Title: Predator-prey interactions are determined by body size and predator hunting traits in diet DNA metabarcoding data of terrestrial invertebrates

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ProcB: 6 MS pages, ~4200 words + 3 figures from abstract to end of literature cited.

**Abstract (max 200 words)**

Predator-prey interactions are shaped by a combination of predator traits, including body size and hunting strategy. However, applying a traits-based approach is challenging for most invertebrate taxa because predator-prey interactions are difficult or impossible to observe directly with traditional approaches. In this study, we combined diet DNA metabarcoding data of 182 individual invertebrate predators from nine species with community body size data to explore how predator traits shape interactions. Using a total of 335 individual predator-prey interactions, we found that 1) prey size scales with predator size, with species-specific variation to a general size scaling relationship and 2) predator individuals of species that use webs to catch or subdue prey (Arachnida: Araneae) consume larger prey proportional to individual predator body size than do predator individuals that do not use webs. Web use was a stronger predictor of this pattern than other hunting traits, including venom use and active versus sit-and-wait hunting modes. Our findings indicate that predator-prey traits are important in shaping trophic interactions in invertebrate food webs and could help predict how anthropogenic biodiversity change will influence terrestrial invertebrates, the earth’s most diverse and biomass-dominant taxonomic group.

**Keywords (3-6 words)**

Food web, arthropod, allometry, spider, insect, functional role, consumptive

**Introduction**

Predator-prey interactions shape the structure and function of ecosystems and their responses to external influences, including anthropogenic global change (McCann 2000, Brodie et al. 2014). Traditionally, predator-prey interactions have been approached from a species-specific framework; specifically, species identity or phylogenetic relatedness shapes feeding interactions (Ings et al. 2009). However, more generalizable predictions of feeding interactions can be made using non-specific traits. Body size, for example, is a key trait that determines feeding interactions between predators and prey across ecosystems (Woodward et al. 2005). Because body size is integral to feeding interactions, both dictating the rate and range of prey a predator can consume, it is one of the primary approaches for predicting the structure of feeding interactions for biological communities, or food webs (Stouffer et al. 2005, Woodward et al. 2005, Gravel et al. 2013, Nakazawa 2017). While body size alone predicts general patterns across food webs in multiple contexts, combining body size with more species-specific characteristics, including species identity, and more broadly, species traits such as locomotion or metabolic group creates food web models that look even more similar to empirically-observed patterns (e.g. Rudolf et al. 2014, Gray et al. 2015, Brose et al. 2019, Pomeranz et al. 2019). Using general traits to describe food web patterns across ecosystems is not only important for the development of generalizable rules describing patterns in biological communities but could also be integral to predicting and mitigating species extinctions given the rate of anthropogenic species loss (Valiente-Banuet et al. 2015).

While a few general rules sometimes predict patterns in empirical food webs (e.g. Gravel et al. 2013), for some predators, in particular small-bodied invertebrate predators for which empirical diet methods (e.g. gut dissections) are impossible or often unfeasible (Sheppard and Harwood 2005, McLaughlin et al. 2010), we have a dearth of observed interaction data from these species in their natural environments with which to validate extrapolated approaches to predicting interactions based on general rules. For these consumers, species interactions are often inferred from literature reports of observed interactions from phylogenetically-related species (e.g. (Simberloff and Wilson 1969, Piechnik et al. 2008, Laigle et al. 2018), based on body size feeding constraints (e.g. Digel et al. 2014, Laigle et al. 2018, Hines et al. 2019), derived from mesocosms or feeding trials which include only pre-defined predator-prey identity pairs (e.g. Rall et al. 2011, Digel et al. 2014, Rudolf et al. 2014). Thus, because these interactions are not empirically observed in natural environments, we do not know whether general patterns that emerge for these interactions are real ecological patterns or artefacts of the rule-based diet assignment methods used to compile them. The lack of empirical interaction data for small-bodied invertebrate taxa is not inconsequential; these taxa represent over 50% of the earth’s animal biomass and a majority of animal species diversity (Mora et al. 2011, Costello et al. 2013, Bar-On et al. 2018, Stork 2018).

In this study, we employ novel diet DNA metabarcoding data from 182 samples of nine terrestrial invertebrate predator species to document predator-prey interactions between these predators and their prey in natural field conditions. We combined these data, which included 335 unique predator-prey interactions, with an extensive dataset of body sizes for both predator individuals and the prey groups identified in their diets. To understand how predator size, species identity, and hunting traits may drive empirical predator-prey interactions, we asked: 1) do larger predator individuals eat larger prey and does this vary by predator species identity? and 2) do predator species traits related to hunting strategy, including whether predators are active or non-active (sit-and-wait), and whether predators use venom or webs to subdue prey, explain variations in prey size selection?

**Methods:**

*Field site and collections*

We conducted this work on Palmyra Atoll National Wildlife Refuge, Northern Line Islands (5º53’ N, 162º05’W). Palmyra Atoll has a well-characterized species list, and like many atolls, is relatively species poor, allowing for detailed characterization of potential diet items (Handler et al. 2007). Predator individuals were collected across habitat types, including different forest types and microhabitats (e.g. understory vegetation, canopy vegetation, and soil habitats). For each of these habitat types, we used a combination of methods, including individual collection during visual surveys for understory and soil collections and canopy fogging with insecticide onto collection sheets for canopy individuals. All individuals were collected individually with sterilized implements (ethanol-burned forceps) in sterilized collection containers containing 95% EtOH to avoid contamination (Greenstone et al., 2011, Miller-ter Kuile et al. *in revision*). All individuals were stored in 95% EtOH at -20ºC before DNA extraction.

We identified all predators to morphospecies using a species list for Palmrya Atoll (Handler et al. 2007, McLaughlin et al. *unpublished data*) and later validated unique species by DNA metabarcoding sequence data. The predators sampled represent the most common predator species found in each habitat location and span a body size range of 0.2 – 928 mg (wet mass, Figure 1, SI Table 1). These predators included five arachnid species (Oonopidaesp., *Neoscona theisi*, *Heteropoda venatoria*, *Smeringopus pallidus*, and *Scytodes longipes*), one dragonfly (*Pantala flavescens*), one predatory katydid (*Phisis holdhausi*), one earwig (*Euborellia annulipes*), and one soil-dwelling centipede species (Geophilomorphasp.). These predators employ various hunting tools, including webs, venom, and grasping forearms and employ several different hunting strategies, including active hunting and non-active hunting (e.g. sit-and-wait or ambush, Supplementary Table 3).

*DNA extraction, PCR amplification, library preparation, sequencing, and denoising*

Our full DNA extraction, PCR amplification, library preparation, sequencing, and denoising methods can be found in the Supplementary Information, though we provide an abridged version here.

To determine the identity of DNA in predator diets, we extracted and sequenced DNA from samples consisting of one or several predator individuals using high throughput sequencing methods. Multiple predator individuals were combined due to small body size (thus, inability to extract ample DNA) based on shared size (mean size difference ± 0.5 mm), species, and sampling period (70%, or 128/181 samples consisted of one predator individual, 53/181 of two or more individuals, Supplementary Methods and Figures 7 & 8). We extracted DNA from predator samples using a modified CTAB protocol and following methods outlined in Krehenwinkel et al. (2017). We amplified the CO1 gene with general metazoan primers (mlCOIintf/Fol-degen-rev; Yu et al. 2012, Leray et al. 2013, Krehenwinkel et al. 2017) and sequenced samples on the Illumina MiSeq platform with 250 paired-end reads. We merged, filtered, and denoised our sequences to amplicon sequence variants (ASVs) using the DADA2 package in R (v1.1.14.0; Callahan et al., 2016, SI Figures 3 & 4). We removed samples from analysis with incomplete sequencing depth using interpolation and extrapolation methods (Hsieh and Chao 2017) and then rarefied all sequencing depths to the lowest sequencing depth of remaining samples (15, 954 reads). We performed these steps in R (version 4.0.2) with the iNEXT (version 2.0.20, Hsieh et al. 2016) and vegan (version 2.5.6) packages.

*ASV taxonomic assignment*

To determine the identity of the sequenced DNA, we compared sequencing data to the GenBank and BOLD taxonomic. GenBank searches were run using the computing cluster at UC Santa Barbara. We chose to combine prey taxonomies at the family level, similar to diet resolution in both metabarcoding and histological methods in this field (e.g. Kartzinel et al. 2015, Brose et al. 2019, Eitzinger et al. 2019) summing the cumulative rarefied read abundances across the ASVs that corresponded to each diet family in each sample. Family-level data provides information comparable to previous studies, additionally, on Palmyra, each family corresponds to an average of 1.9 (± 0.13 SE) species, so a family-level taxonomic assignment may closely mirror species-level assignments. All DNA matching any predator family present on an individual sequencing run was removed as a conservative method to account for potential sequence jumping (van der Valk et al. 2020). We verified ASV specificity based on positive and negative control samples (Supplementary Table 7 & Figure 9)

*Predator and prey size determination*

We measured the length of each predator individual prior to DNA extraction. We converted predator lengths to wet mass using mass-length scaling relationships for each predator species from existing datasets (Yaninek and Gnanvossou 1993, Sohlström et al. 2018, Su et al. 2020, Miller-ter Kuile *unpublished data*, McLaughlin et al. *unpublished data*). Prey masses were taken as the average mass for individuals across species within each family (Supplementary Figure 12).

*Data analyses*

To determine 1) whether individual predator size, species, or both predicted prey size, we fit a linear mixed effects model with the response variable of log10 prey mass (in mg) and predictor variables of log10 predator mass (in mg), species identity, and their interaction, with a random effect of predator individual. Second, to explore 2) whether predator hunting traits may influence predator-prey size ratios, we divided predators based on whether or not the predator species was an active versus non-active (e.g. sit-and-wait) hunter (e.g. Schmitz 2008), uses webs to either capture or subdue prey (n = 5 predator species, 101 individuals that build webs; n = 4 predator species, 81 individuals that do not build webs), or uses venom to subdue prey. We determined the ratio of predator to prey size for each of these interactions (raw predator mass/prey mass) and then built a set of linear mixed models of this ratio (log transformed for data normality) as the response variable, and each type of predator trait as a predictor variable (one model with web-building, venom use, and active versus non-active hunting). In each of these models, predator individual and predator species identity were random effects. We took this approach to avoid trait effect levels that were not completely independent: specifically, all the non-active hunting species used webs, though some active hunters used webs as well.

*Statistical model selection*

For the linear mixed effects models examining how predator size and species identity shape prey size, we performed model selection using the dredge() function in the MuMIn package in R (package version 1.43.17, Barton 2020) to compare nested models (n = 5 models) and chose the model with the lowest AICc value. To compare the three predator trait models, we performed model selection by comparing AICc values for just those three models along with a null model with no predictor variables. For all models, we verified model assumptions for best-fitting models using the DHARMa package in R (version 0.3.3.0, Hartig 2020). For the CCA analysis, we extracted the marginal significance of each predictor in the full model, refit the model removing the least significant (at p-value > 0.05) variables and chose the best fitting model comparing both the full and reduced models with the anova() function in R. The color palette in our figures is from the calecopal package (version 0.1.0, Bui et al. 2020).

**Results**

*DNA extraction, PCR amplification, library preparation, sequencing, denoising, and ASV taxonomy*

Complete results and QC for each step of the DNA sequencing protocol can be found in the Supplementary Information.

Our final analyses were performed on a total of 182 predator samples of nine species. Each predator sample contained 1 – 7 (average 1.86 ± 1.21 SD) prey families. Thirty percent (n = 524 of 1,738 total ASVs) of the total ASVs found in samples received taxonomic assignments from GenBank and BOLD corresponding to prey items at the family level or lower (n = 75 prey families; SI Table 4, SI Figures 11 & 12).

*Statistical results*

The best performing model predicting prey size included the terms of predator mass and predator species identity, but not their interaction (log10(prey mass) = 0.34\*log10(predator mass), with significant variation in by-species intercepts, Figure 2, SI Table 7). Lastly, the predator trait model that most explained variation in predator-prey size ratio was the model that included web-use as a predictor (p-value = 0.05, β = 1.25, Figure 3, SI Table 8). Predator individuals from species that use webs either to capture or subdue prey (five arachnid species) had significantly smaller predator:prey size ratios than predators without web-use traits (median ratios of predator to prey size of 9.71 for non web-builders versus 2.57 for web-builders, with larger numbers corresponding to larger predator in relation to prey).

**Discussion**

For terrestrial invertebrate predators like the ones in our study, comprehensive field-based diet analyses have been nearly impossible or time-prohibitive without genetic methods (e.g. Polis 1991, McLaughlin et al. 2010), so our data provide important empirical examination of food web patterns for these consumers. We found that predator size, species identity, and hunting traits are important drivers of prey size selection and resulting food web patterns. Specifically, 1) we found that larger predator individuals do eat larger prey, however, individuals of some predator species eat proportionally smaller or larger prey than would be expected by one general cross-species relationship. Then, 2) we demonstrate that more general species traits, in particular, the hunting strategy of web use, whether in capturing or subduing prey, enables some predator species to eat proportionally larger prey items. These results highlight that many food web patterns in small, terrestrial invertebrate predator-prey interactions may be explained by a combination of species traits and that not one predator attribute alone predicts all interactions (e.g. approach in Pomeranz et al. 2019).

Our results strengthen the need for combining multiple predator traits, including body size, species identity, or hunting traits for explaining and predicting food web patterns (Raffaelli 2007, Rall et al. 2011, Rudolf et al. 2014). In our results, samples from predator species that may be more limited in diet based on prey that can fit in their mouths (“gape-limited”, e.g. *Pantala flavescens* and *Geophilomorpha* sp.) have smaller prey items on average compared to those of similar or even smaller size that instead use “tools” such as webs (e.g. Oonopidae sp). While both sets of feeding interactions are still constrained by predator and prey size, these constraints vary depending on predator identity, or, more broadly, predator traits related to gape limitation. While these traits (body size and gape limitation) may vary across individuals within a species over its lifespan, our dataset demonstrates that some traits that limit prey size selection, specifically, web use, are conserved across life stages and phylogenetically similar species, lending credence to phylogenetic approaches to inferring feeding interactions (e.g. Gray et al. 2015).

These traits related to predator hunting strategies, such as web and venom use, have already gained attention as important drivers of interactions in invertebrate food webs (Schmitz 2008, 2009, Laigle et al. 2018) and are often a primary way in which interactions are inferred (e.g. Digel et al. 2014, Hines et al. 2019). In our dataset, the fact that individual species deviated from a general predator-prey body size scaling relationship and that hunting tools seem to be one mechanism for relaxing prey size selection constraints, suggest that the relationship between predator and prey size in a given community may be the result of the community average of these traits along with predator hunting traits (e.g. community weighted trait means, Garnier et al. 2004). Our dataset also highlights how empirical field data is key to understanding which traits may matter for constraining feeding interactions. Specifically, predators that use venom, such as centipedes, which are thought to relax prey size constraints (e.g. Digel et al. 2014), fed on only relatively small-bodied prey in our dataset (mean predator-prey mass ratio 247 ± 61:1), and a presumed predatory earwig that uses neither venom or webs fed on relatively large prey (mean ± standard error of predator-prey mass ratio 4.35 ± 1.99:1), either suggesting some other predator trait or reliance on scavenging (Wilson and Wolkovich 2011).

Diet DNA metabarcoding will continue to be an important tool in understanding the biology of small-bodied invertebrate consumers because it allows us to examine invertebrate diets at the individual level, the same resolution as that of the diets of larger-bodied species (Hyslop 1980, Duffy and Jackson 1986, Baker et al. 2014). As databases of DNA sequences continue to grow (Porter and Hajibabaei 2018), these analyses will likely get more specific, potentially surpassing the resolution of other methods (e.g. McElroy et al. 2020). For example, rather than being confined to family-level taxonomic assignments, future studies, or re-evaluations of past data could reveal more specific patterns than those that restrict prey identification to coarser taxonomic levels. While individual body size data had high resolution for the predators included, we are still limited in knowing the abundance of prey items consumed by these predators because read abundance may not accurately correspond to prey biomass (Elbrecht and Leese 2015, Elbrecht et al. 2017). Combining these field-based empirical observations with future experimental feeding trials could help to constrain prey sizes. Combining multiple genetic methods, such as RNA sequencing, could also highlight the hidden and potentially common interaction between predators and scavenged food sources (Nielsen et al. 2018).

Small-bodied invertebrate predators are the most diverse and abundant predators on earth (Mora et al. 2011, Costello et al. 2013, Bar-On et al. 2018) and until now, the predation interactions of these consumers in the wild have been largely unknown. Like other predators in multiple other ecosystem contexts (Brose et al. 2019), the predation interactions of small-bodied predators are driven by a combination of measurable and generalizable traits, including body size and hunting strategy. Using empirical datasets, such as those built by diet DNA metabarcoding data, will be key to determining which traits shape and mediate species interactions. Not only will this build a deeper understanding of the generality of feeding interactions and food webs across environmental contexts and consumer groups, but could be key to predicting and mitigating ongoing biodiversity loss (Borrvall and Ebenman 2006, Valiente-Banuet et al. 2015, Donohue et al. 2017).

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**Figures**

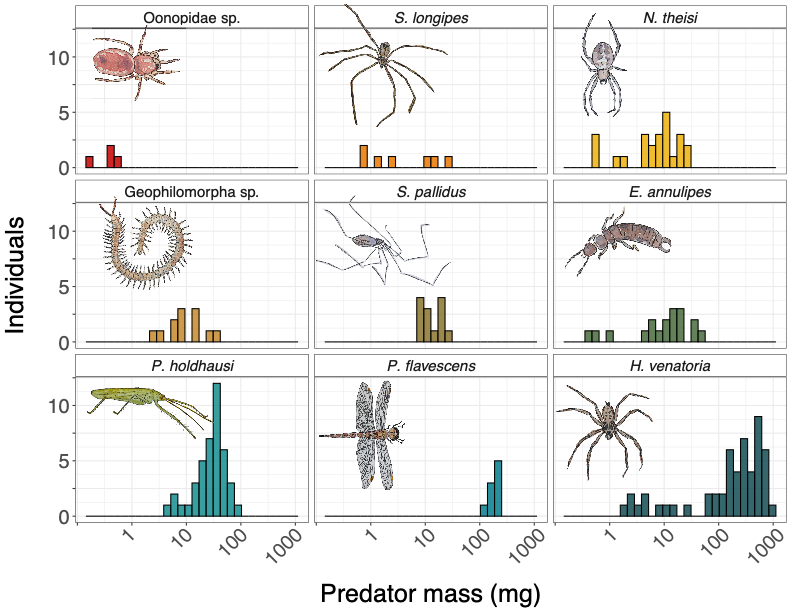
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Figure 1: Predator size distributions across the nine predator species. The x-axis scale depicts absolute values but has been log10 transformed. Predator individuals span from 2x10-1 to 9.3x102 mg in wet weight and the facets in this figure have been ordered by increasing predator species mean size.



Figure 2: Larger predators eat larger prey based on a log10-log10 transformed relationship (panel (a), log10 prey size = 0.34\*log10 predator size), though the effect is mediated by species identity (b). Continuous axis labels represent absolute values but the scale between them has been log10 transformed. In panel (b), “+” and “-“ icons indicate species that either have higher (“+”) or lower (“-“) prey sizes relative to predator body size and the general predator-prey body size patterns. The dashed line in panel (a) represents the 1:1 relationship between predator and prey size.



Figure 3: Web-using traits increase the relative size of prey compared to predators (smaller ratios mean larger prey relative to predator size). Predators with web-using traits can relax gape limitation to access larger prey (p-value = 0.05, β = 1.25). The y-axis is presented with absolute values but displayed on a log10-transformed scale to demonstrate the spread in the data. The dashed line indicates the 1:1 ratio where predators and prey are the same size; any interaction below this line indicates prey items that are larger than predators.