

# DNA Barcoding: The CURE for Citizen Science

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## Exploring Biodiversity using DNA

The DNA Learning Center has developed an inexpensive lab protocol and durable computational infrastructure—DNA Subway—to support student DNA and meta-barcoding research. There is growing enthusiasm for using DNA barcoding as a common platform for CUREs and student citizen science projects. Each year, approximately 4,500 students from 300 high schools and universities around the world do independent barcode research using our methods and tools. James Madison University has scaled a DNA barcoding CURE to engage 800 students taking the core freshman core biology sequence per semester. Students participating in this project published the first DNA barcode inventory of Marine Park, Brooklyn in PLoS One, and identified fraudulent Ginkgo products whose distribution was later halted by the New York State Attorney General's office.

## What is DNA Barcoding?

Like a unique pattern of bars in a universal product code (UPC) identifies each consumer product, a short "DNA barcode" is a unique pattern of DNA sequence that can potentially identify each species.

## Integrated Website and Sample Database

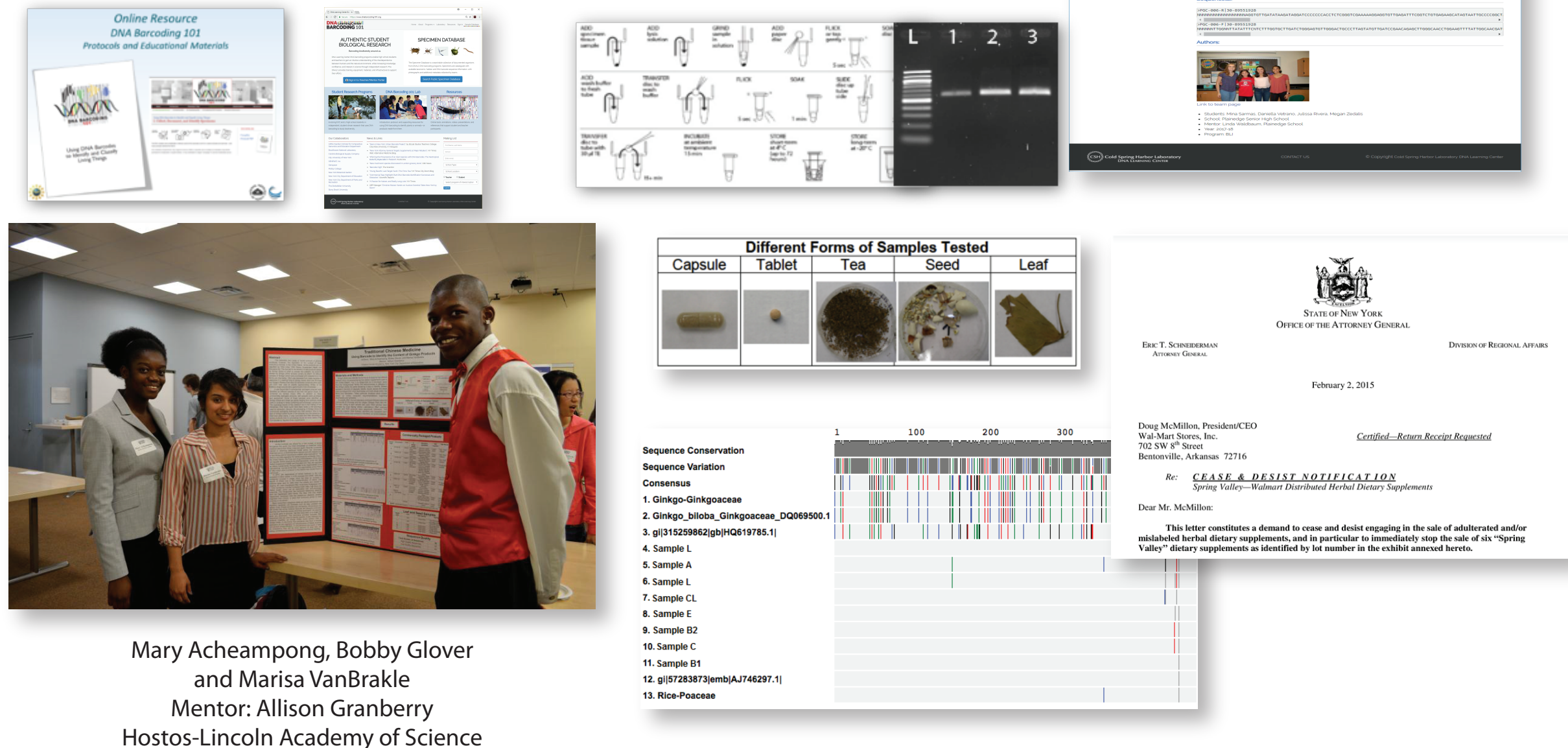
*DNA Learning Center Barcoding 101* is an integrated resource to support DNA barcoding programs. The site includes background, experiment planning, reagent preparation, protocols, instructions for bioinformatics analyses, and multimedia resources. Mentors log in and enroll teams, view guidelines, track team progress, register for Open Labs, and request equipment footlockers. A symposium section features student projects, team information, and results.

The Sample Database allows users to store sample metadata and was updated to include a comprehensive, searchable database of all organisms documented across Long Island, Brooklyn, and Queens. Organisms can be searched by name, habitat, or collection date. Each sample includes organism information, pictures, sequence data, and collection location.

The Blue Line of *DNA Subway* was developed as part of *CyVerse*, an NSF project to develop cyberinfrastructure for life sciences. *DNA Subway* supports bioinformatics analysis of DNA sequence for DNA barcoding. The Blue Line also supports submission of barcode sequences to GenBank, at the NIH National Center for Biotechnology Information.

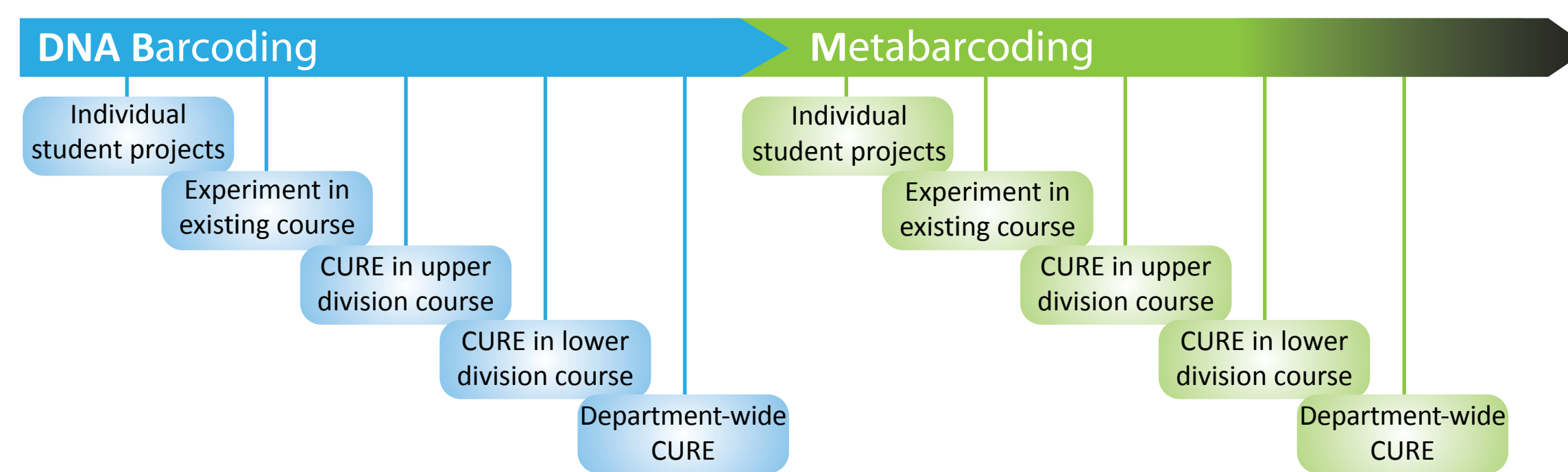
To date, 16 novel sequences and 142 new entries have been published to GenBank; 10 novel sequences are pending submission.

[www.dnabarcoding101.org](http://www.dnabarcoding101.org)



Mary Acheampong, Bobby Glover and Marisa VanBrakle  
Mentor: Allison Granberry  
Hostos-Lincoln Academy of Science

## Moving along a continuum of Barcoding CUREs

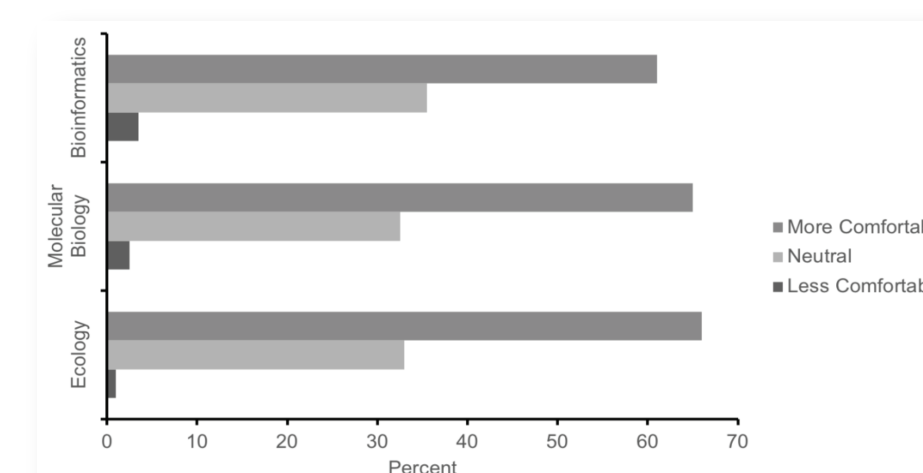
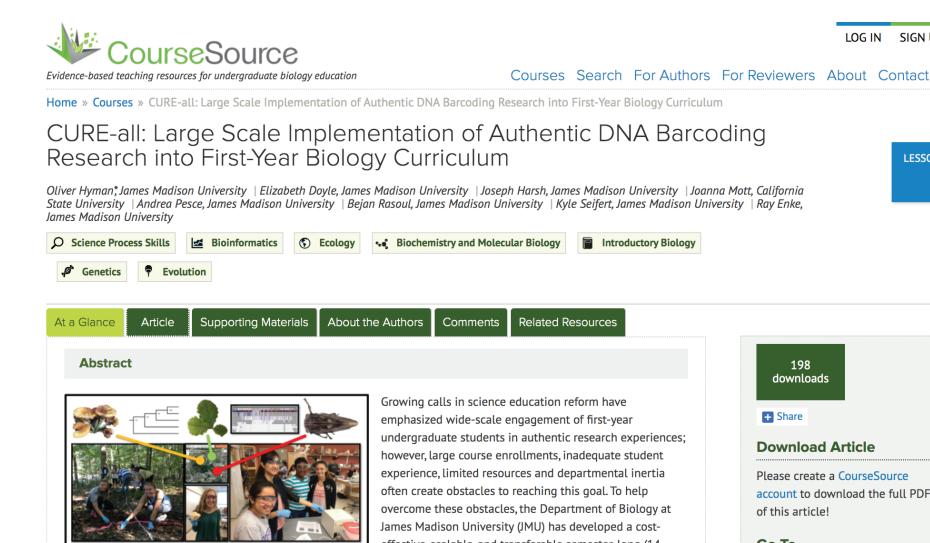


## Developing and Disseminating Barcoding and Metabaroding CUREs

- Collaboration with CUNY, JMU, and Bowie State Faculty
- Refining Biochemical and Bioinformatics Pipeline
- Training Faculty Nationwide

## Highlights:

- Adapted and Piloted Barcoding CURE
- Trained 20 Faculty to implement CURE
- Evaluating impact on faculty and students
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JMU students (n = 430) report the lab experience increased their level of comfort methods from ecology, molecular biology, and bioinformatics?

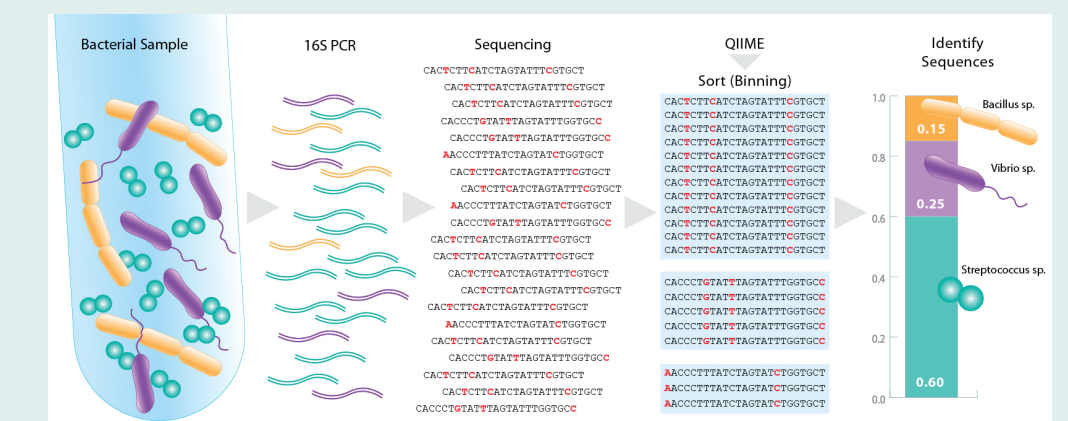
## InnovATEBIO National Center for Biotechnology Education

- Training Community College Faculty in Barcoding and Metabarcoding CUREs
- Developing a Supply Chain Solution:
  - Biotechnology students at HUBs preparing reagents and providing sequencing
- Reducing the cost of barcoding and metabaroding
  - Illumina prep and sequencing  
\$2,000/400 = \$5
  - \$2,000/200 = \$10
  - Reverse engineer DNA isolation kit: \$10 to \$1
  - Pre-indexing: \$20 to \$3
  - Reverse engineer DNA purification kit: \$4 to \$1
  - Goal: \$10-15 per sample



## Metabarcoding

High-throughput analysis of 12S and 16S ribosomal sequences is a natural extension of DNA barcoding. Moving from single barcodes to microbiomes and eDNA perfectly embodies the conceptual transition from single gene to massively parallel genome analysis.



**Aim:** Extend DNA barcoding of single organisms to high throughput analysis of microbial 12S and 16S ribosomal sequences as a launch pad to big data analyses and computer science.

### Objectives:

- Develop a workflow to support microbiome and data science explorations.
- Train and support faculty to implement metabarcoding CUREs
- Evaluate impact on faculty and students.

## Highlights:

- **Adapted** metabarcoding research for students.
- **Developed** Jupyter notebooks to support analysis using QIIME (Quantitative Insights into Microbial Ecology)
- **Optimized** biochemical workflow for distributed microbiome analysis
- **Developed** a user-friendly interface for analysis on *DNA Subway* (the Purple Line)
- **Piloted** metabarcoding CURE at JMU
- **Supporting** metabarcoding in five courses
- **Optimizing** biochemistry to reduce costs and support CUREs
- **Expanding** to support COI for invertebrates

## Example Projects:

**Tick microbiomes contain human pathogens.**

### Lone Star Ticks:

Ehrlichia (2/9), which causes ehrlichiosis.  
Rickettsia (3/9), which causes Rocky Mountain Spotted Fever  
Studied by students from William Floyd High School: Rebecca Ferguson, Jenny Le, Fariyah Chowdhury, and teacher mentor Victoria D'Ambrosia.

### Black-legged ticks:

Borellia (8/12), associated with Lyme Disease  
Studied by students from Connetquot High School: Jacob DeRosa, Dogan Okur, Christopher Picchiello, Giavana Prucha, James Scarabino, and teacher mentor John Halloran.

## Eel grass microbiomes change in unhealthy plants.

Studied by students from William Floyd High School: Elizabeth Scianno, Angela Ochoa, Philip Oriuwa, and teacher mentor Victoria D'Ambrosia

