FINAL REPORT

Assessing Pollinator Communities via Environmental DNA (eDNA) Metacommunity Assay

SERDP Project RC19-1102

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Dr. Mark Davis
Dr. Lynsey R Harper
Dr. Brenda Molano-Flores
University of Illinois Urbana-Champaign

Mr. Joseph Benito
Dr. Matthew L Niemiller
The University of Alabama in Huntsville

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Mark Davis, Brenda Molano-Flores, Lynsey Harper
University of Illinois Urbana-Champaign

Matthew Niemiller,Joseph Benito
The University of Alabama in Huntsville

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Champaign, IL 61820

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14. ABSTRACT
Pollinators provide essential ecosystem services and are critical components of resilient ecosystems. Yet, pollinators are suffering staggering global declines leading to increased listing under the Endangered Species Act. This presents challenges for DoD installations. The technical objectives of this project were to: 1) develop and validate broad-spectrum pollinator eDNA metabarcoding primers, 2) test the efficacy of multiple capture methods to obtain Next Generation Sequencing-ready pollinator eDNA from flowers, and 3) validate eDNA sampling and microfluidic metabarcoding methods in controlled and field experiments with mixed plant/pollinator communities.

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LIST OF ACRONYMS AND ABBREVIATIONS

16s	mitochondrial 16s ribosomal RNA locus
18s	nuclear ribosomal RNA locus
28S	nuclear ribosomal RNA locus
AE	Qiagen elution buffer
AL	Qiagen lysis buffer
ANOVA	analysis of variance
ASV	amplicon sequence variant
ATL	Qiagen tissue lysis buffer
AW1	Qiagen wash buffer
AW2	Qiagen wash buffer
BLAST	Basic Local Alignment Search Tool
BLCA	Bayesian Least Common Ancestor
bp	base pairs
BOLD	Barcode of Life Data System
°C	degrees Celsius
COI	mitochondrial cytochrome c oxidase subunit 1 locus
CRUX	Creating Reference libraries Using eXisting tools
CTAB	cetyl trimethyl ammonium bromide
df	degrees of freedom
DNA	deoxyribonucleic acid
DoD	U.S. Department of Defense
eDNA	environmental DNA
EDTA	ethylenediaminetetraacetic acid
EMBL	European Molecular Biology Laboratory
EtOH	ethanol (ethyl alcohol)
FR	Federal Register
g	gram or gravitation constant
GLM	generalized linear model
hr	hour
IBCP	Illinois Bat Conservation Program
INHS	Illinois Natural History Survey
LCA	least common ancestor
M	million
metaBEAT	Metabarcoding and Environmental DNA Analysis Tool
min	minute
mL	milliliter
mtDNA	mitochondrial DNA
MVDISP	multivariate dispersion
NaCl	sodium chloride

NCBI	National Center for Biotechnology Information
nDNA	Nuclear DNA
ng	nanogram
NMDS	non-metric multidimensional scaling
nt	nucleotide
NGS	next-generation sequencing
OTU	operational taxonomic unit
P	probability value (p-value)
PCI	phenol-chloroform-isoamyl
PERMANOVA	permutational multivariate analysis of variance
PCR	polymerase chain reaction
PRI	Prairie Research Institute
r	correlation coefficient
R^2	coefficient of determination
RNA	ribonucleic acid
RTE	rare, threatened, and endangered
sec	second
SE	standard error
SERDP	Strategic Environmental Research and Development Program
TAE	Tris-acetate-EDTA
TE	Tris-EDTA
T&E	threatened and endangered
UIUC	University of Illinois at Urbana-Champaign
µL	microliter
µM	micromolar
UV	ultraviolet
V	volt
v	version
x	times (multiple of)
χ^2	chi-square

KEYWORDS

Biodiversity, Community Ecology, Environmental DNA, Microfluidic Metabarcoding, Pollinator Communities, Species Richness

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ABSTRACT

Introduction Pollinators provide essential ecosystem services and are critical components of resilient ecosystems. Yet, pollinators are suffering staggering global declines leading to increased listing under the Endangered Species Act. This presents challenges for United States Department of Defense installations. Range closures must occur to facilitate surveys, but conventional sampling is costly, time consuming, and increases range closure time, which erodes mission readiness and decreases lethality. Rapid, efficient, and accurate assessment of pollinator communities is therefore essential to maximize return-on-investment. Here, we assess the potential for environmental DNA (eDNA) metabarcoding as a means to maximize return on investment. Specifically, we test if eDNA metabarcoding can provide a viable method of documenting pollinator communities.

Objectives Our technical objectives were to: 1) develop and validate broad-spectrum pollinator eDNA metabarcoding primers, 2) test the efficacy of multiple capture methods to obtain Next Generation Sequencing (NGS)-ready pollinator eDNA from flowers, and 3) validate eDNA sampling and microfluidic metabarcoding methods in controlled and field experiments with mixed plant/pollinator communities.

Technical Approach We conducted *in silico* and *in vitro* testing on a broad spectrum of arthropod metabarcoding primers. We established a greenhouse flower community, introduced a colony of common eastern bumblebee (*Bombus impatiens*) pollinators, and obtained eDNA samples from four focal flower species (*Monarda, Penstemon, Solanum, Cynoglossum*) via three sampling methods (nectar draws, flower swabs, whole flower heads). Samples were preserved and extracted using two methods, Phenol-Chloroform-Isoamyl and Qiagen DNeasy Blood and Tissue kit, before being subjected to microfluidic eDNA metabarcoding using the validated primer panel. Sequence reads were analyzed with two bioinformatics pipelines for quality and length filtering, merging, dereplication, and taxonomic assignment.

Results *In silico* and *in vitro* testing revealed a panel of 15 primer sets that showed promise for amplifying pollinator DNA. Microfluidic eDNA metabarcoding detected not only the focal taxon, but also beneficial insect species released historically in the greenhouse as well as common arthropods known to occur in the region. In addition, field samples provided preliminary support for *ex situ* validation of methods.

Benefits Our study demonstrates three significant benefits of microfluidic eDNA metabarcoding of pollinator communities: 1) eDNA metabarcoding reduces both time and effort needed to acquire the same level of information as and the financial burden of conventional surveys, 2) eDNA metabarcoding has the potential to detect federally listed species, 3) eDNA sampling requires considerably less time in the field compared to traditional methodologies, minimizing range closure time and increasing mission readiness, and 4) eDNA metabarcoding approaches

can reveal complex networks that undergird critical ecosystem functions and services, ultimately allowing for an assessment of ecosystem resilience.

POLLINATOR eDNA MICROFLUIDIC METABARCODING: REAL WORLD APPLICATION

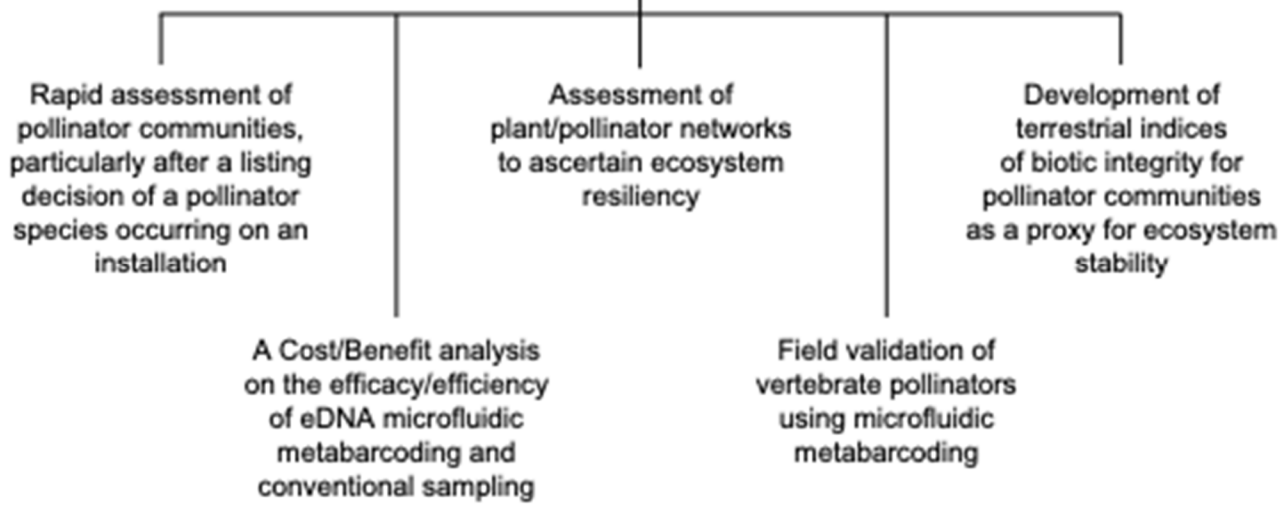
ADDITIONAL WORK NEEDED

Across US Military Installations, pollinator communities can vary to include vertebrates (particularly birds and bats). These species are increasingly afforded protection by the Endangered Species Act.

Can these species be detected using this approach?

Conventional sampling is expensive, time consuming, and often requires prolonged closures on installations, which can reduce mission readiness and decrease lethality.

Does pollinator eDNA metabarcoding offer an approach that is more cost/time effective than conventional surveys?



EXECUTIVE SUMMARY

Introduction Biodiversity is being lost at an alarming rate. Current extinction rates exceed those of the last five mass extinction events, and biodiversity loss cuts across habitats, ecosystems, and geopolitical boundaries (Pimm and Brooks, 2000; Wake and Vredenburg, 2008; Barnosky et al., 2011; Kolbert, 2014). This modern mass-extinction event has been precipitated by anthropogenic activities (Krutzen, 2006), and the impacts have fallen particularly hard on pollinator species (Potts, 2010; Cameron et al., 2011; Lever et al., 2014). Consequently, numerous pollinators have been added to the Federal Register (81 FR 67786, 82 FR 10285) as threatened or endangered, signaling the vital importance of pollinators to North American ecosystems and economies (Southwick and Southwick, 1992; Losey and Vaughn, 2006). The loss of pollinator biodiversity is of substantial concern, as it reduces plant reproductive success (Thomann et al., 2013), erodes ecosystem services provided by pollination (Allsopp et al., 2008; Winfree et al., 2011; Vanbergen, 2013), and ultimately drives staggering economic losses (Kevan and Phillips, 2001; Gallai et al., 2009). Given the above, rapid, efficient, and accurate assessment of pollinator communities is a conservation imperative to inform adaptive management strategies to stanch the loss of this critical component of biodiversity.

Such assessments are both technically difficult and financially costly (Chacoff et al., 2011; Bartomeus, 2013; Plein et al., 2017). Traditional monitoring often involves comparison of a scant number of communities, requires exorbitant time commitments to document pollinator species presence/absence, and is reliant on extensive time and ever dwindling taxonomic expertise adjudicating pollinators observed (Sheffield et al., 2009; Tur et al., 2013; Weiner et al., 2014). Further exacerbating the above is that monitoring is simply unlikely to be performed for the vast majority of pollinator species (Young et al., 2017). It is likely that these problems are further amplified for threatened and endangered species, whose populations tend to be low in numbers and patchily distributed (Goodman, 1987; Menges et al., 1991; Matthies et al., 2004). Yet, pollinator biomonitoring is critical to both monitor the status and trend of rare, threatened, and endangered (RTE) pollinators and evaluate the impacts of biodiversity loss on ecosystem services (Vamosi et al., 2017). Approaches that can assay pollinator biodiversity in a time and cost-effective manner will vastly enhance our ability to develop effective interventions to mitigate further loss.

Environmental DNA (eDNA) analysis has emerged as a viable candidate for such biodiversity assessments (Taberlet et al., 2012; Goldberg et al., 2015; Deiner et al., 2017). Organisms are continually shedding DNA, which persists, albeit temporarily, in their habitats and can be harnessed to identify single species (e.g., RTE species) or entire communities (Dejean et al., 2011; Thomsen et al., 2012). Single-species eDNA assays have been increasingly leveraged as a reliable means of surveying rare or invasive species (Thomsen and Willerslev, 2015), and the United Sates Department of Defense (DoD) has been at the leading edge of the eDNA revolution as a tool to aid in conservation. However, given the costs associated with single-species assays in terms of research and development investments, coupled with the increasing number of imperiled species that require monitoring (particularly in the case of

pollinators), methods that can screen for multiple taxa simultaneously are essential to increase efficiency and ostensibly reduce economic burden.

Coupling pollinator eDNA with microfluidic metabarcoding may in fact provide the mechanism for faster, more accurate, and less costly assessments of invertebrate communities (Taberlet et al., 2012; Ficetola et al., 2015; Valentini et al., 2016; Deiner et al., 2017). eDNA metabarcoding utilizes a very short genetic sequence from a standard part of the genome (typically mitochondrial genome) that possesses conserved primer binding sites across a range of taxa yet enough sequence variability within intervening regions to distinguish among species in an environmental sample, such as soil or water (Hebert et al., 2003). Since the turn of the 21st century, the scientific community has largely adopted a small (~600 bp) subsection of the mitochondrial DNA (mtDNA) cytochrome c oxidase subunit I (COI) region as the standard for DNA barcoding, although shorter fragments are required for Next Generation Sequencing (NGS) platforms. Online genetic repositories like the Barcode of Life Data System (BOLD) and NCBI's GenBank have been populated with vast amounts of DNA barcodes (approximately 1.5 M in BOLD and over 1.9 M in GenBank) cutting across wide swaths of biodiversity. Moreover, the emergence of NGS has elevated the resolution with which molecular genetic approaches can capture snapshots of biodiversity (Yu et al., 2012). In particular, DNA and eDNA metabarcoding have become established as innovative and cost-effective means of rapidly assaying biodiversity (Ji et al., 2013; Aylagas et al., 2016; Elbrecht et al., 2017). Finally, microfluidic metagenomics has emerged as an additional advancement that could elucidate broader communities revealed via eDNA metabarcoding due to simultaneous application of multiple primer sets potentially targeting different taxa, different genes, or different regions of the same gene (Hauck et al., 2019).

Prior to the submission of our proposal, eDNA metabarcoding assays for pollinators had yet to be developed and deployed. Just prior to the initiation of our SERDP Limited Scope Project, the first paper to assess the potential of eDNA metabarcoding to document pollinator communities was published (Thomsen and Sigsgaard, 2019). However, this study merely sought to determine whether or not pollinator eDNA could be detected. Our project builds upon this work investigating the detection of pollinator biodiversity by combining eDNA sampling, microfluidic metabarcoding, NGS, and comparative bioinformatics to assess pollinator networks associated with host plants. Ultimately, our work advances the state-of-the art and expands the knowledge base to facilitate widespread adoption of pollinator microfluidic eDNA metabarcoding across DoD installations.

Objectives Our technical objectives were: 1) develop and validate (both *in silico* and *in vitro*) a panel of broad-spectrum pollinator eDNA metabarcoding primers, 2) test the efficacy of multiple capture methods to obtain NGS-ready pollinator eDNA from flowers, and 3) validate eDNA sampling and metabarcoding methods in controlled and natural field experiments with mixed plant/pollinator communities.

Technical Approach

Greenhouse experiment. A mixed species flowering plant colony was established in the University of Illinois Urbana-Champaign (UIUC) Plant Care Facility (Appendix 1). Plantings were staggered so that a constant supply of pollen and nectar was available (Fig. 1). For our experiment, a subset of flowering plants was moved to a secure room where a Natupol colony (Koppert Biological Systems) of common eastern bumblebees (*Bombus impatiens*) was released (Fig. 1). We then systematically introduced four focal flower species (*Penstemon*, *Monarda*, *Solanum*, and *Cynoglossum*) into the greenhouse. Upon introducing a focal flower species, we observed the flowers for bumblebee visits. When a visit by a bumblebee was observed, and upon the bee leaving the flower, the flower was sampled by one of three methods: 1) whole flower heads were harvested and placed in preservative (*Penstemon*, *Monarda*, and *Solanum*), 2) the flower was swabbed with a flocked cotton swab, and the swab was placed in preservative (*Penstemon* and *Monarda* only), or 3) nectar was extracted from the flower via microcapillary tube and placed in preservative (*Cynoglossum* only). Preservatives included ATL buffer or cetyl trimethyl ammonium bromide (CTAB), and in volumes of 300, 600, 900, or 1200 µL depending on size/type of sample (i.e., large *Monarda* flowerheads preserved in 1200 µL, nectar draws preserved in 300 µL). Twenty-five samples were collected per flower type, sampling method, and preservative. In addition to sampling flowers where bee visits were directly observed, flowers were allowed to remain in the greenhouse for 24 hours after visits and were then randomly sampled to assess the ability to detect pollinator visits in absence of direct observation. Twenty-five samples from each flower type, using each sampling method, and both preservation methods were acquired.

Figure 1. Photos depicting greenhouse colonies. We established a mixed species colony of plants to ensure a constant supply of pollen and nectar (A). A subset of plants was then moved to an isolated greenhouse room where a colony of common eastern bumblebees was established (B).

Field experiment. Two of our four focal flower species (*Penstemon* and *Monarda*) also occur on the UIUC campus, and so we conducted a pilot field component to the greenhouse experiment. Here, we employed a similar approach as in the greenhouse experiment. On days when the weather was suitable (9am, temperatures > 13 ºC and sunny), we observed flowers. When a bee species was observed visiting a flower, the bee was identified, a photo was taken, and after the bee left the flower, the flower was sampled by one of two methods (whole flower harvest or swabbing). The flower was preserved in either ATL buffer or CTAB in volumes of 300, 600, 900, or 1200 µL, depending on size of the flowerhead until 25 flower samples via each sampling method, for each preservation type, and for each flower species were obtained. In addition, 25 random flower samples were acquired via each sampling method, for each preservation type, and for each flower species.

DNA extraction, quantification, and plating. DNA extractions were performed in laboratories at the Collaborative Ecological Genetics Laboratory, Illinois Natural History Survey, University of Illinois Urbana-Champaign, where dedicated labs and established protocols for working with samples of low DNA concentration are in place. Decontamination procedures include regular bleaching of work surfaces, UV-light irradiation of consumables and workspaces, isolated PCR-hoods, and physical separation of pre- and post-PCR work (i.e., a dedicated eDNA "clean room," where no high-copy DNA has been introduced).

DNA was extracted using two methods. First, a modified Qiagen DNeasy® Blood & Tissue approach (per Thomsen and Sigsgaard, 2019) was used for whole flower, swab, and nectar samples preserved in ATL buffer. Lysis was performed in the plastic tubes containing the flowers by adding 60, 100, 200 or µL proteinase K respectively depending on the volume of preservative the sample was originally stored in. Samples were lysed at 56 °C with agitation in a rotor for 3 hr. After lysis, samples were mixed on a vortexer for 10 sec and a total of 500, 800, or 1,500 µL lysis mixture was retrieved respectively. Equal amounts of AL buffer and absolute ethanol (EtOH), corresponding to the volume of retrieved lysis mixture, were added to the tubes and vortexed thoroughly before the samples were added to spin columns and spun through the membrane filters over several rounds (700 µL per round). Columns were washed by first adding 600 µL AW1 and then 600 µL AW2 buffers. Finally, DNA was eluted in 2 × 60 µL AE buffer, each time with a 15 min incubation step at 37 °C before spinning. All spinning steps were performed at 10,000 g. Each extraction batch (n = 23) also included an all-buffers-only negative extraction control. DNA extracts were stored at −20 °C until quantification and plating.

Second, a modified Phenol-Chloroform-Isoamyl (PCI) extraction and ethanol precipitation method was employed (following Renshaw et al. 2015) for whole flower, swab, and nectar samples preserved in CTAB. From original preservation tubes, 450 µL of CTAB was removed and transferred to a sterile, labeled 2 mL microcentrifuge tube and 450 µL Chloroform-Isoamyl alcohol was added, then vortexed, and centrifuged at 15,000 g for 5 mins. After centrifugation, 400 µL of the aqueous layer was transferred to a new, sterile 2 mL microcentrifuge tube, and 350 µL of ice-cold isopropanol and 175 µL of room temperature 5 M NaCl were added. Samples were then allowed to precipitate at -20 °C overnight. Following

overnight precipitation, samples were centrifuged at 15,000 g for 10 mins to pellet the DNA. Liquid was decanted off, then 150 µL of room temperature 70% EtOH was added to wash the pellet, and samples were again centrifuged at 15,000 g for 5 mins. After EtOH was decanted off, 150 µL of room temperature 70% EtOH was again added to wash pellets, and samples were again centrifuged at 15,000 g for 5 mins. After EtOH was decanted off, tubes were inverted and placed on a paper towel for a minimum of 10 mins to remove any excess liquid. Samples were then dried in a vacufuge at 45 °C for 15 mins, followed by air drying until no visible EtOH remained. DNA was then rehydrated with 100 µL of 1x TE buffer.

Extracted DNA samples from both methods were quantified using a Qubit® 3.0 Fluorometer with the Qubit™ dsDNA High Sensitivity Assay (ThermoFisher Scientific). Samples were quantified in triplicate and the average concentration (ng/µL) was used as the final value. Finally, 30 µL aliquots of each sample were plated on a 96-well 0.2 mL optical reaction plate. A total of 42 samples, two PCR positive controls, two field blanks (negative controls), and two extraction blanks (negative controls) were included on each plate. Plates were then stored at -20 °C until submission (typically less than 24 hours) for microfluidic metabarcoding (see below).

Primer selection. We conducted a comprehensive literature review to identify potential primer sets for further testing (Appendix 2), resulting in a total of 60 candidate primer sets across two mtDNA regions: cytochrome oxidase subunit 1 (COI), 16s ribosomal RNA (16S), and two nuclear genes: 18s rRNA (18S), and 28s rRNA (28S). Based upon the parameters of the microfluidic metabarcoding platform, we sought primers with published annealing temperatures of approximately 55 °C and with a mean fragment size of approximately 150-400 bp in length.

Primer sets within these parameters were subjected to for *in silico* (i.e., simulating PCR via the ecoPCR (Ficetola et al., 2010) software package and *in vitro* (i.e., subjecting extracted DNA from field collected bumblebees to PCR and confirmatory gel electrophoresis) validation. This included a total of 15 primer sets designed to amplify regions of the COI and 16S loci (Appendix 2). These primer sets have been used in studies investigating diversity of terrestrial arthropods (Clarke et al., 2014a), freshwater macroinvertebrates (Elbrecht & Leese, 2017; Vamos et al., 2017), freshwater mollusks (Klymus et al., 2017), and marine metazoans (Günther et al., 2018; Leray et al., 2013; Meusnier et al., 2008) as well as diet of various predators (Corse et al., 2019; Zeale et al., 2011). Several of the selected primers were recently vetted by Elbrecht et al. (2019) for terrestrial arthropod biodiversity assessment using DNA metabarcoding, where seven published primers outperformed 35 others that were tested: BF3/BR2 (Elbrecht et al., 2019), BF1/BR2 (Elbrecht & Leese, 2017), fwhF2/fwhR2n (Vamos et al., 2017), and mlCOIintF (Leray et al., 2013). By employing 15 primer sets that amplify different markers for microfluidic metabarcoding, we cast a much wider net of species detection than a single primer set with standard metabarcoding (Hauck et al., 2019).

In silico primer validation. We constructed a reference sequence database for invertebrate species that occur in Illinois using a list of binomial names based on observations by INHS

greenhouse staff, light-trapping data from the Illinois Bat Conservation Program (IBCP), Arthropods and Mollusks catalogued in the INHS Insect Collection (Illinois Natural History Survey Insect Collection, 2015), cicadas recorded by Dr. Catherine Dana (INHS), and T&E priorities provided by Angella Moorehouse (Illinois Nature Preserves Commission). With this list, all available COI and 16S rRNA sequences for Illinois invertebrate species were downloaded from GenBank using Reprophylo v1.3 (Szitenberg et al., 2015) in July 2019. Reference sequences in GenBank format were then converted to ecoPCR database format using obiconvert (Boyer et al., 2016). ecoPCR parameters were set to allow a 50–500 bp fragment and 0, 1, 2, or 3 mismatches between each primer and each sequence in the reference database. ecoPCR results were summarized using Microsoft Excel (Appendix 3).

In vitro primer validation. The subset of 15 primer sets was subjected to standard polymerase chain reaction (PCR) and gel electrophoresis was conducted. Eleven bee pollinator species known to occur in Illinois were selected. Reactions were conducted in 25 µL reactions using the following volumes: 12.5 µL of sterile water, 11.1 µL of GoTaq (ThermoFisher) colorless Mastermix, 0.2 µL 10 µM forward primer, 0.2 µL 10 µM reverse primer, and 1 µL of template DNA. The PCR program consisted of a 5 min 94 °C denaturation step, followed by 40 cycles consisting of a 45 sec 94 °C denaturation step, a 1 min 55 °C annealing step, and a 1 min 30 sec 72 °C extension step. Once these cycles were complete, a final 5 min 72 °C extension step was completed, followed by a hold at 4 °C. We confirmed PCR amplification via gel electrophoresis using 2.0% agarose gels in TAE buffer. Electrophoresis settings were 120 V for 90 minutes. Gels were visualized in a LabNet Systems EnduroGel Gel Documentation System. To account for PCR stocasticity, three replicates were conducted for all combinations. Those comparisons in which 3 of 3 replicates showed amplification were deemed successful. Comparisons in which 1 or 2 of 3 replicates showed amplification were deemed moderately successful, and those in which 0 of 3 replicates showed amplification were deemed unsuccessful.

Microfluidic metabarcoding. We used the Fluidigm 48.48 Access Array™ (Fluidigm, San Francisco, California, USA; Fluidigm Corporation, 2016) to employ generic primers for pollinator amplification. The Access Array uses integrated fluidic circuits and a 4-primer amplicon tagging scheme in which target-specific primer pairs amplify up to 48 different targets, allowing for the simultaneous amplification of barcoded targets in each of 2,304 reaction chambers. We selected primer sets for amplification based on taxonomic coverage (see Appendix 3) and that had Fluidigm compatible annealing temperatures of approximately 55 °C, and target amplicon lengths ranging from 150–400 bp (lower bound to meet post-amplification removal of primer-adapted dimers; upper bound to limit amplicon length for paired-end sequencing). Forward and reverse amplification primers were modified by the addition of 5' common sequence tags (CS1, CS2, www.fluidigm.com) which serve as the binding site for the addition of the P5 and P7 Illumina sequences and dual-index multiplex barcodes. Microfluidic metabarcoding, including Access Array amplification, Illumina sequencing, and demultiplexing, was conducted by the Roy J. Carver Biotechnology Center Functional Genomic Unit at UIUC.

metaBEAT pipeline. The demultiplexed FASTQ files for each primer set were processed using metaBEAT v0.97.11 (https://github.com/HullUnibioinformatics/metaBEAT), which incorporates open-source software for quality filtering, trimming, merging, chimera removal, clustering, and taxonomic assignment. After quality filtering (phred score Q30) and trimming using Trimmomatic v0.32 (Bolger et al., 2014), merging (10 bp overlap minimum and 10% mismatch maximum) using FLASH v1.2.11 (Magoč and Salzberg, 2011), chimera detection using the uchime algorithm (Edgar et al., 2011) in vsearch v1.1 (Rognes et al., 2016), and clustering (97% identity with three sequences minimum per cluster) with vsearch v1.1 (Rognes et al., 2016), non-redundant query sequences were compared against the reference database using BLAST (Zhang et al., 2000). Putative taxonomic identity was assigned using a lowest common ancestor (LCA) approach based on the top 10% BLAST matches for any query matching with at least 90% identity to a reference sequence across more than 80% of its length. Unassigned sequences were subjected to a separate BLAST against the complete NCBI nucleotide (nt) database at 90% identity to determine the source via LCA as described above.

Anacapa toolkit pipeline. The demultiplexed FASTQ files for each primer set were processed using the Anacapa Toolkit v1 (archived version doi:10.5281/zenodo.3064152 at github.com/limey-bean/Anacapa; Curd et al., 2019). The Anacapa pipeline consists of four modules to build comprehensive reference sequence databases and assign taxonomy to raw multilocus metabarcode sequence datasets. The fist module called Creating Reference libraries Using eXisting tools (CRUX) generates a custom reference sequence database by running *in silico* PCR for a primer set using ecoPCR (Ficetola et al., 2010) on the EMBL standard nucleotide database then uses *blastn* (Camacho et al., 2009) to query the seed database against the NCBI non-redundant nucleotide database, retaining only the longest version of each sequence then retrieving taxonomy using *entrez-qimme* v2.0 (Baker, 2016). CRUX generates an unfiltered database with all accessions and taxonomic path information as well as a paired filtered database that excludes accessions with ambiguous taxonomic paths. A *Bowtie2*-formated index library (Langmead and Salzberg, 2012) is also generated. We generated a reference 16s rRNA database using CRUX (NCBI nr/nt databases queried on 16 November 2019).

The second module conducts DNA sequence quality control and amplicon sequence variant (ASV) parsing. ASVs are unique sequence reads that differ by as little as 1–2 base pairs and are resolved without the arbitrary similarity thresholds that define operational taxonomic units (OTUs) (Edgar, 2016; Amir et al., 2017; Callahan et al., 2017). The ASV methods infer biological sequences in a sample from sequences with amplification and sequencing errors using a de novo process and the expectation that biological sequences are more likely to be repeatedly observed in a sample than erroneous samples (Callahan et al., 2016, 2017; Edgar, 2016). ASV methods have been shown to outperform OTU method in the sensitivity and accuracy of correcting erroneous sequences, improving taxonomic resolution and increasing observed diversity in a sample (Callahan et al., 2016; Edgar, 2016; Needham et al., 2017).

First, *cutadapt* (Martin, 2011) and *FastX-toolkit* (Gordon and Hannon, 2010) were used to trim primers, Illumina adapters, and low-quality bases from raw FASTQ files for each sample using the sample quality filtering and trimming settings as in the metaBEAT pipeline. A custom Python script sorted sequence reads into three sets – paired-end, forward only, and reverse only – then processed each set separately through *dada2* v1.14 (Callahan et al., 2016) to denoise, dereplicate, merge paired reads, and remove chimeric sequences. This module generated ASV FASTA files and ASV count summary tables for four read types: merged paired-end reads, unmerged paired-end reads, forward only reads, and reverse only reads.

The resulting ASV FASTA files and count summary tables were inputted into the Anacapa Classifier module, which assigns taxonomy to ASVs using *Bowtie2* and modified version of Bayesian Least Common Ancestor (BLCA) algorithm (Gao et al., 2017). *Bowtie2* was used to query ASVs against the CRUX-generated reference databases using the very-sensitive option to determine up to 100 reference matches. *Bowtie2-BCLA* then was used to process the output, using multiple sequence alignment via *muscle* v3.8.31 (Edgar, 2004), with 100 bootstraps to probabilistically determine taxonomic identity by selecting the lowest common ancestor from the multiple weighted *Bowtie2* hits for each ASV (Curd et al., 2019).

Data analysis. All data manipulation and downstream analysis was conducted in R v3.6.3 (R Core Team, 2020). Datasets for each primer set from both pipelines were combined into one master dataset and contamination in controls assessed (Fig. 1). A false positive sequence threshold was calculated based on the maximum frequency of exogenous DNA from metazoan taxa found in the negative controls (1.17%), i.e., field blanks, extraction blanks, and PCR negative controls. The false positive sequence threshold was applied to the metabarcoding data, and the data filtered to remove non-metazoan taxa before combining with greenhouse and field metadata. We then examined several biotic and technical grouping variables that may influence pollinator detection: 1) flower species sampled, 2) sample type, 3) preservation/extraction method, 4) bioinformatics pipeline, and 5) primer set.

The read count data were converted to site x taxonomy presence-absence matrices using the *decostand* function in the R package vegan v2.5-6 (Oksanen et al., 2019). Presence-absence matrices were used as potential bias introduced by PCR amplification may prevent reliable abundance or biomass estimation from sequence reads produced by DNA or eDNA metabarcoding (Elbrecht et al., 2017). First, taxon richness of eDNA samples according to each grouping variable was compared. Alpha diversity was obtained using the *specnumber* function in vegan (Oksanen et al., 2019). The data were not normally distributed, and the assumptions of a one-way Analysis of Variance (ANOVA) and Generalised Linear Models (GLMs) with different error families and link-functions were violated. Therefore, we compared taxon richness according to each grouping variable using the non-parametric Kruskal-Wallis test and performed multiple pairwise comparisons using the non-parametric Dunn's test.

The R package betapart v1.5.1 (Baselga and Orme, 2012) was used to estimate total beta diversity, partitioned by nestedness (i.e., community dissimilarity due to taxon subsets) and turnover (i.e. community dissimilarity due to taxon replacement), across all samples with the

beta.multi function. These three components of beta diversity (Jaccard dissimilarity) were then estimated for eDNA samples according to each grouping variable (e.g. flower species) using the *beta.pair* function. For each component of beta diversity, we compared the variance in each group of samples by calculating homogeneity of multivariate dispersions (MVDISP) using the *betadisper* function from vegan (Oksanen et al., 2019). Differences in MVDISP between groups of eDNA samples was then statistically tested using an ANOVA. Community dissimilarity for each component of beta diversity was visualized using Non-metric Multidimensional Scaling (NMDS) with the *metaMDS* function and tested statistically using permutational multivariate analysis of variance (PERMANOVA) with the function *adonis* in vegan (Oksanen et al., 2019). Pre-defined cut-off values were used for effect size, where PERMANOVA results were interpreted as moderate and strong effects if $R^2 > 0.09$ and $R^2 > 0.25$ respectively. These values are broadly equivalent to correlation coefficients of $r = 0.3$ and 0.5 which represent moderate and strong effects accordingly (Nakagawa and Cuthill, 2007; Macher et al., 2018).

RESULTS

Primer development and validation. Our literature review revealed almost 120 individual arthropod primers that yielded well over 60 primer combinations across two mtDNA regions and two nuclear genes. A coarse assessment of primer performance for microfluidic metabarcoding (based upon an approximately 55 °C annealing temperature and a 150–400 bp fragment length) yielded a subset of 15 primers for extensive *in silico* and *in vitro* validation. *In silico* and *in vitro* testing revealed that the selected primer sets were largely successful in amplifying bee pollinator DNA, specifically 11 species that occur in Illinois (Table 1). Given these results, we chose to retain the full primer panel for pollinator microfluidic eDNA metabarcoding. More critically, these results reveal that we were successful in our first objective, i.e., to develop and validate, both *in silico* and *in vitro*, a panel of broad-spectrum pollinator eDNA metabarcoding primers.

Contamination. Before false positive threshold application, we detected 712 taxa from 345 eDNA samples. Microfluidic eDNA metabarcoding correctly identified seven out of ten bee species used as PCR positive controls to species-level, with three species identified to genus or family-level. However, the PCR positive controls contained a number of contaminants (Fig. 2) due to the manner in which bee specimens were collected, stored, and preserved by museum staff. In contrast, the negative process controls (field, extraction, and PCR) possessed very little contamination (Fig. 2). A total of 517 taxa were consistently detected below the sequence threshold (1.17%) calculated using our negative process controls. Therefore, the final dataset after threshold application contained 195 taxa for downstream analyses. Among the taxa retained were floral visitors, floral residents, and key pollinator species, such as common eastern bumblebee (*Bombus impatiens*), western flower thrip (*Frankliniella occidentalis*), silverleaf whitefly (*Bemisia tabaci*), aphids (*Aphis* spp.), banded garden spider (*Argiope trifasciata*), and white-lined sphinx (*Hyles lineata*).

Table 1. Heat map depicting the results of *in vitro* primer validation. The subset of primers with approximately appropriate annealing temperature and fragment length were tested with 11 locally occurring bee species using PCR and verified via gel electrophoresis. Blue cells represent comparisons in which all three replicates were positive, gold cells represent comparisons in which one or two replicates were positive, and grey cells represent comparisons in which all three resplicates failed.

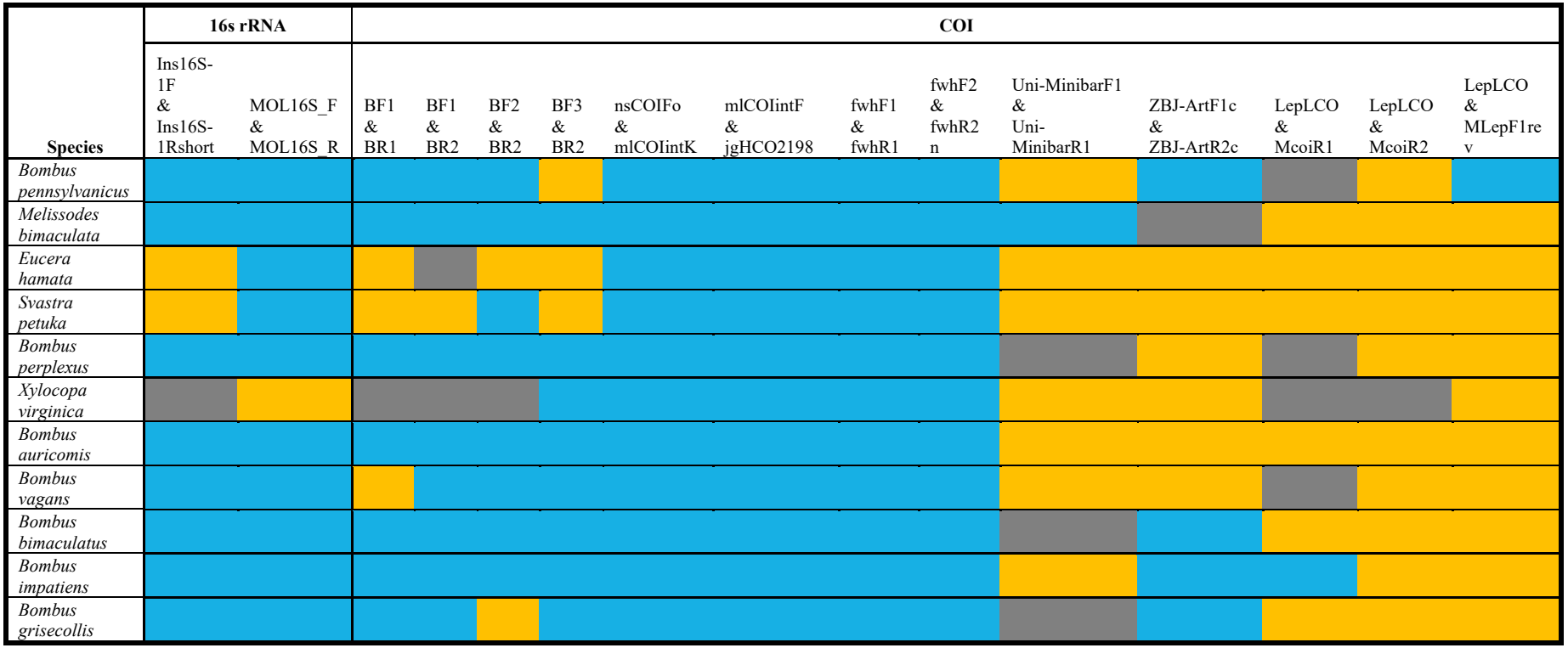


Figure 2. Heat map showing the frequency of contaminants detected in metabarcoding process controls. Assignments that were not detected in a control are colored white with no border.

Greenhouse results. Our target bee species, the common eastern bumblebee (*B. impatiens*) was not detected in any of the baseline eDNA samples collected from flower species before they were introduced to the greenhouse containing the target pollinator species (Fig. 3). Microfluidic metabarcoding successfully detected the common eastern bumblebee (*B. impatiens*) from eDNA samples upon introduction. Both whole flowers (n = 1) and swabs (n = 3) from *Monarda* preserved in CTAB yielded positive detections for the target species, but not samples preserved in ATL buffer. All sample types from *Penstemon, Solanum*, and *Cyngolossum amabile* failed to detect the target species. In addition to the target species, beneficial insects that had been released in the greenhouse as well as other species known to occur in the greenhouse facilities were detected via our microfluidic eDNA metabarcoding approach. Specifically, the insidious flower bug (*Orius insidiosus*), dark-winged fungus gnats (*Bradysia impatiens*), shore flies (*Scatella stagnalis*), western flower thrips (*Frankliniella occidentalis*), and silverleaf whitefly (*Bemisia tabaci*) were detected. However, a number of beneficial arthropod species as well as species known to occur in the greenhouse were not detected, including *Hippodamia convergens, Amblyseius californicus, Encarsia formosa, Phidippus audax, Brasysia coprophilia, Ceuthophilus* spp.*,* Tetranychidae spp.*, Trialeurodes abutiloneus,* and *T. vaporariorum*. Finally, several species not previously known to occur in the greenhouse were detected, including aphids (*Aphis* spp.) and banded garden spiders (*Argiope trifasciata*).

Field results. We observed seven bee pollinator species in the field (*B. auricomus, B. bimaculatus, B. griseocollis, B. impatiens, B. pensylvanicus, Apis mellifera,* and *Xylocopa virginica*). Prior to false positive sequence threshold application, *B. bimaculatus*, *B. griseocollis*, and *B. vagans* were detected at low frequencies from *Penstemon* whole flowers, but not *Penstemon* swabs or any *Mondarda* samples. None of the observed bee species were detected using microfluidic eDNA metabarcoding after application of our false positive sequence threshold. This included the carpenter bee (*X. virginica*) despite widespread observations and extensive evidence of nectar robbing by this species. Pollinators that were not directly observed but were recovered via microfluidic eDNA metabarcoding included white-lined sphinx moth (*Hyles lineata*), cigarette beetle (*Lasioderma serricorne*), *Melanophthalma inermis*, Eastern calligrapher (*Toxomerus geminatus*), common paragus (*Paragus haemorrhous*), house fly (*Musca domestica*), *Paraliburnia kilmani*, *Psychoda alternata*, insidious flower bug (*Orius insidiosus*), western flower thrips (*Frankliniella occidentalis*), and eastern flower thrips (*Frankliniella tritici*).

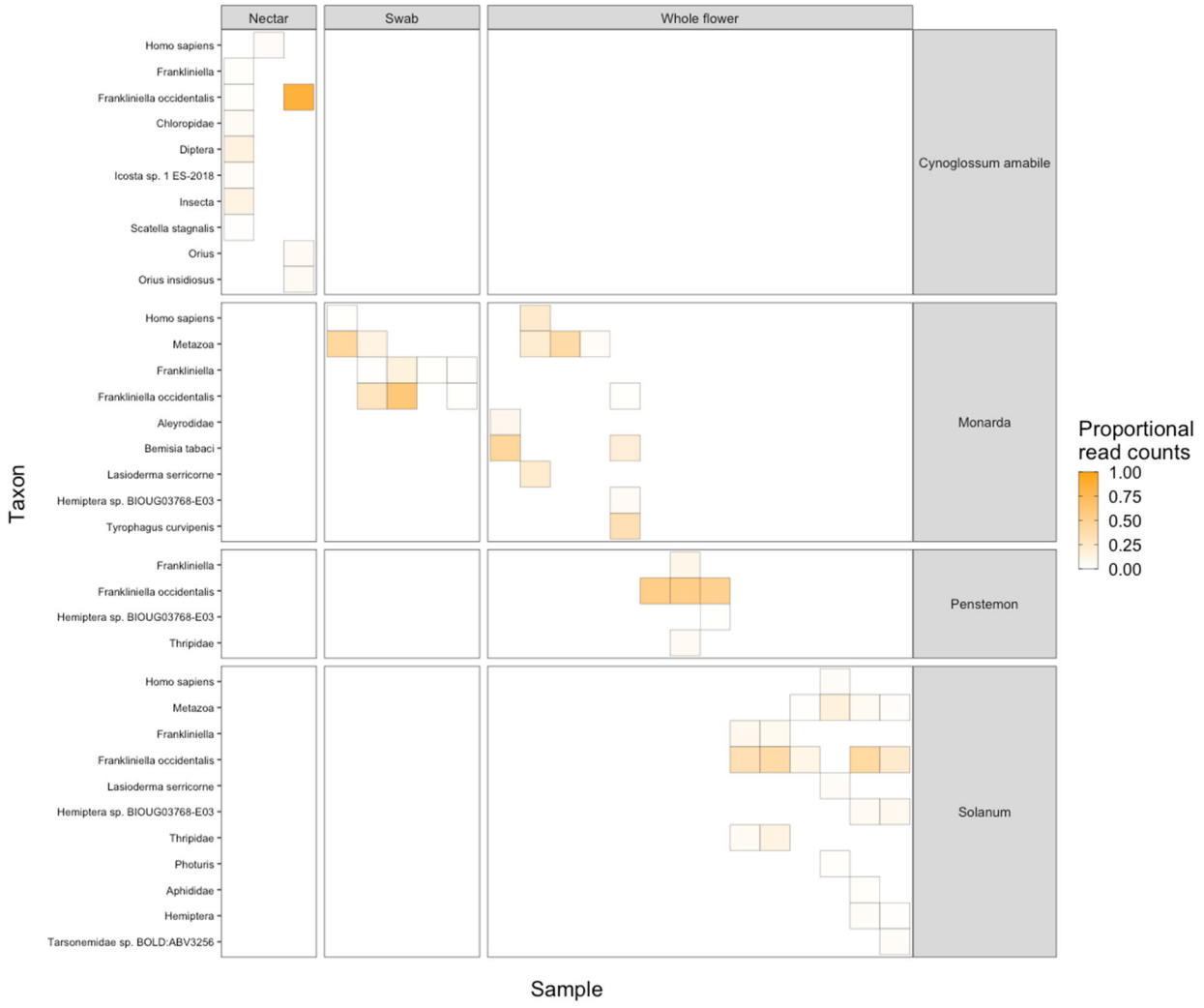


Figure 3. Heat map showing the frequency of taxa detected in baseline samples collected from flower species before they were introduced to the greenhouse containing common eastern bumblebee (*B. impatiens*). Assignments that were not detected in a control are colored white with no border.

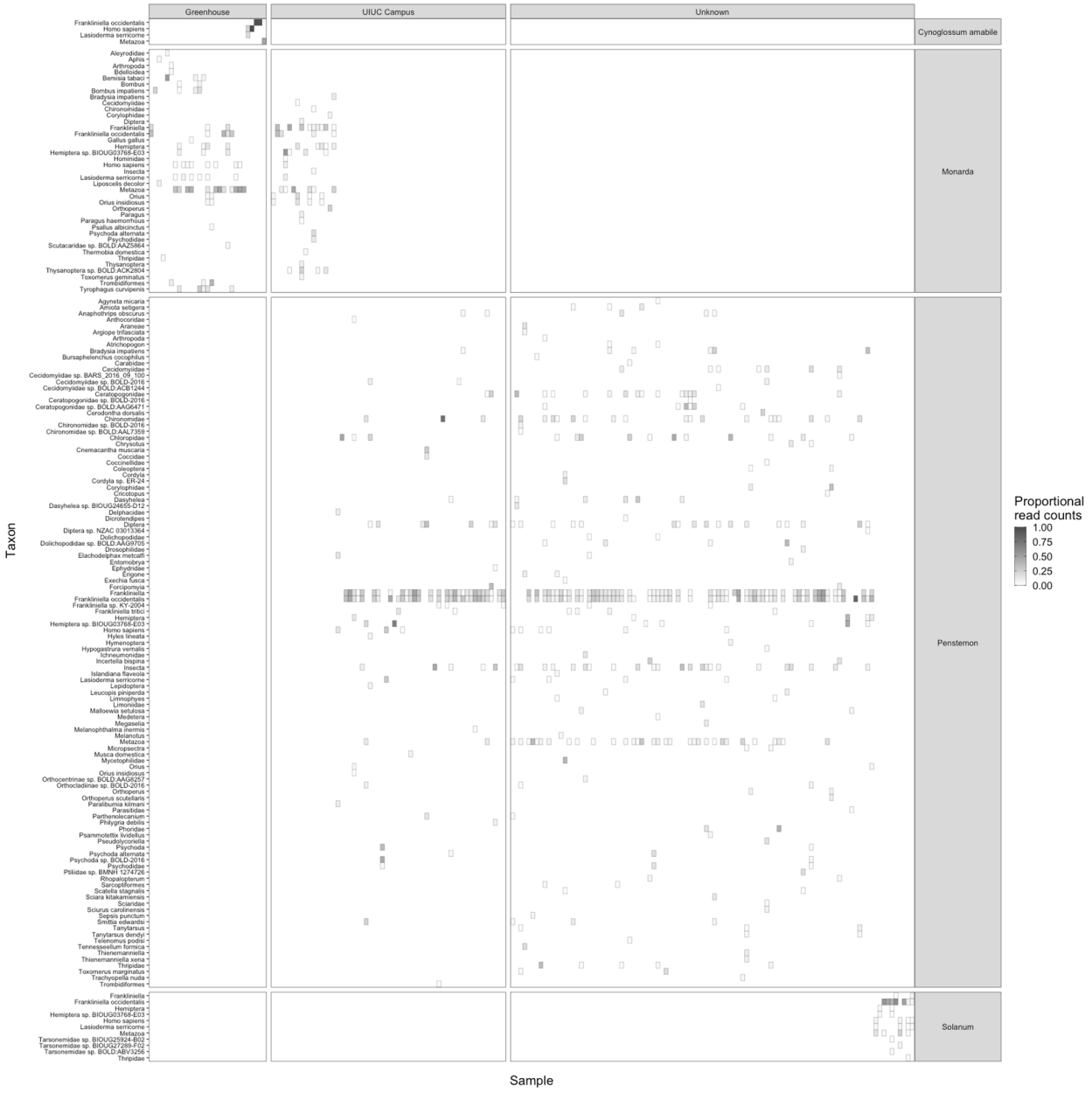


Figure 4. Heat map showing the frequency of taxa detected in greenhouse and field samples collected from our four focal flower species. Assignments that were not detected in a control are colored white with no border.

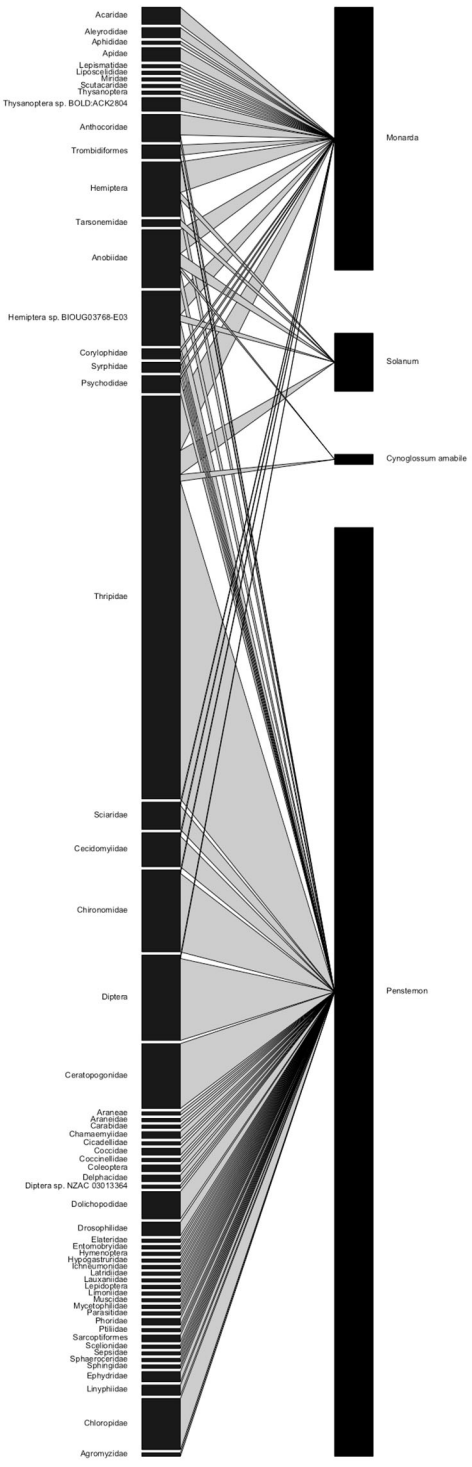


Figure 5. Bipartite network showing interactions between invertebrate families and our four focal flower species. *Monarda* and *Penstemon* possessed the most interactions suggesting that these flower species support more pollinator diversity or retain more pollinator eDNA.

Diversity Across Flower Species. Flower species had a significant effect on alpha diversity of eDNA samples ($\chi^2_3 = 16.328$, $P < 0.001$). Taxon richness for *Cynoglossum amabile* (nectar draws only) was significantly lower than all other flower species (*Monarda* Z = -2.569, $P = 0.010$; *Penstemon* Z = -3.490, $P = 0.001$; *Solanum* Z = -2.044; $P = 0.041$), and greater for *Penstemon* than *Monarda* (-2.058, $P = 0.040$) (Fig. 6). Beta diversity among eDNA samples was largely driven by turnover (99.65%) as opposed to nestedness (0.35%). MVDISP did not significantly differ between flower species for turnover, nestedness, and total beta diversity (Table 2). Flower species had a weak positive effect on turnover and total beta diversity of pollinator communities (Table 2; Fig. 7).

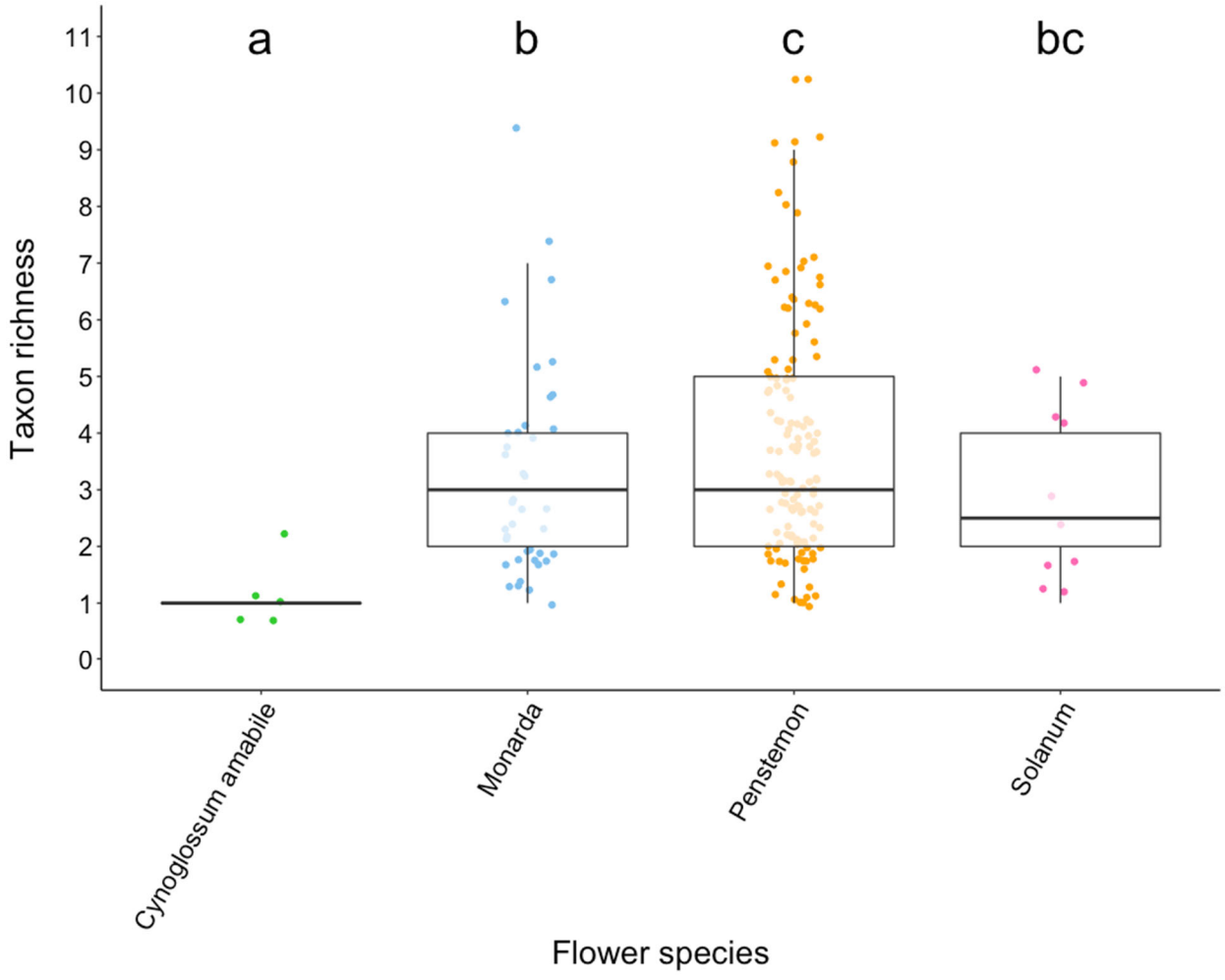


Figure 6. Boxplot showing the number of taxa detected in eDNA samples from different flower species. Taxon richness was significantly different in relation to flower species. Boxes show 25th, 50th, and 75th percentiles, and whiskers show 5th and 95th percentiles.

Table 2. Summary of analyses statistically comparing homogeneity of multivariate dispersions (MVDISP) between the communities of different flower species (ANOVA) and variation in community composition of eDNA samples from different flower species (PERMANOVA).

	Homogeneity of multivariate dispersions (ANOVA)				**Community similarity (PERMANOVA)**			
	Mean distance to centroid ± SE	**df**	***F***	***P***	**df**	***F***	***R^2***	***P***
Turnover		3	2.587	0.055	3	5.582	0.084	**0.001**
Cynoglossum amabile	0.559 ± 0.010							
Monarda	0.582 ± 0.028							
Penstemon	0.449 ± 0.099							
Solanum	0.408 ± 0.060							
Nestedness		3	1.403	0.243	3	-1.512	-0.025	0.958
Cynoglossum amabile	0.138 ± 0.021							
Monarda	0.124 ± 0.016							
Penstemon	0.169 ± 0.024							
Solanum	0.214 ± 0.031							
Total beta diversity		3	1.956	0.122	3	4.394	0.067	**0.001**
Cynoglossum amabile	0.569 ± 0.018							
Monarda	0.629 ± 0.008							
Penstemon	0.550 ± 0.045							
Solanum	0.529 ± 0.014							

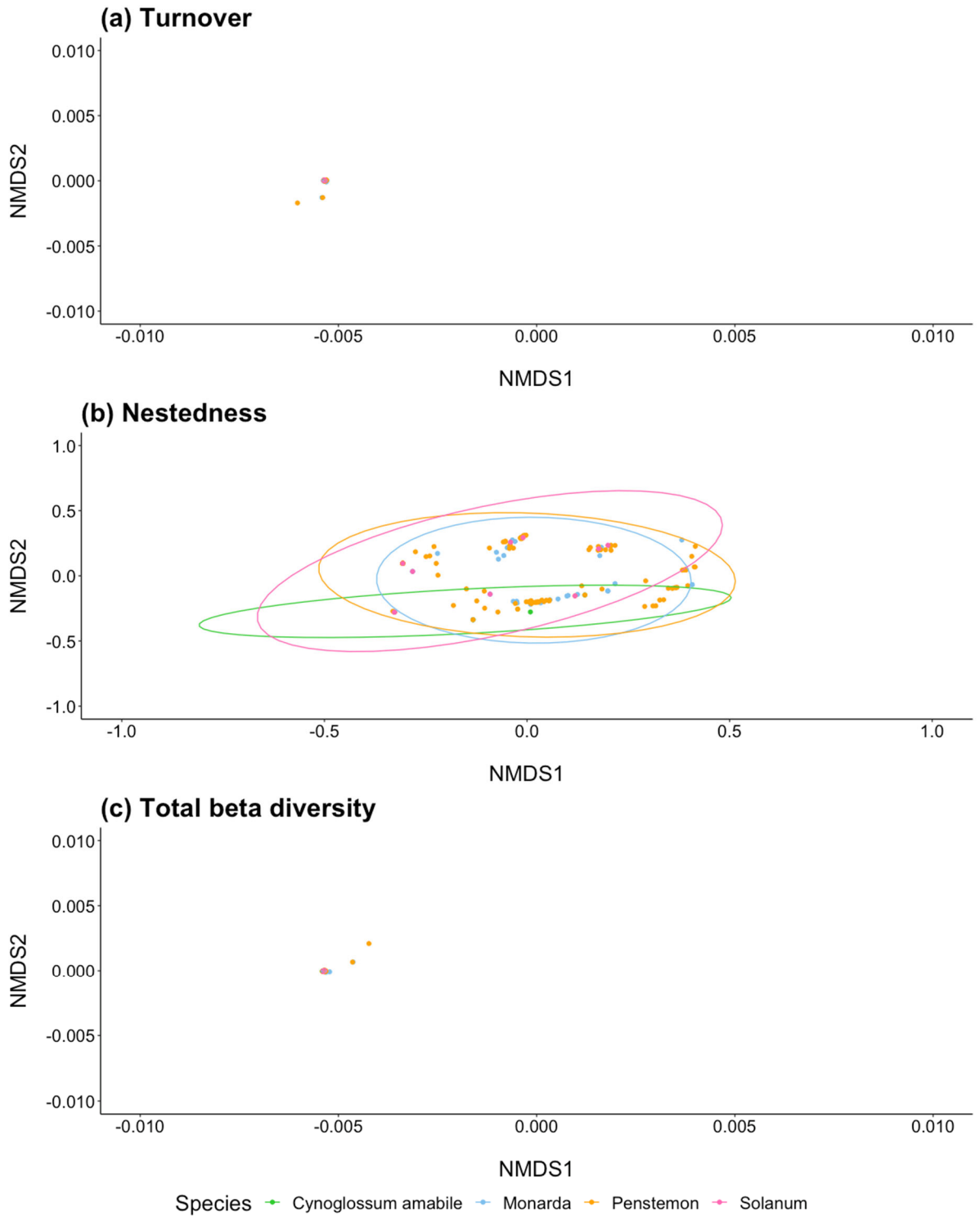


Figure 7. Non-metric Multidimensional Scaling (NMDS) plots of communities (Jaccard dissimilarity) from different flower species (colored points/ellipses). The turnover **(a)** and nestedness **(b)** partitions of total beta diversity **(c)** are shown.

Diversity across sample types. Sample type (i.e., swab, nectar, or whole flower) significantly influenced alpha diversity of eDNA samples ($\chi^2_2 = 14.47$, $P < 0.001$). Taxon richness from nectar draws (*Cynoglossum amabile* only) was lower than swabs (Z = -2.841, $P = 0.005$) and whole flowers (Z = -3.493, $P < 0.001$). Swabs also produced lower taxon richness than whole flowers (Z = -2.001, $P = 0.045$) (Fig. 8). MVDISP did not differ between sample types for turnover, nestedness, or total beta diversity (Table 3). Sample type had a weak positive effect on nestedness of pollinator communities, but not turnover or total beta diversity (Table 3; Fig. 9).

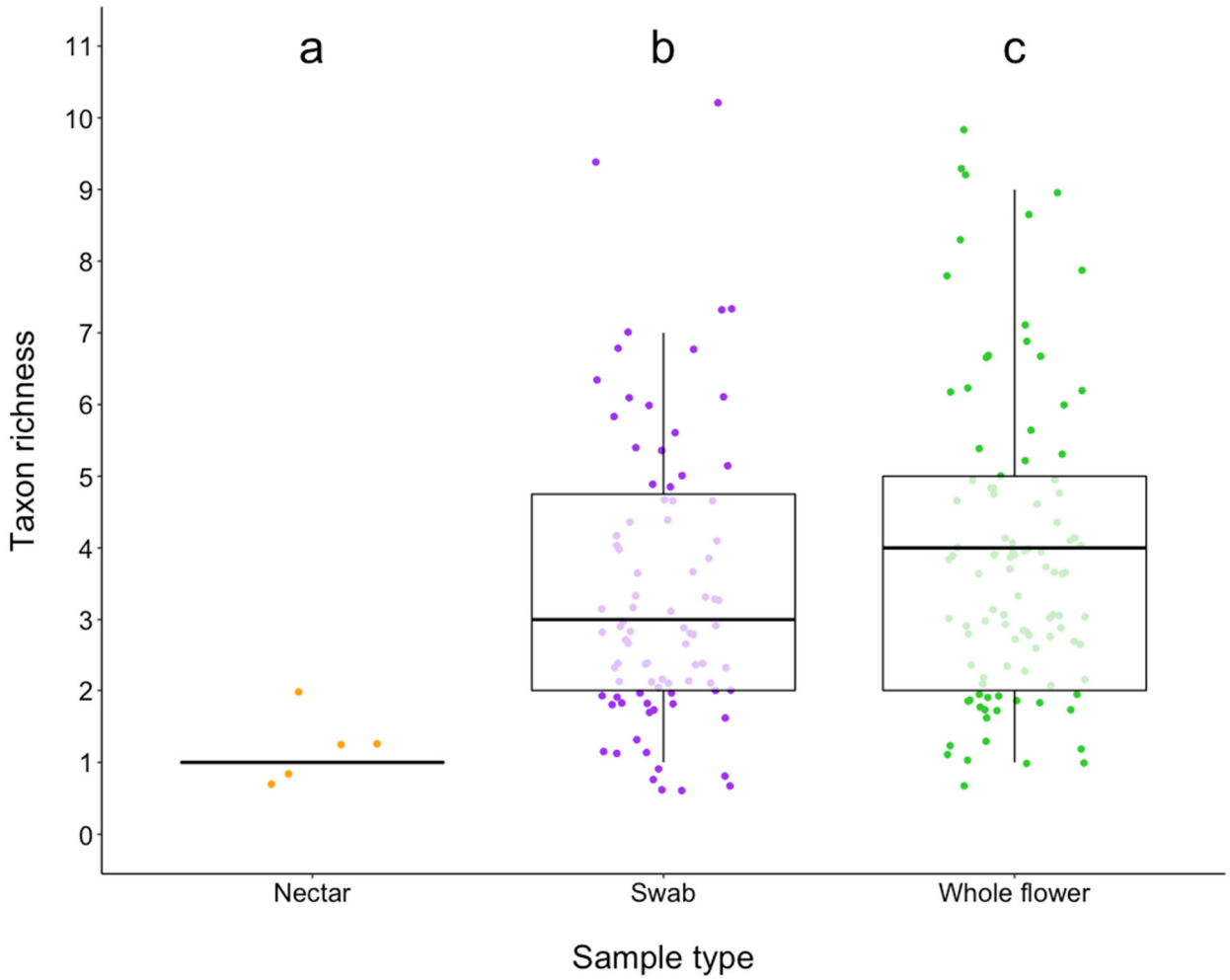


Figure 8. Boxplot showing the number of taxa detected in eDNA samples taken from different sources of plant material. Taxon richness was significantly different in relation to sample type. Boxes show 25th, 50th, and 75th percentiles, and whiskers show 5th and 95th percentiles.

Table 3. Summary of analyses statistically comparing homogeneity of multivariate dispersions (MVDISP) between the communities produced by different sample types (ANOVA) and variation in community composition of eDNA samples sourced from different material (PERMANOVA).

	Homogeneity of multivariate dispersions (ANOVA)				**Community similarity (PERMANOVA)**			
	Mean distance to centroid ± SE	**df**	***F***	***P***	**df**	***F***	***R²***	***P***
Turnover		2	0.398	0.673	2	0.730	0.008	0.707
Nectar	0.560 ± 0.010							
Swab	0.541 ± 0.069							
Whole flower	0.511 ± 0.055							
Nestedness		2	0.842	0.432	2	8.035	0.078	**0.003**
Nectar	0.141 ± 0.022							
Swab	0.131 ± 0.017							
Whole flower	0.158 ± 0.024							
Total beta diversity		2	0.073	0.929	2	1.310	0.014	0.135
Nectar	0.569 ± 0.018							
Swab	0.596 ± 0.037							
Whole flower	0.590 ± 0.022							

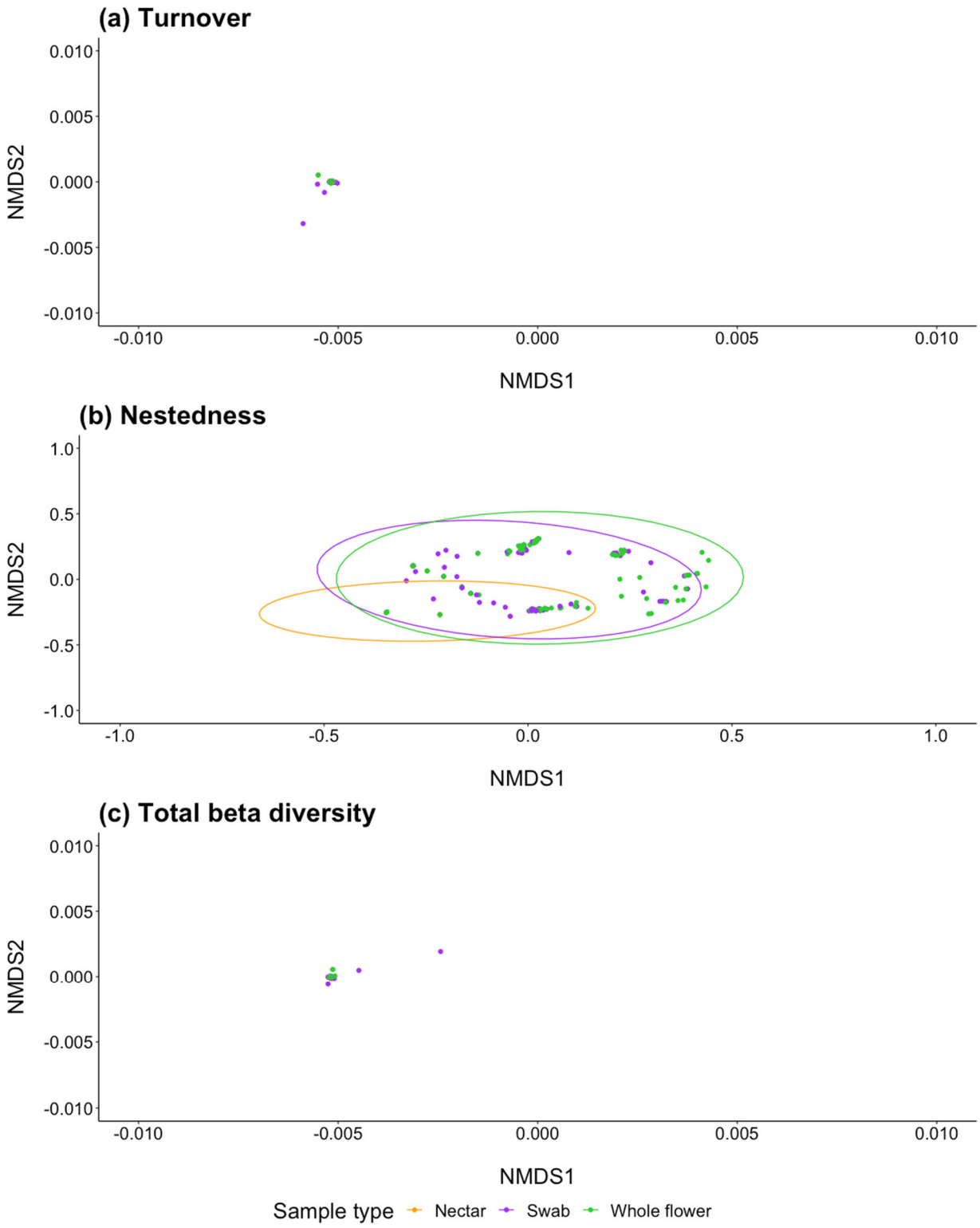


Figure 9. Non-metric Multidimensional Scaling (NMDS) plots of communities (Jaccard dissimilarity) produced by different sample types (colored points/ellipses). The turnover **(a)** and nestedness **(b)** partitions of total beta diversity **(c)** are shown.

Diversity across preservation/extraction method. Preservation/extraction method did not have an effect on alpha diversity of eDNA samples (GLM: $\chi^2_1 = 10.346$, $P = 0.001$). Taxon richness was greater when samples were preserved in ATL buffer and extraction with a commercial Qiagen kit ($Z = 3.217$, $P = 0.001$) as opposed to CTAB and extraction with a PCI protocol (Fig. 10). MVDISP was not different between preservation/extraction methods for turnover, nestedness, or total beta diversity (Table 4). Preservation/extraction method had no effect on turnover of pollinator communities but did weakly and moderately influence nestedness and total beta diversity respectively (Table 4; Fig. 11).

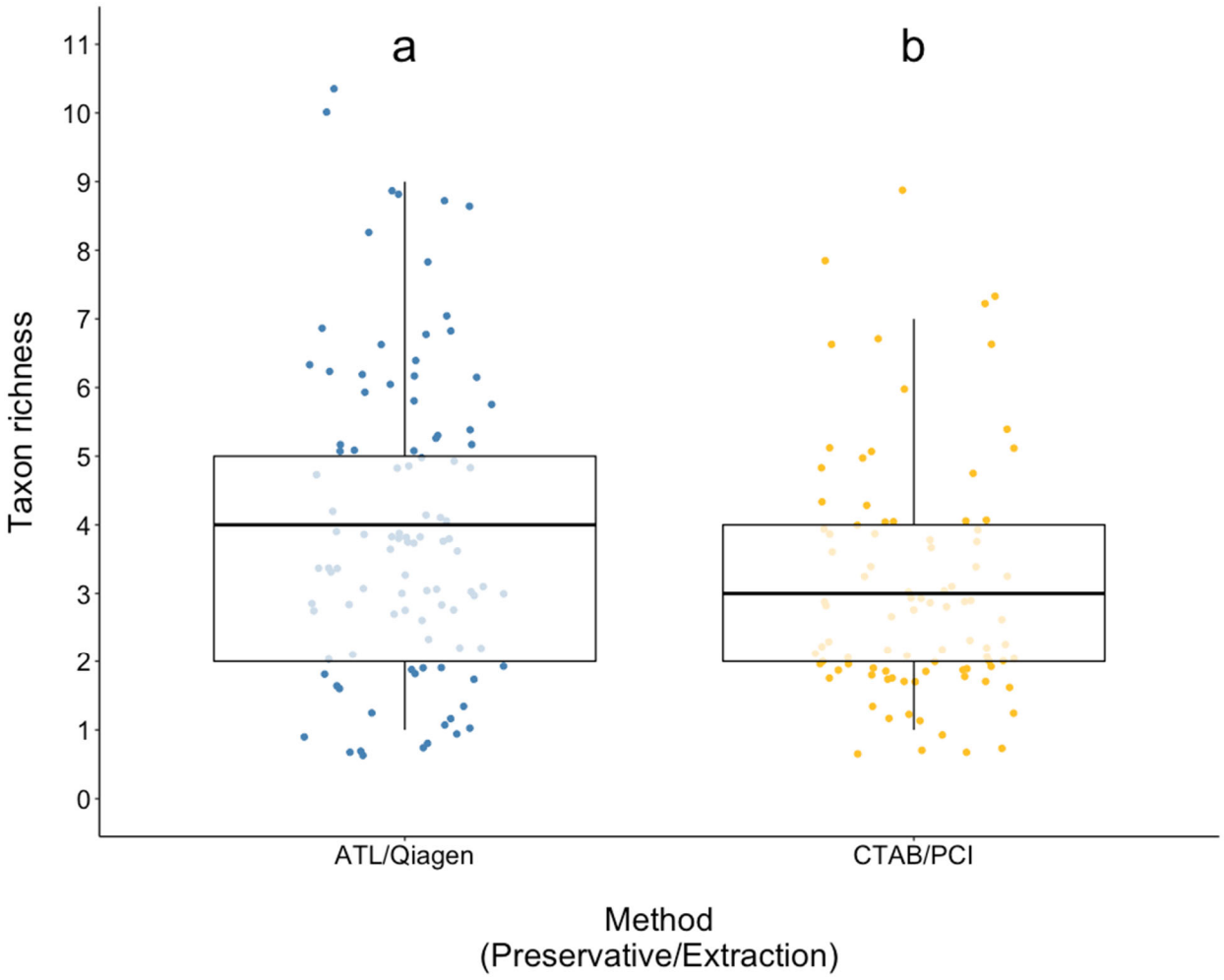


Figure 10. Boxplot showing the number of taxa detected in eDNA samples that were preserved and extracted using different methods. Taxon richness was significantly different in relation to preservation/extraction method. Boxes show 25th, 50th, and 75th percentiles, and whiskers show 5th and 95th percentiles.

Table 4. Summary of analyses statistically comparing homogeneity of multivariate dispersions (MVDISP) between the communities produced by different preservation/extraction methods (ANOVA) and variation in community composition of eDNA samples preserved and extracted using different protocols (PERMANOVA).

	Homogeneity of multivariate dispersions (ANOVA)				**Community similarity (PERMANOVA)**			
	Mean distance to centroid ± SE	**df**	***F***	***P***	**df**	***F***	***R²***	***P***
Turnover		1	0.0001	0.991	1	0.334	0.005	0.473
ATL/Qiagen	0.522 ± 0.045							
CTAB/PCI	0.521 ± 0.098							
Nestedness		1	1.118	0.292	1	21.094	0.099	**0.001**
ATL/Qiagen	0.149 ± 0.023							
CTAB/PCI	0.127 ± 0.019							
Total beta diversity		1	0.192	0.662	1	2.116	0.011	**0.015**
ATL/Qiagen	0.596 ± 0.017							
CTAB/PCI	0.584 ± 0.053							

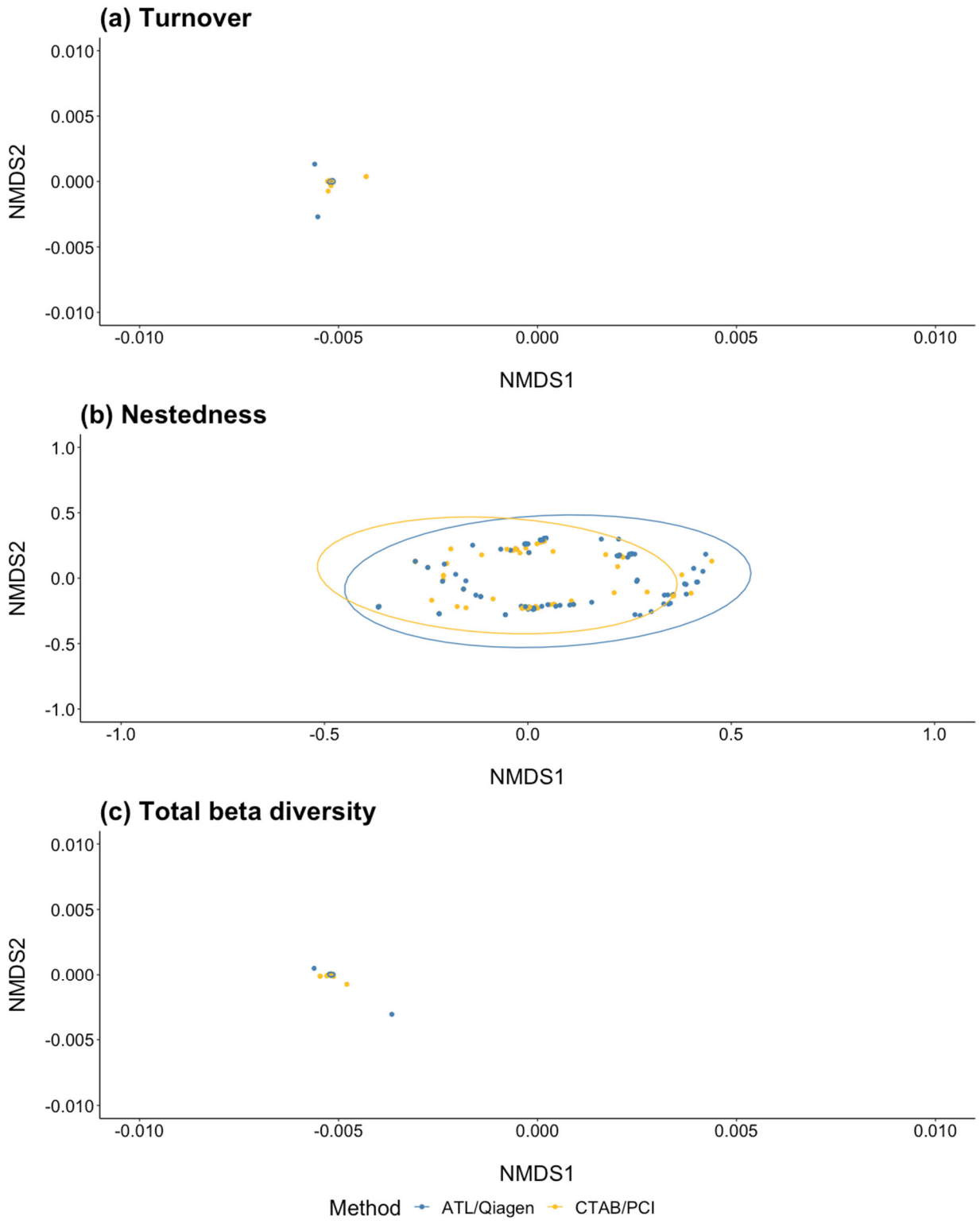


Figure 11. Non-metric Multidimensional Scaling (NMDS) plots of communities (Jaccard dissimilarity) produced by different preservation/extraction methods (colored points/ellipse). The turnover **(a)** and nestedness **(b)** partitions of total beta diversity **(c)** are shown.

Diversity across primer sets. Primer set used for microfluidic eDNA metabarcoding had an effect on alpha diversity of eDNA samples (GLM: $\chi^2_{14} = 352.86$, $P < 0.001$). Overall, taxon richness was higher using BF1/BR2 and mlCOIintF/jgHCO2198, but taxon richness significantly differed between most primer sets (Fig. 12). MVDISP differed between primer sets for turnover, nestedness, and total beta diversity (Table 5). Primer set exerted a moderate influence on turnover and total beta diversity of communities but had no effect on nestedness (Table 5; Fig. 13).

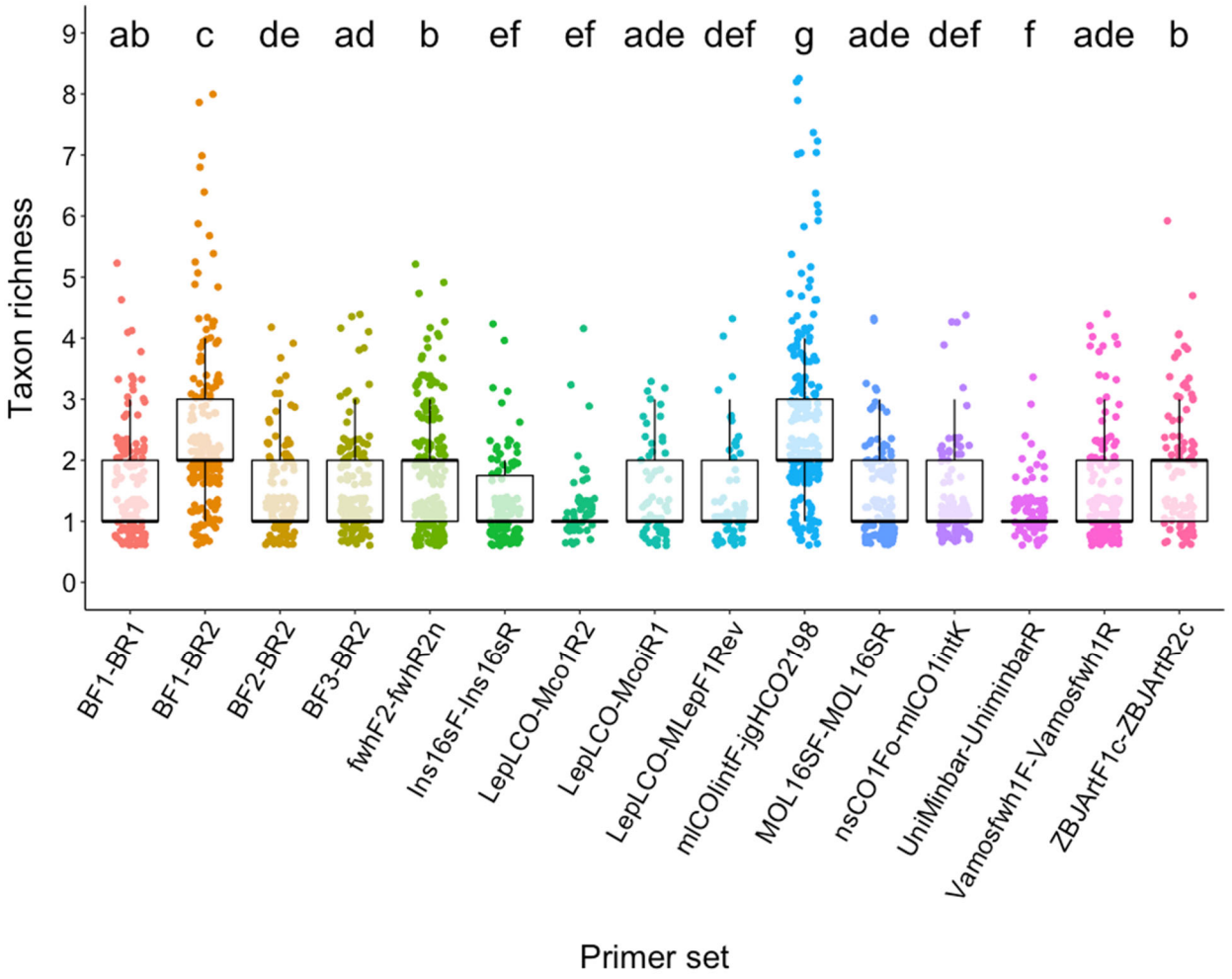


Figure 12. Boxplot showing the number of taxa detected in eDNA samples using different primer sets. Taxon richness was significantly different in relation to primer set used. Boxes show 25th, 50th, and 75th percentiles, and whiskers show 5th and 95th percentiles.

Table 5. Summary of analyses statistically comparing homogeneity of multivariate dispersions (MVDISP) between the communities produced by different primer sets (ANOVA) and variation in community composition of eDNA samples when amplified with different primer sets (PERMANOVA).

	Homogeneity of multivariate dispersions (ANOVA)				**Community similarity (PERMANOVA)**			
	Mean distance to centroid ± SE	**df**	***F***	***P***	**df**	***F***	***R²***	***P***
Turnover		14	10.400	**0.001**	14	24.639	0.162	**0.001**
BF1/BR1	0.375 ± 0.169							
BF1/BR2	0.369 ± 0.195							
BF2/BR2	0.666 ± 0.129							
BF3/BR2	0.404 ± 0.184							
fwhF1/fwhR1	0.499 ± 0.131							
fwhF2/fwhR2n	0.404 ± 0.184							
LepLCO/McoiR1	0.629 ± 0.011							
LepLCO/McoiR2	0.593 ± 0.052							
LepLCO/MLepF1Rev	0.625 ± 0.011							
mlCOIintF/jgHCO2198	0.456 ± 0.143							
nsCO1Fo/mlCO1intK	0.657 ± 0.007							
UniMinbar/UniminbarR	0.549 ± 0.120							
ZBJArtF1c/ZBJArtR2c	0.613 ± 0.019							
Ins16sF/Ins16sR	0.512 ± 0.135							
MOL16SF/MOL16SR	0.477 ± 0.137							
Nestedness		14	9.331	**<0.001**	14	-28.71	-0.291	1.000
BF1/BR1	0.204 ± 0.027							
BF1/BR2	0.147 ± 0.044							
BF2/BR2	0.064 ± 0.006							
BF3/BR2	0.136 ± 0.022							
fwhF1/fwhR1	0.144 ± 0.025							
fwhF2/fwhR2n	0.194 ± 0.029							
LepLCO/McoiR1	0.090 ± 0.011							
LepLCO/McoiR2	0.098 ± 0.017							
LepLCO/MLepF1Rev	0.110 ± 0.013							
mlCOIintF/jgHCO2198	0.158 ± 0.031							
nsCO1Fo/mlCO1intK	0.064 ± 0.005							
UniMinbar/UniminbarR	0.096 ± 0.016							
ZBJArtF1c/ZBJArtR2c	0.128 ± 0.014							
Ins16sF/Ins16sR	0.098 ± 0.022							
MOL16SF/MOL16SR	0.151 ± 0.023							
Total beta diversity		14	6.235	**<0.001**	14	20.123	0.136	**0.001**
BF1/BR1	0.468 ± 0.166							
BF1/BR2	0.482 ± 0.163							
BF2/BR2	0.673 ± 0.005							
BF3/BR2	0.586 ± 0.077							
fwhF1/fwhR1	0.569 ± 0.082							
fwhF2/fwhR2n	0.496 ± 0.178							

LepLCO/McoiR1	0.647 ± 0.005
LepLCO/McoiR2	0.619 ± 0.033
LepLCO/MLepF1Rev	0.647 ± 0.005
mlCOIintF/jgHCO2198	0.548 ± 0.076
nsCO1Fo/mlCO1intK	0.664 ± 0.006
UniMinbar/UniminbarR	0.584 ± 0.091
ZBJArtF1c/ZBJArtR2c	0.646 ± 0.008
Ins16sF/Ins16sR	0.562 ± 0.086
MOL16SF/MOL16SR	0.555 ± 0.073

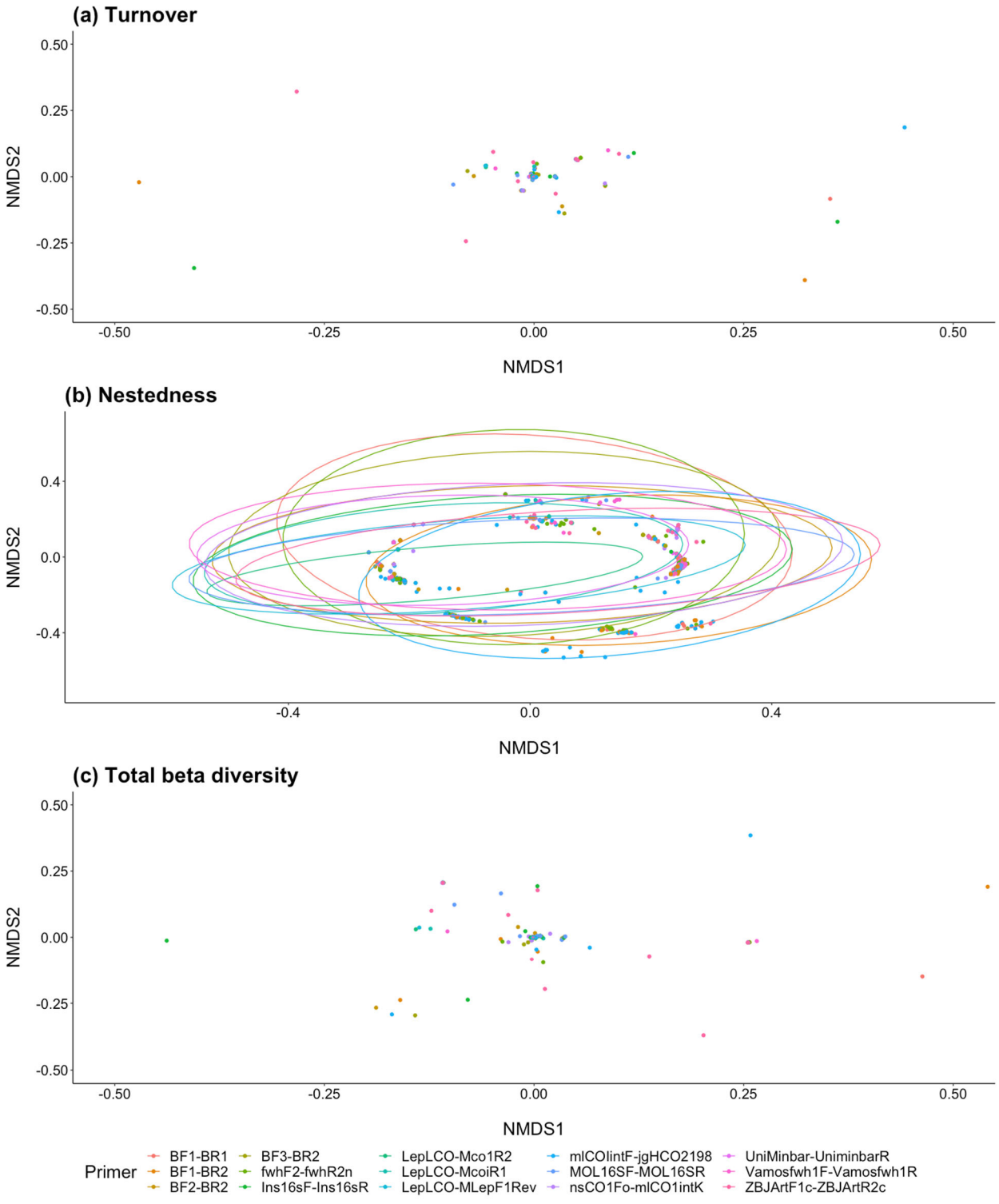


Figure 13. Non-metric Multidimensional Scaling (NMDS) plots of communities (Jaccard dissimilarity) produced by different primer sets (colored points/ellipse). The turnover **(a)** and nestedness **(b)** partitions of total beta diversity **(c)** are shown.

Diversity across bioinformatics pipelines. Bioinformatics pipeline used to process the metabarcoding data influenced alpha diversity of eDNA samples (GLM: $\chi^2_1 = 33.741$, $P < 0.001$). Taxon richness generated by Anacapa was lower than taxon richness generated by metaBEAT ($Z = -5.809$, $P < 0.001$) (Fig. 14). MVDISP was not different between bioinformatics pipelines for turnover, nestedness, or total beta diversity (Table 6). Bioinformatics pipeline exerted a weak influence on turnover and total beta diversity of pollinator communities, but not nestedness (Table 6; Fig. 15).

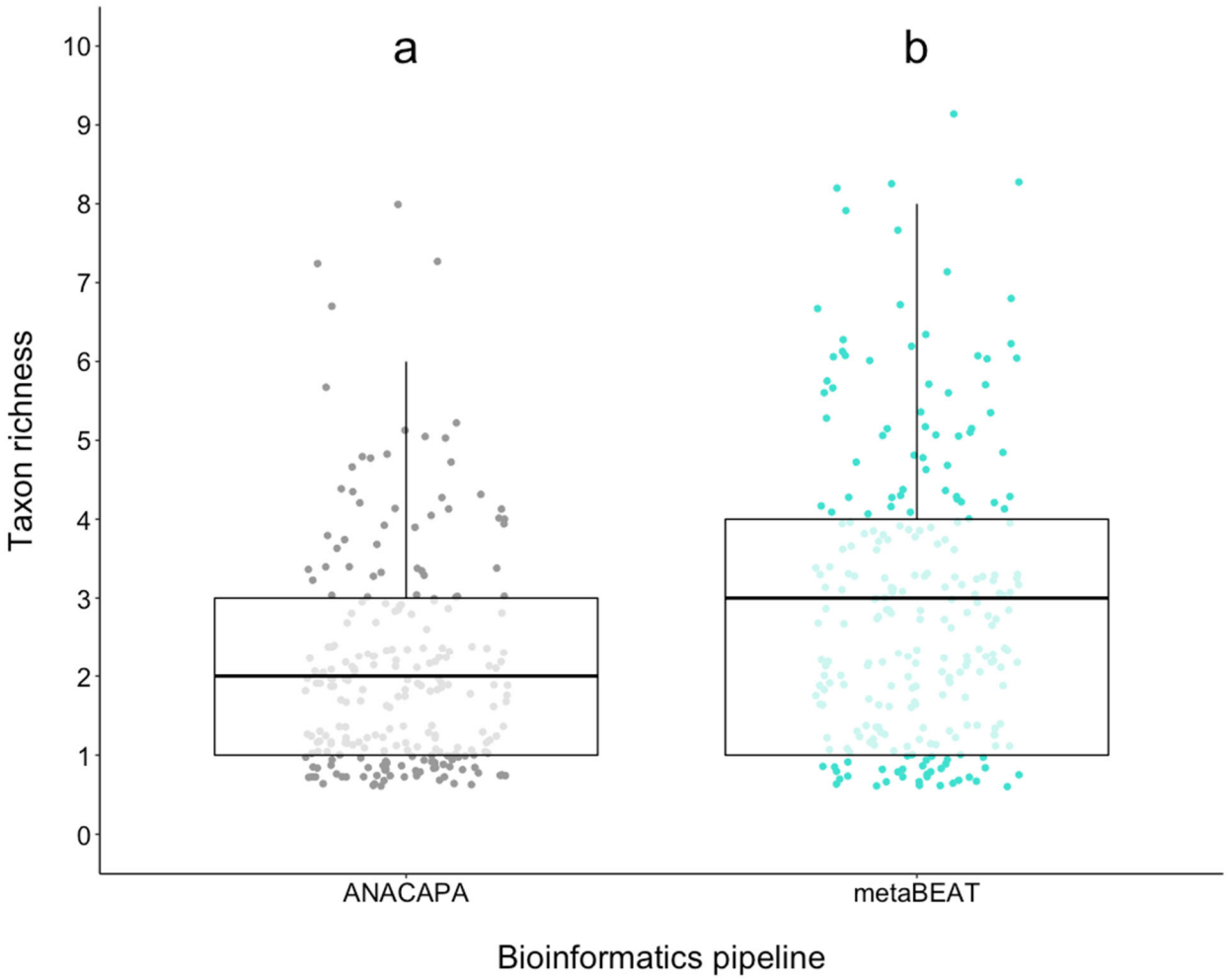


Figure 14. Boxplot showing the number of taxa detected in eDNA samples processed using different bioinformatics pipelines. Taxon richness was not significantly different in relation to bioinformatics pipeline. Boxes show 25th, 50th, and 75th percentiles, and whiskers show 5th and 95th percentiles.

Table 6. Summary of analyses statistically comparing homogeneity of multivariate dispersions (MVDISP) between the communities produced by different bioinformatics pipelines (ANOVA) and variation in community composition of eDNA samples processed using Anacapa or metaBEAT (PERMANOVA).

	Homogeneity of multivariate dispersions (ANOVA)				**Community similarity (PERMANOVA)**			
	Mean distance to centroid ± SE	**df**	***F***	***P***	**df**	***F***	***R²***	***P***
Turnover		1	0.312	0.577	1	39.573	0.076	**0.001**
ANACAPA	0.548 ± 0.073							
metaBEAT	0.536 ± 0.052							
Nestedness		1	3.306	0.070	1	-56.459	-0.132	1.000
ANACAPA	0.143 ± 0.021							
metaBEAT	0.169 ± 0.025							
Total beta diversity		1	0.045	0.832	1	29.059	0.057	**0.001**
ANACAPA	0.612 ± 0.031							
metaBEAT	0.610 ± 0.017							

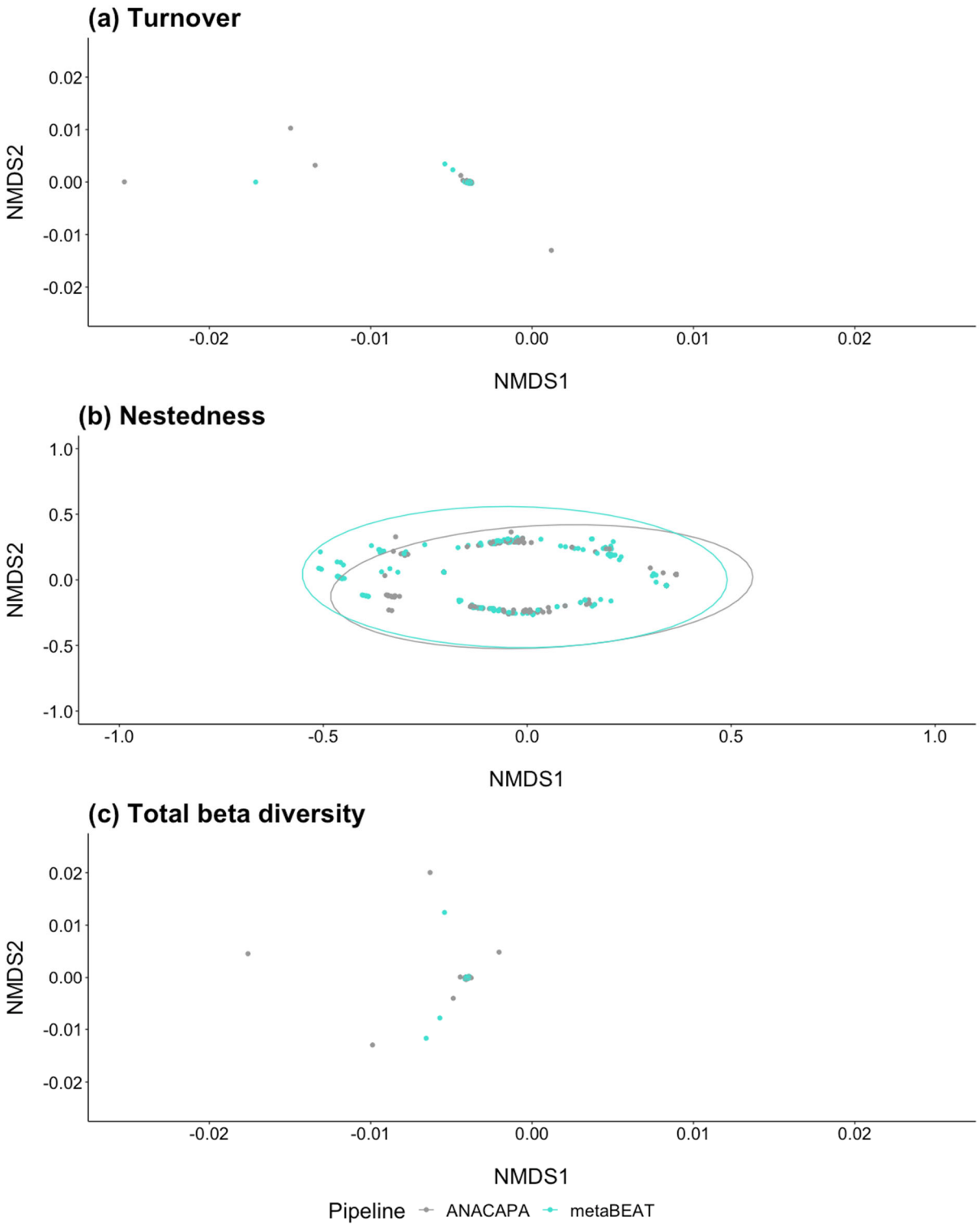


Figure 15. Non-metric Multidimensional Scaling (NMDS) plots of communities (Jaccard dissimilarity) produced by different bioinformatics pipelines (colored points/ellipse). The turnover **(a)** and nestedness **(b)** partitions of total beta diversity **(c)** are shown.

DISCUSSION

Overview. The past decade has yielded remarkable methodological and technological advances to address the critical need to execute rapid, large-scale surveys of pollinators via environmental DNA analysis (Vörösmarty et al., 2010; Dirzo et al., 2014; Steffen et al., 2015; Elbrecht et al., 2019). The emergence of metabarcoding has allowed for the rapid assay of species diversity (Hebert et al., 2003). Next generation sequencing now offers the ability to generate millions of sequence reads (Reuter et al., 2015) and more recently, the advent of microfluidic metabarcoding has allowed researchers the opportunity to "cast a broader net" and to compensate for taxonomic biases or blind-spots inherent to individual primer sets (Hauck et al., 2019).

Our research combines the above technological advances to assess the viability of eDNA metabarcoding as a means of documenting pollinator communities. Our results reveal that eDNA metabarcoding is a viable option to assess pollinator communities, confirming the work of Thomsen and Sigsgaard (2019). Moreover, we have combined multiple approaches in an attempt to develop an optimized strategy for pollinator microfluidic eDNA metabarcoding. Below we contextualize our results and provide a framework for subsequent field research aimed at: 1) further validation of eDNA metabarcoding as a viable tool for assessing all groups of pollinator species (including bats, birds, etc.), 2) the efficacy of pollinator eDNA sampling as a cost-effective alternative to conventional sampling, and 3) the promise of pollinator eDNA metabarcoding to document pollinator/plant networks to ultimately assess ecosystem resilience.

Contamination. Contamination of eDNA samples can arise from many sources, including contamination during sampling or during laboratory work, PCR, or sequencing errors (Ficetola et al., 2015, 2016). Our assessment of contamination revealed low levels of contamination in field and extraction blanks as well as PCR negative controls, yet considerably higher levels of contamination in PCR positive controls. With respect to field blanks, extraction blanks, and PCR negative controls, contamination may well have arisen in the field or in the lab; however, the low levels of contamination suggest that our methodologies, though imperfect, were sound. Nonetheless, it is also possible that contamination occurred during sequencing.

Interestingly, the bulk of contamination was present in the PCR positive controls. DNA for PCR positive controls was obtained from a pinned insect collection housed at INHS. These specimens had been collected in the field, pinned years ago, and have remained in a typical museum drawer setting. Given the above, we speculate that the high amount and composition (including other pollinators, mites, and decomposers) of contamination likely occurred from: 1) contact with DNA from other species in the field prior to sampling (pre-catch), 2) contact with DNA from other species during sampling and preservation (catch), and/or 3) contact with common arthropod species living in museum collections (post-catch). Pre-catch contact is inevitable, as pollinator communities certainly interact, both directly (e.g., via predation, parasitism, and coincidental contact) and indirectly (i.e., utilizing the same flower resources). These interactions are completely uncontrolled but could substantially contribute to

contamination. Contamination during the catch phase will wholly depend on capture and preservation methods. Depending on the trapping method (e.g., malaise traps), samples may have sat in the trap chamber with hundreds of individuals of a diverse species group for extended periods of time (up to days and weeks). If these samples are then bulk preserved, either in ethanol or by freezing, it is highly likely considerable contamination from non-target species will occur. Finally, while museum collections managers devote considerable time and effort to preventing outbreaks of common museum pest species (e.g., book lice, dermestid beetles, and silverfish), these species do occur from time to time. Moreover, the preferred method of dealing with these pests is freezing the entire drawer (Tommy McElrath, *personal communication*), which would not destroy trace DNA left on specimens.

In the case of our PCR positive controls, samples were collected using pan traps, then bulk preserved in ethanol before sorting by hand without sterile gloves in unsterile conditions. The samples were then pinned and stored using standard entomological practices in open drawers. Consequently, each of these three sources may well have contributed to the high frequency of contamination (15.43%) we observed in our PCR positive controls. While the inclusion of PCR positive controls is important to verify microfluidic metabarcoding technology is amplifying target DNA properly, the high levels of contamination from PCR positive controls compared with the low levels of contamination from negative process controls is problematic. Using DNA from specimens that were sample-processed and stored using conventional means (i.e., bulk sampling and processing) as PCR positive controls is inadequate for the purposes of monitoring potential contamination and assessing microfluidic metabarcoding performance. Instead, specimens should be individually collected, processed, and preserved rather than bulk sampled (if possible) or synthesized DNA (e.g., gBlocks) can be employed in place of genomic DNA from preserved specimens as PCR positive controls.

Greenhouse results. The most notable result of the greenhouse experiment is that pollinator microfluidic eDNA metabarcoding was effective in detecting the target common eastern bumblebee (*B. impatiens*) from one of our focal flower species, *Monarda*. However, detection was imperfect as only *Monarda* swabs and whole flowers preserved in CTAB and extracted with PCI yielded positive detections. We swabbed and sampled multiple flowers from each focal species immediately after visits from *B. impatiens*, yet *Penstemon* and *Solanum* did not yield any detections. The positive detections from *Monarda* were flowers that had sat in the greenhouse for prolonged periods of time, suggesting that eDNA may accumulate at high enough levels for detection after repeated visits by pollinator species. This provides important insights for how we design field surveys, suggesting that collecting multiple samples from multiple flower species, and varying sampling both spatially and temporally is required to provide the highest probability of detection (see below). In addition to detecting our target pollinator, we also detected non-target beneficial arthropod species known to occur in the greenhouse facilities, further underscoring the utility of the approach to document pollinator communities. Thus, with well-designed swab and whole flower sampling across multiple plant species differing in morphology

at fine spatiotemporal scales, microfluidic eDNA metabarcoding may sufficiently document arthropod communities.

Field results. Expanding upon the greenhouse experiment, microfluidic eDNA metabarcoding can elucidate pollinator communities and other plant associated arthropods, though with some interesting caveats. Again, targeting our focal flower species (*Monarda* and *Penstemon*), numerous arthropod species were detected, including hymenopteran and lepidopteran species. However, not all observed species were detected, suggesting that inherent characteristics of some pollinator species may make them difficult to detect with this approach. Nevertheless, our limited scope of field sampling suggests that the development of a robust sampling regime across multiple flowering plant species and at varied spatial and temporal scales would yield a robust approach to rapidly assay pollinator communities in diverse ecosystems. We expand upon this below.

Methodological comparisons. Thomsen and Sigsgaard (2019) showed that eDNA metabarcoding could document pollinator communities and other plant associated arthropods. Our study substantially advanced the technical state-of-the art by assessing how different decisions in the workflow can influence the pollinator communities revealed. Specifically, we tested whether or not differences in flower type/morphology, sampling method, preservation and extraction approach, primer choice, and bioinformatics pipeline can affect eDNA-based pollinator community diversity. Our results show that different pollinator communities (and other plant-associated arthropods) are revealed through microfluidic eDNA metabarcoding and are likely driven by a variety of biotic, abiotic, and technical factors operating in concert with one another. Simply put, the decisions researchers make with respect to all facets of a pollinator eDNA metabarcoding study will influence the communities revealed.

After applying the false positive sequence threshold (1.17%), *Penstemon*, *Monarda*, and *Solanum* revealed broadly similar communities, and greater diversity than *Cynoglossum amabile*; however, this is likely due to sampling strategy (swabs/whole flowers vs. nectar draws) and sample size disparity. Prior to applying the false positive threshold, we also recovered more diverse pollinator communities (and other plant-associated arthropods) from *Monarda* and *Penstemon* flowers when compared to *Solanum*. We hypothesize that these differences may arise from several sources. First, flower morphology may play a role in the ability of flower species to capture and preserve eDNA from pollinators. Three of our focal flower species have distinct morphologies (Fig. 16). *Penstemon* has deep, conical flowers that require bees to crawl into the flower to seek pollen and nectar. *Monarda* inflorescences are quite different, with multiple small flowers arrayed in a head-like cluster providing pollen and nectar. *Solanum* flowers are considerably smaller, with petals that do not obscure the stamen and no nectar. Though no research to date has assessed the deposition of pollinator eDNA on flowers of varied morphologies, it is possible that flower morphologies influence eDNA capture and retention. We speculate that the small size, low surface area, and exposed stamens of *Solanum* flowers (and the

buzz pollination strategy of this plant) resulted in less contact with the target common eastern bumblebee, lowering the probability of detection. At the other end of the spectrum, *Monarda* inflorescences are large, complex, have more overall nectar, and thus have a morphology that may be particularly adept at capturing and maintaining pollinator eDNA. *Penstemon* has similar potential as inflorescences are deep resulting in more pollinator contact, and the surfaces that pollinators contact are less exposed to the elements.

Figure 16. Focal flower species morphology. Focal flower species (from left to right) *Penstemon*, *Monarda*, and *Solanum* have distinctly different flower morphologies, sizes, and characteristics. The large, conical flowers of *Penstemon* require pollinators to crawl in to access nectar/pollen. *Monarda* inflorescences are composed of crowded, head-like clusters of flowers providing nectar and pollen. *Solanum*, considerably smaller, are star-shaped with exposed stamensm but no nectar. These morphological differences may influence the ability of the flowers to capture and maintain pollinator eDNA. Photos by Mark Davis and Tiffany Jolley.

Relatedly, morphological differences may yield differential handling time for bee species. Though we did not quantify handling time in this study, our observations suggested that bees spent considerably longer on *Monarda* inflorescences, spent less time on *Penstemon* flowers, and spent the least amount of time on *Solanum* flowers. Our observations comport with numerous studies that have revealed differential handling time by bees across a diversity of flowers (e.g., Ivey et al 2003, Franco et al 2011), which is associated with morphological variation among bee species (Harder 1983). Increased contact and handling time with flowers may confer higher detection probabilities, ultimately influencing the ability of eDNA metabarcoding to recover pollinator communities.

Curiously, some species that were frequently observed left no trace of eDNA on flowers, such as carpenter bees (*X. virginica*). In *Penstemon* flower beds on the UIUC campus, we observed numerous visits by carpenter bees and collected multiple samples immediately after visitation. Moreover, nearly every flower we inspected showed evidence of nectar robbing (Fig. 17), yet no reads were assigned to this species. Reads from a PCR positive control that used carpenter bee DNA were successfully assigned, thus lack of detection was not due to sequencing or bioinformatics error.

Figure 17. A carpenter bee (*Xylocopa virginica*) exhibiting nectar robbing behavior. Here the bee is boring a hole via biting into the base of a *Penstemon* flower to access the nectar. Despite extensive observations and evidence of this behavior, we failed to detect this species. Photo by Mark Davis.

Beyond biological variation in detectability, we found key differences in numerous methodological aspects. First, sampling the entire flower head, irrespective of flower species, documented more diverse pollinator communities than either swabbing or nectar. This method has already been established as an effective means of documenting pollinator communities (Thomsen and Sigsgaard, 2019). Nevertheless, swabbing was able to document pollinators, including our target common eastern bumblebee, albeit this approach produced lower taxon richness than whole flower harvest. Thus, swabbing may be an appropriate means of eDNA sampling in remote locations where it is unreasonable to transport the requisite sampling materials for whole flower harvesting. Nectar draws may be an ineffective method of documenting pollinator communities. First, some flowering plants do not produce nectar, limiting the plant species one might sample eDNA from. Second, we often found that nectar robbing rendered nectar-producing flowers unable to be sampled in the field due to nectar depletion. Finally, volumes of nectar among focal species were variable and, in many instances,

incredibly low which may reduce detection probability. In addition, it is unknown how the dynamics between nectar depletion by a pollinator and nectar regeneration by a plant influences eDNA detection. Our low sample size for *Cynoglossum* and absence of nectar draws from *Penstemon,* and *Monarda* prevented robust quantitative comparisons. However, we recommend that this approach should be further explored with high volume nectar-producing plants pollinated by insects as well as plants that are reliant upon pollination by bats and birds. We provide additional context for this below.

Preservation and extraction methods are known to substantially influence detection of target species in eDNA applications (Renshaw et al., 2014; Turner et al., 2014; Spens et al., 2016). However, studies comparing different methods have largely been focused on aquatic systems where water is filtered to capture eDNA and may not be transferable to pollinator eDNA on flowers (but see Lear et al., 2018). In our study, the choice of preservation and extraction method also influenced pollinator detection and recovered diversity. Overall, we found that ATL preservation in conjunction with a modified Qiagen DNeasy Blood and Tissue Kit extraction (Thomsen and Sigsgaard, 2019) recovered greater taxon richness than and different pollinator communities to CTAB preservation and PCI extraction. This finding largely comports with other, albeit limited, research findings (Djurhuus et al., 2017; Lear et al., 2018).

Taxonomic biases inherent to metabarcoding primers are well established (Clarke et al., 2014; Krehenwinkel et al., 2017), and, thus, it is unsurprising that we observed variation in the communities revealed by different primer sets. It is also unsurprising that variation exists in species diversity between our target loci (i.e., 16S and COI). We recovered a far greater proportion of unassigned reads from 16S than COI. We attribute this largely to the establishment of the COI locus in the early 21st century as the animal "barcoding gene" of choice (Hebert et al., 2003a,b), leading to tremendous amounts of COI sequence data accessioned to online genetic sequence repositories used in metabarcoding bioinformatics pipelines. While 16S has shown promise (Vences et al., 2005), and COI is not without its shortcomings (Deagle et al., 2014), 16S suffers from low representation in online repositories, and therefore its application requires the construction of a local reference database (Elbrecht et al., 2016).

Given that amplification biases are inherent to individual metabarcoding primers, and that biases exist in online DNA sequence data repositories, we argue that the microfluidic eNDA metabarcoding approach we have employed provides a technological mechanism to mitigate some of these biases. However, as new primers targeting both established mtDNA regions as well as new regions emerge, we advocate for continued assessment of primer combinations to maximize the biodiversity recovered to minimize effort and costs associated with documenting pollinator communities.

Finally, choice in bioinformatics pipeline (metaBEAT and Anacapa) influenced the pollinator communities recovered. metaBEAT generated greater taxon richness and produced a dissimilar communitiy to Anacapa. This could be due to the custom reference database for Illinois invertebrates that metaBEAT used for taxonomic assignment as opposed to the broader database produced by CRUX for Anacapa. Alternatively, diversity estimates may be inflated

with metaBEAT due to the clustering step performed instead of ASV parsing with Anacapa. Both pipelines performed equivalently, revealing similar communities. As pipelines continue to be developed for bioinformatic processing and taxonomic assignment of metabarcoding data, and reference sequences continue to accumulate in online repositories, continued validation of bioinformatics pipelines is necessary to account for potential biases that could influence taxon recovery.

Conclusions. Our results, supported by growing body of evidence (Liu et al., 2019), confirm that microfluidic eDNA metabarcoding is a viable means of surveying pollinator communities. Moreover, decisions regarding all workflow aspects, from what to sample, how to sample, preservation and extraction method, primer choice, and bioinformatics pipeline can impact the community diversity elucidated via this approach. In the following section, we will detail a research program to leverage this technology to: 1) improve our understanding of pollinator communities and how they support ecosystem resiliency, 2) maximize return on investment at DoD installations, and 3) enhance mission readiness and lethality by minimizing range closures required to assess pollinator communities.

Recommended workflow. Given our results, we have developed a recommended workflow to optimize documentation of pollinator communities via eDNA microfluidic metabarcoding (Fig. 18). First, given the observed differences in detection across flower types, we recommend that replicate samples from a diverse species assemblage from a given site be established. By maximizing flower diversity (and considering spatial and temporal variation in pollinator communities), one should maximize the probability of detecting a broad pollinator community (and other plant-associated arthropods). Second, we recommend that whole flower heads are sampled. This increases the surface area available for eDNA to be harvested from and may require less time to sample than swabbing or nectar draws.

The ATL buffer + modified Qiagen DNeasy Blood and Tissue Kit approach revealed more diverse pollinator communities. Moreover, this approach tends to recover cleaner, longer-stranded DNA. As such, we recommend this approach for eDNA preservation and extraction. Given the larger volume of COI sequence data available from online repositories, COI performed better than 16S in recovering pollinator communities and minimizing the number of unassigned reads. Furthermore, our multi-locus approach was effective in minimizing taxonomic biases of individual primer sets. We recommend using a diverse suite of COI primers. However, this unlikely to be optimal for other pollinator groups (i.e., bats and birds). Therefore, *in silico* and *in vitro* primer validation should be conducted for all available primer sets across common mtDNA/nDNA metabarcoding regions/genes (e.g., COI, 12S, 16S, and 18S) depending on the pollinator community one seeks to document.

Finally, metaBEAT seemingly recovered more diversity and produced different pollinator communities to Anacapa. Although the same parameters were specified for processing sequence reads produced by each primer set where possible, these pipelines used different reference

databases and divergent tools for bioinformatic processing. The diversity estimates produced by metaBEAT may be real due to use of a database for Illinois invertebrates or inflated due to the clustering approach employed. Therefore, we advise 1) further assessment of these pipelines, and 2) expanded comparisons with other available pipelines.

	FLOWER MORPHOLOGY	SAMPLING METHODS	PRESERVATION/ EXTRACTION	PRIMER SET	BIOINFORMATICS PIPELINE
OPTIMAL WORKFLOW	 **Monarda*** *Ideally a diverse array of flower species with a robust sampling design would be implemented to maximize likelihood of capturing a diverse pollinator community	**Whole Flower Harvesting*** *Swabbing performed well, and could be considered in remote/challenging sampling scenarios and/or when working with TES plant species and whole flower harvesting is prohibited	**ATL + Modified Qiagen DNEasy**	**COI**	**ANACAPA + metaBEAT**
OTHER APPROACHES EXAMINED	**Monarda** **Penstemon** **Solanum (whole flower only)** **Cynglossum (nectar only)**	**Whole flower harvesting** **Swabbing** **Nectar extraction**	**CTAB + Phenol-Chloroform-Isoamyl** **ATL + Modified Qiagen DNEasy**	**COI** **16S**	**ANACAPA** **metaBEAT**

Figure 18. A recommended workflow for pollinator microfluidic eDNA metabarcoding. This workflow was developed based on the results of this study and includes technical recommendations that should yield the most robust estimate of pollinator communities.

IMPLICATIONS FOR FUTURE RESEARCH AND BENEFITS

Implications for future research. The ability to leverage eDNA metabarcoding to document pollinator communities (and other plant-associated arthropods) is an emerging field which can revolutionize our understanding of pollinator biodiversity (Van Zandt et al., 2020), and opens avenues for research at DoD installations in numerous contexts. We believe two subsequent studies are needed to further assess the effectiveness of this technology to benefit installations.

First, while we have demonstrated that pollinator microfluidic eDNA metabarcoding is effective in documenting arthropod pollinator communities, there are also many vertebrates (particularly bats and birds) that are key pollinators and are increasingly afforded protections under the U.S. Endangered Species Act. Yet, controlled lab studies using these pollinator species are difficult. As such, we propose research at Fort Huachuca, Arizona, to assess whether or not our approach is able to detect the federally listed lesser long-nosed bat (*Leptonycteris yerbabuena*) and the broader pollinator community from cacti flowers and an assessment of bird pollinator networks (in collaboration with Dr. Jinelle Sperry) on DoD land holdings on Oahu, Hawaii. These studies will validate this approach for non-arthropod and yet critically important pollinator species.

Second, we propose a study to compare our approach with conventional methods to document pollinator networks in natural settings. Specifically, we propose a study of grassland pollinator communities at Fort McCoy in Wisconsin, home to the karner blue butterfly (*Lycaeides melissa samuelis*), federally listed as endangered. In this study, a robust sampling design that samples diverse flower species at multiple temporal and spatial scales will be used to document pollinator communities via microfluidic eDNA metabarcoding. We will pair this with a conventional observational assessment of pollinator communities. Here, we will compare and contrast both the economic cost of each approach as well as the time investment required to document pollinator communities. This will allow us to both understand which approach yields a greater return on investment, and which approach minimizes range closure times on installations.

In addition to the critical studies identifed above, we propose deploying this methodology in real-world applications to provide actionable information to DoD installations, and we provide examples below. First, as concerns over the loss of pollinator biodiversity have grown (e.g., Potts et al., 2016), species are increasingly being afforded protection under the U.S. Endangered Species Act. As such, pollinator eDNA metabarcoding can be rapidly deployed on large spatial scales to provide a preliminary screening for these species. This will allow for high intensity conventional sampling to be strategically targeted to locations with a high likelihood of success and maximizing return-on-investment.

Secondly, biodiversity is essential for resilient ecosystems (Oliver et al., 2015a,b), and pollinators deliver critical ecosystem services (Hein, 2009; Vanbergen, 2013; Winfree, 2013). In the interest of promoting installation resilience, assessing the health of plant and pollinator networks is essential. By coupling our approach with microfluidic metabarcoding of pollen sacs,

critical information of plant-pollinator interactions can be provided, ultimately serving as a proxy for resilience.

Benefits. We believe the benefits of our approach are three-fold. First, conventional measuring and monitoring of pollinator communities is both costly and time consuming. Researchers with expert taxonomic knowledge (an increasingly rare commodity) must spend large amounts of time observing pollinator/plant interactions. Reducing the time and effort needed to acquire the same information reduces the financial burden of surveying. This has an added benefit in that once species of conservation concern are identified, intensive monitoring and adaptive management can be strategically targeted. Thus, in both phases (data and information acquisition and adaptive management) costs are reduced, thereby maximizing return-on-investment.

Second, we believe that eDNA sampling requires much less time in the field, resulting in reduced range closure time, increasing mission readiness, and ultimately lethality. To provide real-world context, PI Mark Davis led an eDNA study at the U.S. Army Joint Readiness Training Center at Fort Polk assessing imperiled freshwater crayfish and mussels (Davis et al., 2019). Using conventional sampling (timed searches), we were able to survey a total of 9 sites over three days. Using eDNA sampling, we were able to sample a total of 29 sites over an identical three-day period. The rapidity with which eDNA sampling proceeds often provides a distinct advantage to conventional sampling, which minimizes range closures, maximizing mission readiness, and ultimately increasing lethality.

Finally, integrated pollinator microfluidic eDNA metabarcoding approaches (as above) can reveal complex networks that undergird critical ecosystem functions and services, and ultimately allow for an assessment of ecosystem resiliency. By combining data from pollinator microfluidic eDNA metabarcoding with, for example, standard metabarcoding of pollen sacs using plant genetic markers (e.g., rbcL, ITS2, trnL), we can begin to formally assess plant/pollinator networks. Moreover, by assessing a gradient of sites (from degraded to restored/enhanced/protected to protected/pristine) we can develop indices of biotic integrity to use as a proxy for ecosystem functions and services, ultimately providing insights into the resilience of ecological systems on DoD land holdings.

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APPENDICES

Appendix 1. Flower species that comprised the greenhouse community. These flowering plants provided a constant supply of pollen and nectar to the introduced common eastern bumblebee (*Bombus impatiens*) established in the greenhouse.

Botanical Name	Common Name
Nemophila menziesii	Baby Blue Eyes
Gypsophila elegans	Baby's Breath
Linaria maroccana	Baby Snapdragon, Moroccan Toadflax
Eschscholzia californica	California Poppy
Cynoglossum amabile	Chinese Forget-Me-Not
Centaurea cyannus	Cornflower
Helianthus annuus	Dwarf Sunflower Sunspot
Clarkia amoena	Farwell-To-Spring, Godetia
Mirabilis jalapa	Four O-Clock
Gilia capitata	Globe Gillia, Blue-Thimble-Flower
Clarkia unguiculata	Elegent Clarkia, Mountain Garland
Gaillardia pulchella	Indian Blanket
Lupinus	Lupine
Silene armeria	None-So-Pretty, Sweet William Catchfly
Coreopsis tinctoria	Plains Coreopsis
Calendula officinalis	Pot Marigold
Ammi majus	Queen Anne's Lace
Papaver rhoeas	Red Poppy, Common Poppy
Delphinium ajacis	Rocket Larkspur
Lavatera trimestris	Rose Mallow
Linum grandiflorum "Rubrum"	Scarlet Flax
Cosmos sulphureus	Sulphur Cosmos
Cosmos bipinnatus	Garden Cosmos

Appendix 2. Details of the primer panel selected for pollinator eDNA microfluidic metabarcoding.

Primer set			Details			% species amplified *in silico* (N = 5313) mismatches			
Name	**Forward primer (5' - 3')**	**Reverse primer (5' - 3')**	**Marker**	**Fragment size (bp)**	**Target taxa**	**1**	**2**	**3**	**4**
Ins16S-1F & Ins16S-1Rshort	TRRGACGAGAAGACCCTATA	ACGCTGTTATCCCTAARGTA	16S	156	Invertebrates	1.45	8.02	10.20	10.90
MOL16S_F & MOL16S_R	RRWRGACRAGAAGACCCT	ARTCCAACATCGAGGT	16S	183-310	Molluscs	3.65	6.61	9.71	10.75
BF1 & BR1	ACWGGWTGRACWGTNTAYCC	ARYATDGTRATDGCHCCDGC	COI	217	Invertebrates	29.68	43.93	46.19	46.45
BF1 & BR2	ACWGGWTGRACWGTNTAYCC	TCDGGRTGNCCRAARAAYCA	COI	316	Invertebrates	7.06	11.67	12.35	12.67
BF2 & BR2	GCHCCHGAYATRGCHTTYCC	TCDGGRTGNCCRAARAAYCA	COI	421	Invertebrates	6.08	7.91	8.85	9.94
BF3 & BR2	CCHGAYATRGCHTTYCCHCG	TCDGGRTGNCCRAARAAYCA	COI	418	Arthropods	7.27	9.62	9.82	9.98
nsCOIFo & mlCOIintK	THATRATNGGNGGNTTYGGNAAHTG	GGRGGRTAWACWGTTCAWCCWGTWCC	COI	124	Invertebrates	16.83	33.99	42.10	44.02
mlCOIintF & jgHCO2198	GGWACWGGWTGAACWGTWTAYCCYCC	TAIACYTCIGGRTGICCRAARAAYCA	COI	313	Metazoans	0.00	0.00	0.00	11.71
Vamos_fwh1	YTCHACWAAYCAYAARGAYATYGG	ARTCARTTWCCRAAHCCHCC	COI	178	Invertebrates	2.88	4.20	4.69	4.74
Vamos_fwh2n	GGDACWGGWTGAACWGTWTAYCCHCC	GTRATWGCHCCDGCTARWACWGG	COI	205	Invertebrates	19.73	39.02	44.91	46.23
Uni-MinibarF1 & Uni-MinibarR1	TCCACTAATCACAARGATATTGGTAC	GAAAATCATAATGAAGGCATGAGC	COI	127	Metazoans	0.00	0.00	0.00	0.17
ZBJ-ArtF1c & ZBJ-ArtR2c	AGATATTGGAACWTTATATTTTATTTTTGG	WACTAATCAATTWCCAAATCCTCC	COI	157	Arthropods	0.26	1.32	2.88	4.40
LepLCO & McoiR1	RKTCAACMAATCATAAAGATATTGG	AATCCBCCRATTAWAATKGGTAT	COI	~150	Invertebrates	0.23	1.05	2.09	3.33
LepLCO & McoiR2	RKTCAACMAATCATAAAGATATTGG	CCBCCRATTAWAATKGGTATHAC	COI	~150	Invertebrates	0.24	1.13	2.03	3.20
LepLCO & MLepF1rev	RKTCAACMAATCATAAAGATATTGG	CGTGGAAAWGCTATATCWGGTG	COI	~150	Invertebrates	0.02	0.26	1.07	2.99

Appendix 3. Results of *in silico* primer testing for each primer pair considered. The total number of species and the proportion of species that amplified out of a 5313 Illinois native pollinator species database are depicted.

		Total Amplified (mismatches)				Proportion Amplified (mismatches)			
Primer Set	**Region**	**0**	**1**	**2**	**3**	**0**	**1**	**2**	**3**
Corse_LepLCO-McoiR1	COI	12	56	111	177	0	1	2	3
Corse_LepLCO-McoiR2	COI	13	60	108	170	0	1	2	3
Corse_LepLCO-MLepF1rev	COI	1	14	57	159	0	0	1	3
Corse_MFZR	COI	0	0	7	63	0	0	0	1
Elbrecht_BF1-BR1	COI	1577	2334	2454	2468	30	44	46	46
Elbrecht_BF1-BR2	COI	375	620	656	673	7	12	12	13
Elbrecht_BF2-BR2	COI	323	420	470	528	6	8	9	10
Elbrecht_BF3-BR2	COI	386	511	522	530	7	10	10	10
Galan_MG	COI	48	140	232	244	1	3	4	5
Gunther_nsCOIFo-mlCOIintK	COI	894	1806	2237	2339	17	34	42	44
Leray_Geller	COI	0	0	0	622	0	0	0	12
Meusnier_Uni-Minibar	COI	0	0	0	9	0	0	0	0
Shokralla_Ill-B-F-HCO2198	COI	0	0	0	353	0	0	0	7
Shokralla_LCO1490-Ill-C-R	COI	0	0	0	0	0	0	0	0
Vamos_fwh1	COI	153	223	249	252	3	4	5	5
Vamos_fwh2	COI	71	1795	2336	2449	1	34	44	46
Vamos_fwh2n	COI	1048	2073	2386	2456	20	39	45	46
Zeale_ZBJ-Art	COI	14	70	153	234	0	1	3	4
Clarke_Ins16S	16s	77	426	542	579	1	8	10	11
DeBarba_16SMAV	16s	0	1	1	1	0	0	0	0
Klymus_MOL16S	16s	194	351	516	571	4	7	10	11
Klymus_SPH16S	16s	0	0	0	3	0	0	0	0