

Life Sciences Reporting Summary

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► Experimental design

1. Sample size

Describe how sample size was determined.

The sample size for the mesocosms was determined by the availability of these large floating mesocosms (55000m³). From the total number of 10 being available, 5 were used for control and 5 were used for high CO₂ treatments. For the chlorophyll data, samples were taken from each mesocosm every 2 days to be able to follow the developmental patterns. Zooplankton samples were taken every 8 days from each mesocosm. A more intense sampling scheme was not possible, since it would have affected the mass balance determinations from other experiments connected to this study too much. Numbers of fish eggs were calculated based on estimated survival rates with the aim of having 50 -100 herring larvae surviving at the end of the experiment.

2. Data exclusions

Describe any data exclusions.

No data were excluded from the analyses

3. Replication

Describe whether the experimental findings were reliably reproduced.

The experimental setup using 10 mesocosms and two treatments led to 5 replicates for all parameters analysed.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

The mesocosm were randomly distributed in the study area in the fjord. The striped spawned herring egg from the different parents were randomly distributed on each of the egg plates allowing for a random distribution of the larvae in the mesocosms .

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

Blinding was not possible, since CO₂ manipulation of selected mesocosms was needed.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a Confirmed

- ☐ ☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
- ☐ ☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☒ ☐ A statement indicating how many times each experiment was replicated
- ☐ ☒ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
- ☒ ☐ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
- ☐ ☒ The test results (e.g. *P* values) given as exact values whenever possible and with confidence intervals noted
- ☐ ☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
- ☐ ☒ Clearly defined error bars

See the web collection on [statistics for biologists](#) for further resources and guidance.

► Software

Policy information about [availability of computer code](#)

7. Software

Describe the software used to analyze the data in this study.

All statistical analyses were run in the programs R (Version 3.3.2) (R Core Team (2016). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. www.R-project.org) and RStudio (Version 1.0.136) (RStudio Team (2015). RStudio: Integrated Development for R. RStudio, Inc., Boston, MA, USA, www.rstudio.com). Graphics were done in the R package ggplot2 (H. Wickham. ggplot2: Elegant Graphics for Data Analysis. Springer Verlag New York, 2009).

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* [guidance for providing algorithms and software for publication](#) provides further information on this topic.

► Materials and reagents

Policy information about [availability of materials](#)

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

There are no restrictions on material availability

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

No antibodies were used.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

No cell lines were used.

b. Describe the method of cell line authentication used.

Describe the authentication procedures for each cell line used OR declare that none of the cell lines used have been authenticated OR state that no eukaryotic cell lines were used.

c. Report whether the cell lines were tested for mycoplasma contamination.

Confirm that all cell lines tested negative for mycoplasma contamination OR describe the results of the testing for mycoplasma contamination OR declare that the cell lines were not tested for mycoplasma contamination OR state that no eukaryotic cell lines were used.

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

Provide a rationale for the use of commonly misidentified cell lines OR state that no commonly misidentified cell lines were used.

► Animals and human research participants

Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

The brood stock herring originated from the Oslo-Fjord close to the Biological Station Drøbak, University of Oslo and were caught using a gillnet on April, 22nd 2013 at a depth of ~30m, at the southern tip of Søndre Kaholmen, roughly located at 59°40'29" N and 10°36'22" E. The dead ready-to-spawn herring were transported on ice to the Sven Lovén Centre, where fertilization was performed four hours later.

Policy information about [studies involving human research participants](#)

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

There was no human research participation.