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**Larger but younger fish when growth compensates for higher mortality in warmed ecosystem**

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Abstract

Ectotherms are often predicted to “shrink” with global warming, in line with the temperature-size rule (TSR), which states warming leads to smaller adult body sizes. But the TSR also predicts faster growth rates. As such, whether the average size of a population declines with warming depends on the mortality rates. We used data from an artificially heated (+8C) lagoon to analyze how warming has affected body growth, mortality rates and population size-structure of Eurasian perch (*Perca fluviatilis*). Compared to a reference area, we found that the size was larger for all ages and growth was faster for all sizes, to the extent that the size-spectrum slope was larger (indicating a higher proportion of large fish in) – despite the increased mortality rates. General size-temperature rules derived from experimental studies may not always translate to natural populations, and thus predictions of climate change impacts should incorporate a wider range of demographic parameters.

Introduction

It is commonly predicted that global warming will cause ectotherm species to shrink. Body size is a key trait that shapes rate of metabolism, growth and mortality, as well as feeding interactions (Ursin 1973; Blanchard *et al.* 2017; Andersen 2020). Because these biological and ecological processes scale with size, it is important to not only assess if the average size in population changes, but also which sizes and by which mechanism? Do the larger individuals in a population become rarer or smaller (Ohlberger 2013), and how does that interplay with the commonly observed faster growth rates?

The size-spectrum, or the individual size-distribution, is the relationship between number of individuals in a body-size class and the average size of that class, and the size-spectrum slope () is the often-linear relationship between the two variables on a log-log scale (White *et al.* 2007; Edwards *et al.* 2017). Hence it implicitly captures ecological processes such as body growth, mortality and recruitment (Blanchard *et al.* 2017; Heneghan *et al.* 2019), and moves beyond the average size in the population as a metric. However, despite being driven by individual processes that we know are temperature dependent, relatively few studies evaluate changes in the species size-spectrum and its drivers in higher ectotherm organisms, compared to e.g., changes in size-at-age.

Which sizes? It can refer to the the competitive ability of smaller sized species, or changes within species (changes towards smaller individuals within species). However, mean sizes can be unaffected by temperature if e.g., juvenile growth is positively affected by temperature and adult size is negative. Yet changes in the size-distribution like these could have strong impacts as size is a key trait. And we know from observations and experiments that some warming usually speeds up growth rates, likely because species live at temperature below those that maximize growth. In fact, in terms of size-at-age, this is close to the prediction by the temperature size rule. TSR predicts faster growth and development but smaller adult or asymptotic sizes. This could partly be due to the lower optimum temperature for growth in larger fish (Morita *et al.* 2010; Lindmark *et al.* 2021).

Because of these size-dependent responses, it is important to evaluate indicators that integrate over sizes, including how growth changes over size or length-at-age, or for population metrics, using e.g., size-spectra instead of mean size.

Faster growth rates could make the size spectrum slope shallower if it leads to an overall increase in size-at-age. However, with a TSR-like response would result in a steepening of the slope as large individuals become relatively scarcer (Heneghan *et al.* 2019). In the absence of temperature effects on growth, increased mortality can also affect the size spectrum slope by shifting the population to younger and thus smaller individuals. *Within*-species assessments of temperature-effects on mortality arerelatively rare, but together with predictions from metabolic theory and *across*-species studies, there is some support for mortality increasing with temperature (Pauly 1980; Brown *et al.* 2004; Thorson *et al.* 2017; Wang *et al.* 2020). Even with increased growth rates this can occur if mortality is size-dependent (e.g., if mortality increases mostly for large organisms). In other words,

This study uses data from the unique large-scale semi-natural experiment that is the Biotest lake to quantify body growth, mortality and the size structure in a non-commercially exploited population of Eurasian perch (*Perca fluviatilis*, henceforth perch) that was enclosed and exposed to temperatures 5-10 above the normal for 23 years, in relation to the reference outside the enclosure. The Biotest lake is a 1 km2 artificial enclosure of Swedish Baltic Sea archipelago that since the 1980’s has received warm cooling water from the nuclear power plant in Forsmark (Map Fig.) in 1977 (Adill *et al.* 2013; Huss *et al.* 2019). All types of fishing (apart from the regular surveys) have been banned since the construction (Huss *et al.* 2019). A grid at the Biotest outlet together with the strong current prevented fish larger than 10 cm from migrating in and out of the area (Adill *et al.* 2013; Huss *et al.* 2019), and genetic studies confirm the reproductive isolation between the two populations during the time period (Björklund *et al.* 2015). However, since the grid removal in 2004, fish growing up in the Biotest lake can easily swim out, meaning we cannot be sure fish in the reference area did not recently arrive from the Biotest lake. Several studies have been conducted in this system, including analyses of heat tolerance (Sandblom *et al.* 2016), sex-specific responses to warming (van Dorst 2020), reconstructed time series of growth (Huss *et al.* 2019), and the immediate effects of warming on life history traits (Sandström *et al.* 1995). In this study, we use years after the onset of warming to omit transient dynamics and acute responses (i.e., ensuring we use cohorts that were born into the heated area, i.e., post 1981) until the populations were no longer separated, resulting in data (X length-at-age from Y individuals in Z nets). Using hierarchical Bayesian models, we quantify differences in key individual-and population level parameters, such as body growth, asymptotic size, mortality rates and size-spectra while treating years or cohorts as random effects.

Results

Results

Discussion

What happens when a population gets larger but older?

Materials and Methods

*Data*

The Biotest lake and the reference bay outside (henceforth the warm and cool area) have been scientifically sampled using survey-gillnets since the construction of the enclosure. We use data from fishing events that took place in October in the Biotest lake and in August in the reference area when temperatures are most comparable between the two areas (Huss et al., 2019). The catch was recorded by 2.5 cm length classes during 1987-2000, and into 1 cm length groups between 2001-2003. To express lengths in a common length standard, 1 cm intervals were converted into 2.5 cm intervals. The unit of catch data is hence number of fish caught per 2.5 cm size class per night per net (i.e., a catch-per-unit-effort [CPUE] variable). All data from fishing events with disturbance affecting the catch (e.g., seal damage, strong algal growth on the gears, clogging by drifting algae, boat traffic or other human inference) were removed (this mean removing years 1996 and 1999 from the warm area in the catch data).

Age and length-at-age was reconstructed for a semi-random length-stratified subset of individuals each year. This was done using annuli rings on the operculum bones (with control counts done on otoliths), and an established power-law relationship between the distance of annual rings and fish length: , where is the length of the fish, the operculum radius, *k* the intercept of the line, and *b* the slope of the line for the regression of log-fish length on log-operculum radius (Thoresson 1996). Back-calculated length-at-age were obtained from the relationship , where is the back-calculated body length at length , is the final body length (body length at catch) and is the distance from the centre to the annual ring corresponding to age . Since perch exhibit sexual size-dimorphism, and age-determination and back calculation was only done for males in select years, we only used females for our analyses.

To focus on the long term differentiation between the two areas, and to ensure that we had enough back-calculated length-at-age observation within individual fish born after the onset of heating, we avoided the initial years of warming (when mortality rates increased only to decline again (Sandström *et al.* 1995), and used data from 1987-2003. 2003 corresponds to the year before the populations were no longer reproductively separated, and when the back-calculation parameters potentially changed.

*Statistical Analysis*

The differences in size-at-age, growth, mortality, and size structure between the two areas in the period after the onset of warming and before the removal of the barrier were quantified using hierarchical linear and non-linear regression models fitted in a Bayesian framework. First, we describe each statistical model and then we provide details of model fitting, model diagnostics and comparison.

We fit the von Bertalanffy growth equation (VBGE) describing length as a function of age to evaluate differences in size-at-age and asymptotic size: , where is the length at age (, years), is the asymptotic size, is the Brody coefficient (). We used only age-and-size at catch as the response variables (i.e., not back-calculated length-at-age). This was to have a simpler model and not have to account for parameters varying within individuals as well as cohorts (mean sample size per individual was only ~5). Eight models in total were fitted (with area being dummy-coded), with different combinations of shared and area-specific parameters. We evaluated if models with area-specific parameters led to better fit and quantified the differences in area-specific parameters. The model with all area-specific parameter can be written as:

where we lengths are distributed to account for extreme observations, , and represent the degrees of freedom, mean and the scale parameter. Henceforth, subscripts and are used for the warm and cold area, respectively (except in figure legends where subscripts are spelled out for clarity). and are dummy variables such that and if it is the cold area, and vice versa, and and subscripts indicate area-specific parameters. The multivariate normal distribution in Eq. 3 is the prior for the cohort-varying parameters , ,and (for cohorts …,1997) (note that cohorts extend further back in time than the catch data), with hyper-parameters , , , describing the non-varying population means and a covariance matrix with the between-cohort variation along the diagonal (note we did not model a correlation between the parameters hence off-diagonals are 0). The other seven models include some or all parameters as common parameters, e.g., substituting and with etc. To aid convergence of this non-linear model, we used informative priors chosen after visualizing draws from prior predictive distributions (Wesner & Pomeranz 2021) using probable parameter values (see *Supporting Information)*. We used the same prior distribution for each parameter class for both areas to not give introduce any other sources of differences in parameter estimates between areas. We used the following priors for the VBGE model: , (uniform to facilitate convergence and because it is strictly positive), and . *,* , , , were given a prior.

We also compared how growth scales with *size* (in contrast to length vs age) in the two areas, because length-at-age is by fitting allometric growth models describing how specific growth rate scales with length: , where, the specific growth, is defined as: and is the geometric mean weight: . Here we also used back-calculated length-at-age, meaning multiple observations within individuals. As with the VBGE model, we dummy coded area in order to compare models with different combinations of common and shared parameters. We assumed growth rates were distributed, and the full model can be written as:

We assumed only varied across individuals and cohorts, and compared two models, one with a common and one with an area-specific . We used the following priors, after visual exploration of the prior predictive distribution: , and . , and were all given a prior.

We estimated total mortality by fitting linear models to the natural log of catch (CPUE) as a function of age (catch curve regression), under the assumption that in a closed population, the exponential decline can be described as , where is the population at time , is the initial population size and is the instantaneous mortality rate. This equation can be rewritten as a linear equation: , where is catch-at-age , if catch is assumed proportional to the number of fish (i.e., ). Hence, the negative of the slope of the regression is . To get catch-at-age data, we constructed area-specific age-length keys from the sub-sample of the total catch that was age-determined. Age length-keys describe the age-proportions of each length-category (i.e., a matrix with length category as rows, ages as columns). Age is then estimated for the total catch based on the “probability” of fish in each length-category being a certain age. With fit this model with and without an --interaction, and the former can be written as:

where and are the intercepts for the cold and warm areas, respectively, is the age slope (i.e., -) for the cold area and is the interaction between and . All parameters vary by cohort (for cohort ) and their correlation is set to 0 (Eq. 12). We use the following (vague) priors: and . and were given a prior.

Lastly, we quantified differences in the size-distributions between the areas using size-spectrum slopes. We follow (Edwards *et al.* 2017, 2020) and estimate for each year and area using their likelihood approach for binned data, i.e., the *MLEbin* method in the R package *sizeSpectra* (Edwards 2020). This method explicitly accounts for uncertainty in body masses *within* size-classes (bins) in the data and has been shown to be less biased than regression-based methods or the likelihood method based on bin-midpoints (Edwards *et al.* 2020). We then fit a linear model of the size-spectrum slopes with and (and their interaction) as predictors, after initial exploration revealed clear trends over time. The model with the - interaction for the size-spectrum slopes can be written as:

where the response is assumed to be normally distributed, and represent each areas’ intercept, is the year effect for the cold area and is the difference in slope between the cold and the warm area. We use a prior for the intercepts and , which in this model represent the size-spectrum slopes at the beginning of the time series. is the size-spectrum slope predicted by (Andersen & Beyer 2006) based on individual-level processes under the assumption of size-independent average satiation levels. To include uncertainty around this average we use a large standard deviation. We use a prior for and a prior for and .

All analyses were done using R (R Core Team 2020) version 4.0.2. The packages within the *tidyverse* (Wickham *et al.* 2019) collection were used to processes and visualize data. Models where fit using the R package *brms* (Bürkner 2017)*.* When priors were not chosen based on the prior predictive distributions, we used the default priors from *brms*. We used 3 chains and 4000 iterations in total per chain. Sub-models were compared by evaluating their expected predictive accuracy (expected log pointwise predictive density) using leave-one-out cross-validation (LOO-CV)(Vehtari *et al.* 2017) while ensuring pareto values < 0.7, in the R package *loo* (Vehtari *et al.* 2020)*.* Results of the model comparison can be found in the *Supporting Information*. *bayesplot* (Gabry *et al.* 2019) and *tidybayes* (Kay 2019) were used to process and visualize model diagnostics and posteriors. Model convergence and fit was assessed by ensuring potential scale reduction factors () where <1.1 (suggesting all three chains converged to a common distribution) (Gelman *et al.* 2003), and by visually inspecting trace plots, residuals QQ-plots and with posterior predictive checks (*Supporting Information*).

Code and Data Availability

All data and R code can be downloaded from a GitHub repository (<https://github.com/maxlindmark/warm_life_history>) and will be archived on Zenodo upon publication.

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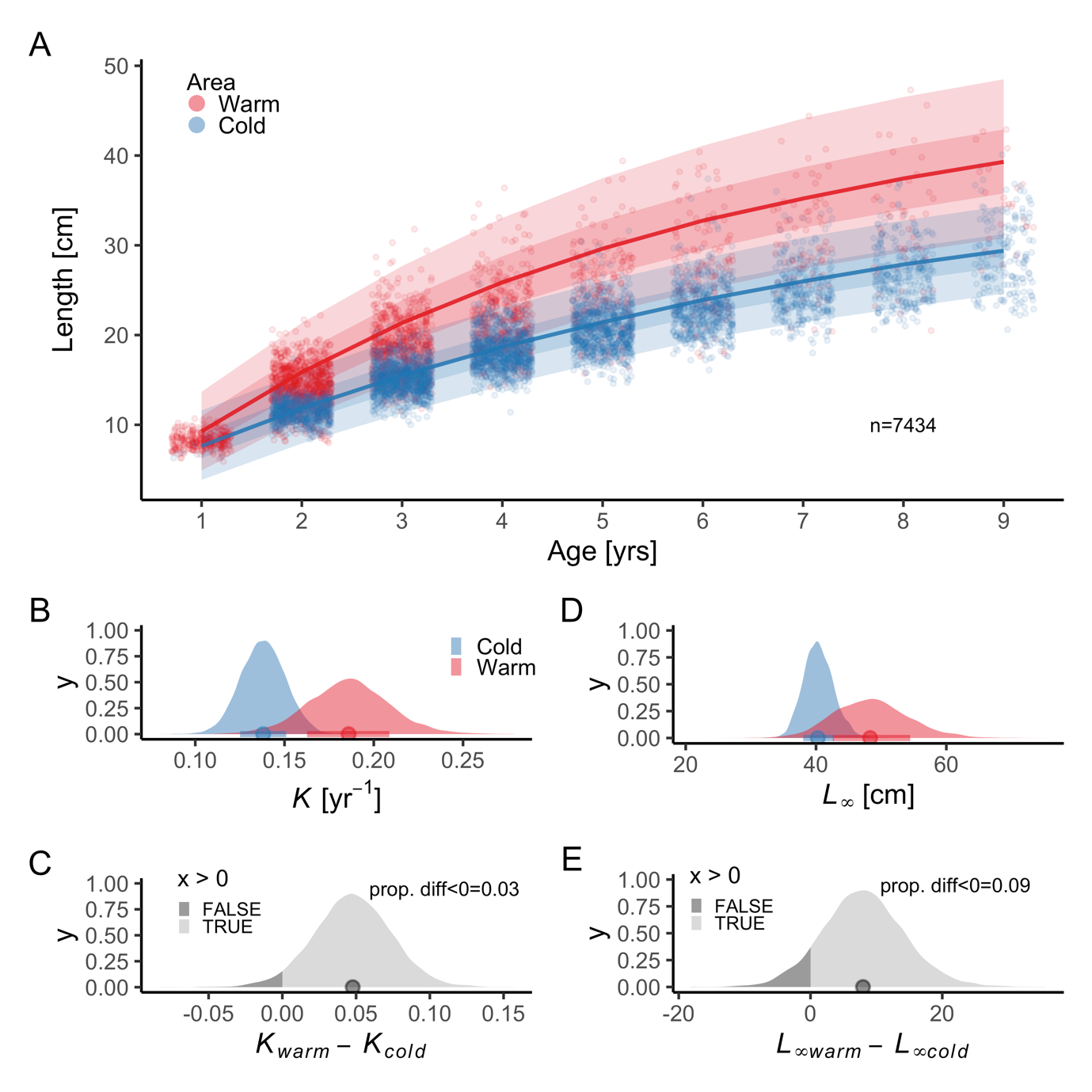
We thank all staff involved in data collection.

Author Contributions

ML conceived the idea and designed the study and the statistical analysis. Data-processing, initial statistical analyses, and initial writing was done by MK and ML. AG contributed critically to all mentioned parts of the paper development. All authors contributed to the manuscript writing and gave final approval for publication.

Tables

Figures



**Fig. 1.** The average length-at-age is larger for all ages in the warm (red) compared to the cold (blue) area. Points in panel (A) depicts individual-level length-at-age and lines show the global posterior prediction without group-level effects (i.e., cohort) from the von Bertalanffy model with area-specific coefficients. The shaded areas correspond to 50% and 90% credible intervals. Panel (B) shows the posterior distributions for parameters and and panel (C) shows the distribution of differences. Panel (D) shows the posterior distributions for parameters and , and panel (E) shows the distribution of differences.

Diagram

Description automatically generated

**Fig. 2.** The faster growth rates in the warm area are maintained as fish grow. The points illustrate specific growth estimated from back-calculated length-at-age (within individuals) as a function of length (expressed as the geometric mean of the length at the start and end of the time interval). Lines show the global posterior prediction without group-level effects (i.e., individual within cohort) from the allometric growth model with area-specific coefficients. The shaded areas correspond to the 90% credible interval. The equation uses mean parameter estimates. Panel (B) shows the posterior distributions for parameters and , and panel (C) shows the distribution of differences. Panel (D) shows the posterior distributions for parameters and , and panel (E) shows the distribution of differences.

Chart

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**Fig. 3.** The instantaneous mortality rate is higher in the warm area. Panel (A) shows the as a function of , where the slope corresponds to the global . Lines show the posterior prediction without group-level effects (i.e., cohort) and the shaded areas correspond to the 50% and 90% credible intervals. The equation uses mean parameter estimates. Panel (B) shows the posterior distributions for parameters and , and panel (C) shows the distribution of differences.

Chart

Description automatically generated

**Fig. 4.** The warm area has a larger proportion of large fish, illustrated both as histograms of proportions and the generally smaller size-spectrum slopes (which also increased over time in both areas). Panel (A) shows mean annual size-spectrum slopes as points and their 95% confidence interval, estimated using maximum likelihood. Lines and shaded areas correspond to the median and 90% credible interval. The equation uses mean parameter estimates. Panel (B) shows the posterior distributions for parameters and (i.e., the intercepts in the model shown in panel (A) of size-spectrum slopes as a function of year), and panel (C) shows the distribution of differences. Panel (D) illustrates histograms of length groups as proportions (for all years pooled).