d)

PAm.t = PAm \* Tc # Maximum area specific assimilation rate (J/ d / mm^2)

PM.t = PM \* Tc # Volume somatic maintenance costs (J/d/mm^3)

Kj.t = Kj \* Tc # Maturity maintenance rate coefficient (d^-1)

Phi.t = Phi \* Tc

# Parameters functions of primary parameters

Em = PAm.t/v.t # Maximum reserve density (J/mm^3)

g = Eg / (Kappa \* Em) # Energy investment ratio

Km.t = PM.t / Eg # Somatic maintenance rate

Linf = (v.t / (Km.t\*g)) \* 1/Shape # Maximum physical length (mm)

Lm = (v.t / (Km.t\*g)) # Maximum structural length (mm)

# Reserve density

Qn.t = inputb(t)

f = (Qn.t / (Phi.t \* L^2 \* 0.5)) / ( 1 + (Qn.t / (Phi.t \* L^2 \* 0.5)) )

freal = ifelse(Eh < Ehb, 0, f)

dE = (PAm.t / L ) \* (freal - (E/Em) )

# Growth

e = E/Em

dL =(v.t / (3 \* (e+g))) \* (e - (L/Lm))

# Maturity

PC = ((g\*E)/(g+e))\*(v.t\*L^2 + Km.t\*L^3)

temp.Eh = ((1-Kappa) \* PC) - ( Kj.t \* Eh)

dEh = ifelse (Eh <= Ehp, temp.Eh, 0)

# Cumulated eggs

temp.dr = (Kr/Eegg )\*( ((1-Kappa)\* PC) - ( Kj.t \* Ehp) )

dR = ifelse (Eh >= Ehp, temp.dr, 0)

# Output model

ParSim = round(c(Linf=Linf, Tc=Tc, g=g, Km.t=Km.t, Em=Em, Texp.t=Texp.t),digits=4)

list(Sim = cbind(dE, dL, dEh, dR),

Parameter = ParSim,

f=freal) })

}

# (I.2) Simulation

#~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

ModelE3EF = function(

# Value of parameters (Qn and Texp should be adapted in function of the food and temperature scenarios as well as the time of simulation given by Timesdata)

Qn = 100000 \* 3.73, # "Chironomus" 3.73 J/mg wet weigt – Default value

Phi = 15.31, # J/mm^2

# energy

PAm = 2.42, # Maximum area specific assimilation rate

v = 1.33, # Energy conductance (mm /d)

Kappa = 0.757, # fraction of energy to growth/somatic

# growth

Shape = 0.250, # shape coefficient for adults V = zota \* L ^3

PM = 0.111, # Volume somatic maintenance costs (J/d/mm^3)

Eg = 1.10, # Cost of synthesis of a unit of structure J/mm^3

# reproduction

Ehb = 1.33, # Cumulated energy at birth (J)

Ehp = 442, # Cumulated energy at puberty (J)

Kj = 0.003, # Maturity maintenance rate coefficient (d^-1)

Kr = 0.978, # Reproduction efficiency

Eegg = 5.61, # Energy in an egg (J)

Legg = 0.563, # Size of primordial cell in physical length (mm)

# temperature (from Hovel et al. 2015)

Tmax = 25, # water temperature above which consumption ceases

Topt = 23, # the laboratory-derived temperature preferendum

Cq = 3 , # approximates the rate at which the function increases over low temperatures.

Texp = 16, # –Default value

# Time step and initial points

Timesdata = seq(1,8,0.01), # –Default values

E.init = NULL, # Energy density at t0

Eh.init = NULL, # Energy maturity at t0

L.init = NULL # Length at t0

){

# (I.3) Simulation - Compute differential equations

#~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

parameters = c(Tmax=Tmax,Topt=Topt, Cq=Cq,

Kappa=Kappa, Qn=Qn, Phi=Phi, Eg=Eg,v=v,PAm=PAm,Shape=Shape,

Ehp=Ehp,Kr=Kr,PM=PM,Kj=Kj,Ehb=Ehb,

Legg=Legg, Eegg=Eegg ,

L.init=L.init, E.init=E.init, Eh.init=Eh.init )

# Starting points:

Km = PM/Eg

Em = PAm/v

g = Eg/(Kappa\*Em)

# Initialization

L.0 = ifelse( is.null(L.init), Legg \* Shape , L.init \* Shape )

Eh.0 = ifelse(is.null(Eh.init), 0 , Eh.init)

E.0 = ifelse(is.null(E.init), (Eegg/(Legg\*Shape)^3) , E.init)

R.0 = 0

# temperature scenario

if( length(Texp)>1){

times = seq(0,length(Texp)-1, 1) #Attention : on considère des températures/jours (pas de temps=1)

import = Texp

}else{

times = Timesdata

import = rep(Texp, length(times)) }

Scenario = data.frame(times = times, import = import )

Texp.Scenario = approxfun(Scenario$times, Scenario$import,rule = 2)

# food scenario

if( length(Qn)>1){

times = seq(0,length(Qn)-1, 1)

import = Qn

}else{

times = Timesdata

import = rep(Qn, length(times)) }

Scenariof = data.frame(times = times, import = import )

f.Scenario = approxfun(Scenariof$times, Scenariof$import,rule = 2)

#plot(f.Scenario)

state = c(E=E.0, L=L.0, Eh=Eh.0, R=R.0)

out = ode(y=state,

times=Timesdata,

func=debF,

parms=parameters,

inputa = Texp.Scenario,

inputb = f.Scenario,

method="lsode")

# (I.4) Simulation function - Output data

#~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

Sim = out[,1:5]

Sim[,3] = out[,3] \* 1/Shape # physical length

colnames(Sim) = c("Time", "Energy", "Size", "Maturity", "Reproduction")

L\_mat = Sim[Sim[,4] >= Ehp,3][1]

tps\_mat = Sim[Sim[,4] >= Ehp,1][1]

ParSim= out[nrow(out), 6:ncol(out)]

return(list( Sim=Sim,

Init.values = c(E0 =E.0, L0.Structural=L.0, Eh0=Eh.0, R0=R.0),

Par=parameters,

food=out[ ,ncol(out)],

L\_mat = L\_mat,

tps\_mat=tps\_mat,

ParSim=ParSim))

}

**R Script of the DEB model for males (R 3.3.1 software)**

Type R metabolic acceleration:

* alpha = 0.082 is added as parameter (calibrated value with laboratory experiments)
* Parameter called Kappa is replaced by KappaM which is defined in (I.3 – starting points) by the following script:

KappaM = ifelse(Eh.0 >= Ehp, (Kappa - alpha), Kappa)

**Possible variation of R Script for males (not used in the article):**

Type A metabolic acceleration:

* beta = 0.219 (calibrated value with laboratory experiments)
* Parameter called PAm is replaced by PAmM which is defined in (I.3 – starting points) by the following script:

PAmM = ifelse(Eh.0 >= Ehp, (PAm - beta), PAm)

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