

Global imprint of climate change on marine life

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Past meta-analyses of the response of marine organisms to climate change have examined a limited range of locations^{1,2}, taxonomic groups^{2–4} and/or biological responses^{5,6}. This has precluded a robust overview of the effect of climate change in the global ocean. Here, we synthesized all available studies of the consistency of marine ecological observations with expectations under climate change. This yielded a meta-database of 1,735 marine biological responses for which either regional or global climate change was considered as a driver. Included were instances of marine taxa responding as expected, in a manner inconsistent with expectations, and taxa demonstrating no response. From this database, 81–83% of all observations for distribution, phenology, community composition, abundance, demography and calcification across taxa and ocean basins were consistent with the expected impacts of climate change. Of the species responding to climate change, rates of distribution shifts were, on average, consistent with those required to track ocean surface temperature changes. Conversely, we did not find a relationship between regional shifts in spring phenology and the seasonality of temperature. Rates of observed shifts in species' distributions and phenology are comparable to, or greater, than those for terrestrial systems.

Despite the ocean having absorbed >80% of the heat added to the global climate system, the ocean's thermal capacity has led to surface waters warming three times slower than air temperatures over land⁷. Nevertheless, isotherms at the ocean surface have migrated at comparable or faster rates than isotherms over land during the past 50 years (1960–2009)⁸. Winter and spring

temperatures, over both the ocean and land, are warming fastest, which might advance phenological events such as the start of growing seasons and the timing of reproduction⁷. In addition, anthropogenic CO₂ uptake by the oceans is altering seawater carbonate chemistry, which can reduce calcification rates and impact physiological processes in some marine organisms^{9,10}. Given these findings, we expect marine organisms to have responded to recent climate change, with magnitudes similar to or greater than those found for terrestrial species.

We investigated the peer-reviewed literature that addresses the question of whether or not climate change impacts marine ecological phenomena, and found 208 studies of 857 species and assemblages. From these, we extracted 1,735 observations (median time span = 41 yr, range = 19–343 yr, Supplementary Fig. S1, plus two subfossil comparisons spanning >12,000 yr) of the following types of response: distribution, phenology, abundance, community change, calcification and demography. We included responses irrespective of whether they were consistent with expectations under climate change or not, as well as null responses (Fig. 1). Data were available for every ocean (Fig. 1a), although most reports were from Northern Hemisphere temperate oceans (Fig. 1b).

We analysed this meta-database to estimate mean shifts in distribution and phenology among marine taxonomic or functional groups (data subset given in Table 1). We assessed relationships between the magnitude of observed changes in distribution and spring phenology with regional temperature shifts, and evaluated whether there is a global imprint of climate change on changes in marine life, by comparing consistent and inconsistent observations

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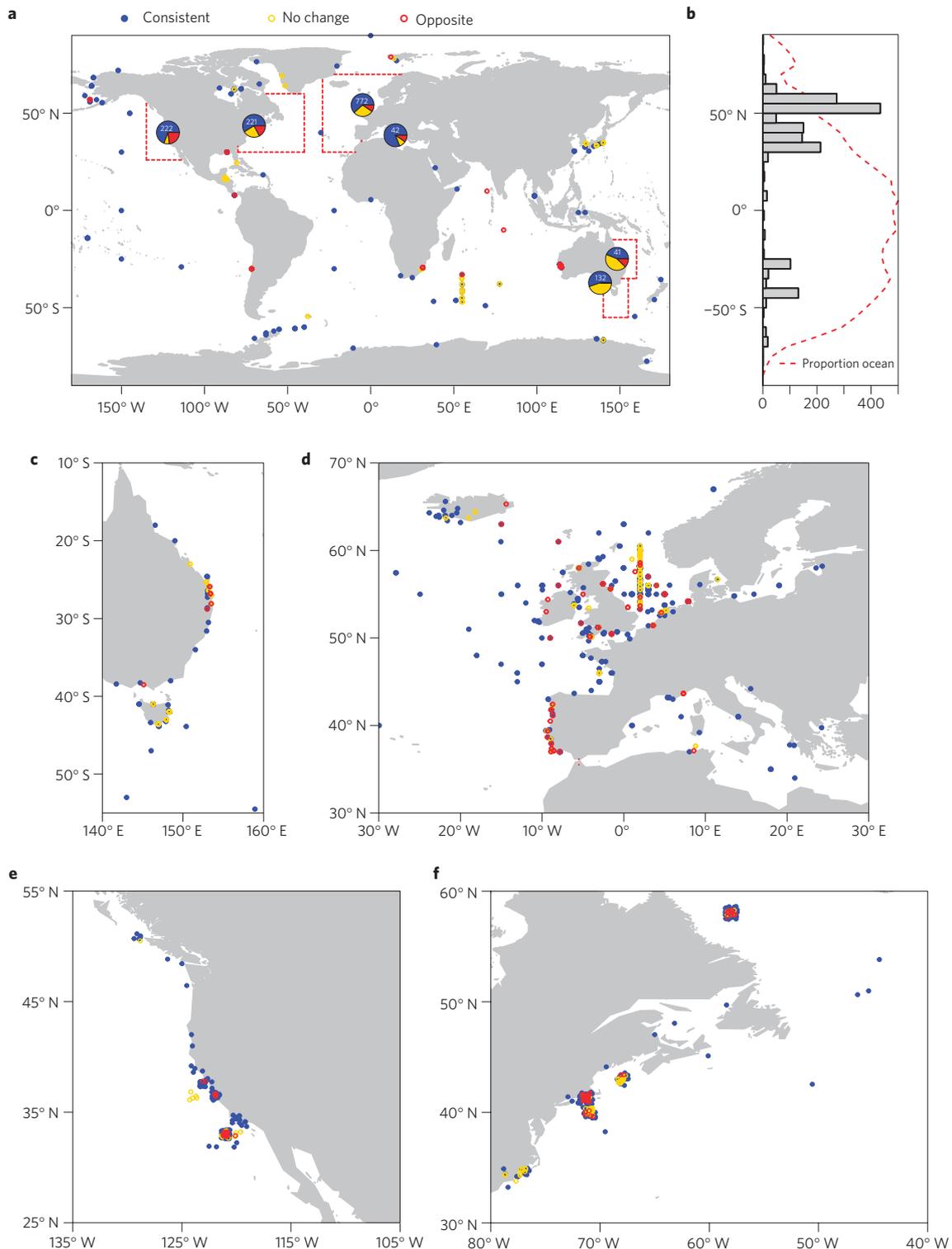


Figure 1 **a**, Observed responses ($n = 1,735$) of marine organisms to climate change from 208 single- and multi-species studies showing responses that are consistent with climate change (blue, $n = 1,092$), opposite to expected (red, $n = 225$) or are equivocal (yellow, $n = 418$). Each circle represents the centre of a study area. Where points fall on land, it is because they are centroids of distribution that surround an island or peninsula. Pie charts show the proportions within regions bounded by red squares and in the Mediterranean Sea; numbers indicate the total (consistent, opposite plus equivocal) observations within each region. **b**, Frequency of observations and ocean area by 5° latitudinal bins; red dotted line shows the proportion of ocean area within each latitudinal bin. **c**, Observations from the California Current. **d**, Northeast Atlantic, North Sea and Mediterranean Sea. **e**, Southwest Pacific. **f**, Northwest Atlantic.

1 across all types of response. The inclusion of single-species
 2 studies in meta-analyses of climate change impacts might result
 3 in positive publication bias due to possible under-reporting of
 non-responses^{11,12}. However, our meta-database contains only 181
 observations (<11%) from single-species studies and many of
 these are from fisheries-driven studies that were designed to detect

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Table 1 | Rates of change in phenology and distribution from this study (marine) compared to results from previous studies in both marine and terrestrial systems.

Study	Observation	Shift (mean \pm s.e.m.)	<i>n</i> studies	<i>n</i> observations	Realm (% studies)	Data criteria
Phenology						
This study	Summer	-4.4 ± 0.7 days dec^{-1}	10	51	Marine 100%	Single [†] and multi-species studies, climate change inferred
This study	Spring	-4.4 ± 1.1 days dec^{-1}	17	52	Marine 100%	Single [†] and multi-species studies, climate change inferred
Ref. 20	Spring	-1.1 to -3.3 days dec^{-1}	n/a	1,634	Terrestrial 100%	Long-term observations of plant phenology from NECTAR [‡] database
Ref. 12 (ref. 11)	Spring	-2.8 ± 0.35 days dec^{-1}	9	203	Terrestrial 91%, Fresh water 8%, Marine 1%	Multi-species studies, climate change inferred
Ref. 3	Spring	-5.1 ± 0.1 days $\text{dec}^{-1\text{s}}$	61	169	Terrestrial 86% Fresh water 10% Marine 4%	Minimum 10 yr time span from 1951 to 2001; observed shift >1 day dec^{-1} or >1 day $^{\circ}\text{C}^{-1}$, single and multi-species studies
Distribution						
This study	Leading and trailing edges plus centre	30.6 ± 5.2 km dec^{-1}	36	360	Marine 100%	Single* and multi-species studies, climate change inferred
This study	Trailing edge	15.4 ± 8.7 km dec^{-1}	11	106	Marine 100%	Single* and multi-species studies, climate change inferred
This study	Leading edge	72.0 ± 13.5 km dec^{-1}	27	111	Marine 100%	Single [†] and multi-species studies, climate change inferred
Ref. 11	Leading edge	6.1 ± 2.4 km dec^{-1}	4	99	Terrestrial 100%	Multi-species studies, climate change inferred
Ref. 2	Leading edge	19.7 ± 3.7 km $\text{dec}^{-1\text{ll}}$	3	16 groups (336 species)	Terrestrial 83%, Fresh water 15% Marine 3%	Multiple species studies (≥ 4) that infer climate change, average response of taxonomic or functional group in a region
Ref. 4	Leading edge	13.8 ± 4.8 km dec^{-1}	11	85	Marine 100%	Multi-species studies

The number of studies and number of observations (taxonomic or functional groups) from studies are given, together with a breakdown of studies by realm and biome. The criteria for data inclusion are outlined for each study. Seabirds, anadromous fish and polar bears were counted as marine, given their dependence on marine food sources, and wading birds were considered as freshwater birds. Minimum time span of observations within studies is 19 or 20 years, unless stated otherwise. * $<4\%$ of total number of observations from single-species studies. [†] $<10\%$ of total number of observations from single-species studies. [‡]The network of ecological and climatological timings across regions. [§]Correcting for methodological differences compared with ref. 11 gives a revised estimate of 3.1 days dec^{-1} (ref. 12) that was not significantly different from the estimate reported in ref. 11. ^{ll}Recalculated using leading-edge (cold limit) observations spanning ≥ 19 yr, and with data after 1990.

changes other than climate change and are therefore likely to have been published irrespective of whether they detect climate change impacts or not. Although this suggests that our database is relatively robust to publication bias, we nevertheless give all results both with and without single-species studies.

Characteristics common among marine organisms, such as high rates of propagule production and dispersal by ocean currents, might lead to faster expansions in distribution than observed for plants and animals on land, even at latitudes where velocities of isotherm migration over the ocean and land surfaces (1960–2009) have been comparable⁸ (Supplementary Table S4). Evidence of faster spread rates for marine than terrestrial organisms was previously shown for expansions of both native and introduced species⁶. Here, focusing on responses to climate change, the mean rate (\pm s.e.m.) of expansion at the leading range edges for marine species was 72.0 ± 13.5 km dec^{-1} (Fig. 2a, 54.6 ± 11.7 km dec^{-1} excluding single-species studies) about an order of magnitude faster than rates reported for predominately terrestrial species (6.1 ± 2.4 km dec^{-1} ; Table 1). We find the fastest leading-edge expansions in highly mobile or dispersive pelagic organisms: phytoplankton (469.9 ± 115.3 km dec^{-1}), bony fish (277.5 ± 76.9 km dec^{-1}) and invertebrate zooplankton (142.1 ± 27.8 km dec^{-1}). We find the magnitude of distribution change differed by taxonomic or

functional group ($p < 0.0001$, $F = 11.51$, $df = 8$) and range edge ($p < 0.0001$, $F = 16.01$, $df = 1$; two-way analysis of variance with df residuals = 206; no significant interaction between taxa and range edge). In the latter case, trailing-edge range contractions (15.4 ± 8.7 km dec^{-1}) were significantly slower than leading-edge expansions (72.0 ± 13.5 km dec^{-1}).

Recent analysis suggests that both leading and trailing range edges for ectothermic marine organisms are equally responsive to warming¹³. Thus, our faster leading-edge shifts might be driven by stronger regional warming there compared with trailing-edge locations. Thirty-eight per cent of our leading-edge observations were from latitudes warming strongly⁸ ($>40^{\circ}$ N), whereas only 15% of trailing-edge observations were from temperate and polar regions. Hence, differences in expansion at leading and trailing edges may be explained by differences in regional climate change at the polar and equatorial edges of biogeographic distributions. A link between global warming patterns and the magnitude or frequency of multiple biological responses has been shown previously for predominately land species^{2–4}, but not for marine species⁵. However, new indices, such as the velocity of temperature change^{8,14} and seasonal shift in temperature⁸, describe the pace and direction of climate change and thus provide improved expectations for biological shifts¹⁵.

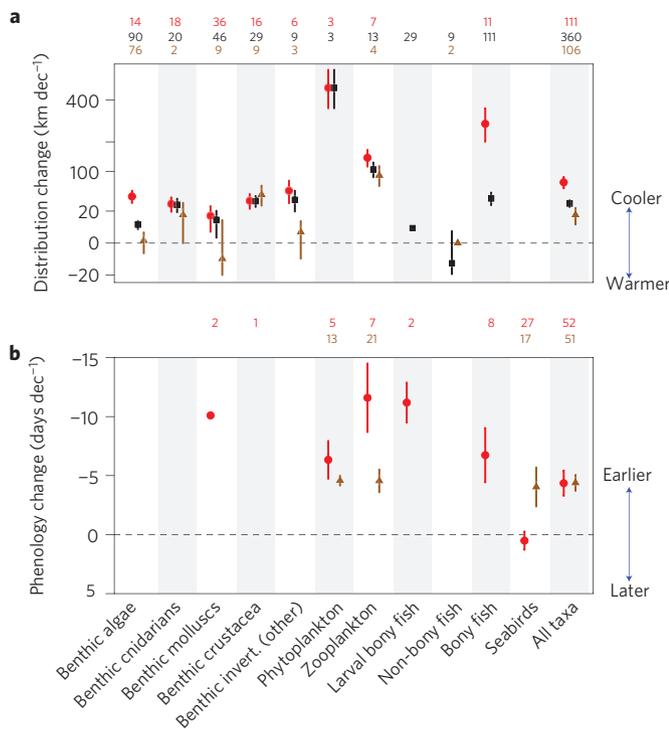


Figure 2 | a, b. Rates of change (means \pm s.e.m.) of marine taxonomic or functional groups in distribution (km dec^{-1}) at the leading edges (red circles), trailing edges (brown triangles) and from all data regardless of range location (black squares) (**a**), and phenology (days dec^{-1}) during spring (red circles) and summer (brown triangles) (**b**). Axis scaled on square-root for display, so standard errors are asymmetric. Negative phenological changes (generally earlier) and positive distribution changes (generally poleward into previously cooler waters) are consistent with warming. Sample sizes (n) are given above each taxon or functional group (**a**, leading edges upper row, trailing edge lower row; **b**, spring upper row).

1 For each quantified shift in distribution in our database, we
 2 generated corresponding quantitative expectations based on the
 3 decadal rate of temperature velocity for the period 1960–2009⁸ (see
 4 Supplementary Methods). Taking the distance shifted by species
 5 that show a response ($n = 279$); those that did not show a response
 6 were not included because failure to detect a change in distribution
 7 may have several causes, including barriers to dispersal, poor
 8 sampling resolution or the dominance of alternative drivers of
 9 change¹¹), and weighting by the numbers of years during which
 10 observations were made, yields a significant relationship with rates
 11 of isotherm shift (regression using fourth-root transformed data of
 12 observed shifts against shifts expected from velocity multiplied by
 13 time span: $y = 1.460 + 0.514 \cdot x$, $R^2 = 0.11$, $P < 0.0001$, $n = 279$).
 14 Thus, faster distributional shifts generally occur in regions of faster
 15 isotherm shift. However, many distribution shifts seem not to be
 16 keeping pace with isotherm movement; biological responses lead
 17 or lag isotherms in ways that vary among and within taxonomic or
 18 functional groups (Fig. 3).

19 Differences between expected size of response and observed
 20 shifts may arise owing to mismatches between the spatial and
 21 temporal scales of the temperature data set and the local
 22 climate that the species is responding to, mismatches between
 23 the climate variable and biological measurement arising from
 24 poor understanding of mechanistic drivers, biases in data sets,
 25 and idiosyncratic species' responses^{16,17}. For example in the
 26 Bering Sea, the extent of the cold pool ($<2^\circ\text{C}$ water) located
 27 on the Bering Sea shelf separates Arctic and subarctic fauna.
 28 Ref. 18 presents evidence of a community-wide northward shift

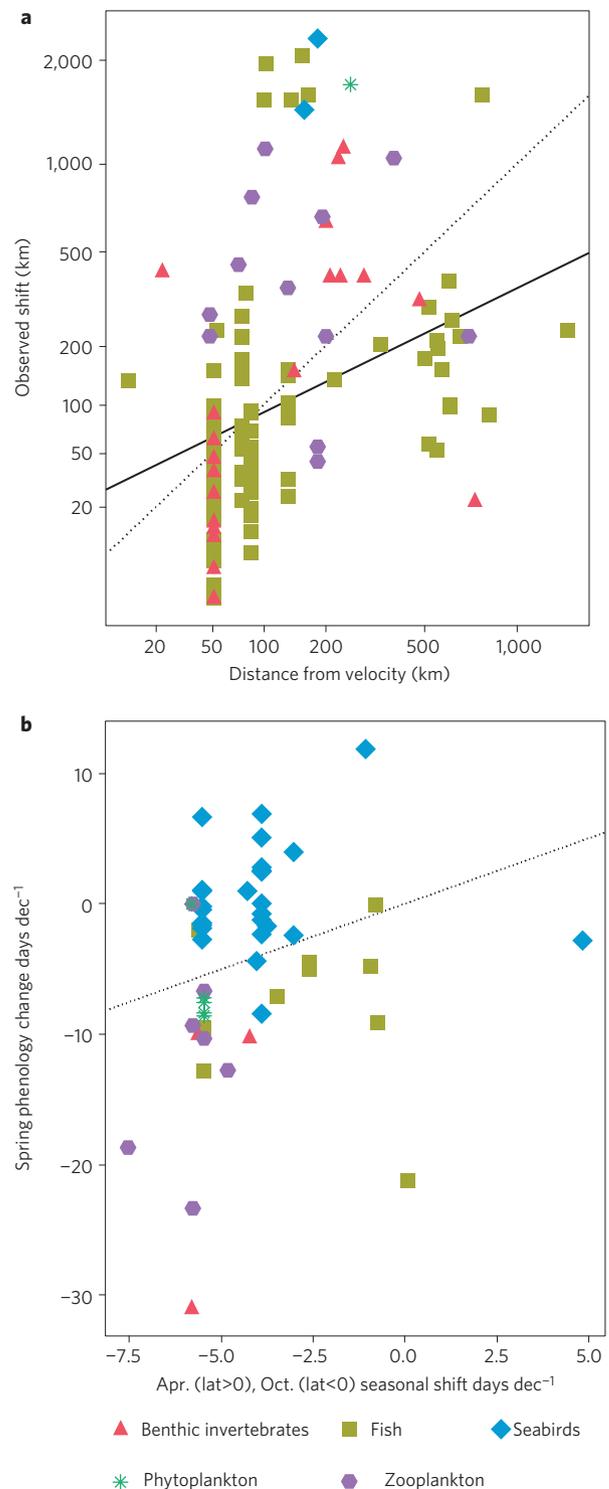


Figure 3 | a, Magnitude of observed shifts in species distributions (km dec^{-1}) for marine taxonomic or functional groups against expected magnitude. Two hundred and seventy-nine observed shifts taken from 36 published studies (null responses excluded). **b,** Observed shifts in spring phenology (days dec^{-1}) for marine taxonomic or functional groups against expected shift in spring phenology taken as shift in seasonal sea surface temperatures. Fifty-one observed shifts taken from 17 published studies. Expected distributional and phenology shifts over 1960–2009 calculated using the Hadley Centre data set (HadISST 1.1) and methods presented in ref. 8. April temperatures used for Northern Hemisphere spring phenology and October temperatures for Southern Hemisphere phenology.

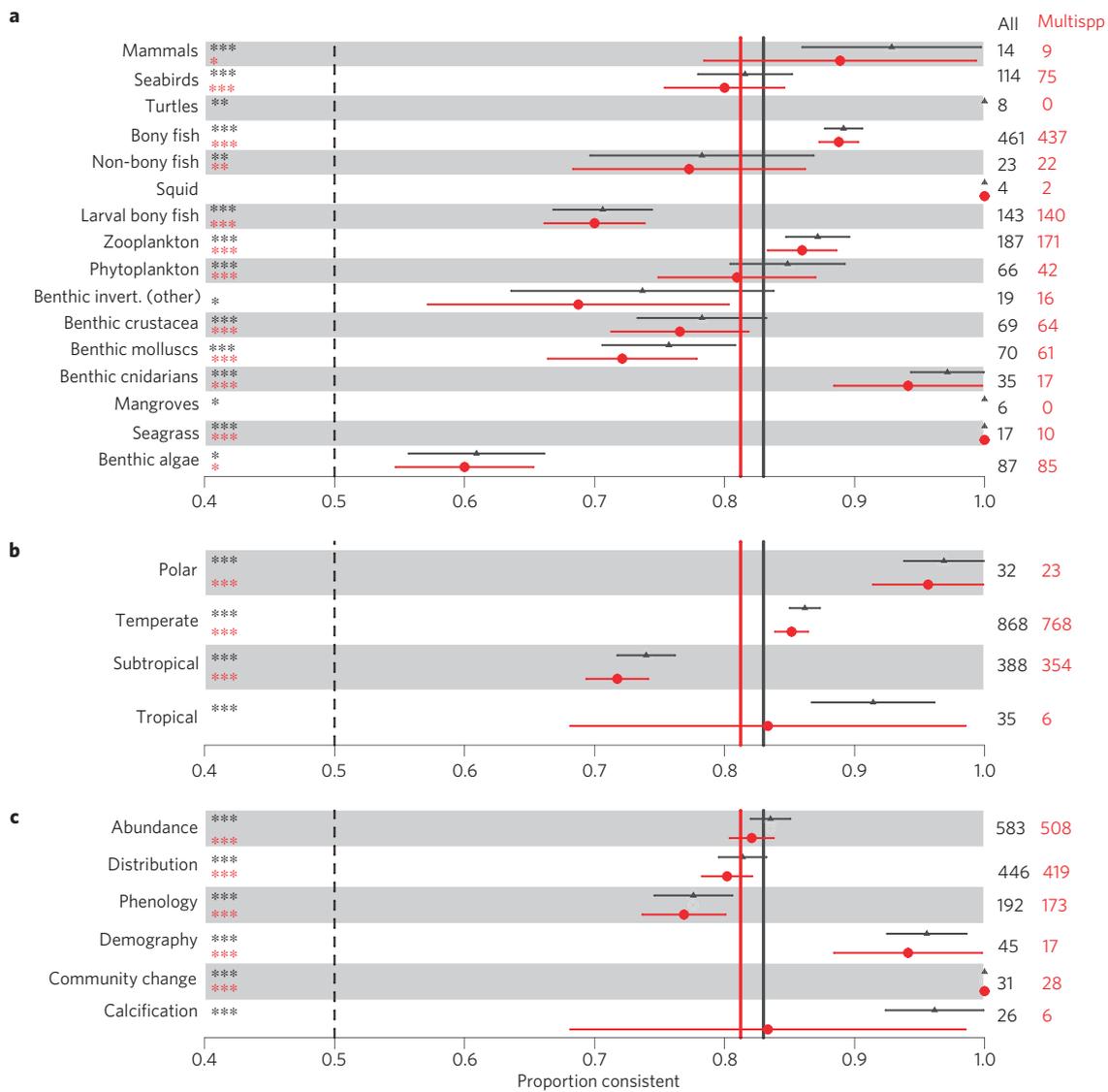


Figure 4 | Proportion of marine observations consistent with climate change predictions using observations from both single- and multi-species studies (all, black, $n = 1,323$) and multi-species studies alone (red, $n = 1,151$). **a–c**, Mean and standard error of responses by taxonomic or functional group (**a**), latitudinal zone (**b**) and response type show significantly higher consistency than expected from random as determined by binomial tests for each estimate against 0.5 (dashed line at 50% consistency; **c**). The solid line is the mean across all observations. Significance of results is listed next to labels (***, $p < 0.001$; **, $p < 0.01$; *, $p < 0.05$). Sample sizes are listed to the right of each row.

1 in demersal fauna related to loss of sea ice and northward
 2 retreat of this cold pool. However, variable responses among
 3 individual species in the community (some leading, some lagging
 4 temperature change and some not responding) are probably the
 5 result of interacting factors such as population size, dispersal
 6 ability, dependence on habitat or prey availability, resource
 7 competition, migratory strategy, latitudinal gradient in light regime,
 8 and fisheries impacts.

9 Observed shifts in seasonal timing of spring temperatures
 10 (1960–2009) are generally greater over the ocean than over
 11 land at high latitudes⁸ (above 45°). Given that the bulk of
 12 the quantitative phenological data are from higher latitudes, we
 13 expected that rates of response would be similar to or greater than
 14 those for terrestrial species. We found spring phenology in the
 15 ocean has advanced by 4.4 ± 0.7 days dec^{-1} (4.7 ± 1.1 days dec^{-1}
 16 excluding single-species studies) and summer phenology by
 17 4.4 ± 1.1 days dec^{-1} (4.0 ± 0.6 days dec^{-1} excluding single-species
 18 studies; Fig. 2b and Table 1). Our results contrast with slower
 19 estimates, between 2.3 and 2.8 days dec^{-1} (Table 1), of spring

phenological advancement on land¹², also predominately from
 Northern Hemisphere temperate regions.

The strength of the phenological response to climate change
 for both marine and terrestrial species varies among taxonomic
 or functional groups¹² (Fig. 2b). Phytoplankton, the main primary
 producers in the oceans, can respond rapidly to environmental
 changes compared with most terrestrial trees and plants, given their
 short generation times, sensitivity to temperature and advection
 of organisms within water masses¹⁹. The timing of phytoplankton
 blooms advanced much faster (6.3 ± 1.6 days dec^{-1} for multi-
 species assemblages) than that of plants on land (1.1–3.3 days dec^{-1} ;
 refs 12,20). Fastest rates of spring advancement were for pelagic
 animals (invertebrate zooplankton 11.6 ± 2.9 days dec^{-1} , and larval
 bony fish 11.2 ± 1.7 days dec^{-1} and Fig. 2b). However, phyto- and
 zooplankton groups both show slower, and similar, advancement
 of summer phenology (phytoplankton: 4.6 ± 0.4 days dec^{-1} ; inver-
 tebrate zooplankton: 4.6 ± 1.0 days dec^{-1}). These variable responses
 across biological communities and seasonal cycles imply temporal
 mismatches between food requirements and availability²¹.

1 Previous meta-analyses focusing on terrestrial species showed
2 only weak relationships with shifts in seasonal temperature using
3 latitude as a proxy^{3,12}. We produced quantitative expectations
4 for spring phenology shifts ($n = 34$ phyto- and zooplankton
5 plus $n = 17$ seabirds; mostly from the North Atlantic), but
6 found no relationship between these and corresponding seasonal
7 temperature shifts (Fig. 3 and Supplementary Information). In
8 marine ecosystems, nutrient availability, mixing (turbulence),
9 solar irradiance, water-column stratification and grazing pressure
10 combine to regulate the timing and magnitude of plankton
11 blooms^{22,23}, so the timing of seasonal temperatures may be too
12 simple an indicator for these events.

13 Our final challenge was to evaluate global consistency in
14 observed biological responses to climate change. Global coherence
15 of biological responses such as changes in distribution, abundance,
16 phenology and community structure, over the period during
17 which climate change has been unequivocally linked to the rise of
18 greenhouse gases, infers that anthropogenic climate change is, in
19 part, a causal driver^{11,24}. We extracted consistent and inconsistent
20 observations (as identified by each study's authors) from our
21 database across all response types ($n = 1,323$). These were used
22 to test the hypothesis that marine responses were equally likely
23 in either direction, as assessed by a binomial test against 0.5, the
24 value expected if changes were random (Supplementary Methods).
25 We excluded null responders, because apparent null responses can
26 arise from a number of causes, such as poor data resolution, lags
27 in species' responses, barriers to dispersal, or species' responses
28 that are not driven by climatic factors¹¹. Eighty-three per cent of
29 observed changes were in the direction expected under climate
30 change, and 81% ($n = 1,151$) if data from only multi-species studies
31 were selected (Fig. 4), well above the value expected by chance ($P <$
32 0.0001). Proportions of observations consistent with climate change
33 were significantly greater than 50% for all taxonomic or functional
34 groups (Fig. 4a), biomes (Fig. 4b) and response types (Fig. 4c), but
35 with substantial variability (see Supplementary Results). Our results
36 corroborate those of a regional marine synthesis¹ and also syntheses
37 from predominately terrestrial species with global consistencies of
38 81–90% (refs 3,4,11).

39 A major potential criticism of climate meta-studies is that
40 supporting evidence may contain biases¹². To investigate these,
41 we compared analytical results from subsets of the database that
42 were less prone to bias. We show above our results are robust to
43 publication bias (Fig. 4). We selected subsets of observations that:
44 span 30 yr or more, reducing biases introduced through decadal-
45 scale variability (78% consistency, $n = 776$, Supplementary Fig.
46 S5); and specifically discounted other drivers of change, reducing
47 the influence of non-climate drivers (79% consistency, $n = 379$,
48 Supplementary Fig. S6). These results show that our conclusions are
49 robust when major known biases are accounted for.

50 Diagnostic fingerprints are uniquely predicted by twentieth-
51 century climate trends and provide convincing evidence that
52 climate change is the primary driver behind the observed biological
53 changes, strengthening attribution^{11,24}. Such fingerprints include:
54 opposing responses in warm-water and cool-water species within
55 a community, or at leading and trailing range ranges; and
56 similar responses from discrete populations at the same range
57 edge (for example northwest Atlantic and northeast Atlantic
58 populations). We find numerous examples of these in our database
59 (see Supplementary Information). For example, for 33 species,
60 observations were available from both leading and trailing range
61 edges, or from distant, leading-edge populations. Twenty-four of
62 these showed responses at all sites that were consistent with climate
63 change, namely expansion or increased abundance at leading edges,
64 and/or contraction or decreased abundance at trailing range edges.

65 In conclusion, recent climate studies show that patterns
66 of warming of the upper layers of the world's oceans are

67 significantly related to greenhouse gas forcing^{25,26}. Global responses
68 of marine species revealed here demonstrate a strong fingerprint
69 of this anthropogenic climate change on marine life. Differences
70 in rates of change with climate change amongst species and
71 populations suggest species' interactions and marine ecosystem
72 functions may be substantially reorganized at the regional scale,
73 potentially triggering a range of cascading effects²⁷. Significantly,
74 24% of the species in our database showed no response,
75 which may arise from diverse circumstances including limited
76 observational resolution, poor process understanding, antagonistic
77 and synergistic interactions among multiple drivers of change, and
78 evolutionary adaptation. A focus on understanding the mechanisms
79 underpinning the nature and magnitude of responses of marine
80 organisms to climate change can help forecast impacts and the
81 associated costs to society and facilitate adaptive management
82 strategies effective in mitigating these impacts. This study not only
83 provides compelling evidence for widespread impacts of climate
84 change in the ocean, but also predicts future reconfiguration of
85 marine ecosystems, and the services they provide.

86 Methods

87 We reviewed the published literature to compile a global database of observations
88 of marine biological responses to regional and global climate change, including
89 null responses and studies where expectations of climate change responses
90 were considered and rejected (Fig. 1). We searched ISI Web of Science using
91 key words including climate change, warming, acidification, calcification and
92 phenology. We define an observation as a single biological response (classified
93 into phenology, distribution, abundance, community composition, demography
94 or calcification) that was tested, or at a minimum discussed, in relation to
95 expected impacts of recent climate change. These included cases where biological
96 responses were consistent with regional climate change, and where regional climate
97 change did not explain biological responses (inconsistent) or there was a lack
98 of biological response (null responders). Ninety-six per cent of the observations
99 in our database identified temperature as the primary climate change driver,
100 with the remainder relating biological change to pH, sea ice extent, sea level rise
101 or climate oscillations.

102 To be included in our database, a study had to meet three criteria: authors
103 inferred or directly tested for trends in biological and climatic variables; data
104 after 1990 were included; and to minimize the chance of bias resulting from
105 short-term biological responses to natural climate variability, observations
106 spanned at least 19 years. We included data from continuous data series
107 (number of observations, $n = 1,096$, >48,000 data points), intermittent data
108 series ($n = 271$) and comparisons of two periods in time ($n = 368$), if they
109 met our criteria. From each study we extracted data on the characteristics
110 of observations including location and duration of study, the number of
111 data points collected, and the direction of observed change in the biological
112 parameter (if any; Supplementary Table S1). Where species were encountered
113 more than once, we retained only the observation from the longest time series
114 or most robust analysis, unless the observations were from separate regions
115 or of different types (for example, distribution and phenology). We did not
116 restrict our search to only studies that applied a statistical test of a relationship
117 between observed climate change and observed biological response. Most studies
118 supplied multiple lines of evidence from theory, process-understanding, historical
119 overview and experimental and field results, to contextualize findings of a
120 response to climate change.

121 We categorized each observation as no change ($n = 418$) in response to climate
122 change, consistent ($n = 1,092$), or inconsistent ($n = 225$) with climate change
123 on the basis of the original authors' interpretations (Supplementary Methods).
124 Examples of expectations consistent with climate change are poleward distribution
125 shifts, earlier timing with warming and declining calcification rates. However,
126 we also captured responses that were contrary to general expectations under
127 climate change, such as equatorward range contractions, but consistent with
128 regional climate change such as areas of cooling. Quantitative estimates of shifts
129 in distributions and phenology were taken directly from the papers, calculated
130 from information in figures and tables, or, in some cases, supplied on request by
131 the authors of the study.

132 We extracted subsets of data to address three questions. We used data reported
133 as kilometres per decade or days per decade or to examine mean rates of shifts
134 in distribution ($n = 362$) and spring ($n = 52$) and summer phenology ($n = 51$).
135 We included negative and null responses in these analyses as we were focused
136 on global response to climate change across all species and taxonomic groups¹².
137 We then used this subset to determine whether responses in distribution and
138 spring phenology were tracking changes in regional temperatures. We excluded
139 null responses (23% distribution and <2% phenology observations) to avoid
140 over-inflation of zero data. For distribution change, we took the absolute distance

1 shifted, irrespective of direction. For each quantitative shift in our database for
 2 distribution and phenology, excluding null observations, expectations regarding the
 3 velocity of temperature isotherms (VoCC) and the shift in seasonal temperatures
 4 (SCS) were produced using the data sets and methods described in ref. 8 over
 5 the period 1960–2009. Distribution shifts were matched to VoCC values by
 6 averaging all values from 1° grid cells within a circular buffer distance (size of
 7 reported shift) from each observation. Spring phenology responses were similarly
 8 matched to SCS values for April (Northern Hemisphere) and October (Southern
 9 Hemisphere). The buffer radius was set as the square root of the reported area of
 10 each observation, divided by π .

11 Finally, to show a global coherence of biological responses to climate change,
 12 we applied the vote-counting approach^{4,5,11} using consistent and inconsistent
 13 observations to test for a coherent pattern in responses across regions, taxonomic
 14 or functional groups, using all available data ($n = 1,323$) and only multi-species
 15 studies ($n = 1,151$).

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Author contributions

E.S.P. and A.J.R. led the NCEAS working group. E.S.P., A.J.R., C.J.B., P.J.M., S.A.T.
 and W.J.S. extracted data from publications for the database. E.S.P., A.J.R. and C.B.
 undertook quality-control of the database. E.S.P., C.P. and W.J.S. wrote the first draft
 of the paper. W.K., C.J.B., A.J.R., M.T.B., E.S.P. and D.S.S. ran analyses and produced
 figures and tables. All authors contributed equally to discussion of ideas, development of
 the database and analyses, and commented on the manuscript.

Additional information

The Marine Impacts Database (NCEAS 12449: Richardson and Poloczanska E. 2013:
 Towards understanding marine biological impacts of climate change, National Center for
 Ecological Analysis and Synthesis. Impacts of Climate Change on Marine Organisms) is
 available at <http://knb.ecoinformatics.org/knb/metacat/nceas.1000.1/nceas>.

Supplementary information is available in the online version of the paper.

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Competing financial interests

The authors declare no competing financial interests.

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