



Department of
Environmental
Conservation

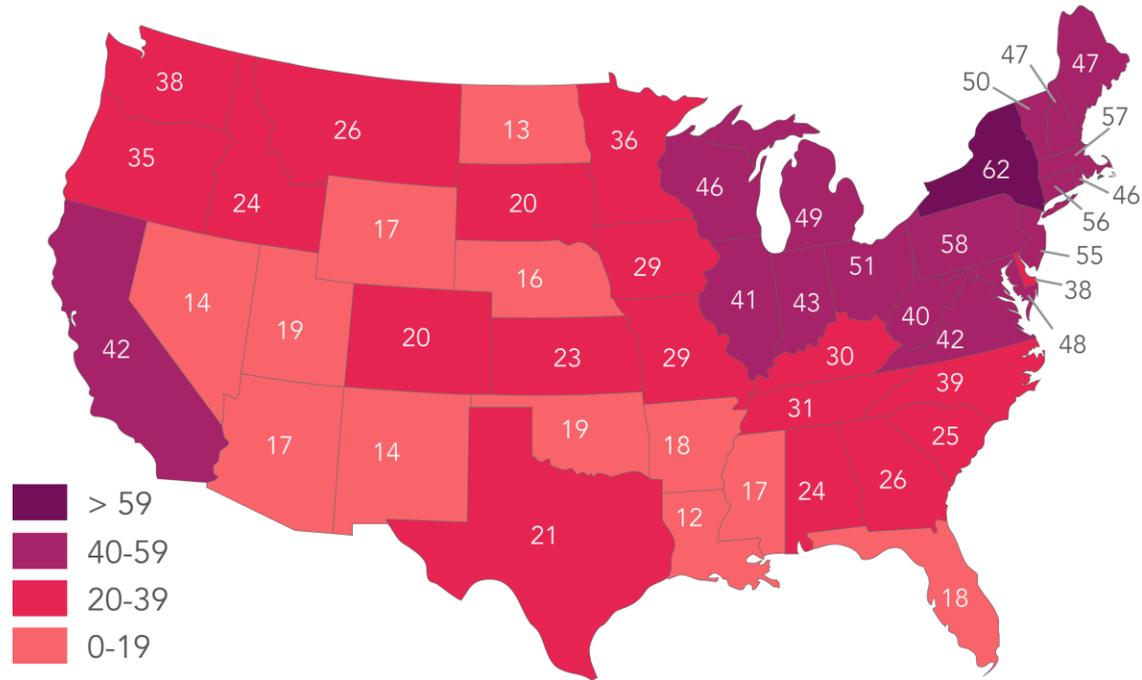
Barcoding Bycatch: **Exploring Techniques to Maximize** **Knowledge Gained from Trapping Efforts**

Amanda Dillon- Forest Health Research Lab Manager

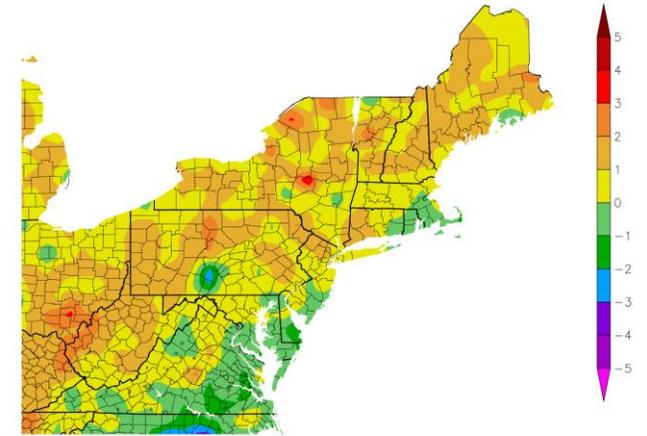
October 22, 2025

Changing climate and geography

IMPORTED FOREST PESTS OCCUR IN EVERY STATE IN THE US



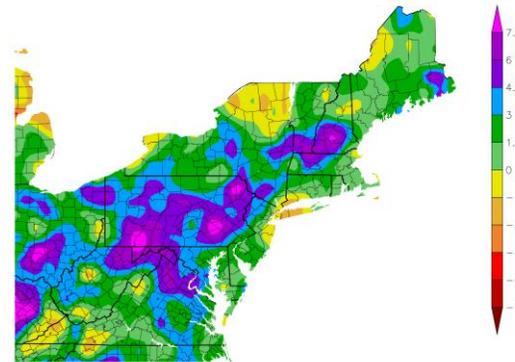
Departure from Normal Temperature (F)
7/1/2025 - 9/30/2025



Generated 10/10/2025 using provisional data.

ACIS Web Services

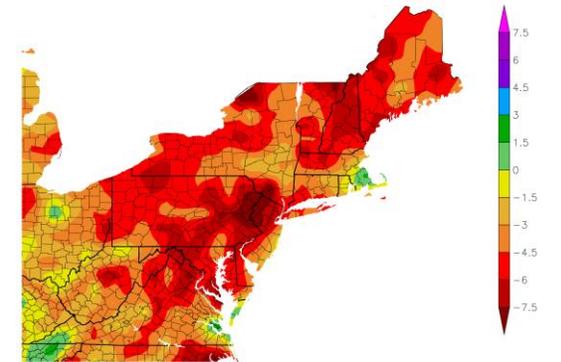
Departure from Normal Precipitation (in)
4/1/2025 - 6/30/2025



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ACIS Web Services

Departure from Normal Precipitation (in)
7/19/2025 - 10/16/2025

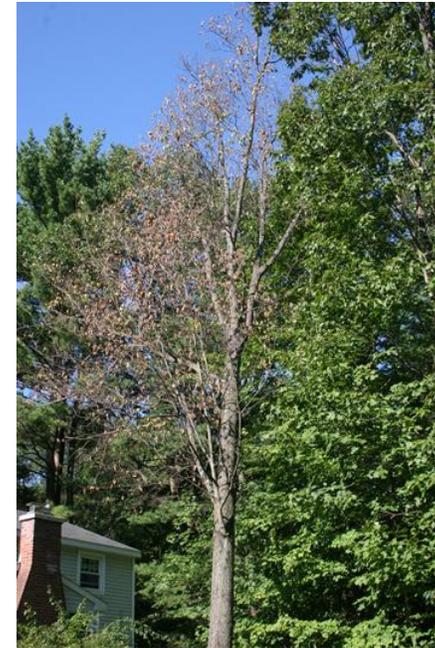


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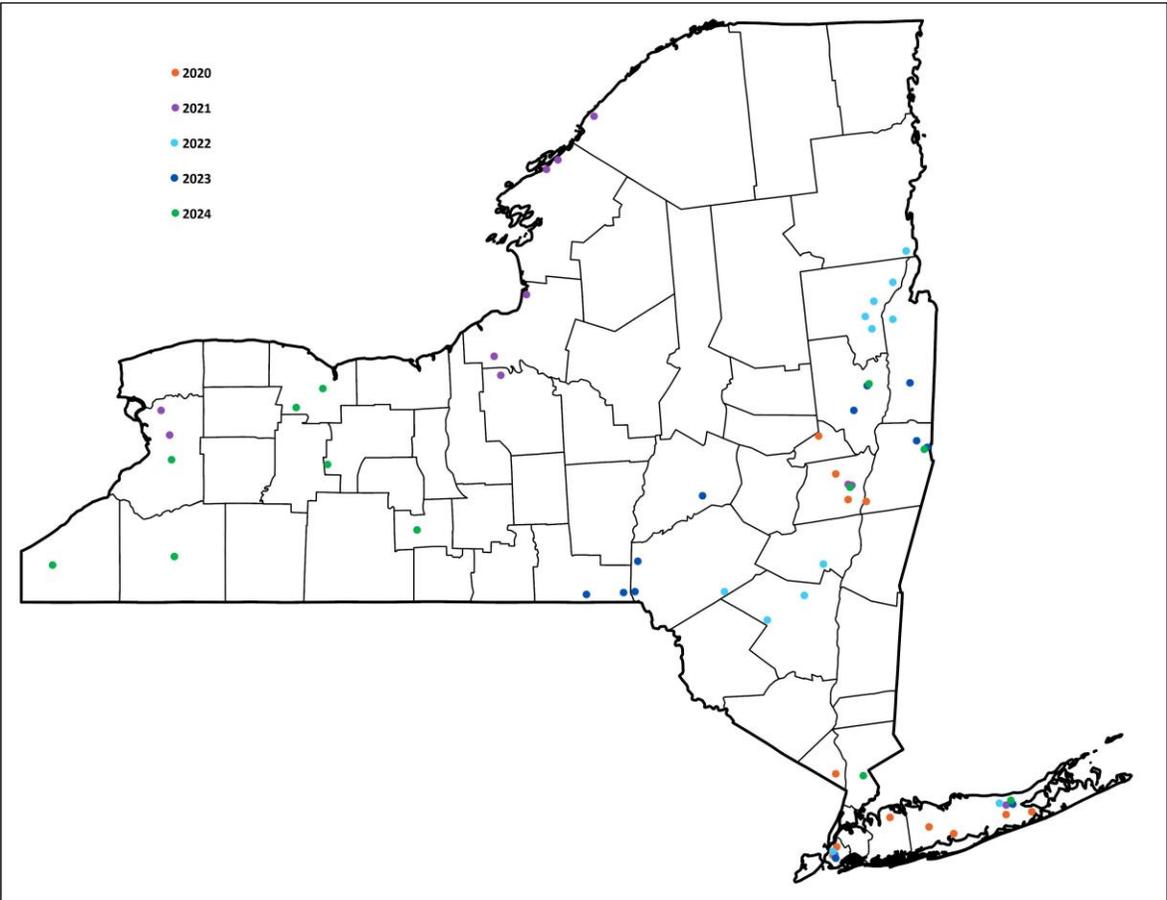
ACIS Web Services

Impacts on Forest Health

- Introduction of novel species
- Range expansions of forest pests
- Conditions favoring pathogenic fungi
- Temperatures increasing degree days
- Draught stress



Monitoring for novel introductions



Studies of management and restoration efforts



Bycatch

- Specimens are consolidated and sent to USFS Durham Field Office for identification of target species
- Bycatch
 - Non-target groups
 - Taxonomic bottleneck
 - Records for other species of concern, data-deficient insects, or rare species of interest
 - Large volume

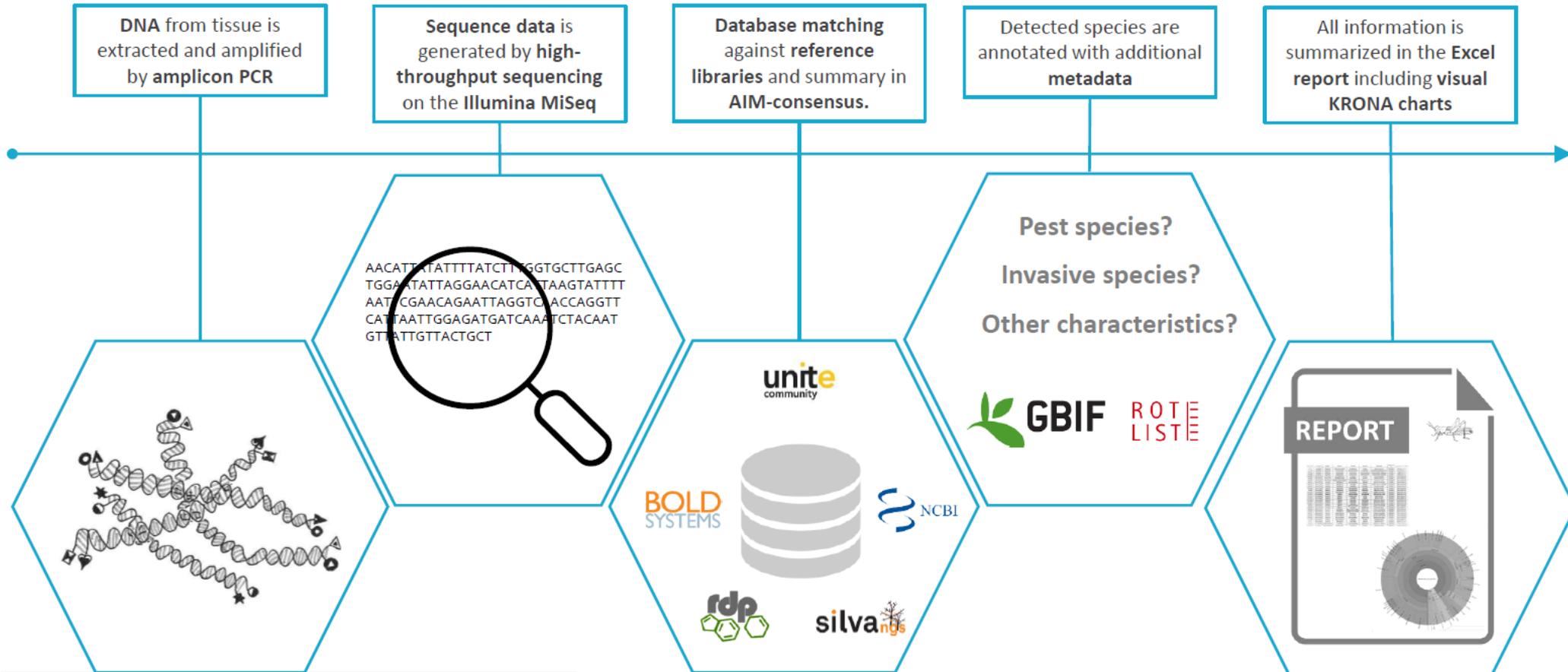


Genetic barcoding with AIM Lab



OUR DYNAMIC BIOINFORMATICS

Our bioinformatics is dynamic and starts where other labs send the raw data.



THE REFERENCE DATABASES - ANIMALS (CO1)



BOLD – Barcode of Life Database

The BOLD database is the world's only curated database for genetic data. BOLD provides important metadata in addition to species assignments and includes the BIN system, which allows conclusions about genetic species diversity in mixed samples even without species assignments. BOLD is used by default for the BLAST for our CO1 and ITS2 - metabarcoding.

Advantages: curated entries, BIN system

[Click here](#) for the database.

NCBI Genbank

NCBI Genbank represents the world's largest repository of genetic sequence data. It contains genetic sequences of most of the described organisms. Thus, the database is suitable for a search for animals, plants, fungi & bacteria.

Advantages: most comprehensive database

Disadvantages: not curated

[Click here](#) for the database.

RDP Classifier

The **RDP Classifier** (Ribosomal Database Project Classifier) algorithm (Porter & Hajibabaei 2018) allows to inspect OTUs in more detail, which do not achieve a clear hit when matched against the other databases. The classifier allows to match each hierarchical level of an OTU sequence against the databases. In this way it is possible to inspect specific target taxa without genus and species assignment.

[Click here](#) for the publication.



THE RESULTS - LAYOUT OF THE ANNOTATED OTU TABLES (EXCEL FILE)



BOLD BLAST	Consensus taxonomy	Consensus score & GBIF link	Sequence sums	NCBI BLAST	RDP Classifier	Taxonomy comparison	BOLD metadata	Red list metadata
Results of the Barcode of Life Database – BLAST (BOLD - www.boldsystems.org)	Consensus of taxonomic classification across databases	Consensus score & link to Global Biodiversity Information Facility (GBIF) website of the identified species	Summed sequence numbers per sample and species	Results of the NCBI Genbank BLAST (www.ncbi.nlm.nih.gov/genbank)	Taxonomy of the Ribosomal Database Project Classifier algorithm	Hit comparisons between the three databases	Additional information of the BOLD database	German species records and endangerment status

The data

Multi-state barcoding results - Saved to this PC

File Home Insert Page Layout Formulas Data Review View Automate Help

Clipboard Font Alignment Number Styles Cells Editing Analysis Sensitivity Add-ins

AH4 Run2023_06_EC_2022_274_009_E224

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
1	BOLD database BLAST – grade-%ID-adjusted taxonomy (August 2022)												consensus taxonomy						
2																			
3																			
4	BOLD_Process_ID	BOLD_BIN_uri	BOLD_HIT%ID	BOLD_Grade%ID	BOLD Hit_Seq_Length	adjusted_Phylum_BOLD	adjusted_Class_BOLD	adjusted_Order_BOLD	adjusted_Family_BOLD	adjusted_Genus_BOLD	adjusted_Species_BOLD	OTU_ID;cluster_size	consensus_Domain	consensus_Phylum	consensus_Class	consensus_Order	consensus_Family	consensus_Genus	consensus_Species
5	CERGL139-08	BOLD-ACE8452	100.0%	100.0%	313	Arthropoda	Insecta	Coleoptera	Cerambycidae	Aseum	Aseum_striatum	OTU_330;size=52735	Eukaryota	Arthropoda	Insecta	Coleoptera	Cerambycidae		

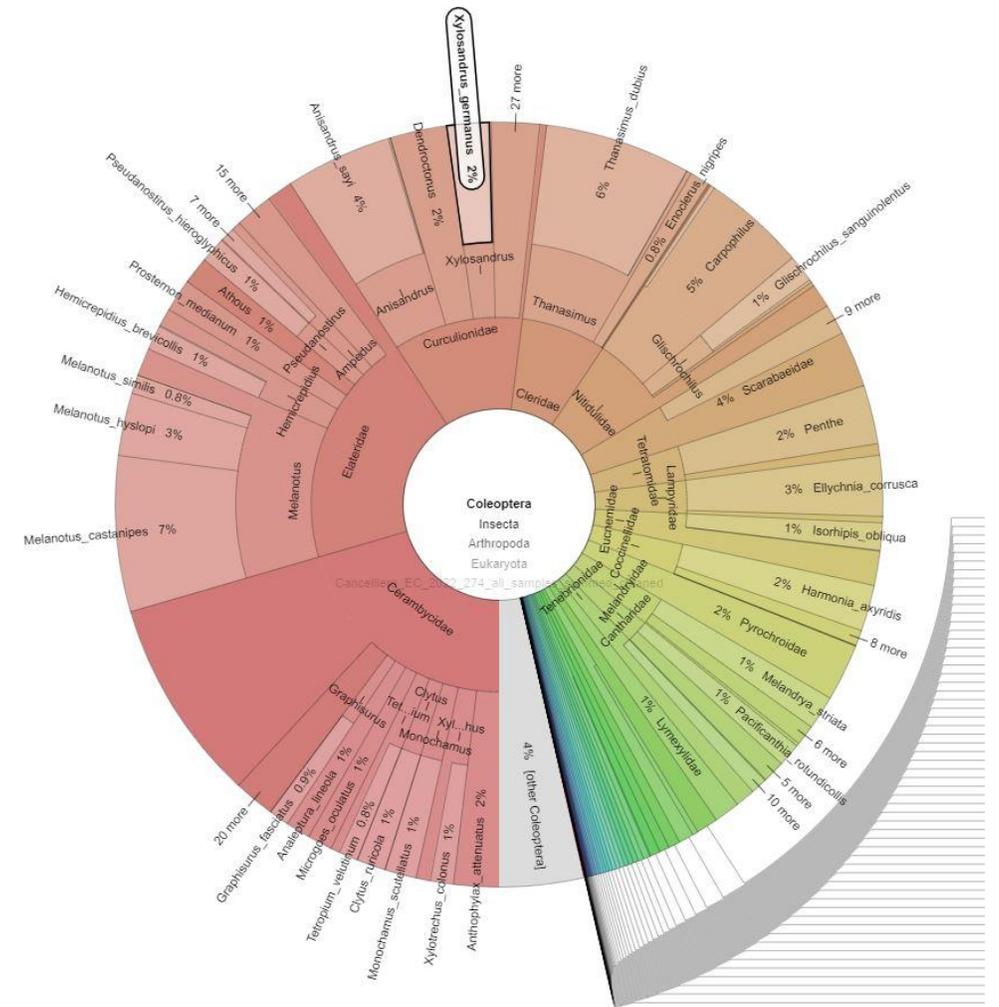
Ready Accessibility: Investigate

Methods improvement

- Limited by databases
- Sampling is destructive
- Results can send us back out to trap more

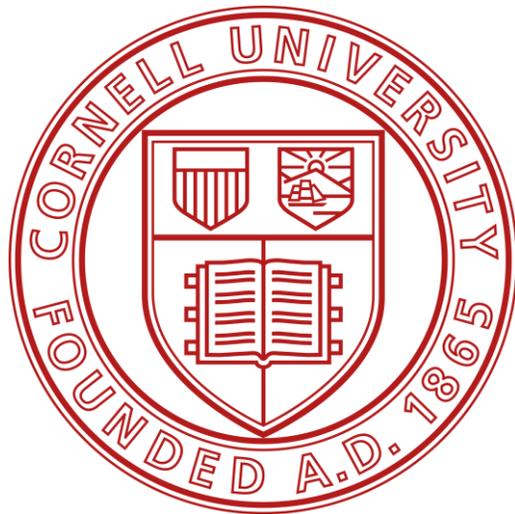


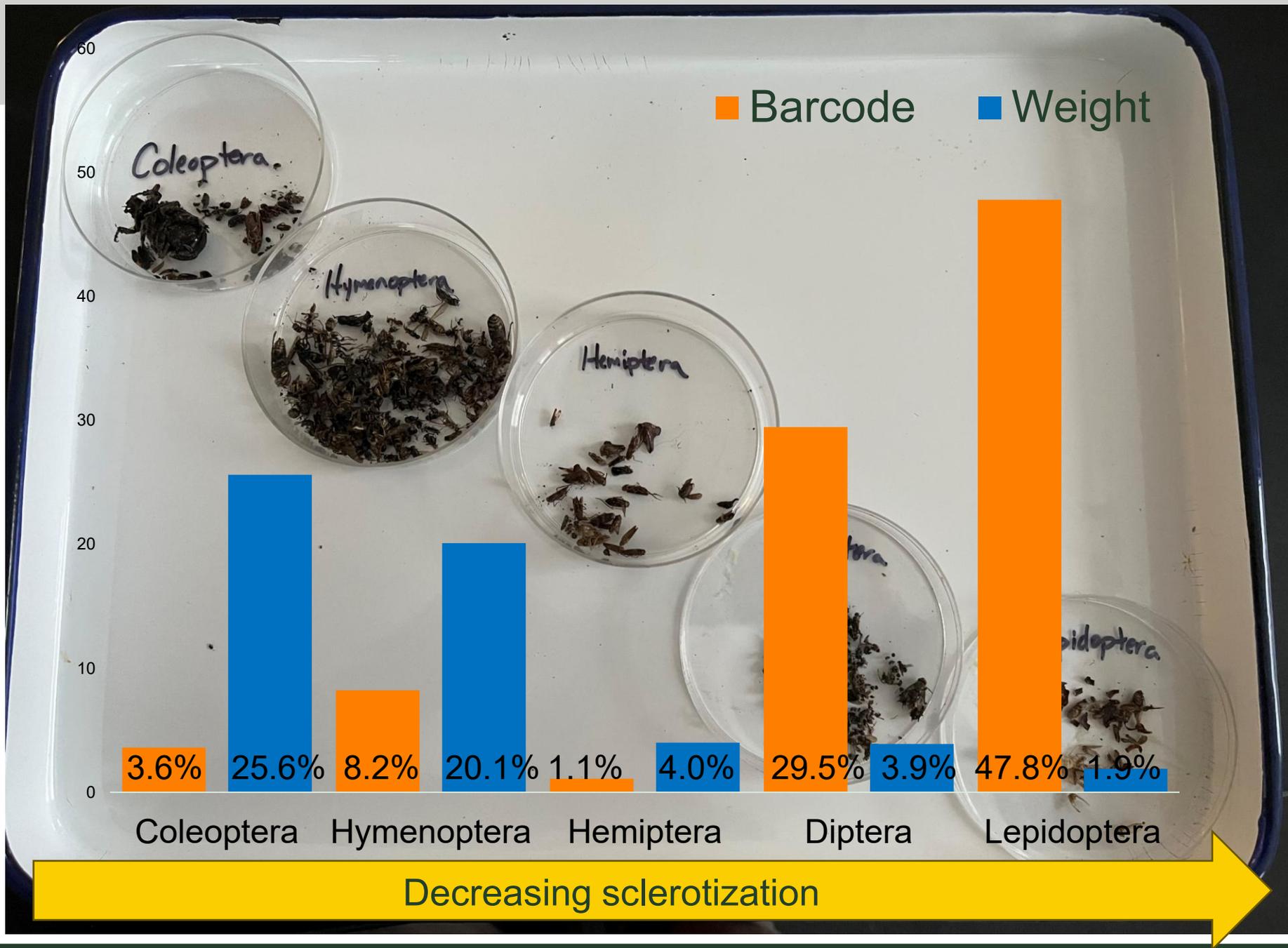
Preserved silver Y moth specimen. Photo: Julieta Brambila, USDA APHIS PPQ, Bugwood.org

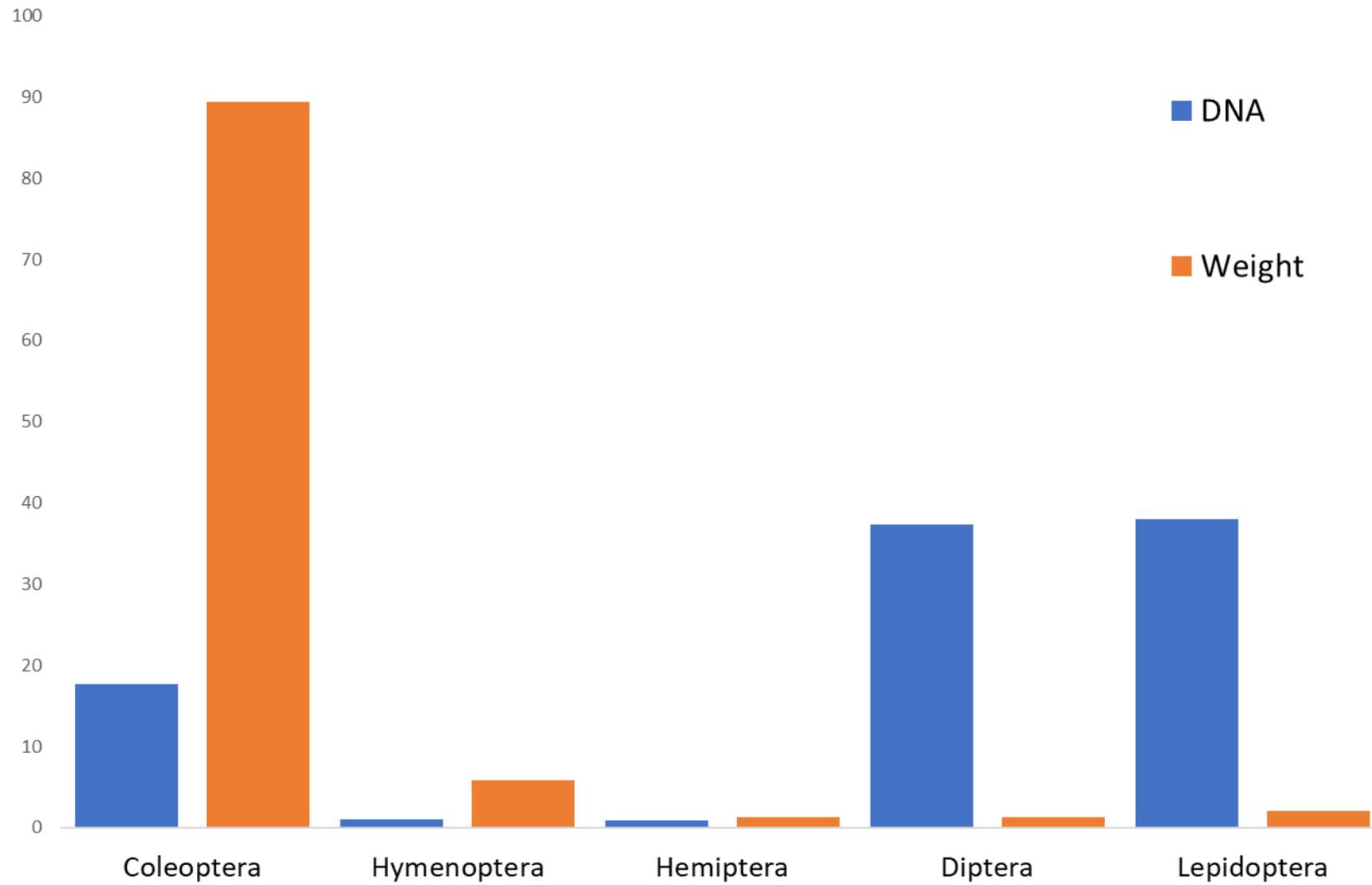


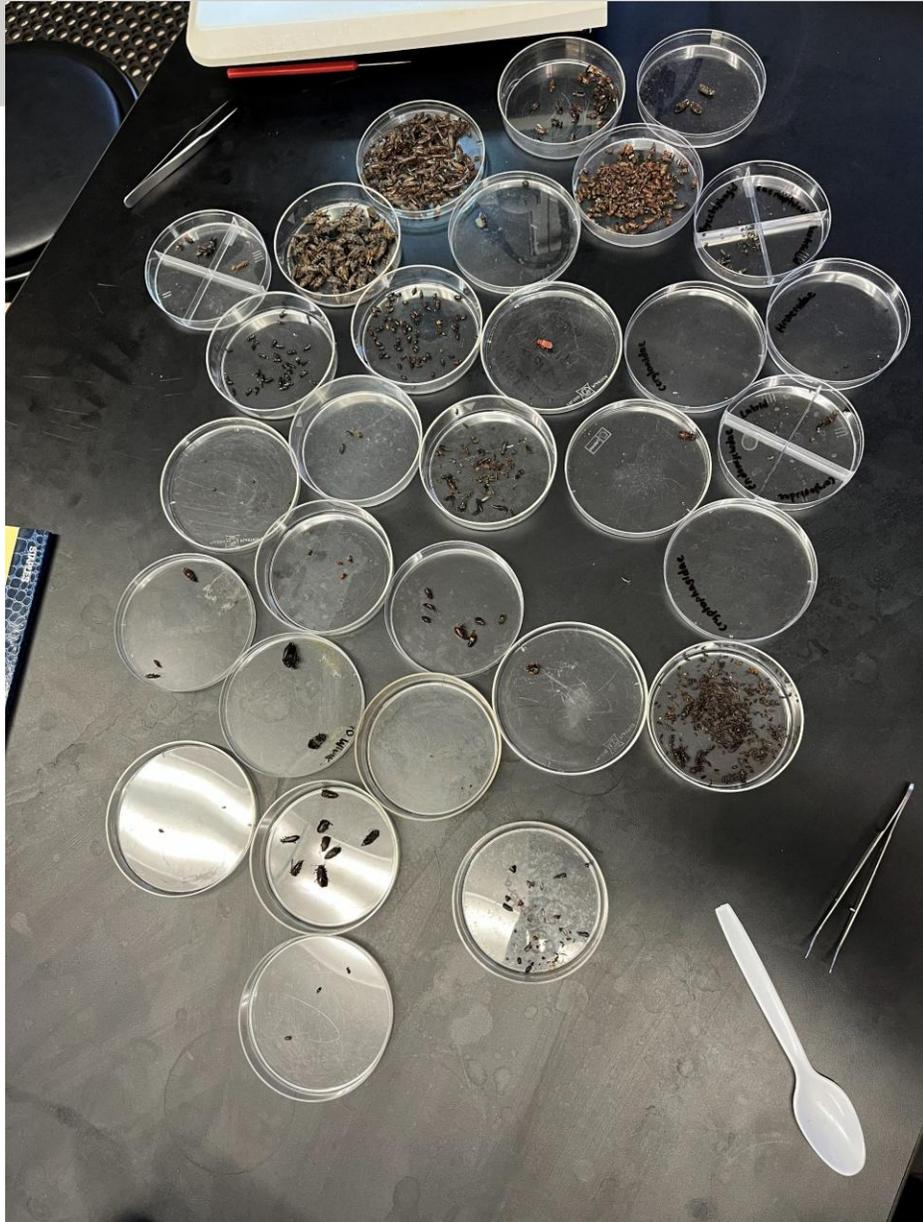
New approach

- Methods development with Cornell University
 - Environmental DNA and Genomics Core Facility
 - Soaking specimens in lysis buffer
 - Maintain integrity of specimens for subsequent examination





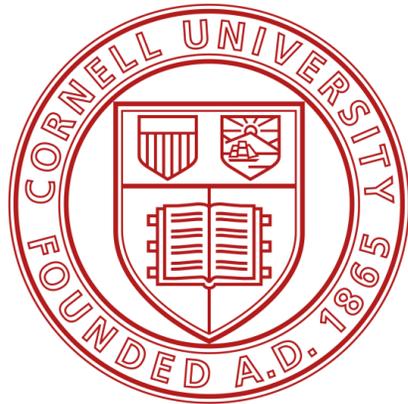




	Barcode	Morpho
Coleoptera		
Cantharidae	Y	Y
Carabidae	Y	Y
Cerambycidae	Y	Y
Ciidae	Y	Y
Cleridae	Y	Y
Curculionidae	Y	Y
Elateridae	Y	Y
Lampyridae	Y	Y
Latridiidae	Y	Y
Leiodidae	Y	Y
Melandryidae	Y	Y
Nitidulidae	Y	Y
Scarabaeidae	Y	Y
Scraptiidae	Y	Y
Silphidae	Y	Y
Staphylinidae	Y	Y
Tenebrionidae	Y	Y
Cucujidae		Y
Chrysomelidae		Y
Thanerocleridae		Y
Histeridae		Y
Trogossitidae		Y
Passandridae		Y
Attelabidae		Y
Coccinellidae		Y
Endomychidae		Y
Eucnemidae		Y
Stenotrachelidae		Y
Laemophloeidae		Y
Lucanidae		Y
Mycetophagidae		Y
Cryptophagidae		Y
Salpingidae		Y
Cerylonidae		Y
Tetratomidae		Y

Hymenoptera	Barcode	Morpho
Andrenidae		Y
Apidae		Y
Chrysididae		Y
Cynipidae	Y	Y
Formicidae		Y
Icheumonidae	Y	Y
Orussidae		Y
Siricidae	Y	Y
Tenthredinidae	Y	Y
Trigonalidae	Y	
Vespidae	Y	Y

Goldilocks Experiment





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Questions?

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