Taking the Pulse of Natural History Collections During COVID-19 Series: Where are we now?

September 16: Collections’ perspectives

John Bates, The Field Museum
Emily Braker, University of Colorado Boulder
Brian Atkinson, The University of Kansas
Mare Nazaire, California Botanic Garden
The Field Museum in the time of Covid-19
The New Museum “Normal”

- Decreased attendance
- Budget shortfalls
- Staff reductions
- Salary reductions
- Frozen searches

- Little collections access
- Reduced lab access
- No fieldwork
- Working from home
- Zoom fatigue
- Reopening strategies
The Field Museum: 126 years of Biodiversity collections and research
The “New” Museum

- Working from home (the upside)
- Honest discussions of I.D.E.A.
- Virtual Meetings (global access)
- Virtual Educational Activities (broader local and regional access)
- Virtual interactions with donors (no need to drive to the museum)
- Realizing the benefits of digitization
Issues of societal concern.

Closed for the pandemic, the Field Museum of Natural History hosted a socially-distanced blood drive in its empty, cavernous halls. SCOTT OLSON/GETTY IMAGES

Shuttered natural history museums fight for survival amid COVID-19 ‘heartbreak’
Inclusion, Diversity, Equity, and Accessibility: So much to do
¿Cómo pueden surgir especies por cambios en el comportamiento migratorio?

Valentina Gómez-Bahamón
Field Museum Botany: Increased access of the web site
The Extended specimen: Genotype

Long-term archival of genetic resources available at multiple facilities (thousands/millions of specimens) for scientific research
GenBank sequence downloads for the last 12 months
The extended specimen realized: phenotype

NSF supported CT-scanning of vertebrates

Figure 1. Diversity of data and analyses resulting from traditional computed tomography (CT) and diffusible iodine-based contrast-enhanced CT (diceCT) of a formalin-fixed, ethanol-stored frog specimen (genus *Hemisus*). A, qualitative morphology of skeleton; B, isolated cranium with, C, inner ear endocast; D, density analysis; E, Finite Element Analysis (10) showing distribution of stresses when force applied (red arrow); F, wall thickness analysis; G, 3D printed model of skull; H, external surface anatomy (similar to photogrammetry of specimens); soft-tissue anatomy including, I, skeletal muscles and glands, J, nervous system, K, cardiovascular system, and, L, intrinsic tongue muscles (blue, m. genioglossus; red, m. hyoglossus); natural history 'by-catch': M, eggs in oviducts, and, N, endoparasites (nematodes).
Quarterly downloads of Morphosource 3-D specimen data
Our “New” Museum

- Working from home if you can
- Virtual Meetings (global access)
- Virtual Educational Activities (broader local and regional access)
- Virtual interactions with donors (no need to drive to the museum)
- Continued digitization
- Beyond discussions of I.D.E.A.
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COVID Operations and Interim Outcomes
VERTEBRATE COLLECTIONS
University of Colorado Museum of Natural History
• Boulder, Colorado
• Student population ~35,000
• 5 million natural history specimens
  • Anthropology
  • Botany
  • Diatoms
  • Entomology
  • Paleontology
  • Zoology
• 50,000 visitors annually. Audiences:
  • K-12
  • University students
  • General public
• Museum and Field Studies (MFS) Graduate Program
Current campus operating mode = EXPANDED

- Limited in-person research and teaching
- Online course offerings
- Remote work for noncritical staff
- Infrastructure mitigation - HVAC improvements
- Formal 'return to campus' request process
- Daily online health assessment
- Limited COVID testing (dorms, waste streams)

Mandatory mask wearing, social distancing, enhanced custodial and sanitation practices

Have you completed your daily health form?

| Colorado University Boulder | Colorado Daily Health Form |
Collections Operations (March – August 2020)

- Museum closure
- Remote work
- Tiered furloughs, anticipated budget cuts
- Critical In-House Functions (collections):
  - Building security
  - Collections checks
  - Caring for live organisms
Preparation for Return to Campus

- Campus COVID Task Force coordination
- PPE and cleaning supply distribution
- Directional & safety signage
- Building security – after-hours campus police sweeps due to extended class schedule (7am-10pm)
Vertebrate Collections – Current Operations

- Hybrid mode: In-house and remote tasks
- Hiatus on visiting researchers and volunteers
- Reduced occupancy: 1 person per room
- Increased sanitation practices
Positive Outcomes
I. Priority Reshuffling: *Rise of the backburners*

- Collections Policy revision
- Data improvement projects
  - Georeferencing
  - Taxonomy updates
- Data Linkages:
  - Citations 📚
  - GenBank sequences
  - Exchanged materials
- Media Linkages:
  - Ledger pages
  - Field notes

![Image of 27 ledgers and 40+ field notebooks scanned]

![Image of arctos database interface with citations and persistent IDs/URLs]
II. Increased Collaboration

• Collections Managers
  • Sharing strategies
  • Continuity of Operations Planning (COOP)
  • Collaborative student training

• Institutional
  • Virtual Exhibits
  • MFS virtual tours and panel discussion
  • Museum Unlocked podcast
  • Gallery space for in-person classes

Museum gallery Mammalogy Lab – gloves required, traffic guides on floor, socially distanced lab stations.
III. Opportunistic Continuity Tools

- Video Tutorials
  - Zoom recordings
  - Annotated specimen prep videos

- COOP – Hotspot Maps

- Remote Work – possible, even for collections people!
Lessons & Tips

- Consider collaborative training opportunities
- Video conferencing
  - Regular check-ins with remote staff
  - Record - Good for current and future technicians
  - Even when in person, database training is easier over Zoom (for social distancing)
- Scan archives! University collections may be able to partner with libraries
- Invest in laptops for staff when possible
- **Adaptability**
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COVID-related operations from the perspective of a faculty curator teaching classes with a virtual lab

Brian Atkinson
Asst. Professor, Ecology and Evolutionary Biology Department
Curator, Division of Paleobotany, Biodiversity Institute
University of Kansas
Email: brian.atkinson@ku.edu
Break down of this report:

a. Introductions: myself, KU Paleobotany personnel, research, and collections
b. Status of KU Paleobotany before and during covid
c. Teaching a lab based course in a virtual format
d. Outlook
Active field program along the western coast of North America and Antarctica
Collection and Research Strengths:

400,000 specimens: Pre-Cambrian-Recent

Largest North American repository for Antarctic fossil plants (>35,000 specimens, Permian-Jurassic)

NSF Sanctioned Repository for Antarctic fossil plants

Anatomically preserved plants from crucial time intervals

Currently digitizing our specimens via Specify
COVID-19, the Novel Corona Virus

News and information for the ERA-EDTA community and kidney patients.
Managing a research program and collection in the middle of a pandemic???
Research within the division:
Everyone has scopes at home

Remote access to fast computers for Ct-imaging processing

Dedensifying the lab

Collections management:
Loans are still out and normal operations have resumed
Teaching

Diversity and History of Organisms (lecture and lab)

Co-taught: Myself (everything except Metazoa); Rich Glor (Metazoa)

Lab has traditionally been a hands-on specimen based experience
Teaching a biodiversity class in the middle of a pandemic???
Given the current situation and a prioritization of safety. What do we want the students to walk away with this year?

Richard Glor
Professor & Curator

Walter Tapondjou
PhD Student & Graduate TA

Keana Tang
PhD Student & Graduate TA

Anna Krause
Undergrad Rschr. & Undergrad TA

Phylogenetic Tree Literacy
Asynchronous pre-recorded lectures
Synchronous recitations, 2 sections per week
Open book exams (24 hrs to take exam)
Online labs:

Tree thinking exercises using iTOL

Hopefully: diversity surveys via iNaturalist
Reconstructing the history of traits that can be gained and lost using parsimony is not difficult, but does require us to learn a simple algorithm known as Fitch parsimony. Fitch parsimony was invented as a solution to solving parsimony questions a half century ago and remains widely used today. In this lab you will use Fitch parsimony’s signature downpass/uppasp algorithm to infer the evolutionary history of a game-changing evolutionary innovation: photosynthesis (Fig. 2). For details on using Fitch parsimony, see Box 1 below.

Goals: Learn how to use Fitch parsimony to reconstruct trait evolution.

Exercise 1: Good idea! I’ll take it!

Background: A important goal of this week’s lab is to learn how to reconstruct the evolution of traits that may exhibit reversible evolution via Fitch parsimony. A secondary goal is to learn more about another explanation for why a trait might be scattered across the tree of life. Last week, we learned that complex multicellularity evolved repeatedly in distantly related groups via convergent evolution, and always from ancestors that had themselves independently evolved simple multicellularity.

A second way that organisms in different parts of the tree can obtain similar traits is via horizontal transfer, or, put another way STEALING ([3, 3]). We will define horizontal transfer broadly as any instance where one organism acquired a trait from another, regardless of whether the trait was lost by the donor or retained by the recipient.

Box 1: Reconstructing Evolution of Reversible Traits Using Fitch Parsimony

The goal of parsimony is to reconstruct the evolutionary scenario(s) with the fewest possible evolutionary changes. In the case of relatively small trees, where traits change infrequently, and where changes are irreversible, it is often possible to infer the most parsimonious solution “by eye” without the aid of any specific rules or algorithms (this is what you did last week with much smaller trees). In many real-world scenarios, however, we need to apply simple algorithms designed to efficiently identify the most parsimonious solution. The purpose of this box is to explain how to apply the Fitch parsimony algorithm.

The Fitch parsimony algorithm works by stepping through the tree one node at a time and making decisions about possible ancestral states that ensure the most parsimonious solution(s). The algorithm involves two steps. First, you complete a downpass, where possible ancestral states are reconstructed from the tips down to the root. During this downpass, the ancestral state at some internal node may be reconstructed as ambiguous, meaning that the node could be either a photosynthetic or non-photosynthetic. Second, you complete an uppass by working backwards from the root to the tips to resolve ambiguous nodes inferred during the downpass. During both the downpass and uppass, character states are reconstructed following two simple rules. Once you have completed the downpass and uppass, you can assign trait changes to branches in your tree.

Rule 1: If the descendants of an ancestral node share any common traits, assign those shared states to the ancestral node. Here are a few examples of how this rule is applied: (A) If your downpass starts with two descendants that are both photosynthetic, you would assign photosynthesis to the ancestor. (B) If one descendant is classified as ambiguous (i.e., either photosynthetic or non-photosynthetic) and the other as photosynthetic, you would assign photosynthesis to the ancestor. (C) If both descendants are classified as ambiguous, the ancestor would also be classified as ambiguous.

Rule 2: If the descendants of an ancestral node do not share traits in common traits, assign both the possible states to the ancestral node. For example, if one descendant has photosynthesis and the other does not, you would reconstruct the ancestor as ambiguous. For every node where you apply Rule 2, you will ultimately infer a trait change along one of the two descendant branches.

Figure 2. A sample of bryophyte diversity. The top two images show the liverwort, Marchantia. At the top right, we can see the elongated archegonial(gynaec) that contain the egg and eventually the sporophyte. The bottom image shows an expand moss gametophyte bearing small unbranched sporeophytes.

Exercise 1a: Evolution of Alternative Generations Under the Classic Tree

Background: Our first goal is to evaluate how the two different life history strategies involving alternation of generations - gametophyte and sporophyte dominant - evolved under the classic phylogenetic hypothesis - where bryophytes are paraphyletic. To do this we will use parsimony to reconstruct the evolution of the two alternative life histories on a phylogenetic tree that includes broad sampling of major embryophyte lineages.

Exercise 1b Goals: Reconstruct evolution of alternation of generations under the classic phylogenetic hypothesis involving paraphyly of bryophytes.

1. Open ITOL and upload the tree file - Lab4_Exercise1a_Tree1.nw (Fig. 4). This file is a simple text document that contains a NEWICK formatted tree. Note: this lab includes several files with similar names, please be sure to carefully read and check the file name(s) to avoid the trouble that results from carelessly picking the wrong one (one of your instructors may have made this mistake while testing the lab).

2. Download and save the file that contains annotations for several major clades of embryophytes - Lab4_Exercise1a_MajorClades.txt. Drag and drop this file into the ITOL window. You should see shaded boxes that indicate the following seven clades of embryophytes: mosses, hornworts, liverworts, lycophytes, ferns, gymnosperms, and angiosperms. You can view the names associated with each of these clades using the Datasets tab in the Controls window of ITOL (Fig. 4).

3. Download the file that contains data on whether the gametophyte is dominant or whether the sporophyte is carried by the wind (rather than water as seen in their aquatic and marine algal relatives). In some cases, such as in the liverworts (Marchantia) the gametophyte grows specialized structures that raise the female sex organs (archegonia) and and their short-lived sporophytes.

4. Before going any further, we need to mention that land plants are divided into two major groups - the bryophytes and the polyporangiophytes (vascular plants are the only survivors of this later group). Bryophytes are characterized by having a sporophyte life cycle with alternation of generations where the gametophyte is the dominant multicellular form (Fig 2); in this group, the sporophyte is simple, short-lived, unbranched, and has just one sporangium. Polyporangiophytes (polyporangiophyte - multiple sporangia - “spore plant”), meanwhile, are characterized by having a sporophyte life cycle with alternation of generations where the sporophyte is the dominant multicellular form. In this case the sporophyte is long-lived, complex, branched, and has multiple sporangia (see Fig 2). As polyporangiophytes began to become more abundant and diverse, competition and natural selection drove increases in height that allowed plants to disperse their spores further (stay tuned for Part 2) and obtain more sunlight than competitors.

Recent major changes to the embryophyte tree of life have major implications for our understanding of early land plant evolution (Fig 3). Historically, bryophytes were thought to be paraphyletic with respect to polyporangiophytes. In fact, the latest edition of the Raven textbook includes this arrangement. However, within the past few years (like basically everywhere else in molecular phylogenetics), there have been major changes to the bryophyte tree. In this lab, we will consider the implications of these new results for understanding trait evolution along the embryophyte tree of life, and by extension, how we study the traits that lead to the success of land plants.

Part 1 Goal: Analyze the evolution of the sporophyte life cycle and alternation of generations across two phylogenetic hypotheses for Embryophytes.

Figure 3. Two of the new studies - de Sousa et al. 2018 and Harris et al. 2020 - that recovered monophyly of Bryophytes.
Reflections teaching during Covid:

Class enrollment is virtually the same as compared to previous years

KU undergraduate biology program enrollment is up

Overall students have appreciated the flexibility in our class format and are learning

Rich and I are happy to share our lab material
Outlook:

Specimen based research will continue

Fieldwork will resume next summer and beyond

Grant proposals focusing on collections based work are being written
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California Botanic Garden’s Collections and COVID: Creating the Silver Lining

Mare Nazaire, Herbarium Administrative Curator
Chair, Collections Committee
COVID-19: Challenges

- Budget constraints
- Reduced staffing
- No volunteers
- No fieldwork
- Delays: collecting permits
- Non-essential tasks on hold
- Staggered schedules
- Inside vs. outside work
How do we connect students to collections when they cannot visit in person?
Surveyed the academic community:
- Previous visitation and tours
- Determine interest in virtual tours
- Determine interest in supplementing coursework
The Collections Connection

Educational module:

Plants in a changing world: California Diversity, Species Distributions, and Climate Change

This work is supported by the Hispanic-Serving Institution’s Education Grants Program, grant no. 2015-38422-24058/project accession no. 1007104, from the USDA National Institute of Food and Agriculture.
Dataset: RSA-VascularPlants
Taxa: Encelopsis cavillei (Encelopsis argophylla var. grandiflora, helianthella cavillei)
Search Criteria: has images; excluding cultivated/captive occurrences

RSA - California Botanic Garden Herbarium

Encelopsis cavillei (A. Nutt.) Blake
RSA0891889 - B. C. Telohar, s.n. 1887-08-14
United States, California, Inyo County, Bishop Canyon, (Below Guard ledge), 36.11081°N 117.10069°W, 762m

Full Record Details
For more info:
https://www.calbg.org
Break-out room discussion

What are the top three positive outcomes experienced by collections as we adapt to new COVID-aware workplace guidelines?


Break-outs (15 minutes) • Review (5 minutes) • Discussion
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September 17: Moving Forward: Communities Response and Opportunities for the Future: Presentations and Panel Discussion/Q&A

Speakers: Rob Gropp, Pam Soltis, Scott Miller, Roland Roberts
Please help by providing feedback about this webinar series!

Survey link: https://ufl.qualtrics.com/jfe/form/SV_aVL7wEfLYUXcbFb