**Working Title:**

**Effects of environmental contamination on diet metabarcoding data of invertebrate consumers in mesocosms and natural environments**

**Target Journal: *Molecular Ecology Resources (8000 words excluding references, unclear if this means including components after references)***

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**Abstract ( ≤ 250 words)**

Background: Consumptive interactions shape ecosystems and DNA metabarcoding is an emerging tool to explore interactions in new environments and consumer groups.

In many of these contexts, the small body size of consumers requires DNA extraction from full body parts, and so surface contamination could alter diet measures.

Methods: We look at different measures of diet (consumption frequency, abundance, diversity, and composition) in two different environments (mesocosm = offered a known diet item; natural = allowed to feed on naturally-occurring diet items) with a group of invertebrate consumers. We surface sterilized half of the consumers using washes in 10% commercial bleach solution followed by deionized water, leaving the other half unsterilized. We examine how surface contamination may alter measures of diet and whether environmental context may matter for these outcomes.

Results: We found that surface contaminants do not alter any measure of diet (consumption, abundance, diversity, or composition) for consumers collected in a natural environment. In a mesocosm environment, we saw evidence that potential surface contaminants from the offered diet item inflated estimates of consumption, though the statistical results were marginally significant (p-value = 0.07, 50% to 91% detection).

Conclusion: Surface contamination does not seem to be a pervasive challenge for DNA metabarcoding of full body parts of invertebrate consumers. However, our equivocal results by environment type suggest that considering and mitigating (through surface sterilization) environmental conditions that increase the likelihood of surface contamination should be a first step in any diet DNA metabarcoding study of invertebrate consumers.

**Introduction**

Biological communities and ecosystem function are shaped by the interactions between organisms (Brown et al. 2001, Hooper et al. 2005, Delmas et al. 2019, Schleuning et al. 2015). Among the many interaction types (e.g. mutualism, consumption, competition), consumptive interactions (including herbivory, predation, and parasitism) can shape the stability of biologically diverse communities (Ings et al. 2009, Delmas et al. 2019). Until recently, these consumptive interactions could only be measured by visual observations of feeding or by dissection or inspection of fecal contents. (Hylsop 1980, Nielson et al. 2018, Baker et al. 2014, Duffy and Jackson 1986). However, this dependence on visual identification or observations is unfeasible or impossible for many consumer groups. Specifically, for consumers that are too small for dissection and food identification, have feeding habits which render food items unidentifiable, have food items that contain few components which pass through digestion in recognizable form, or have cryptic habits that prevent them from being observed in large enough numbers for diet analyses, to name a few (Sheppard and Harwood 2005). For these applications, the use of high-throughput sequencing methods for determining gut contents is one of the most promising approaches. High-throughput sequencing (or DNA metabarcoding) can identify a suite of diet species at once and provides a comprehensive and efficient method for determining intraspecific, intra-population, and interspecific diets (Pompanon et al. 2012, Lucas et al. 2018, Soininen et al. 2015, Quemere et al. 2013). These methods have already illuminated interesting new interactions and ecological trends in a variety of environments (e.g. host-parasitoid: Wirta et al. 2014; plant-herbivore: Kartzinel; host-parasite: Schnell et al. 2012, predator-prey: Toju et al. 2018).

As diet DNA metabarcoding methods have continued to advance, however, they need to be validated so that the ecological inference made from them is robust. Specifically, for organisms where small body size has limited other diet analysis methods, DNA diet analyses often necessitate the extraction of diet data from full organisms or body parts without dissection, and so the possibility of surface contamination altering the detection and species composition of presumed diet items is an important consideration. Surface sterilization is systematically used in other fields to reduce the risk of contamination in DNA metabarcoding datasets (e.g. fungal endophyte research; Zimmerman and Vitousek 2012, Burgdorf et al. 2014), but has not been systematically used in diet metabarcoding studies. While some fields have developed informed protocols based on decades of research into best practices and study-specific considerations (e.g. physical treatments such as sonication for strong tissues or chemical treatments that vary in strength depending on the permeability of tissues; Brown et al. 2018, Hallman et al. 1997), due to its relative infancy, the field of diet-based DNA metabarcoding has not developed a similarly systematic approach (e.g. ethanol washes in Doña et al. 2019, bleach washes in Anslan et al. 2016, no sterilization in Wirta et al. or Jacobsen et al. 2018). The lack of systemic surface sterilization in diet metabarcoding when using full individuals may be due to the desire to avoid destruction of DNA in relatively permeable animal cells (compared to plant cells; eg. degradation in Greenstone et al. 2012). However, without considering surface sterilization as a treatment for surface contamination, we have limited ability to confidently assign DNA sequences to ingested diet items and to help discern broad and study-specific approaches to reducing surface contamination effects (e.g. likelihood of contamination or sensitivity of different consumer species to sterilization-induced degradation; Greenstone et al. 2011/12, Linville et al. 2002).

In addition to the open question of whether surface sterilization should be common practice in diet DNA metabarcoding, it is important to consider how different environmental, ecological, and methodological factors may contribute to the importance of whether to surface sterilize consumers prior to DNA metabarcoding. In more closed environments, DNA can persist in the environment for months to years, increasing the likelihood that relic DNA could alter DNA metabarcoding data (Strickler et al. 2015, Barnes et al. 2014, Neilson et al. 2007, Carini et al. 2016). Conversely, in open environments with high nutrient cycling, UV light, or biological activity, DNA does not persist past a day or two, suggesting low risk of abundant relic DNA (Collins et al. 2018, Strickler et al. 2015). In mesocosms, a common closed environment used to study the effects of consumptive interactions (e.g. Gao 2017, Rudolf et al. 2014), the DNA that persists in the environment could be that of potential diet items that have not been ingested by consumers, which could inflate measures of consumption. The ecological interpretation of diet data with surface contamination could alter the interpretation of these data regardless of the diet measure in question (e.g. rate of consumption versus diversity of interactions). If diet data are being used to ask questions about the species-, population-, or community-level rate of consumption of a diet item or items (e.g. detection or DNA abundance of a diet item or items across a group of individuals; Kaunisto et al. 2020), then surface contaminants could either inflate (i.e. contaminants are potential prey) or depress (i.e. contaminants are not potential prey) estimates of consumption (e.g. evidence from mass-collected arthropods, Greenstone et al. 2011/12). Similarly, if diet data are being used to ask questions about a range of interactions between groups of organisms (e.g. diet diversity or composition; Kartzinel et al.), then surface contaminants could introduce false diet diversity or hide real diet diversity, especially if this diet diversity is low abundance because of small body size or infrequent consumptive interactions (Macias-Hernandez et al, Elbrecht et al. 2017).

In this study, we look at the effects of surface contamination on our understanding of consumer diets where the DNA of full organisms is used in analyses. We use high throughput sequencing results of the CO1 gene from the full body parts (opisthosomas) of invertebrate consumers (the spider, *Heteropoda venatoria*) from two environments – a “contained” mesocosm environment in which we offered consumers a potential diet item, and a natural environment in which consumers could feed on naturally-occurring diet items. In each environment, we surface sterilized half of the consumers prior to DNA extraction using a series of washes in a 1:10 dilution of bleach (10% commercial bleach) and deionized water; we left the other half of consumers unsterilized. These two environments represent two common contexts in the study of consumptive interactions and so we wanted to know whether environmental contamination poses a risk in studies aiming to use diet DNA metabarcoding in these environments. Specifically, we ask: Does surface sterilization alter 1) detection of offered (mesocosm environment) or all potential (natural environment) diet items or 2) the proportion of offered or all potential diet DNA, suggesting that contaminants either hide or inflate diet consumption amount? Last, 3) Does surface sterilization alter the richness or composition of potential prey items in a natural environment, suggesting that surface contamination could alter ecological interpretations of community-scale species interactions? Examining how surface contaminants may contribute to estimated diet metrics for studies of consumptive studies is an important step for verifying and standardizing these methods in future studies.

**Materials and Methods**

*Field site and collections*

We conducted this work on Palmyra Atoll National Wildlife Refuge, Northern Line Islands (5º53’ N, 162º05’W). We targeted a generalist, active hunting spider species (*Heteropoda venatoria*) as the consumer for this project because this species occurs in high abundance on the atoll and is therefore easy to collect and observe. Palmyra Atoll has a well-characterized species list, and like many atolls, is relatively species poor, allowing for relatively easy characterization of potential diet species (Handler et al. 2007, Food webs if published). We collected consumer individuals during two summers. In 2017, we collected consumer individuals which we kept in mesocosm environments in the lab (explained below). In 2015, we collected individuals in natural habitats across the atoll. All individuals were collected individually in sterilized collection containers to avoid contamination (Greenstone et al. 2011).

*Mesocosm consumer set-up and feeding*

In 2017, we conducted mesocosm trials (n = 26) because we were interested in testing whether DNA metabarcoding would detect DNA from potential diet items a consumer was offered in a common “contained” environment (mesocosms) often used in studies of feeding interactions (e.g. Gao 2017, Rudolf et al. 2014, Srivistava et al. 2004). We created feeding mesocosms out of one-liter yogurt containers with holes for air transfer. We placed an individual *H. venatoria* in each of these mesocosms. After a 12-hour period alone in the mesocosms, all *H. venatoria* individuals were offered one individual of a large grasshopper species (*Oxya japonica*), which is a common introduced species on the island (Handler et al. 2007). While many mesocosm experiments include natural “habitats” for consumers and diet to hide, we did not include anything in mesocosms to avoid contamination from DNA on these items. We left all mesocosms for 24 hours, after which we immediately froze *H. venatoria* individuals which had killed (though ingestion was not confirmed) an *O. japonica* individual at -20°C. All mesocosms were cleaned between each trial with a 10% bleach solution and kept closed to avoid contact with other organisms with the inside of the mesocosms.

*Natural environment consumer collection*

In 2015, we collected consumers (n = 47) in natural environments because we were interested in whether DNA metabarcoding would detect diet DNA from consumers occurring in natural environments which fed on available diet items and came into contact with natural environmental surfaces. We collected and froze all individuals in separate containers at -80°C immediately following collection until surface sterilization and DNA extraction in 2019.

*Both mesocosm and natural environment consumers: surface sterilization*

Because we planned to extract DNA from entire consumer individuals or from the opisthosoma of larger individuals (following methods from Krehenwinkel et al. 2016 and Macias-Hernandez et al. 2018), we wanted to determine whether contaminant DNA on the outside of *H. venatoria* consumer individuals altered potential diet DNA detection, and for consumers from a natural environment potential diet item richness and composition. We used a surface sterilization treatment to remove possible contaminants from some consumer individuals while leaving some individuals unsterilized. We used surface sterilization techniques common in other fields of molecular ecology (i.e. plant endophytes Schulz et al. 1993, Burgdorf et al. 2014) by submerging and stirring each sample in 10% commercial bleach by volume (0.5% sodium hypochlorite) for 2 minutes and then washing each sample by submerging and stirring in deionized water for 2 minutes. We surface sterilized mesocosm consumers (2017) in the lab on the atoll following freezing at -20°C and then stored each sample in individual vials of 80% ethanol because no long-term refrigeration was available on the atoll at the time (n = 10 surface sterilized; n = 14 not surface sterilized). Natural environment consumers (2015) had been frozen at -80ºC since collection; these consumers were surface sterilized in a sterilized laminar flow hood in 2019 just before DNA extraction (n = 22 surface sterilized, n = 25 not surface sterilized; Table). Prior to DNA extraction, all samples from both 2015 and 2017 were allowed to dry for 1-3 hours in a sterilized laminar flow hood.

*DNA extraction and removal of consumer DNA with Ampure XP beads*

We extracted DNA from each *H. venatoria* consumer individual following a modified CTAB extraction protocol (Fulton et al. 1995). At least twenty-four hours following extraction, we quantified DNA using a Qubit (Invitrogen) fluorometer and the high sensitivity DNA quantification kit with 1L of DNA per reaction. We used methods developed by Krehenwinkel et al. (2016) to remove a proportion of lower molecular weight consumer or prey DNA prior to PCR steps. To do this, we diluted each DNA sample to 20ng/l (a total of 40L per sample), bead cleaned each sample using Ampure XP beads (0.75x bead ratio), keeping the supernatant from the bead cleaning step. Because Ampure XP beads preferentially bind to heavier molecules, during this step, more intact consumer or prey DNA binds to the beads (Supp figure). Thus, by keeping the supernatant, we aimed to work with a sample that had a larger proportion of heavier molecular weight diet DNA after removing some consumer DNA that bound to beads (Krehenwinkel et al. 2016). With the supernatant, we repeated the CTAB protocol steps for precipitating DNA pellets with isopropanol and 5M potassium acetate and cleaning DNA pellets with ethanol washes. Waiting at least another twenty-four hours, we quantified DNA again using a Qubit fluorometer and high sensitivity kit with 1L of DNA per reaction tube and diluted all samples to 10ng/L prior to PCR steps. All DNA pellets were stored in and diluted with TE buffer.

*PCR amplification, library preparation, and sequencing*

The CO1 gene is well-represented in the GenBank sequencing database (Porter et al. 2018), so we chose to amplify this gene using general metazoan primers (Krehenwinkel et al. 2016, Yu et al. 2012, Leray et al. 2013). We performed all PCR amplification steps in a UV-sterilized biosafety cabinet. We used a standard desalted primer set tested by Krehenwinkel et al. (2016) for use in diet analyses of invertebrate predatory consumers (Table). Our primers included overhang adapters compatible with the Illumina indexing PCR (Illumina 2009).

We PCR amplified the CO1 gene in our samples with a 25L reaction volume, including 9L nuclease free water, 12.5L GoTaq Green Master Mix (Promega Corp.), 1.25 L of each of the primers, and 1 L of DNA template (at 10ng/L). When DNA concentrations were lower than 10ng/L, we added more DNA to the sample to equal 10ng of total template and reduced the amount of water added. Each sample was run in duplicate until after the Illumina indexing PCR, and we ran a duplicated negative sample each PCR run. We ran each reaction with an initialization step at 95°C for 3 minutes, and then 35 cycles of a denaturation step at 95°C for 30 seconds, an annealing step at 46°C for 30 seconds, an elongation step at 72°C for one minute. We ended each run with a final elongation step at 72°C for 5 minutes and then held samples at 4°C until placed in a 4°C refrigerator until attaching Illumina indices via an additional PCR step. To remove reaction dimer, we performed a bead cleaning step with Ampure XP beads at a 0.8x bead ratio prior to the Illumina index PCR. Samples were re-suspended from beads using a 10mM TRIS resuspension buffer.

We then attached Illumina index primers with an additional PCR step (Nextera XT Index Kit v2). Each total reaction volume was again 25L, with 5L of nuclease free water, 12.5L GoTaq Green Master Mix, 1.25L of each primer, and 5L of PCR product. These were run in a standard PCR protocol for these primers: an initialization step at 95°C for 3 minutes, followed by 10 cycles of a denaturation step at 95°C for 30 seconds, an annealing step at 55°C for 30 seconds, and an elongation step at 72°C for 30 seconds. We ended each run with a final elongation step at 72°C for 5 minutes and then held samples at 4°C until placed in a 4°C refrigerator.

We verified PCR amplification by visualizing 3-4 L of each PCR product in a 1.5% agarose gel using GelRed (Biotium) at 100V and 170mA for 30-40 minutes. Gels were visualized with a Bio-Rad Gel Doc XR+ imager using Image Lab 5.0. We kept samples for which both duplicates successfully amplified during the PCR steps and only kept samples on PCR runs in which both negative control duplicates resulted in no product detection. For successful samples, we combined duplicates and bead cleaned with an Ampure XP bead ratio of 0.7x. We determined the average length of the gene region using an Agilent TapeStation with a D1000 ScreenTape System following the standard protocol from the quick start guide. We then quantified these final PCR products using a Qubit fluorometer and a high sensitivity kit with 1L of sample per reaction tube and diluted each sample in 10mM TRIS to a final concentration of 5nM.

We multiplexed all samples along with one negative control and two positive controls (cloned fungal species of the ITS gene region; GenBank accession numbers: MG840195 and MG840196, Apigo and Oono 2018; Toju et al. 2012). We submitted multiplexed samples for sequencing at the University of California, Santa Barbara Biological Nanostructures Laboratory Genetics Core. Samples were run on an Illumina MiSeq platform (v2 chemistry, 500 cycles, paired end reads) with a 15% spike-in of PhiX. Following sequencing, samples were demultiplexed using Illumina’s bcl2fastq conversion software (v2.20) at the Core facility.

*Sequence merging, filtering, and clustering with UNOISE3*

We merged, filtered, and denoised (clustered) our sequences around exact amplicon sequence variants (ASVs) using the UNOISE3 algorithm (unoise3 command in the open-source USEARCH 32-bit version 11.0.667; Edgar 2016). This ASV denoising approach incorporates sequence abundance, quality, and error rates to cluster reads in high throughput sequencing data into a smaller subset of real biological units (Supp Figure). We also repeated analyses with the DADA2 algorithm run through R (dada2 package version 1.1.14.0; Callahan et al. 2016) and with a data cleaning step run through BBSplit (Bushnell 2018) to remove consumer DNA prior to ASV assignment (since ASV assignment is abundance-sensitive); however, UNOISE3 assigned more sequence reads to positive controls (on average, 3x as many per positive control), so we chose to continue analyses from this algorithm only (summary and comparisons in Supplement).

Prior to denoising, we used cutadapt (version 1.18, Martin 2011) to remove primers from each sequence. With trimmed sequences, we ran UNOISE3 in USEARCH with a maximum error rate of 1 in the filtering step. From the output, we created a list of unique ASVs and a matrix of ASV abundances across samples. We matched ASVs to taxonomies both in the GenBank and BOLD databases. For GenBank, we used BLAST (version 2.7.1) with the blastn command for taxonomic assignment of each ASV using the computing cluster at UC Santa Barbara, comparing against the GenBank nucleotide database with an evalue of 0.01 (downloaded on November 20, 2019). We visualized and exported taxonomic alignment using MEGAN Community Edition (version 6.18.0, Huson et al. 2016), selecting the subtree with all possible diet items for this species (Kingdom: Animalia, Clade: Bilateria). For taxonomies which were not assigned below the order level (n =24), we submitted each ASV individually to the BLAST Basic Local Alignment Search Tool and assigned them a family based on the best sequence match in the database, given this match was (%) aligned (OR STATS HERE?) with the sequence (CITE THIS ASK AUSTEN). For BOLD taxonomic assignment, we used the BOLD IDEngine of the CO1 gene with Species Level Barcode Records (accessed February 5-16, 2020; 3,825,490 Sequences, 216,704 Species, and 95,537 Interim Species in database) to match each ASV list to taxonomies. We combined taxonomic assignments from both programs and discarded taxonomic assignments that were mismatched at the family level or higher (Elbrecht et al. 2017).

*Detection of potential diet items*

For consumers from both mesocosm and natural environments, we wanted to know whether surface contamination altered the detection of potential diet items for each consumer (either by increasing detection because of “false” diet detection or by decreasing detection because of abundance of non-diet DNA). For mesocosm consumers, we focused our detection analysis on the potential diet item we had offered the consumers in the mesocosm environment (*O. japonica*, which all consumers were observed to have killed, but not necessarily ingested). For natural environment consumers, we examined all potential diet items (which could represent either real diet or surface contaminants). Samples were rarefied (McKnight et al. 2018) because sequencing depth (total number of DNA sequences assigned) can vary considerably across samples in high throughput sequencing runs. We did this using the rrarefy() function in the vegan (version 2.5.6) package in R and we rarefied based on the sample with the lowest sequencing depth (but which had been sequenced with 95%+ sampling completeness based on iNEXT (version 2.0.20) interpolation and extrapolation methods (Hsieh and Chao 2017). We rarefied to 55,205 reads per sample for the mesocosm and 16,004 reads per sample for the field consumers. We rarefied these separately because samples had been preserved in different ways and for different times, which can have large effects on DNA extraction outcomes (Murphy et al. 2002).

Following rarefying, we selected all ASVs which matched to the known potential diet item for the mesocosm consumers (species: *Oxya japonica*, genus: *Oxya*, family: Acrididae), and all potential diet items for the natural environment consumers (Kingdom: Animalia; Clade: Bilateria, excluding consumer DNA). In addition, for all consumers, because BLAST and BOLD matched multiple ASVs to the same taxonomies (e.g. at species, genus, or family level), we concatenated all ASVs based on shared taxonomic assignment. All ASVs received a family-level taxonomic assignment, and family-level analyses are common in DNA metabarcoding studies (e.g. Kartzinel et al.), so we chose to concatenate at the family level. We did this by combining ASVs which matched at the family level into one potential diet item with cumulative read abundance (i.e. all ASVs matched to *diet family A* were combined into one *diet family A* taxonomy with cumulative read abundance). For both mesocosm and field consumers, we assessed per sample detection of potential diet (offered diet item (*O. japonica*) for mesocosm consumers, all potential diet items for field collected consumers) using generalized linear models with potential diet item detection (presence-absence per sample) as the response variable, surface sterilization treatment as a fixed effect, and a binomial distribution.

*Proportion of potential diet DNA*

Because potential diet DNA can represent a rare subset of total sequence abundance in DNA metabarcoding studies (e.g. 0.03 – 8.43 percent of all sequencing reads in one study; Krehenwinkel et al. 2016), we also wanted to determine whether surface sterilization altered this proportion of reads assigned to possible diet. Again, because contaminants can represent artificial diet or can be non-diet items, surface contamination, and therefore, surface sterilization, could lead to either an increase or decrease in the proportion of reads representing potential diet. To test whether surface sterilization altered the proportion of DNA representing potential diet items, we assessed per sample potential diet DNA proportion for both sets of consumers (mesocosm and natural environment) separately. For this analysis, we subset only consumer individuals for which we detected diet DNA (n = 14 out of 19 for mesocosm; 33 of 37 for natural environment), since we were interested in whether contaminants alter diet abundance only when potential diet DNA is present. We assessed diet proportional abundance in consumers using generalized linear models with the number of potential diet DNA reads per sample (only *O. japonica*, the offered potential diet item, for mesocosm consumers, all potential diet DNA for natural environment consumers) as the response variable, surface sterilization treatment as a fixed effect, total read abundance of the sample (constant across all) as an offset term, and a Poisson or negative binomial distribution (to correct for overdispersion when needed). We also examined the proportions of other potential diet items for the mesocosm consumers as well as DNA which was sequenced but was not diet (e.g. fungi and potential endoparasites) and results are in the Supplement.

*Diet richness and composition in natural environment consumers*

In addition to allowing detection of diet items, DNA metabarcoding also enables the analysis of diet communities, allowing explorations of individual-, population-, and species-level diet richness and composition. If surface contaminants alter these metrics, ecological interpretation of these community-level data could be misleading, either by increasing the number of consumptive interactions attributed to a consumer, or by hiding interactions that occur more rarely or further back in time (e.g. Marcias-Hernandez et al. 2018, MacKenzie et al. 2002). We assessed whether surface contamination altered richness and composition of potential diet items in our natural environment consumers. For per sample potential diet richness, we used ASVs concatenated at the family level and assessed differences in per sample potential diet richness among sterilization treatments using generalized linear models with the number of potential diet items per sample as the response variable, surface sterilization treatment as the fixed effect and a Poisson or negative binomial distribution (to correct for overdispersion when needed). We assessed differences in potential diet item composition between surface sterilized and unsterilized consumers using a presence-absence PERMANOVA model fit with a binomial mixed effects model with surface sterilization treatment as a fixed effect, a random intercept term for potential diet item, and a random slope term for surface sterilization treatment. Incorporating a random intercept term for potential diet item combined with a random slope term for surface sterilization treatment allows the effect of surface sterilization treatment to vary by potential diet item, such that some potential diet items may increase in presence with surface sterilization (i.e. hidden by contaminants), while others may decrease in presence (i.e. potential diet item is a contaminant; Zurr). We repeated the field consumer potential diet item PERMANOVA with abundance data, conducted both presence-absence and abundance based PERMANOVA analyses on all potential diet items (including offered item) for mesocosm consumers, and repeated each analysis using the adonis() function from the vegan package (version 2.5.6) in R (dist = “jaccard” with binary = TRUE for presence/absence and dist = “bray” for abundance; Supplement).

*Model selection*

For all generalized linear models, we performed model selection by comparing the full model (including the fixed effect of surface sterilization treatment) to a null model without this effect. All models were called in the glmmTMB package (version 1.0.0, Brooks et al. 2017) in R (version 3.6.1) We chose the best fitting model based on size corrected AIC values (MuMIn package version 1.43.15). For responses for which the best model included the surface sterilization treatment term, we examined the model summary to determine the standardized coefficients () and p-value of the significance between marginal means of the levels of the surface sterilization fixed effect. We assessed model fit using diagnostics in the DHARMa package (version 0.2.7), including tests for heteroskedasticity, and for count models (Poisson or negative binomial), zero inflation and overdispersion (Zurr, Bolker citations here). All raw data, data cleaning, and data analyses can be found in the data (CITE data here).

**Results**

*PCR success, sequence merging, filtering, and clustering with UNOISE3 and DADA2*

Amplification success across all samples was 78%, with 56 of 72 initially extracted samples successfully amplified and sequenced (mesocosm: n = 8 surface sterilized, n = 11 unsterilized; field: n = 18 surface sterilized, n = 19 unsterilized). The Illumina MiSeq run yielded 33,332,804 unpaired reads and had a Q30 quality score of 78.03%. After quality filtering and denoising with UNOISE3, we had a set of 8,029,959 paired-end reads that corresponded to 176 ASVs. Seventy-three percent (128 of 176) of the ASVs matched to a taxonomic assignment. Twenty-three percent of these taxonomies corresponded to potential prey items (41 of 176) and eight percent (14 of 176) corresponded to consumer DNA. Eighty-five percent of the potential prey ASVs received a species-level taxonomic assignment (35 of 41) from either the BLAST or BOLD taxonomic assignments, and every potential prey species received a family-level and order-level taxonomic assignment. There were no conflicting taxonomic assignments at the family level or higher between the BOLD and BLAST assignments.

*Detection of potential diet items*

We detected offered known diet (*O. japonica*) in 74% (14 of 19) of mesocosm consumers and diet of all species in 89% (33 of 37) of field-collected consumers. For mesocosm consumers, one ASV matched to the known diet (*O. japonica*), and the best model for diet detection included the fixed effect of surface sterilization treatment with a marginally significant difference between marginal means (( = -2.3; p-value = 0.07). Based on this model, known diet detection decreased with surface sterilization treatment from a detection in 91% (10 of 11) of all consumers when unsterilized to 50% (4 of 8) of all consumers when surface sterilized. For field consumers, concatenated ASVs corresponded to 20 families. The best model for diet detection was the null model that did not include surface sterilization treatment as a fixed effect (Figure). (Supplement).

*Proportion of potential diet DNA*

Offered known diet DNA sequence reads (*O. japonica*) represented 0.8% (± 0.7% SE) of total per-sample DNA sequence abundance for mesocosm consumers; all potential diet DNA sequence reads represented 2.0% (± 1.0 %) of total per-sample DNA sequence abundance for natural environment consumers (Figure). For both the mesocosm and natural environment consumers, the null models which did not include surface sterilization treatment as a fixed effect were the best models of prey DNA read abundance.

*Diet richness and composition in natural environment consumers*

For natural environment consumers, the best model for per sample diet richness was the null model which did not include surface sterilization treatment as a fixed effect. Diet richness per consumer was an average 2.08 (± 0.26) diet families per individual sample, with a maximum of 5 diet families in one consumer diet (Figure). The best model for potential diet composition also did not include surface sterilization treatment as a fixed effect. Diet composition consisted of twenty families from ten arthropod orders (*Class Insecta*: Dermaptera, Diptera, Blattodea, Lepidoptera, Orthoptera, Odonata, Hymenoptera; *Class Arachnida*: Araneae, Scorpiones; *Class Chilopoda*: Geophilomorpha; Figure; Supplement).

**Discussion:**

**[Main takeaways]**

Surface contamination does not appear to systematically introduce erroneous or hide diet items into DNA metabarcoding data for the predatory consumer *H. venatoria*. In a natural environment, all measures of DNA diet (diet detection, abundance, richness, and composition) were not altered by surface sterilizing consumers prior to DNA metabarcoding, suggesting the potential diet DNA extracted from these individuals represents consumed diet items (including 19 species from nine arthropod orders and one insect infraclass). In a contained mesocosm environment, we found potential evidence of surface contamination with a marginally significant reduction in detection of an offered diet item with surface sterilization (a reduction of offered diet item in 91% to 50% of the population, p-value = 0.07). This outcome suggests that some environments may be more prone to surface contamination that could alter the ecological interpretations of diet metabarcoding data. Surface sterilization did not appear to have negative effects on diet DNA detection, abundance, or richness (diet detection in 74% of consumers with a fed diet item, 86% with natural-fed diet items). This, tied with our observation of possible contamination in a mesocosm environment, suggests that surface sterilization may be an appropriate validation step prior to conducting a diet DNA metabarcoding study in a new environment, especially in contained environments. The diet data revealed in our dataset suggest a wide range of continued and future applications for diet DNA metabarcoding studies across a range of scales and environments. (e.g. individual- and population-level consumption rates via detection and abundance of diet DNA; Kaunisoto et al. 2020; population- and community-level consumption patterns via abundance, diversity, and composition of diet DNA; Quemere et al. 2013, Kartzinel et al.).

**[Surface sterilization broadly]**

The field of diet DNA metabarcoding has not universally adopted surface sterilization practices into common protocols, especially for studies including DNA extraction of full organisms (Doña et al. 2019, Anslan et al. 2016, Wirta et al., Jacobsen et al. 2018). We demonstrate that surface sterilization may not be necessary in these types of studies in the future, but that researchers may want to consider aspects of their study system and validate a lack of surface contaminants prior to diet DNA metabarcoding studies. This evident lack of surface contaminants that hide or inflate diet detection or diversity in DNA metabarcoding studies contrast with obvious surface contaminants altering ecological interpretations in other fields that use high-throughput sequencing methods to determine community diversity (e.g. fungal endophytes, , Burgdorf et al. 2014). The reasons for this difference are numerous, but foremost is that fungal spores and bacterial cells are widespread on and in the surfaces of most environments and organisms (Despres et al. 2012, Philippot et al., Colston et al. 2016) and so likely to contaminate studies targeting specific subgroups of these communities. Indeed, even in our dataset, many sequences matched to fungal reference sequences from both GenBank and BOLD (Supplement). The fact that these non-target sequences did not alter our DNA metabarcoding data by hiding target diet DNA (even with the relative rarity of diet DNA compared to consumer DNA; 0.006 – 26% of each sample, similar to other studies; Krehenwinkel et al. 2016), is likely due to the differences in biomass of these sources of DNA in our samples and the specificity of our PCR amplification protocol; diet items are likely in greater biomass in consumers than any single fungal species and more directly targeted by the primer set selected for our study (Leray, Yu, Elbrecht et al. 2017). Therefore, in studies where contaminants and diet are likely to be similar in biomass, or where diet are widespread organisms (e.g. fungi or bacteria), surface sterilization may be an important consideration.

**[Surface sterilization by environment]**

While we saw no widespread evidence of environmental contamination in our study, we did observe some evidence that more contained environments (here, mesocosms) may be more prone to contamination than open terrestrial environments. This outcome highlights that the decision to surface sterilize prior to DNA metabarcoding may matter more in some environments and experiments than others. Mesocosms, either built or natural, are a widely used type of environment in studies of consumptive interactions (e.g. built mesocosms: Gao 2017, Rudolf et al. 2014; ponds, lakes, and natural microcosms: Srivistava et al. 2004, De Meester et al. 2005) and DNA metabarcoding in any of these environments may benefit from surface sterilization. Any environment is shaped by both abiotic and biotic factors, and these may play out in complicated ways to influence the risk of environmental contamination. In aquatic and marine eDNA environments, some abiotic conditions are attributed to DNA persistence (e.g. pH and salinity; Collins et al. 2018, Strickler et al. 2019), while others are not or show inconclusive results (e.g. sunlight; Machler et al. 2018, Pilliod et al. 2014). Others attribute biotically-mediated responses to the environment in DNA persistence (e.g. microbial growth due to ideal abiotic conditions: Nielson et al; Strickler et al. 2014). Any aspect of an environment that alters the persistence of DNA is likely to alter the risk of environmental contamination. Ecological factors of an environment or consumer could shape contamination risk as well, including diet density, consumer-diet population ratios, consumer-diet body size ratios, and interaction frequency, which can alter contact probability and handling times as well as the likelihood that high-biomass contaminants will hide diet items that were consumed farther back in time (Greenstone 2011 and 2012, Scharf et al. 1998, Jeschke et al. 2002, Samu and Biro 1993, Marcias-Hernandez et al., Abrams and Ginzberg 2000). Considering these aspects of any environment prior to performing a DNA metabarcoding study is key in confidently assigning consumptive interactions and could help build predictive frameworks of when surface sterilization may be necessary.

**[When, how, what to sterilize]**

Why not to sterilize? How do we sterilize, and how can we figure out when/how to sterilize and for what purposes.

Austen comment: This may be hard to find, but for methods-type papers of surface sterilization, it might be nice to include the rationale for the different treatments/chemicals. Bleach kills DNA, whereas sonication physically removes contaminants, etc. in the methods or intro if you think that’s appropriate.

**[what we learn broadly from diet studies and why new tools are important]**

DNA metabarcoding is providing the first glimpse at comprehensive diet for a suite of consumers important to the field of food web ecology and to the maintenance of biodiversity on the planet (Nielson et al. 2018). DNA metabarcoding could be used in combination with other diet methods to understand how consumptive processes that scale from between individuals to between functional groups may regulate ecosystems and their functions (Birhofer et al. 2017, Kaunisto et al. 2020). Like any method for determining consumptive interactions in nature, DNA metabarcoding needs refinement (e.g. discussion in Zinger et al. 2019). As DNA methods become more standardized and cost-efficient (including extending to metagenomics, which can differentiate individuals of a species in a sample; Gomez-Rodriguez et al. 2017), online taxonomy databases become more complete (Kvist 2013), and new techniques arise (e.g. real-time field sequencing with MinION technology; Jain et al. 2015), DNA-based diet approaches may surpass many other methods (e.g. Riccioni et al. 2018). Being able to determine consumptive interactions for many species and environments for the first time will only continue to build a better picture of the complex structure of nature, and how species interactions can scale up to create unique ecosystems and ecosystem functions (Pilosof et al. 2017, Ives et al. 2005, Rudolf and Lafferty 2011, Brophy et al. 2017, Dunne et al.). In addition to building more realistic models of community interactions, a more complete picture of how consumptive interactions shape ecosystems could be key to predicting and curbing future biodiversity loss due to human change (Tylianakis et al. 2008, Harvey et al.2017).

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**References**

Will be putting in after some rounds of edits.

**Data Accessibility**

Data will be available on Dryad and I will be uploading my sequence data to GenBank.

**Author Contributions**

AM-tK, AA, and HY conceived the idea for this study. AM-tK collected field samples and conducted mesocosm study. AM-tK and AA designed laboratory analyses for this study. AM-tK performed all lab processing and data analyses for the study. AA and HY provided feedback on data analysis methods. AM-tK led the writing of the manuscript. All authors contributed to editing of the manuscript.

**Figures and Tables:**

Table: Sample sizes for successfully DNA extracted and PCR amplified samples of surface sterilized and unsterilized *H. venatoria* individuals in the mesocosm and field environments. Bold numbers indicate final sample sizes for analyses.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | *Surface sterilized* |  | *Unsterilized* |  |
| *Environment* | Extracted | Amplified | Extracted | Amplified |
| Mesocosm | 10 | **8** | 14 | **11** |
| Field | 22 | **18** | 25 | **19** |

Table: Primers with Illumina overhang adapters (in bold) used to amplify the CO1 region in this study.

|  |  |  |
| --- | --- | --- |
| Primer | Sequence (5’ – 3’) | Source |
| mICOIintF | **TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG**GGWACWGGWTGAACWGTWTAYCCYCC | Yu et al. 2012 |
| Fol-degen-rev | **GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG**TANACYTCNGGRTGNCCRAARAAYCA | Leray et al. 2013 |



Figure: a) Detection of fed diet (*Oxya japonica*) DNA in mesocosm consumers that were and were not surface sterilized. Significant decrease with surface sterilization. B) Detection of all diet DNA in natural-environment consumers that were and were not surface sterilized. Non-significant difference.

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Figure: a) In mesocosm consumers for which the fed diet was detected, the proportional abundance of DNA from that diet item in individual spiders. The difference is significant, but driven by one very high data point, and when that is removed, the difference is no longer significant. b) In field-collected consumers for which diet DNA was detected, the proportional abundance of DNA from that diet item in individual consumers. The difference is non-significant.

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Figure: Diet richness (number of unique diet taxonomic assignments) for field collected consumers that were and were not surface sterilized. There is no significant difference.

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Figure: Presence (indicated by a colored box) and abundance (indicated by color depth) of diet items in field-collected consumers that were and were not surface sterilized. Neither presence- or abundance-based community metrics demonstrate a significant difference between these two groups of consumers. Because of the wide range of abundances per diet item, color depth is divided by quartiles of DNA sequence abundance.

**Supplementary Info and Figures:**

Data: Raw data files as well as code for each step of the cleaning and analysis process.

Supplement A: model outputs for GLMMs in main text

Supplement B: Full DNA extraction and PCR protocol

Supplement C: Comparison of UNOISE3 and DADA2 in diet DNA detection

Supplement D: Additional figures and statistical analyses, including consumer and other diet DNA abundance for mesocosm consumers, by-species presence and composition effect graphs from both mesocosm and field PERMANOVA analyses.

A picture containing dark, man, holding, standing

Description automatically generated

Supp Figure: Ampure XP bead cleaning of DNA to remove consumer DNA, motivated by results from Krehenwinkel et al. 2016.



Supp Figure: Library prep, starting with attaching the CO1 primer pair with Illumina tag to diluted, bead-cleaned DNA. Then, this PCR product is bead cleaned at a 0.8x ratio and run through a subsequent PCR step to attach Illumina tag, index, and P5/P7 identifiers. This PCR product is then cleaned again at a 0.7x bead ratio, diluted to 5nM, and pooled for sequencing on an Illumina MiSeq.

A picture containing screenshot, food

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Supp Figure: Denoising algorithms like UNOISE3 and DADA2 take into account DNA sequence abundance and error rates to assign groups of similar sequences to one amplicon sequence variant (ASV).



Supp Figure: Sequencing depth determined via interpolation and extrapolation in the iNEXT package in R. All samples were sequenced to 99-100% sequencing depth.

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Supp Figure: Consumer DNA read abundances from A) mesocosm consumers and B) field-collected consumers, potential diet DNA reads from C) mesocosm consumers and D) field consumers, and non-diet DNA read abundance for E) mesocosm consumers and F) field-collected consumers that were and were not surface sterilized. The surface sterilized/not surface sterilized treatment groups are not significantly different for any type of other DNA, suggesting that the reduction in offered diet item detection for mesocosm consumers is due to surface contamination as opposed to a relic of the DNA extraction, amplification, or sequencing process.



Supp Figure: The composition by-species of other diet in the mesocosm consumers, demonstrating that both presence- and abundance-based diet communities did not shift with surface sterilization treatment. (more positive means more present/abundant in unsterilized; more negative means more present/abundant in sterilized). Species are ranked by their overall presence in the population (A) or their overall abundance in the population (B) to demonstrate that there is no skew for relatively abundant or rare species.



Supp Figure: The composition by-species of diet in the field consumers, demonstrating that both presence- and abundance-based diet communities did not shift with surface sterilization treatment. More positive values mean more present/abundant in non-sterilized; more negative values mean more present/abundant in surface sterilized consumers). Species are ranked by their overall presence in the population (A) or their overall abundance in the population (B) to demonstrate that there is no skew for relatively abundant or rare species.