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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see Authors & Referees and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	Calcium ions flurescence data were collected using Leica LAS AF software. Chlorophyll flurescence data were collected using Walz imagingWin software. Instantaneous velocity data were collected INSIGHT™ 4G software.
Data analysis	SPSS v.22, R 3.5.1

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	Using a six-level, CO2 gradient experiment, we investigated the changes in the velocity of Microglena sp. under laboratory microscale. Field mesoscale experiments were investigated using three-level CO2 gradient. Changes in the expression of motility-related genes was investigated. The effects of three-level CO2 gradient experiment on Dunaliella salina and Chlamydomonas reinhardtii velocity have also been done. See manuscript for full details.
Research sample	Microglena sp., Chlamydomonas reinhardtii and Dunaliella salina were used in this study. These three species were semi-continuously cultured in aerated 500 ml conical flasks containing 400 ml of medium in a 12-h/12-h light/dark cycle and at 6 °C, 20 °C, 20 °C, respectively. All following experiment assays were performed using cells in the light period (6~8 h after the light came on) after the five-year acclimation.
Sampling strategy	Microglena sp., Chlamydomonas reinhardtii and Dunaliella salina were measured for motility in the light period (6~8 h after the light came on) after the five-year acclimation. Motility-related genes expression of Microglena was 6 hours after illumination.
Data collection	Y.T.W., D.X., X.W.Z. and W.T.H collected the data.
Timing and spatial scale	All data of Microglena sp., Chlamydomonas reinhardtii and Dunaliella salina were done after five-year acclimation expect for SNP data which lasting from the first year to the fifth year .
Data exclusions	No data has been excluded.
Reproducibility	Before the formal experiment, we did many pre-experiments to make sure that our operation is correct and the experiments are repeatable. In addition, three algae species were used and short-term and long-term experiments were conducted, which output similar results.
Randomization	Randomised sampling strategies were used in all sampling , with replicates analysed in random order.
Blinding	Complete blinding of data analysis was used.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	Temperatures were approx. 5.0 - 7.0°C. Daily light cycle was 11:13 h light:dark.
Location	The experiment was carried out in the sea , approx. 1 km offshore , Qingdao (36.05° N, 120.36° E).
Access and import/export	The site where field experiments were conducted is a public area and open to everyone.
Disturbance	The field experiments were conducted in an enclosure system, which minimized the disturbance to local ecosystem.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Microglena sp. was obtained from the Algae Culture Collection at the Institute of Yellow Sea Fisheries Research Institute (YSFRI). Chlamydomonas reinhardtii was obtained from Freshwater Algae Culture Collection at the Institute of Hydrobiology, Chinese Academy of Sciences. Dunaliella salina was obtained from the National Institute for Environmental Studies (NIES Collection, Tsukuba, JAPAN).
Authentication	We identified atpB, psaA, psaB, psbC and rbcL genes and classified the polar marine alga into the genus of Microglen (Demchenko, E., Mikhailyuk, T., W. Coleman, A. & Pröschold, T. Generic and species concepts in Microglena (previously the Chlamydomonas monadina group) revised using an integrative approach. European Journal of Phycology - EUR J PHYCOL 47, 264-290, doi:10.1080/09670262.2012.678388 (2012).). Chlamydomonas reinhardtii is numbered Chlamydomonas reinhardtii FACHB-2217 in FACHB. Dunaliella salina is numbered Dunaliella salina NIES-2257 in NIES.
Mycoplasma contamination	Using transcriptome and genome data, we found that the results of Mycoplasma contamination were negative.
Commonly misidentified lines (See ICLAC register)	There is no commonly misidentified cell lines used in the study.