

# Supporting Materials and Methods

**The Food Web Data Set.** Data Set 1 contains the food web with interaction strengths, the list of species, and the list of the 10 species with a higher number of strongly interacting simple trophic chains and omnivory chains as top predators and as species at the base.

**Data: Strengths and Limitations.** We have compiled and analyzed a large quantitative food-web. First, while the bulk of previous studies use food-webs with a number of species ranging from 25 to 94 (only one food web has as much as 181 species), our food web has 249 species. Second, in the previously published food-webs the level of aggregation is really high (nodes of the web correspond to trophic species, not taxonomic species). In contrast, the bulk of species in our food web correspond to taxonomic species (but see below). Third, almost all previously studied food-webs are qualitative, while we present quantitative information. However, our data have still weaknesses which need to be acknowledged to put our conclusions in perspective. There are two potential limitations: the variability in diet and biomass estimates and the unequal level of resolution.

First, calculations of interaction strength are based on estimates of diet preferences, biomass (calculated as the average number of individuals per square meter times their average body mass), and the number of times an age-structured population of predator  $j$  consumes its own weight per day  $(Q/B)_j$ . One has to make some simplifying inferences when estimating body mass and densities. As noted in the main text, body mass is estimated as the average body mass of adults (a well

known amount) multiplied by a correction factor describing the age structure of the population (the average body mass is reduced, assuming that the bulk of individuals are juveniles; see ref. 1 for details). This correction factor is, however, common for all species, and could be improved by considering species-specific age-structure data.

When analyzing stomach contents, the standard deviation of the number of fishes per species is quite high (29.03). Fifty-four species are represented by 10 or less individuals. Variability of estimates for these species has to be considered high, and future studies should focus on these less represented species. Two species of Carcharhinidae (*Galleocerdo cuvier* and *Negaprion brevirostris*) are represented by only two individuals, and Opitz (1) complements this information based on accounts in ref. 2.

Despite the limitations of diet data, they stand as the best resolved studies for fish feeding habits in the Caribbean, and for some species “may be regarded as definitive expression of their food habits” (3). Randall’s study (3) is extremely detailed, which helps in reducing the weakness of this approach. Specifically, it addresses the fact that some species may feed in different habitats. As an example, one can read on page 671 of ref. 3:

Many species of reef fishes occur in diverse habitats, and their food habits may differ profoundly from area to area ... For this reason an effort was made in the present study to collect in all environments in the Virgin Islands and Puerto Rico in which the fishes were encountered.

Randall’s study also overcomes the possible diet bias when studying intestine contents:

One source of error ... is the result of the varying rate of digestion of the different food organisms... The inevitable result is a bias in the data towards the less digestible organisms. Such a bias is greater if working with intestinal contents than with stomach contents; for this reason, only stomach-content analysis were made except for a few fishes such as the diodontids and *Lachnolaimus maximus* which feed almost exclusively on invertebrates with shells or exoskeletons (3, pp 671).

But variability is, probably, still high. This variability may affect the calculations of interaction strength, but it is quite unlikely that is the responsible for the seven orders of magnitude of observed variability. Data errors are likely going to represent white, unbiased noise, with a variance increasingly reduced because of the aggregate nature of these measures. Before most detailed data is available, the results have to be look in the perspective of these weaknesses, but we do not expect this variability is going to bias in any qualitative way the results shown in the paper. Future work should look at smaller sets of species with higher levels of resolution.

In relation to the temporal resolution, data on food habits were collected throughout the whole period of study by Randall (from July 1961 to October 1965), which tends to reduce any possible bias due to seasonal variation in food habits (3). As noted by Randal, tropical marine fishes would not be expected to show significant variation in their diet with season, although some variation may be expected from local fluctuations in the abundance of preys. He also noted that marked changes may be expected for most fishes as they grow to adults, and that most data from his study was obtained for adult individuals.

Second, the level of resolution is not homogeneous through all ecological groups. Fishes are resolved at the species level, but other species are still highly aggregated: zooplankton, microfauna, sponges, stonycorals, octopuses, echiuroids, amphipods, tanaids, isopods, shrimps, spiny lobster, scyllarid lobsters, hermit crabs, crabs, and echinoids. To what extent results may be affected by this biased level of resolution? This is a difficult question to answer (4, 5), and future studies are needed to be able to understand how aggregation may affect results on food webs. In our case, the aggregated groups are basal species in 56% of the strongly interacting tritrophic chains (intermediate species in 20.5%, and top species in 1%), but they are basal species in only 23% of the strong omnivory chains (intermediate species in 10%, and top species in 1%).

**Derivation of the Measure of per Capita Interaction Strength.** This supporting information describes the derivation of the measure of per capita interaction strength used in the paper. Pauly (6) defined  $(Q/B)_j$  as the number of times an age-structured population of species  $j$  consumes its own biomass per day.  $B_j$  is the biomass of this age-structured population, calculated as the average number of individuals per square meter times their average body mass (see refs. 1 and 3 for details). The product of the above two terms  $((Q/B)_j \times B_j)$  defines the biomass that an age-structured population would require per day to persist.  $DC_{ij}$  is the percentage in volume of prey  $i$  in the diet of predator  $j$  (3). The product of the previous three terms  $((Q/B)_j \times B_j \times DC_{ij})$  is thus the biomass of prey  $i$  consumed daily by an age-structured population of species  $j$ . To make this last expression per capita, we divide by the biomass of predator:

$$\frac{(Q/B)_j \times B_j \times DC_{ij}}{B_j} = (Q/B)_j \times DC_{ij}$$

Dividing the last expression by prey biomass  $B_i$  we obtained our measure of per capita interaction strength, as the proportion of prey population consumed daily by a predator biomass unit:

$$\frac{(Q/B)_j \times DC_{ij}}{B_i}$$

Unifying structural and dynamic (theoretical) measures of interaction strength and using biologically realistic parameter values is still an open problem. Acknowledging the similarities and differences in different measures will provide a way to bridge between independent ways to understand the relationship between structure and dynamics in food-webs.

**Food Web Model: Parameter Fit and Robustness.** Here we provide additional information on the parameter fit of the food-web model described in the paper (see *Materials and Methods*; 7-9) and assess the robustness of the dynamic results presented in the paper by exploring other biologically realistic parameter combinations. The average body mass ratio between basal and intermediate species ( $R : C$ ) was 0.135, a value obtained by averaging the body mass of basal and intermediate species present in all the food chains in the food-web. Specifically, the median body mass was 10 g. and 188 g. for basal and intermediate species, respectively. The average body mass ratio between consumers and predators ( $C : P$ ) was 0.06, with a body mass' median for top predators of 27090 g. The most frequent top predators were ten species of sharks of the Carcharhinidae and Sphyrnidae fam-

ilies, which are included in 48% of all the strongly interacting tritrophic food chains and 80% of all strongly interacting tritrophic food chains with strong omnivory (see species names in Dataset). The average body mass ratio between resources and predators ( $R : P$ ) is 0.009.

The mass-specific metabolic rate  $X_{ij}$  was estimated using the above body mass ratios following the equation (9):

$$X_{ij} = \frac{a_T}{a_i f_i} \left( \frac{M_i}{M_j} \right)^{0.25}$$

where  $M_i$  and  $M_j$  are the average body mass of prey and predator, respectively.  $a_T$  is the respiration rate, set in this case for ectothermic vertebrates to  $2.30 \text{ kg (kg yr)}^{-1} \text{ kg}^{0.25}$  (10).  $a_i$  is the maximum possible production-to-biomass ratio for ectothermic vertebrates (9) and is equal to  $a_i = a_J - a_T$ , where  $a_J$  is the maximal ingestion rate of ectothermic vertebrates or the limit to the amount of energy that can be consumed, processed, and converted into either production or respiration and is equal to  $8.9 \text{ kg(kg yr)}^{-1} \text{ kg}^{0.25}$ . Therefore,  $a_i = 6.6 \text{ kg (kg yr)}^{-1} \text{ kg}^{0.25}$  in ectothermic vertebrates (9).  $f_i$  is the fraction of total time allocated to absorbing and processing food. For example,  $f_i = 1$  means that there are no interferences in metabolizing food, and so that physiology limits the capacity of the population to metabolize food. Running away from predators, for example, would decrease  $f_i$ . In here,  $f_i$  has been set to 0.7, a conservative value for resources and consumers (9, 11). Using the above values,  $X_{RC} = 0.27$ ,  $X_{CP} = 0.21$  and  $X_{RP} = 0.15$ .

Similarly,  $Y_i$  ( $i = C, P$ ) has been estimated using the equation by Yodzis and Innes (9):

$$Y_i = \frac{f_J a_J}{a_T},$$

where  $f_J$  is defined as  $f_i$  and is set to 1, that is, physiology and no other ecological factors limit the capacity of population  $i$  to metabolize food.  $a_J$  and  $a_T$  are as defined above.  $Y_i = 3.87$  with values defined above.

Here we explore three possible functional responses: Holling type II ( $n = 1$ ,  $c_i = 0$ , Fig. 4a), Holling type III ( $n = 2$ ,  $c_i = 0$ , Fig. 4b), and predation interference ( $n = 1$ ,  $c_i > 0$ , specifically  $c_C = 0.005$  and  $c_P = 0.35$ , Fig. 4c). For each functional response, we compare the magnitude of the trophic cascade as top predators are fished for strong tri-trophic food chains (continuous line) and strong omnivory chains (broken line). Four values are explored for each module and each functional response, illustrating a range of strong interaction strength values. Each combination corresponds to a line in Fig. SI and is obtained by combining the following parameter values:  $Y_i = Y_C = Y_P$  is either 3.7 or 3.9;  $X_{CP} = X_{RP}$  is either 0.1 or 0.2. Other parameter values are  $X_{RC} = 0.2$ ,  $X_{AC} = X_{AP} = 0.05$ ,  $r = 1$ ,  $K = 1$ ,  $R_o$ ,  $R_{o2}$ , and  $C_o = 0.75$ .

The magnitude of the trophic cascade (measured as the resource log ratio) is always greater for strongly interacting tritrophic food chains without omnivory (continuous line) with the exception of predation interference (Fig. 4c). Thus, the results presented in Fig. 3 are robust to changes in interaction strength values and functional responses with a single exception.

Little is known about the specific functional response for the bulk of species in this community. In the face of this lack of data, we have decided to explore a wide range

of possibilities (type II, type III and predator interference functional responses). Our results stand for two out of three such possibilities. Top predators in this system show low abundances, and on this basis one could suggest that predator interference does not probably play an important role.

Allochthonous inputs  $A$  capture the fact that resources and consumers feed on other species. Thus, our modules are not completely isolated from the food-web. Assuming these inputs come from a large number of species whose fluctuations are asynchronous and cancel out, it is reasonable to describe them as a fixed amount  $A$ . It would be very convenient to extend this modeling exercise by considering larger trophic modules. However, a modeling approach using much more species is complicated. As reviewed in ref. 12, “most published dynamic food web models were limited to relatively few species... Persistent dynamics for systems beyond six species are difficult to generate without using biologically unrealistic species and interaction parameter values.” These problems should be sorted out in order to make progress in this direction.



## References

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