**Supplementary methods of “*Biological trade-offs underlie coral reef ecosystem functioning*”**

We first assembled a global species list based on an openly accessible database of reef fish abundances and sizes; all data were collected via belt transects on SCUBA1. We then used individual-based bioenergetic models to estimate key fish-mediated functions in each transect. We used a subset of data (see methods) and included 1,110 species that belong to 25 families: Acanthuridae, Balistidae, Bothidae, Chaetodontidae, Cirrhitidae, Fistulariidae, Haemulidae, Holocentridae, Kyphosidae, Labridae, Lethrinidae, Lutjanidae, Monacanthidae, Mugilidae, Mullidae, Ostraciidae, Pempheridae, Pomacanthidae, Pomacentridae, Sciaenidae, Scorpaenidae, Serranidae, Siganidae, Tetraodontidae, Zanclidae. To apply bioenergetic models and estimate fluxes of carbon (C), nitrogen (N), and phosphorus (P) for all species in the database across their entire temperature range, a number of parameters are required (Table 1)2. Here, we describe how these parameters were quantified for all 1,110 species through a combination of primary literature, empirical measures, and Bayesian models.

All protocols related to the capture and handling of fish complied to the ethical standards of the Centre for Island Research and Environmental Observatory (CRIOBE), and the University of California Santa Barbara’s Institutional Animal Care and Use Committee (IACUC #915 2016-2019). Collection and transport of samples were approved by the government of French Polynesia. All analyses were carried out in R v.3.6.3, and Bayesian models were run using Stan3 and the R package *brms*4.

**Table 1.** Overview of input parameters required by *fishflux*, detailed in Schiettekatte et al. (2020)2. VBGC = von Bertalanffy growth curve.

|  |  |  |
| --- | --- | --- |
| Symbol | Description | Unit |
| , , | Element-specific assimilation efficiency | \_ |
|  | Total length of individual at time t | cm |
|  | Asymptotic adult length (VBGC) | cm |
|  | Growth rate parameter (VBGC) |  |
|  | Age at settlement (VBGC) |  |
|  | Parameter length-weight relationship |  |
|  | Parameter length-weight relationship | \_ |
| , , | Element-specific body content percentage of dry mass | % |
|  | Wet body mass | g |
|  | Metabolic normalisation constant independent of body mass |  |
|  | Mass-scaling exponent | \_ |
|  | Activity scope | \_ |
|  | Environmental temperature | C |
|  | Trophic level | \_ |
|  | Aspect ratio of caudal fin | \_ |
|  | Mass-specific turnover rate of N |  |
|  | Mass-specific turnover rate of P |  |
|  | Ratio of dry mass and wet mass of fish | \_ |
| , , | Element-specific diet content percentage of dry mass | % |

### 1. Growth parameters

The bioenergetic model uses the von Bertalanffy growth function to estimate daily growth2. This growth function relies on three parameters: (i.e. the population asymptotic body length of a fish), (i.e. the rate at which a fish in a population, on average, approaches its population asymptotic body size), and (i.e. the theoretical age at which length is zero). For , we used a standardized coefficient that describes the potential growth trajectory of an individual if were equal to its maximum lengthi.e., , 5. For simplicity, we kept constant at 0 for all species.

***1.1 Data compilation***

We first compiled maximum lengths for all species using Fishbase6 and used these lengths for the . Then, we extracted the available data for from Morais & Bellwood (2018), which are estimated using growth curve parameters from Fishbase, standardized to the maximum length.5 We selected the species that occured in our species list and only included the estimates from otolith studies. In total, this selection process resulted in 439 observations of for varying species and temperatures. Furthermore, we used an openly accessible otolith dataset, gathering 669 individuals belonging to 44 species, sampled around five French Polynesian islands7. This dataset includes total length measurements to the nearest millimeter and fish weights to the nearest 0.1 grams. Further, it includes distances between annual growth increments, measured by two independent researchers to prevent biases induced by a single observer. These data were used to estimate growth rate parameters using a two-step approach: back-calculation to achieve individual-level size-at-age data and hierarchical regression to fit the von Bertalanffy growth curve7.

Specifically, we used the Modified Fry back-calculation model (MF)8 to estimate fish lengths at previous ages. We adapted the traditional model to also estimate the uncertainty around the obtained length estimates and allow for the inclusion of missing values using a Bayesian approach. Then, we fitted the von Bertalanffy growth model to all species at each location for which there were at least 3 individuals, using Bayesian hierarchical regression models. Both steps of this procedure were carried out using the developed R package *fishgrowbot*.9 The package also automatically estimates the parameter .

After combining the two datasets, we obtained 496 estimates of for 181 species across varying temperatures.

***1.2 Data analysis and extrapolation***Aside from phylogeny, is mostly determined by body size and temperature5. We therefore fitted a Bayesian phylogenetic regression to predict based on body size, temperature, and phylogeny.

We extracted the phylogenetic position of all species included through the Fish Tree of Life10. We retrieved 100 synthetic stochastically resolved phylogenies where missing taxa were placed according to the highest level of taxonomic resolution using the function *fishtree\_complete\_phylogeny()* in the R package *fishtree*11. For each tree, we then calculated the correlation matrix and averaged each element across 100 matrices to obtain one correlation matrix for the regression model.

We then fitted the Bayesian phylogenetic regression to predict the growth rate parameter of fishes depending on body size, temperature, and phylogeny using the R package *brms*4 :

where represents the natural log-transformed value, is the predicted average, is the standard deviation, is the fixed-effect intercept, is the random-effect coefficient that accounts for the residual intercept variation, based on the relatedness as described by the phylogeny, is the slope for the natural transformed maximum body size, and is the slope for SST. We used uninformative priors and ran the model for 2,000 iterations with a warm-up of 1,000 iteration for 4 chains.

The model fit confirmed a negative relationship of with maximum body size ( = -0.76, 95%CI: -0.96;-0.57 ), and a positive relationship with sea surface temperature ( = 0.02, 95%CI: 0.00;0.05 ). We verified model convergence and fit by checking the posterior predictive plot, inspecting parameter trace plots, and checking the R statistic. The Bayesian R2 of the model was 0.738 (95%CI: 0.702;0.769).

The phylogenetic heritability (equivalent to Pagel’s) was estimated as the proportion of total variance, conditioned on the effects attributable to the phylogeny (i.e., ). This calculation resulted in a phylogenetic signal of 0.74 (95% CI: 0.70;0.77). This means that most of the variation, independent of the effect of body size and SST, is explained by phylogeny.

We extrapolated for all species across the full SST range for species that occur in the database, with SST rounded to the degree (°C), which results in 4,712 unique SST and species combinations. There is currently no streamlined method to make predictions for new species from a phylogenetic regression model. We circumvented this issue by extracting draws of the phylogenetic effect, , for each species included in the model. We subsequently predicted these phylogenetic effects for missing species with the help of the function *phyEstimate* in the R package *picante*12. This function uses phylogenetic ancestral state estimation to infer continuous trait values for new species on a phylogenetic tree by rerooting the tree to the parent edge for the node to be predicted13. We repeated this for all 100 trees and 1,000 draws. For each draw, we averaged the extrapolated values per species for the 100 trees. Then, by combining the predicted phylogenetic effects with the global intercept and slopes for body size and temperatures for each draw, we predicted for each species. We only used one chain in order to keep computational time within reason. Finally, we summarized all predictions per SST per species by taking the mean and standard deviation across the 1000 draws.

Finally, we tested our phylogenetic extrapolation approach by performing a leave-one-out cross validation. Specifically, we conducted the above-described approach 496 times, each time removing one species from the analysis and extrapolating to that species. We then compared the extrapolated values for to the predicted values based on the full model. These values were positively correlated with a correlation coefficient of 0.88.

### 2 Body stoichiometry

***2.1 Data collection***

We collected 1633 individuals of 108 species and 25 families between 2015 and 2017 in Mo’orea14 , the Caribbean15 , and Palmyra (Table 2). Their gut contents were removed and the whole body was freeze-dried and ground to powder with a Precellys homogenizer. Whole body elemental proportions () were measured in the lab using standard methods. Specifically, ground samples were analyzed for %C and %N content using a CHN Carlo-Erba elemental analyzer (NA1500); samples were analyzed for %P using dry oxidation-acid hydrolysis extraction followed by a colorimetric analysis16. Elemental content was calculated based on dry mass.

**Table 2.** Overview number of species and individuals per fish family used for body stoichiometry analysis. For each species, there was a minimum sample size of 4.

|  |  |  |
| --- | --- | --- |
| Family | # Species | # Individuals |
| Acanthuridae | 10 | 188 |
| Balistidae | 5 | 104 |
| Bothidae | 1 | 6 |
| Chaetodontidae | 11 | 129 |
| Cirrhitidae | 1 | 26 |
| Fistulariidae | 1 | 6 |
| Haemulidae | 4 | 54 |
| Holocentridae | 9 | 123 |
| Kyphosidae | 1 | 4 |
| Labridae | 19 | 308 |
| Lethrinidae | 2 | 31 |
| Lutjanidae | 6 | 146 |
| Monacanthidae | 1 | 5 |
| Mugilidae | 1 | 8 |
| Mullidae | 4 | 50 |
| Ostraciidae | 1 | 5 |
| Pempheridae | 1 | 10 |
| Pomacanthidae | 3 | 20 |
| Pomacentridae | 15 | 201 |
| Sciaenidae | 1 | 5 |
| Scorpaenidae | 1 | 12 |
| Serranidae | 4 | 132 |
| Siganidae | 2 | 14 |
| Tetraodontidae | 3 | 41 |
| Zanclidae | 1 | 5 |

***2.2 Data analysis and extrapolation***

The CNP content of organisms is highly conserved within taxa14,15. We therefore used phylogeny to extrapolate these values to species with unknown body stoichiometry. We fitted C, N and P contents (%) through a hierarchical phylogenetic multivariate normal model with phylogenetic effects and random effects per species.

where , and are the % content of , , and , respectively, represents the average % content of element (, , and ) per species, is the covariance matrix of the residual errors of , , and , is the fixed-effect intercept for each element , is the random-effect coefficient that accounts for the intercept variation, based on the relatedness as described by the phylogeny per element , is the random-effect coefficient that accounts for the residual species-level intercept variation per element k.

We used uninformative priors and ran the model for 2,000 iterations with a warm-up of 1,000 iteration using 4 chains (i.e., a total of 4,000 posterior draws). The Bayesian R2 of the model was 0.39 (95%CI: 0.36-0.42), 0.50 (95%CI: 0.48-0.53), and 0.43 (95%CI: 0.40-0.46) for C, N, and P respectively. The phylogenetic heritability was 0.41 (95%CI: 0.28-0.55), 0.58 (95%CI: 0.4-0.66), and 0.57 (95%CI: 0.46-0.69) for C, N, and P, respectively.

We used 1,000 fitted draws for each species, and 100 phylogenetic trees to extrapolate to all species with unknown body stoichiometry, similar to the above methods. Specifically, we used the *phylopars* function from the *Rphylopars* package17. This function uses ancestral state reconstruction and Brownian motion, and takes the correlation among C, N, and P into account.

Finally, we tested the phylogenetic extrapolation approach by performing a leave-one-out cross validation, similar to the methods described in section 1.2. The extrapolated species-level estimates were correlated with the mean species-level estimates from the full model with correlations of 0.61, 0.67, and 0.67 for C, N, and P, respectively.

### 3 Diet

***3.1 Data collection***

We collected 571 adult individuals of 51 species between 2018 and 2019 in Mo’orea, Tetiaroa, and Mangareva, three French Polynesian islands. We extracted the stomach content and stored it in a 2ml tube. After freezing the samples, we dry-froze all samples for at least 24 hours, then we ground them to powder. Samples were sent to the lab for CNP content analysis using similar methods as described above for the fish body stoichiometry.

***3.2 Data analysis and extrapolation***

Using trophic guilds defined by Parravicini et al. (2020)18 , we fitted a multivariate Bayesian regression model to summarize CNP content data per trophic guild with random effects at the species level. This model had a median Bayesian R2 of 0.62, 0.62, and 0.48 for C, N, and P, respectively. Next, we extracted 1,000 draws of the predicted CNP content per trophic guild. Parravicini et al. (2020)18 provides the probabilities of reef fish species to be assigned to each of the eight defined trophic guilds(i.e. sessile invertivores; herbivores, microvores, and detrivores; corallivores; piscivores; microinvertivores; macroinvertivores; crustacivores; planktivores). By combining these probabilities with the predicted CNP contents per trophic guild, we finally estimated the diet CNP content for each species in our database. Essentially, we performed a weighted average of CNP content across diet groups for each species, where the weights represent the probability of being in a certain trophic guild. We then took the average and standard deviation across all 1,000 draws. While we recognize the bias of using diet CNP content estimates of a dataset from a single region, we argue that variability between food categories (e.g. animal versus plant material) is likely higher than regional differences within trophic categorizations. Further, the trophic guild classification includes probabilities that belong to each group, so variation is included when the trophic categorization is not well known. For example, if a species has a 50% probability of being herbivore and a 50% probability of being a sessile invertivore, this uncertainty will be reflected in the estimation of the CNP content of the diet.

### 4 Metabolic parameters

***4.1 Data collection and lab experiments***

To quantify standard metabolic rate (SMR) and maximum metabolic rate (MMR), we carried out intermittent-closed respirometry experiments19,20. Between 2018 and 2019, we collected 1,393 individuals across 61 species and 18 families with a minimum sample size of 3 individuals per species in Mo’orea, French Polynesia. Fishes were captured on SCUBA using hand nets and clove oil and immediately transported to the laboratory in coolers with ambient seawater and oxygen stones. After an acclimatization and a fasting period of 48 h in aquaria, the fishes were individually transferred to a water-filled tub at 28°C (ambient sea water temperature) and manually chased by the experimenter until exhausted21,22. Then, they were placed in respirometry chambers submersed in an ambient and temperature-controlled tank, where they were left for approximately 23 h. The intermittent respirometry cycles started immediately after a fish was placed in its respirometry chamber. The cycles consisted of a measurement (sealed) period followed by a flush period during which the respirometry chambers were flushed with fully aerated water from the ambient tank. Fishes were exhausted immidiately before entering the respirometry chambers, so we measured the approximate MMR. Depending on fish size, 8 respirometry chambers ranging in volume from 0.4 to 4.4 L (including tubes and pumps) were run in parallel, and measurement and flush periods lasted between 3 to 15 min and 3 to 5 min, respectively. SMR was calculated as the average of the 10 % lowest values measured during the entire period, after the removal of outliers (defined as < mean – 2 s.d.)23. MMR was calculated from the slope of the first measurement period.

***4.2 Data analysis and extrapolation***

To retrieve the parameters (Metabolic normalisation constant independent of body mass; ), (mass-scaling exponent), and (factorial activity scope), we fitted a normal Bayesian mixed effects model predicting the log10-transformed metabolic rate using the log10-transformed biomass including random effects of family, species, and metabolic rate type (SMR or MMR) on both the intercept and slopes using *brms*4 :

We ran the model for 4000 iterations, with a warm-up of 2000 iterations, and four chains. Further, we used an informative prior, for the slope (), based on previous work24. The model had a Bayesian R2 of 0.973 (95%CI: 0.972-0.974). We then predicted the family-level by summing the slope of the model with the effects of the family on the slope of the SMR. We did this for all iterations, then we took the mean and standard deviation. Similarly, we extracted the family-level intercept for SMR and MMR, then we quantified mean and standard deviation of after the back-transformation of all iterations of the intercept (i.e., the intercept for SMR).

Finally, we estimated as follows, based on the assumption that, on average, fishes rest 12h a day and they spend the remaining 12 hours at a metabolic rate that is the average of their SMR and MMR:

where all iterations of the back-transformed family-level intercepts were used for SMR and MMR. We then summarized these predictions by taking the mean and standard deviation. We used the family-level estimates of these parameters for all species in our database. We used the average across all families for families that were not represented in our respirometry dataset, (Bothidae, Chaetodontidae, Fistulariidae, Haemulidae, Kyphosidae, Lethrinidae, Lutjanidae, Mugilidae, Ostraciidae, Pempheridae, Sciaenidae, and Siganidae).

The parameter was adjusted for each temperature in the varying locations in the database, following24 :

where is the Boltzmann’s constant (), is the activation energy (0.59 eV, extracted from Barneche et al. (2014)24 ), is the value of the metabolic normalization at a fixed reference temperature (301.15 K), and is the temperature of interest (K).

### 5. Additional parameters

We retrieved the parameters , , , and for each species from Fishbase6. For the mass-specific turnover rates for N and P (; ), we used the estimates provided in Schiettekatte et al. (2020)2.

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