Smithsonian

NATIONAL MUSEUM of NATURAL HISTORY

Department of Botany Specimen Preparation Volunteer Handbook

Revised May 2025

This handbook belongs to:

Start Date: ______________________________

CONTENTS

INTRODUCTION 4

Getting to Know You 5

Welcome Message 6

Code of Conduct 7

Conflict Resolution Policy 8

Equal Employment Opportunity Policy Statement 9

Prevention of Workplace Harassment Policy Statement 10

Emergency Information 12

FLOOR-PLAN MAPS 14

5th Floor Map 15

4th Floor Map 16

3rd Floor Map 17

INFORMATION ABOUT THE HERBARIUM 18

General herbarium rules and specimen handling instructions 19

Our Collections 21

History of the US National Herbarium: A Timeline 23

List of historical expedition specimens in our collection 24

Department of Botany Staff Directory 25

MOUNTING BOTANICAL SPECIMENS 26

Selecting specimens to mount 27

List of supplies for Mounting Botanical Specimens 28

Mounting procedure for new herbarium specimens 29

Drop Tag Information 34

Recording Sheet Numbers from Drop-tag Using iPad 35

EVALUATIONS 41

First Bundle Mounting Evaluation 42

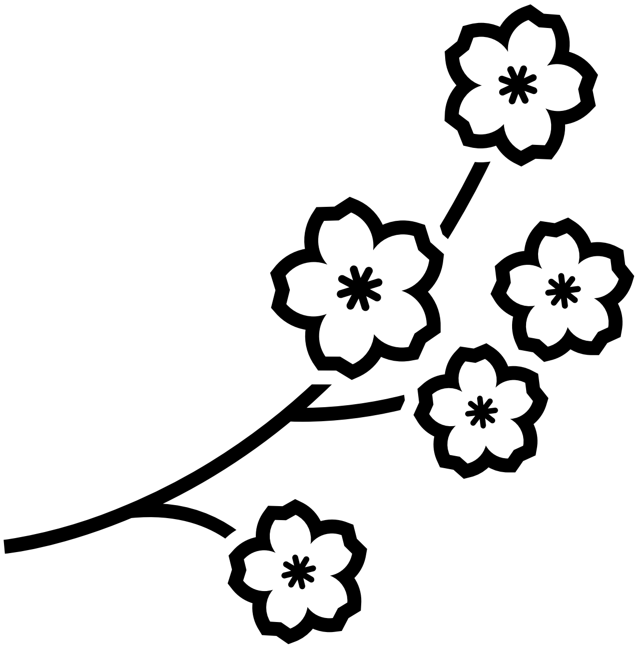
Six month Mounting Evaluation 45

Six Month Volunteer Review Questionnaire 48

SUPPLEMENTAL INFORMATION 50

Appendix A. 51

100 Uses for an Herbarium (Well at Least 72) 51
Appendix B. 55
Collections-based science in the 21st Century 55



INTRODUCTION

Getting to Know You

Please complete this form and return it to your supervisor.
(Questions are optional. Emergency contact information is required.)

Volunteer Information

Full Name: ____

Start Date (Volunteering): _____________________________

Just for Fun (Optional):

Favorite Color: _______________________________________

Favorite Plant: ____

Favorite Food: ____

Hobbies or Interests: ___________________________________

Do you have pets? ☐ Yes ☐ No

If yes, what kind? _____________________________________

Do you have children? ☐ Yes ☐ No

Your Birthday (Month/Day): _________________________________

Emergency Contact Information (Required):

Contact's phone number:

____

Emergency contact's name:

____

Welcome Message

Dear Volunteer,

On behalf of the Department of Botany, we are thrilled to welcome you to our volunteer team! You are about to embark on a meaningful journey where you will contribute to the long-standing tradition of preserving botanical specimens for scientific research.

The practice of collecting botanical specimens dates back to the Renaissance era, and some of these historical collections are still preserved today. The specimens you prepare for our collection will serve researchers for years to come, with the potential to remain accessible for the next century or more.

Your role is invaluable to both our department and the museum. Without your dedication and support, our backlog would be unmanageable, and researchers would be unable to make the significant discoveries that drive scientific advancement.

Thank you for joining our specimen preparation team. We look forward to collaborating with you and getting to know you better as you contribute to this important collection.

Welcome aboard!

Sincerely,

Erika M. Gardner
Museum Specialist, Volunteer Supervisor

Code of Conduct

“Volunteers, like museum staff and leadership, should be held to the same standards of conduct and behavior” -Van Hoven, K., 2016. *Recruiting and Managing Volunteers in Museums.*

The Hatch Act: Some Civil Service employees (many people on staff at the Smithsonian) must take an oath under the Hatch Act. Although volunteers are not under oath, please use your best judgement and discretion.

Mindfulness: The Department of Botany comprises people from different backgrounds. It is in the best interest of everyone if we accept everyone for who they are even if their beliefs/values or ideologies are different from our own. This is a unique workplace where few restrictions are placed upon the staff’s ability to express themselves via clothing, tattoos, piercings, and hairstyles. This is truly an amazing place to learn from each other and grow as an individual and a team.

Sexual Harassment: The Smithsonian has a zero-tolerance policy when it comes to sexual harassment. If you feel you have been sexually harassed on Smithsonian property, please report the incident as soon as possible to the Volunteer Coordinator or OPS. If you are in violation of such misconduct, you will be permanently banned from volunteering and charges can be filed against you.

Violence: Safety is the highest priority for both visitors and staff (including: volunteers and interns). If you see or hear something that can potentially put others in danger, please report it immediately to OPS. The Smithsonian has a zero-tolerance policy for violence. If you are overheard making a threat(s) or found with a weapon(s), you will be permanently banned from the premises. Such conduct can result in a felony conviction.

Reporting intimidation or other concerning behavior: The SI Civil Program is a resource that Smithsonian employees and affiliated persons may use to report harassment, threats of violence, incidents of intimidation, or other concerning behaviors, and get information about appropriate next steps. The goal and mission of SI Civil is to empower employees and affiliated persons to communicate workplace concerns and facilitate the resolutions of those concerns as quickly as possible.

It is the responsibility of Smithsonian managers and supervisors to maintain a harassment-free and safe work environment and to take prompt and effective action when situations covered by the policies arise. The success of the SI Civil Program requires the commitment of all Smithsonian employees and affiliated persons.

Conflict Resolution Policy

Volunteers are encouraged to promptly address any concerns regarding their working conditions. If a volunteer believes that any aspect of their assignment is unsuitable or presents a challenge, they are advised to report the issue to the individual they believe is most appropriately positioned to assist in resolving the matter.

Should a volunteer supervisor determine that a volunteer's behavior may pose a risk to themselves or others, the supervisor is required to notify the Volunteer Office immediately. Volunteers who exhibit disruptive or uncooperative behavior may be subject to removal from their position or dismissal from the institution.

Failure to comply with program expectations including repeated absences without prior notice, failure to complete required online trainings, or not logging volunteer hours, may result in the deactivation of the volunteer's badge.

Contact information:

Volunteer Supervisor: Erika Gardner

Phone: 202-633-0936

Email: gardnere@si.edu

Volunteer Coordinator: Agustin Baldioli

Phone: 202-633-4485

Email: baldiolia@si.edu

Smithsonian Institution

Date: January 12, 2023

Equal Employment Opportunity Policy Statement

Equal Employment Opportunity at the Smithsonian Institution means opportunity for all. The Smithsonian is committed to ensuring that all employees and affiliated persons (e.g., interns, research associates, fellows, and volunteers) are treated equitably in an environment that is free from discrimination based on race, color, religion, sex (including gender identity, gender stereotyping, pregnancy, and sexual orientation), national origin, age, disability, genetic information, parental status, or marital status and reprisal for reporting workplace harassment.

Together, as a team, it is our responsibility to attract talented leaders, researchers, curators, educators, and employees in every area of endeavor and to ensure that our employees and affiliated persons are aware that EEO covers all personnel and employment programs, management practices, and decisions, including, but not limited to, recruitment, hiring, merit promotions, transfers, reassignments, training and career development, benefits, and separations.

We are collectively responsible for supporting equal employment opportunity, diversity, inclusion, and access. Moreover, we must work to eliminate behaviors or practices that discriminate or create barriers for any members of our workforce so that everyone will have the freedom to compete on a fair and level playing field.

All managers and supervisors will be held accountable through annual performance appraisals for ensuring that their staff are made aware of this policy and the requirements of Smithsonian Directive 214. Equal Employment Opportunity. Additionally, every supervisor must complete EEO for Supervisors training and non-supervisory employees must complete Basic EEO training. Every employee, regardless of the level of responsibility, must complete refresher training every three years.

This document is your insurance policy that the Smithsonian is committed to equality, diversity and inclusion in the workplace. In our diversity lies our greatest potential and I want to assure you of my commitment to an organizational culture of mutual respect where each of us feels welcomed, comfortable, and safe.

Working together, we will continue to cultivate a place that is accessible, inclusive, and diverse. A place where individuals, regardless of their background, come together and support each other as we affirm and celebrate the value of being One Smithsonian. I am grateful to all of you, as we each play a critical role in creating the type of workplace where everyone can thrive.

Lonnie Bunch

Lonnie G. Bunch III

Secretary

Smithsonian Institution

Date: September 30, 2021

Prevention of Workplace Harassment Policy Statement

Enhancing and maintaining a workplace that is conducive to safety and success for all is among my highest priorities. The Smithsonian Institution prohibits workplace harassment. Unlawful harassment based on race, color, religion, sex (including gender identity, gender stereotyping, pregnancy, and sexual orientation), national origin, age, disability, genetic information, parental status, or marital status and retaliation for reporting workplace harassment will not be tolerated.

Workplace harassment is defined as unwanted or unwelcome conduct, whether verbal, written, or physical in nature that a reasonable person would find denigrating or objectionable when:

- Enduring the offensive conduct becomes a condition of continued employment; or
- Such conduct is severe and or pervasive enough to create a work environment that a reasonable person would consider intimidating, hostile, or abusive.

Employees, contractors, and affiliated persons (e.g., interns, research associates, fellows, and volunteers) are responsible for appropriate professional conduct and behavior and cooperating in the enforcement of this policy. Supervisors and sponsors are responsible for maintaining a work environment free of harassment. Individuals engaging in conduct that violates this policy will be subject to appropriate disciplinary measures up to, and including, removal or disassociation from the Smithsonian.

To achieve the goals of this policy, every supervisor must complete the EEO for Supervisors training and non-supervisory employees must complete Prevention of Workplace Harassment training. Every employee, regardless of the level of responsibility, must complete refresher training every three years.

To prevent and remedy incidents of workplace harassment, the Smithsonian must be made aware of the conduct or behavior. The Smithsonian will protect the privacy of individuals and the confidentiality of information related to allegations of harassment to the extent possible. Information will be provided only to those who have a need to know to carry out their responsibilities.

Reported workplace harassment will be addressed immediately. Individuals who believe they are being harassed on the job are encouraged to:

- Tell the harasser (orally or in writing) to stop, keep a record of the events, report the behavior to a supervisor or manager, and cooperate in the inquiry; or

- Immediately discuss the issue with someone in their supervisory chain to determine the course of action.

Individuals who do not feel comfortable discussing the issue within their immediate chain of supervision are encouraged to contact the Office of Equal Employment and Supplier Diversity (OEESD), the Employee Assistance Program (EAP), the Ombuds, the union, or SI Civil Coordinator at (202) 633-6379 or sicivil@si.edu, the SI Civil Hotline at (202) 633-6620.

The new SI Civil Program, implemented in January, has provided a platform for employees and affiliated staff to communicate workplace concerns and facilitate the resolution of those concerns as quickly as possible. The SI Civil Program manages both Smithsonian Directive 217, *Workplace Violence Prevention Policy* and the new Smithsonian Directive 225, *AntiHarassment Policy*, the associated handbook, and other guidance materials. SI Civil was developed as a resource that employees and affiliated staff may use to report threats of violence, incidents of intimidation, or harassment, and get information about appropriate next steps. Raising an allegation with the SI Civil Program is not equivalent to or in lieu of filing an EEO complaint of discrimination or a grievance under the administrative or negotiated procedures included in the applicable Collective Bargaining Agreement. Individuals are encouraged to visit the SI Civil website to learn more about this program and how to report incidents of workplace harassment.

Additional guidance is available in Smithsonian Directive 214, *Equal Employment Opportunity Program* and the associated handbook. Related questions or requests for services and information should be directed to the Office of Equal Employment and Supplier Diversity, 600 Maryland Avenue, S.W. Suite 7078, (MRC 521), Washington, DC 20013-7012; (202) 633-6430.

The Smithsonian Tropical Research Institute (STRI) has a separate complaint process available for their employees and applicants who are outside of the U.S. and are not US citizens. For more information, please contact the STRI Office of Human Resources and/or the SI Civil Program to learn more about the STRI reporting process.

The Smithsonian is committed to being a welcoming, inclusive, and safe place for all. We will never waver from that commitment. I am inspired by what is possible when we all work together toward our shared future.

Lonnie G. Bunch III

Secretary

Emergency Information

Fire:
Calmly evacuate from the building using the stairs and leave personal belongings behind. Never use the elevator. Each floor has a designated Safety Officer. Follow the directions from this person. They will escort everyone out of the building to the designated meeting location on the east side of the mall. If you require assistance to evacuate the building, please let the safety office know.

Flood:
Move to higher ground, avoid taking elevators and do not go into the basement. If a pipe bursts, locate the closest staff member to section off the collection and evacuate the area immediately. Notify the Department Chair and/or the Collection Manager.

Inclement weather (tornado or hurricane):
Shelter in place in the designated location on the floor which you are currently on. Leave personal belongings behind. Each floor has a designated Safety Officer, follow the directions from this person.

If herbarium cabinet(s) falls over:
If you can get away from the fallen or unstable case, find and alert the closest staff member to section off the collection and locate the Department Chair and/or the Collection Manager. If you are trapped under a case, call out for help and do not try to move the case off of yourself. These cases can weigh over 500 lbs.

Active shooter:
Run, hide, or fight, depending upon the situation. If you are a safe distance from the situation, try to evacuate immediately- leave excessive personal belongings behind. If you are unsure if you are close to the danger, try to find a hiding spot out of sight from the shooter. In the worst case, if you are unable to hide or run from the shooter, try to disarm, or fight if you are able. When you can get to a safe location notify security or call 911 immediately.

See something? Say Something:
If at any time you feel concerned about your safety or the safety of others, contact the Office of Protective Services (OPS) immediately- see listed phone numbers at end of this document. If they do not answer call 911. Please inform your supervisor, the Department Chair, or the Collection Manager.

In the event of an injury:
If you are hurt and ambulatory, please notify the closest staff member, your supervisor, a Safety Officer, the Collection Manager, or the Department Chair. Your supervisor will need to fill out an illness/injury report in the Automated Incident Reporting System (AIRS) for you by providing all the necessary information for the Office of Occupational

Health and Safety (OHS). You will be escorted to the OHS office to be evaluated and treated if emergency medical procedures are not required for your injury.
If your injury requires you to go to the hospital, your injury must be reported to OSHA within 24 hours and to the Safety Officer for the Department of Botany.

If you find someone injured on-site, report the incident to the nearest staff member. If the person is in distress, call for emergency help by calling 911 or the Office of Protective Services (OPS). Do not attempt to move the injured person.

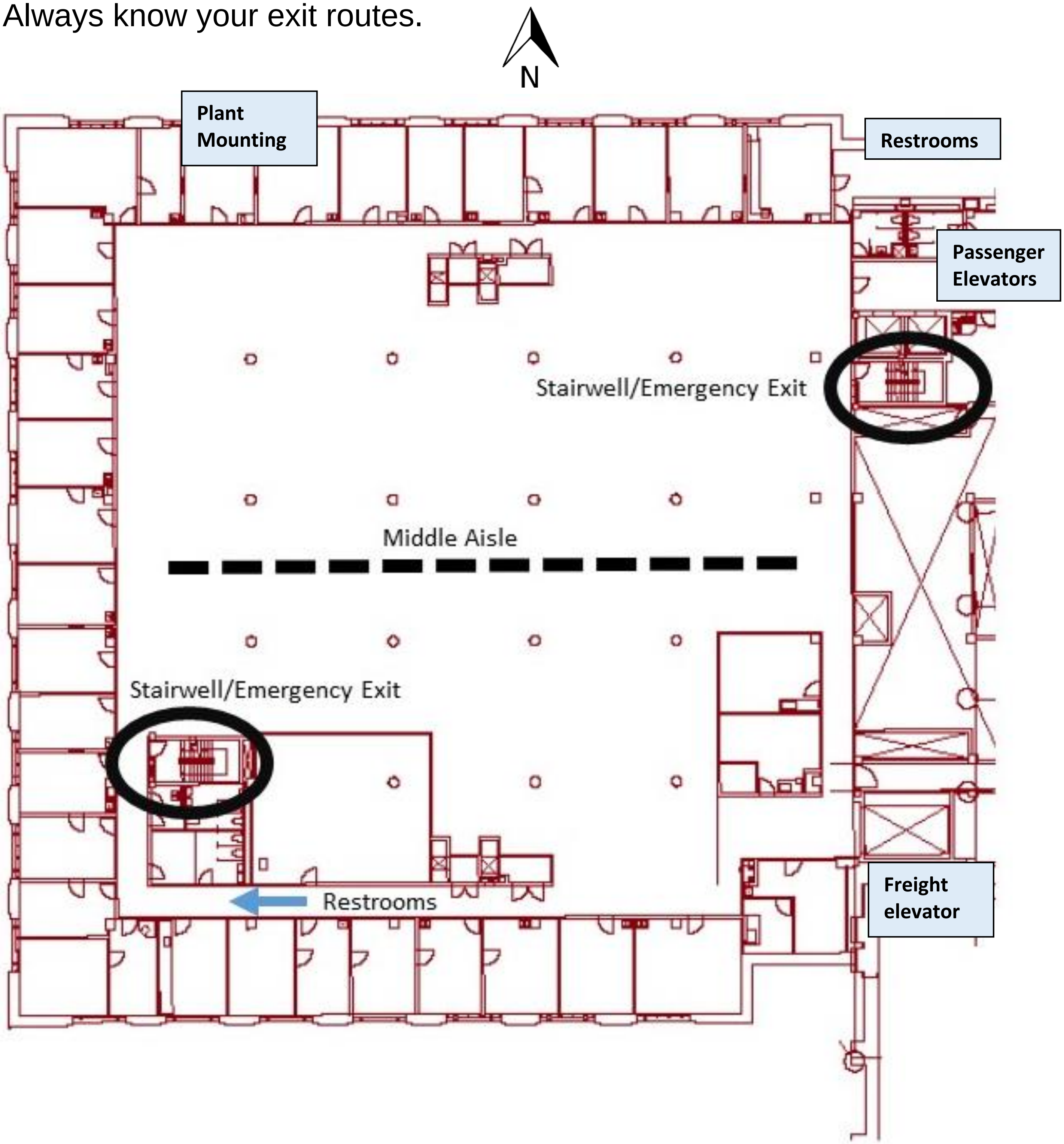
Emergency contact numbers:

- Security Sub-Office 202-633-31605 (Open during the hours of the museum)
- NMNH Control Room (24 hours) 202-633-2086
- Office of Health and Safety: 202-633-9355
- OSHEM: 202-633-2530

FLOOR-PLAN MAPS

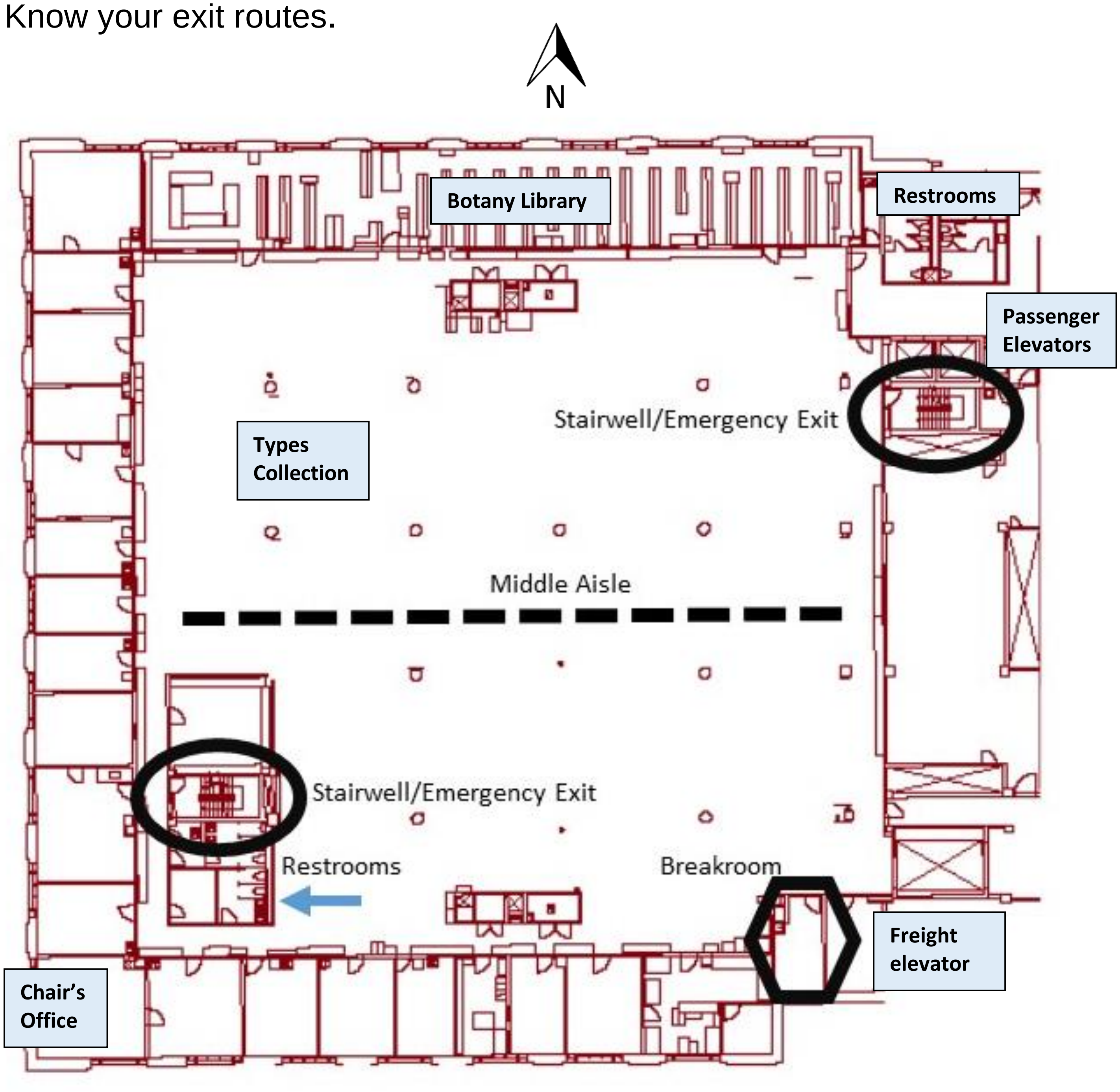
5th Floor Map

Always know your exit routes.



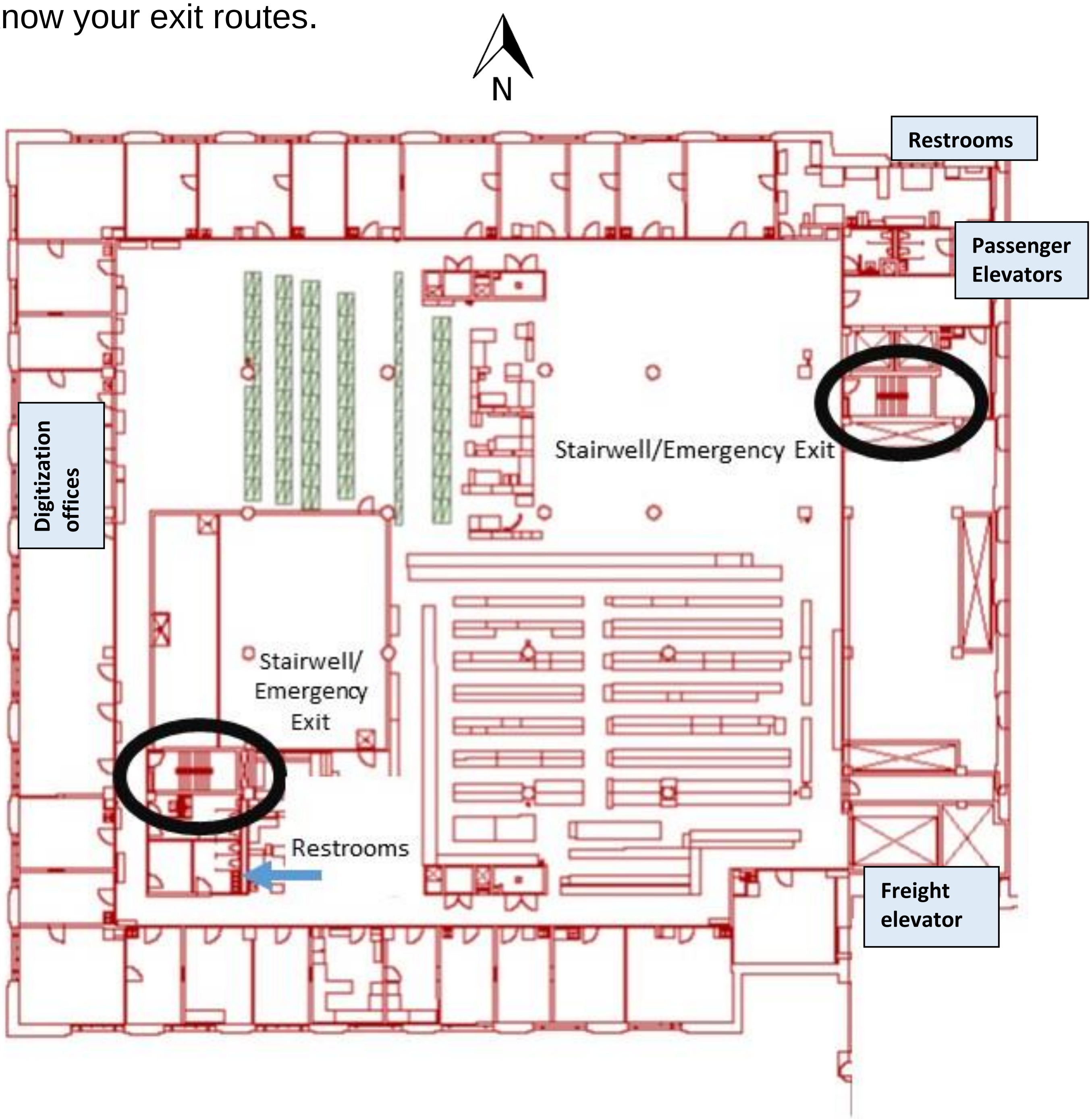
4th Floor Map

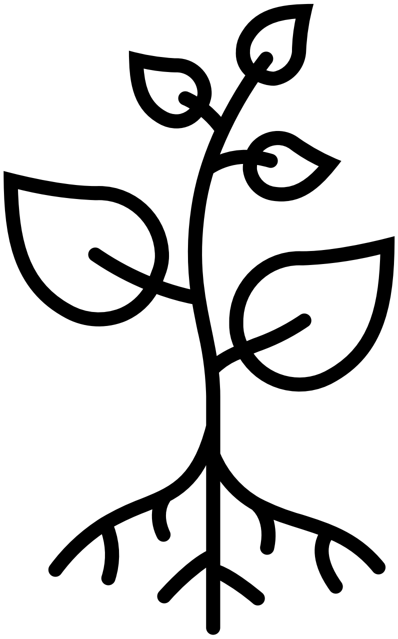
Know your exit routes.



3rd Floor Map

Know your exit routes.





INFORMATION ABOUT THE HERBARIUM

General herbarium rules and specimen handling instructions

1. No food or drink (including water, chewing gum or candy) may be consumed in areas where specimens are being handled. This includes the herbarium and imaging workstations.
2. Handwashing before and after working with herbarium specimens is highly recommended for personal hygiene and safety. Nitrile gloves will be provided if requested.
3. When opening a herbarium case, step back for 30 seconds to allow the captured atmosphere to dissipate. Some cases tend to accumulate mercuric chloride vapor, but in a very short time, the breathing zone is clear.
4. All work surfaces should be clean and provide sufficient space to perform the task at hand. After working in an area, sweep excessive debris from your workspace.
5. Always handle specimens, folders of specimens, and species covers containing specimens with both hands. Do not squeeze, crunch, or bend bundles of specimens. Hold specimens parallel to the floor, not tilted or vertically, and ALWAYS facing up.
6. Do not forcefully push folders into cabinet or cart slots. Reduce the amount of impact by gently sliding folders into the slots.
7. Do not turn specimens over like the pages of a book. Do not "thumb through" folders of specimens while stored in a herbarium case.
8. Any fragment that occurs when handling specimens can be returned to the sheet ONLY if there is no doubt from which sheet it came. If there is any doubt at all, the fragment should not be saved. This is also true of material that is commonly found in the spine of genus covers and species covers.
9. Specimens should never be refiled by inserting it directly into a genus folder or species cover while those folders are in the herbarium case.
10. Rigid "gray boards" are available for transporting loose specimens for any distance.
11. Specimens should never be left exposed at the end of a workday. Always keep specimens in carts when not working extracting, imaging, or refiling them, and close each cart at the end of the day.
12. Specimens are NEVER permitted on the floor.

13. Be sure to replace each specimen in the folder/cover you used to extract them. This ensures that specimens will be returned to the exact same location from which they were removed.

14. Any specimen that needs significant repair, should be placed in a REPAIR folder provided by Core Collections Management, and stored in a designated case. Specimens will be repaired and refiled by CCM.

Our Collections

The United States National Herbarium is the 10th largest herbarium in the world and the 4th largest in the United States. Our acronym provided by Index Herbariorum is, **US**. Anytime you see the acronym US on documentation it is about our collection.

We store over 5 million+ specimens in our collections! These range from pressed specimens (4 million) to wood samples (32,000), anatomy slides, algae, pollen slides, bulky bamboos, mosses, and lichens.

Each year we mount about 10,000-12,000 specimens and we accept about 12,000-15,000 unmounted specimens. We also loan our specimens to other herbaria, similar to a library lending its books. We send out about 8,000 specimens a year on loan and we borrow specimens from other herbaria for our researchers.

An important part of our collection is our Type Herbarium. Over 115,000 Types are in our holdings. Each year we acquire about 15-25 Type specimens. Types are specimens which describe a new species to science.

We also house the D.C. Herbarium. It is one of the most comprehensive botanical collections of the DC region, spanning across Maryland and Virginia counties near DC.

The Botany Library is a wonderful resource located on the 4th floor of our department. The subjects range from botanical science journals to gardening. It is one of the largest libraries dedicated to botanical literature. If you have time and need a place to take a break, be sure to check out this amazing collection of books.

Notable research conducted in our Herbarium.

Taxonomic research

- Algae
- Dinoflagellates
- Euphorbiaceae, Malvaceae, Onagraceae, Poaceae, Vitaceae, and ferns.

Geographic research

- Biological Diversity of the Guiana Shield
- Flora of Puerto Rico and the Virgin Islands
- Flora of the Washington-Baltimore Area
- Marquesas Islands
- Micronesia
- The Guiana Shield
- West Indies

Specialties research

- Lianas and Climbing Plants of the Neotropics

Current Research Areas

Research staff in the Department of Botany study plant systematics and floristics of plant communities across the globe. Both modern and fossil species of many plant groups, including algae, mosses, ferns, and flowering plants, are currently being studied. Smithsonian botanists conduct field studies globally.

Uses for herbarium specimens:

After mounting a few specimens, you might ask, "what happens after a specimen is mounted? Who uses these specimens? Why are there so many? Do we really need all of them?"

The answer to these questions can be found in Vicki Funk's 2004 Article, "*100 Use for an Herbarium: Well at Least 72."* Check it out in Appendix A. There are so many interesting uses for herbarium specimens. They can facilitate science, art, history, genealogy and much more!

History of the US National Herbarium: A Timeline

1838-1842: First collections accessioned were from *The United States Exploring Expedition* (over 50,000 specimens collected by the U.S. Navy) and the U.S. South Pacific Exploring expedition, under the command of Lt. Charles Wilkes, U.S.N.

1848: Earliest expedition sponsored by the Smithsonian, the explorations of Charles Wright in Texas and New Mexico.

1868: All specimens collected for the Smithsonian up to this time were housed off-site with Dr. Torrey at Columbia College. Dr. Torrey could no longer care for the specimens and Joseph Henry, the first secretary, made arrangements for the specimens to go to the USDA.

1881: Smithsonian published Lester F. Ward's, paleobotanist, *Guide to the flora of Washington and vicinity*.

1883: Spencer F. Baird, the second secretary of the Smithsonian, arranged for the Smithsonian collections at the USDA and the USDA's collections to be housed at the Smithsonian. March 28, 1983, Frederick Vernon Coville was appointed Honorary Curator of the National Herbarium.

1894: Dr. Joseph N. Rose, became the first full-time curator, studied Cactaceae and carried out extensive field work in the **West Indies**

1986: The collection contained about 250,000 specimens.

1910: National Museum of Natural History building opened its doors of March 17th.

1923: Mary Agnes Chase becomes an assistant Botanist to Alfred Hitchcock. In 1936 she succeeded Chase after his death and to become the Senior Botanist in charge of Agrostology.

1942: Robert Fosberg and William C. Steer travel to Colombia to collected Cinchona samples to treat for malaria.

2024: Angiosperm collections reorganized according to APG classification

List of historical expedition specimens in our collection

- 40th Parallel Expedition
- Byrd Antarctic Expedition
- California Geological Survey
- Cinchona Missions
- Colorado Exploring Expedition (Ives Expedition)
- Death Valley Expedition
- First Voyage of Captain James Cook
- Fremont Expedition
- Harriman Expedition
- Hassler Expedition
- Hayden U.S. Geological Survey, 1872
- Hayden's US Geological Survey – Colorado
- International Boundary Commission
- J. W. Powell Colorado Exploring Expedition, 1868
- J.W. Powell Survey
- La Plata Expedition
- Macomb's San Juan Exploring Expedition
- Mexican Boundary Survey
- Nicollet Expedition
- Peary's Expedition to Greenland
- Smithsonian African Expedition
- Stevens Pacific Railroad Survey
- U.S. North Pacific Exploring Expedition
- U.S. Typhus Commission
- Western Union Extension Telegraph Exploring Expedition
- Whipple Pacific Railroad Survey
- Whitney Expedition
- Williamson Pacific Railroad Survey

To find out more information about these expeditions, please check out the departmental website at:

https://naturalhistory.si.edu/research/botany/about/historical-expeditions

Department of Botany Staff Directory

Area code for the National Mall: **(202)**

Botany Phone List (24 Feb 2020)

Acevedo, Pedro – 633-0963, W404

Ballantine, David – 633-0959, W527

Brooks, Barrett – 633-0970, W323

Brothers, Leslie – 633-0938, W503

Dorr, Laurence J. – 633-0964, W416

Everly, Robin – 633-2146, Botany Library

Gardner, Erika – 633-0936, W525

Gulledge, Rose – 633-0973, W415

Johnson, Gabriel – 301-238-1098, MSC-E1412

Kelloff, Carol L. – 633-0953, W510

Khan, Nancy – 633-0943, W514

Krupnick, Gary – 633-0940, W407

Lin, Ingrid Pol-yin – 633-0908, W314

Lutz, Sue – 633-0901, W526B

Orli, Sylvia – 633-0911, W317

Peterson, Paul M. – 633-0975, W410

Schuettpelz, Eric – 633-0914, W521

Soreng, Robert J. – 633-0981, W408

Strong, Mark – 633-0966, W404

Tangerini, Alice – 633-0915, W519

Toner, Meghann – 633-0904, W525B

Tuccinardi, Chris – 633-0900, W316

Wagner, Warren L. – 633-0968, W504

Wen, Jun – 633-4881, W500

Wurdack, Kenneth – 633-0916, W512

Algae Lab – 633-0976, W528

Botany Department Office – 633-0920, W405

Botany Meeting Room – 633-0946, W516

Botany Sort Center – MSC – 301-238-1066, E1102

FAX Machine (Botany NMNH) – 202-786-2563, Mach. Room

Functional Morph. Lab – 633-0979, W531

Greenhouse – 301-238-1060, MSC Greenhouse

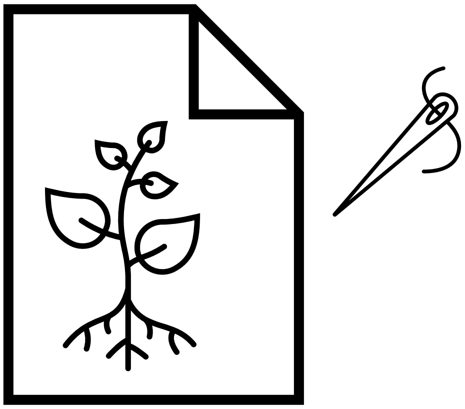
Library, Botany – 633-2146, W422

MSC Botany Fax – 301-238-3492, A1004

Plant Anatomy Lab – 633-0977, W529, W529A

Records Room/Photocopy Machine – 633-0945, W409

Shipping Room – 633-0947, W500A-B



MOUNTING BOTANICAL SPECIMENS

Selecting specimens to mount

MOUNTING PRIORITY:

1- Type specimens
   - Specialists' material
   - Field collections by current staff
   - Purchases
2- Tropical localities both New World and Old World
3- North America, Europe; temperate areas of Asia, Africa, South America, Australia
4- Material requires additional attention before mounting.
5- Attributes of material make it the lowest mounting priority.

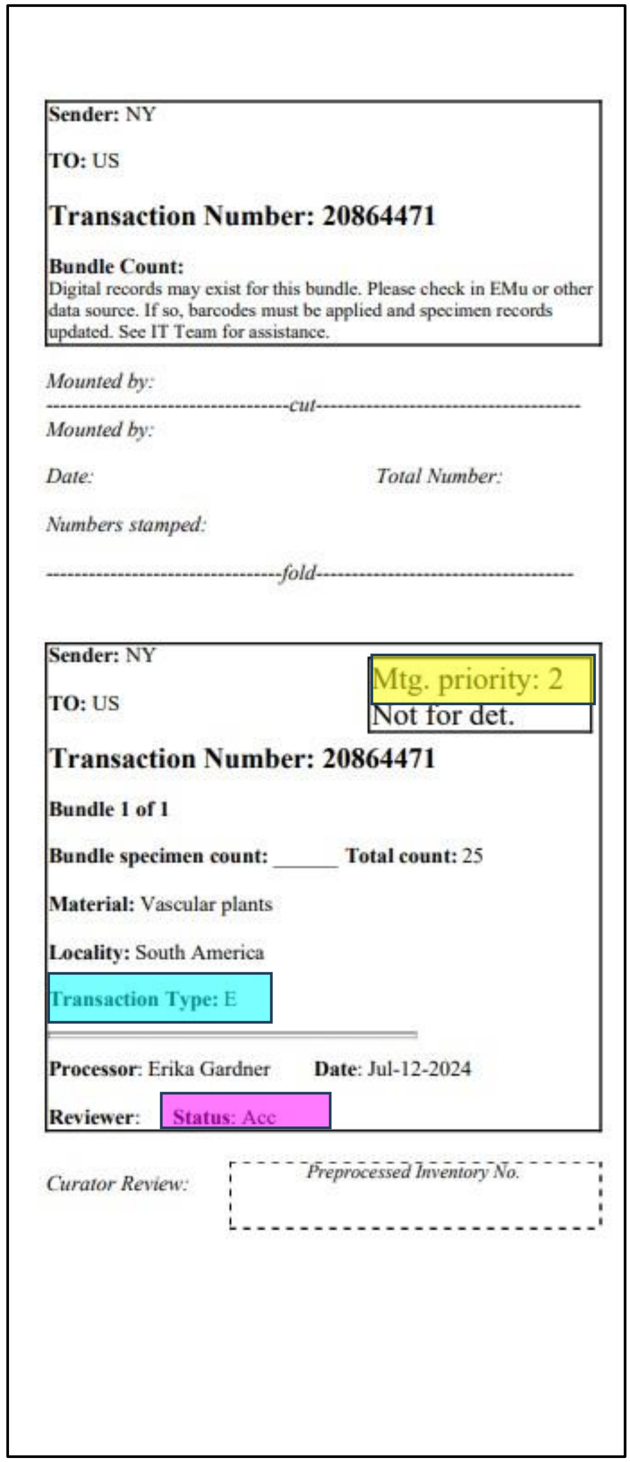
TRANSACTION TYPE:

E- exchange
G- gift
F- field collection
P- purchase
T- transfer
B- bequest
TC- Temporary custody

STATUS:

Acc. – Accessioned
Pending – Not yet accessioned; status to be det.
Non-Acc. Acq. – Non-accessioned acquisition; material will be maintained but not part of main collection
Dispose – Material will be sent elsewhere

Retyped September 2015. Erika Gardner



Sender: NY
TO: US
Transaction Number: 20864471
Bundle Count:
Digital records may exist for this bundle. Please check in EMu or other data source. If so, barcodes must be applied and specimen records updated. See IT Team for assistance.

Mounted by:
--------------------------------cut------------------------------------
Mounted by:
Date: *Total Number:*
Numbers stamped:
--------------------------------fold----------------------------------

Sender: NY
TO: US
Mtg. priority: 2
Not for det.
Transaction Number: 20864471
Bundle 1 of 1
Bundle specimen count: ______ **Total count:** 25
Material: Vascular plants
Locality: South America
Transaction Type: E
Processor: Erika Gardner **Date:** Jul-12-2024
Reviewer: Status: Acc

Curator Review: *Preprocessed Inventory No.*

List of supplies for Mounting Botanical Specimens

- Mounting Paper, 100% rag, unbuffered, (caliper .01 2-.01 5)
  - pH neutral paper board (for bulkier/heavy specimens)
- Alkaline buffered paper, 100% rag (fragment packet paper)
- pH neutral bond paper, 100% rag (for labels)
- Gummed paper hinging tape (Lineco) 1 inch width
- pH neutral linen tape with gummed backing for strapping
- Bone folder, 6 inches
- Brass weights
- Cellulose sponge
- Watch glass or petri dish
- Kim wipes (tissues)
- Linen or cotton thread, size 8
- Plastic paper clips
- Polyester film
- Polyethylene bags, zippered closure
- Glue. Polyvinyl acetate emulsion adhesive, pH neutral
- Sewing needles (embroidery/crewel suggested)
- Needle threader
- Thimble
- Sewing scissors
- Needle-nose tweezers
- Dissecting probe
- Wax paper
- Bubble wrap (11 inches x 17 inches)
- Soft paint brush
- Archival pen or pencil

Mounting procedure for new herbarium specimens

Author: Katherine Boyd Rankin

Purpose

The purpose of mounting dried plant specimens onto archival herbarium sheets is to preserve the specimens by minimizing damage by handling. Mounted specimens are more safely handled and stored because brittle and fragile parts are supported, and all parts are secured against loss. A mounted specimen provides a means for data to be repeated via examination.

Description

The system described here is appropriate for mounting vascular plants (flowering plants, ferns, and conifers). Algae, lichens, and bryophytes are “mounted” using other methods. An herbarium specimen comprises a pressed, dried plant specimen affixed to a thick sheet of paper. The collection information relating to the specimen is contained on a label. This method involves securing specimens to the paper with thin cloth straps backed with a water activated adhesive, as well as sewing with heavy-duty cotton or linen thread.

Construction

Positioning and Arrangement of Specimen.

DO NOT GLUE ANYTHING until you know everything will fit on the sheet.

Carefully examine both sides of the specimen. Arrange the specimen on the sheet to expose as many of the diagnostic characters as possible (e.g., flowers, fruits, petiole attachment, upper and lower surface of leaves, etc.). Some of the plant material can overlap if the important features are not obscured.

Determine if the entire specimen will fit on one sheet (always try to mount on a single sheet). If multiple sheets are necessary to adequately represent the specimen, annotate the sheets as follows: “Sheet 1 of 2”, “Sheet 2 of 2” with an archival pen. Then scan and make a copy of the specimen label for the second sheet.

If there is too much plant material for one sheet and a 2nd sheet is not warranted, set the extra plant material aside in the newspaper. Scan and print a duplicate label. Cut the label out and place it with the duplicate plant in the newspaper. Write the transaction number from the drop-tag onto the newsprint and give the specimen to the plant mounting supervisor.

Separate clumps of plants, spread them out, remove excess soil and keep the plants aligned in the same orientation (usually base near the bottom and apex near the top). However, not all specimens should be mounted with the heaviest and bulkiest section near the base. If all specimens are mounted using this orientation, the general storage becomes lopsided.

Avoid crowding the specimen into corners or placing it too close to the edges of the sheet where the specimen may be more vulnerable to damage. Keep in mind that when the specimen is filed away and is stored in species and/or genus covers, which open from right to left, more pressure is applied on the left edge of the sheet.

Label

A specimen label, which bears the collection information, should always accompany a specimen and the specimen should not be mounted until a label is provided. Allow room for attaching the specimen label to the bottom right corner of the sheet. This is customary practice in herbaria worldwide, and it allows for easy reading when kept inside the genus cover.

Position the collection label in place with paper clips and arrange the specimen and fragment pocket (explained in the next section) on the page. Ideally the label should be completely adhered. If the specimen is particularly large and the label could become obscured by the specimen, attach the label only along the right edge, allowing it to be pulled back to view the specimen.

Before affixing, examine the label(s) and check both sides for information. If information is included on the reverse side, photocopy it on alkaline buffered paper and mount it with the other label information or place it in the fragment pocket.

When affixing the label with glue, place a sheet of waxed paper over the label to avoid smearing the print when pressure is applied by hand or a bone folder.

Mount other labels or annotations above the specimen label leaving some space in between. Place the most recent annotation at the very top. If there are no additional labels, leave space above the main label to place additional labels in the future. If there is no room directly above, affix additional labels as close as possible to the left of the collection label.

Specimen tags, which bear the collection number, may be left attached to the specimen or can be mounted on the specimen sheet. As an alternative, they can be removed and placed in the fragment pocket.

Deteriorated labels or labels on poor quality paper should be photocopied or reprinted, using alkaline buffered 100% rag paper. Place the original label in the fragment pocket.

Fragment Pockets

Determine the correct size of a “fragment” pocket needed to accommodate what is *detached or is likely to become detached in the future and allow room for it on the herbarium sheet. The pocket size may vary depending on the amount of fragments. The pocket, which is adhered to the sheet, will hold specimen fragments, whole leaves, flowers, and small fruits that have become detached from the specimen, in addition to other items already mentioned. Every sheet must have a pocket, even if there are no loose parts at the time of mounting. Use pH neutral 100% rag folder paper for the pockets.

Place bulky fruits that do not fit easily into paper pockets in bags with zippered closures which are sewn onto the herbarium sheet, space allowing.

Segregate loose bulky fruits above a certain size from the sheet specimen to optimize storage space. Place the bulky specimen with a duplicate label in plastic bags with zippered closures and store in the “bulky collection” of the herbarium.

To assure reunion of the parts of a single collection, duplicate the label and place it in the bag. Make a cross reference on both labels indicating each part of the collection, i.e., mark the sheet “bulky collection” and mark the duplicated label (placed in with the bulky fruit) with the sheet number of the specimen.

Mounting or attaching the specimen

Strapping

After the specimen is arranged on the sheet and space is ensured for the other items, place weights on the specimen to hold it in place while mounting. It is best to begin mounting a specimen from the bottom and working up. Unless the specimen is very thick.

Cut small straps of varying widths from gummed linen tape. The width may vary from 1-5 mm. Thin straps are used on finer plant parts and thicker straps over heavier or bulkier areas.

Moisten the gum-backed straps by running them over a damp sponge. It is very important to keep sponge and hands clean while mounting to avoid soiling the page.

Place straps over most plant parts, taking care not to obscure flowers. Because flowers and fruits are critical structures for study they should not be obscured by straps;

nevertheless, they should be secured. To secure the flowers, use very narrow straps, sparingly, and avoid covering up the reproductive structures. Always bear in mind not to conceal important features such as leaf tips, leaf bases, flower structures, small inflorescences, etc.

Place straps approximately 8 cm to 15 cm apart (avoid over strapping) and wherever possible, place straps at right angles to the stems, leaves, flowers, and fruits.

Allow about 7-10mm of the strap to extend on each side of the plant part that is being fastened, after snugly fitting the strap against the plant. The tip of a pair of closed scissors, dissecting probes or tweezers are useful tools for doing this. It is important to have the specimen secure on the sheet to avoid the specimen sliding and abrading on the sheet.

Sewing

Sewing is the preferred way to secure thick parts (e.g. woody stems, bulky fruits still attached to the specimen) and is generally done to provide extra security for heavier specimens.

Sew large, leathery leaves or numerous, overlapping leaves, making certain that the stitch goes over the edge of the leaf to flatten and secure it to the sheet. Stitches should not be longer than 1-2 inches; and try to use existing holes in leaves to make the stitches.

For extremely heavy specimens, adhere the herbarium sheet to a card stock (same size as the herbarium sheet), which will provide extra support to the specimen. Mount as usual but using a stronger needle for sewing.

For shattering parts and flyaway inflorescences, cover the specimen or parts of specimens with small pieces of polyester film and sew it over the specimen.

Make stitches using a sturdy needle threaded with cotton or linen thread and knot it on the back side of the herbarium sheet. Use double strands of thread to provide extra strength. When all the sewing is completed, cover the knots with alkaline buffered paper tape to prevent the strings from snagging on other specimens during storage.

Adhering

Use adhering techniques only for affixing the label and the fragment pocket, never on the specimen or any of its parts.

A water soluble, white, pH neutral adhesive or methyl cellulose is recommended.

Comments

Other techniques for mounting plants exist, such as directly bonding the specimen to the paper with adhesive. The method described here has been selected over adhering the specimen directly to the herbarium sheet because it is a completely reversible mounting process and allows for the expansion and contraction of the plant specimen due to changes in environmental conditions.

Drop Tag Information

After a mounter finishes a bundle, the mounter will need to provide information on the drop tag. The information should be included in the appropriate space provided on the droptag.

Please include the following information:

1. The mounter's name.
2. The date bundle was completed.
3. The sheet number range.
4. The total number of sheets mounted.

This information will need to be recorded on the iPad.

Follow the directions on the next page

Sender: NY

TO: US

Transaction Number: 20864471

Bundle Count:
Digital records may exist for this bundle. Please check in EMu or other data source. If so, barcodes must be applied and specimen records updated. See IT Team for assistance.

Mounted by:

---------------------------------cut---------------------------------

Mounted by:

Date: *Total Number:*

Numbers stamped:

---------------------------------fold---------------------------------

Sender: NY

TO: US

Mtg. priority: 2
Not for det.

Transaction Number: 20864471

Bundle 1 of 1

Bundle specimen count: ______ **Total count:** 25

Material: Vascular plants

Locality: South America

Transaction Type: E

Processor: Erika Gardner **Date:** Jul-12-2024

Reviewer: **Status:** Acc

Curator Review: *Preprocessed Inventory No.*

Recording Sheet Numbers from Drop-tag Using iPad

Required Items

- Drop-tag from bundle
- iPad
- Mounting Tag Input Form (accessed via Safari)

---

1. Prepare the iPad

- Turn on the iPad and unlock with provided code.
- Tap the **Safari** icon to open the browser.

---

2. Access the Mounting Tag Input Form

- If the **Mounting Tag Input Form** is not already open:
  - Tap the **Bookmarks** icon (open book symbol).
  - From the list, select: **Mounting Tag Input Form**.
  - To close the bookmarks panel, tap the bookmark icon again.

---

3. Enter Information in the Form

Fill out each of the following fields:

- **Mounting Date**:
  Tap *Select Date* and choose the appropriate date from the calendar.
- **Mounter Full Name**:
  Select your name from the dropdown list.
- **Sender**:
  Enter the sender's name as it appears on the drop-tag.
- **Transaction Number (OR number)**:
  Enter the transaction or OR number exactly as shown on the tag.
- **Sheet Number From**:
  Enter the first sheet number in your series.
  - If only entering one sheet, use the same number for both fields.

- **Sheet Number To**:
  Enter the last sheet number in your series.
- **Notes**:
  Include any relevant additional information (optional).

---

4. Submit the Form

- Tap **Submit**.
- A confirmation message will appear when the record is successfully added.

---

5. Recording Multiple Number Ranges for One Transaction

If a transaction has more than one sheet number range:

1. On the Mounting Tag Input Form page, tap **Add Another Mounting Tag**.
2. Repeat the steps in Section 3, using the new range of sheet numbers.
3. Tap **Submit** after each entry.

---

6. Correcting a Record

To modify or delete a submitted record:

a. Access the Query Page

- Tap **Query the Mounting Data Table**.
- If closed, reopen it via **Bookmarks** > **Mounting Tags**.

b. Search for Your Record

Fill in one or more of the following fields:

- **Mounted by**: Select your name.
- **Sent by**: Enter sender's name (if known).
- **Transaction Number**: Enter if available.
- **Mounting Done in the Last**: Choose a timeframe from the dropdown.

Tap **Submit**.

c. Edit or Delete

- Click the **Trans No.** for the record you want to change.

- Make necessary edits in the form.
- Tap **Submit** to save changes or tap **Delete this Record** to remove it.

---

7. Final Steps

- Turn off the iPad and return it to the locker.
- If the battery level is below 10%, plug it in to charge.

NOTES:

Entering Hours in the VSys Volunteer Portal
Smithsonian Institution Volunteer Guide

---

1. Logging In

Portal URL: vol.si.edu
Username: Your full email address
Password: As set during initial setup

First-Time Users:
You will receive an email from the Smithsonian to create your password. Your username will be your full email address.

Forgot Your Password?
Use the "Forgot password" link on the login page to reset it.

After Logging In:
You'll see a navigation menu at the top, including the **Action Box**, a **Calendar** displaying your assigned shifts/enrichments, and a **News Bar**.

To return to the main page from any other section, click the **Home** button in the upper right corner.

---

2. Action Box

The Action Box provides quick access to key features:

- **Check In/Check Out:** Start and end your shifts
- **Update My Info:** Modify your contact information and preferences
- **My Info:** View hours, awards, and training history
- **Report Past Hours:** Submit hours for previous volunteering sessions

---

3. Calendar Overview

Your calendar displays current assignments and is color-coded for clarity:

- **Light Blue:** Volunteer Shifts
- **Purple/Pink:** Enrichments and Field Trips
- **Yellow:** Today's Date
- **Blue Border:** Required Data
- **Gray Border:** Optional Data

Hover over dates for more info or use calendar views (day, week, month). You can also cancel shifts or send messages directly from the calendar.

---

4. Check In/Check Out

You can check in/out from any computer while onsite:

- **To Check In:**
  - Log in at vol.si.edu
  - Click **Check In/Check Out** in the Action Box
  - Select your opportunity and check in
  - Log off after use
- **To Check Out:**
  - Click **Check In/Check Out** again
  - Add mileage or comments as needed
  - Click **Check Out**
  - Log off after completion

---

5. EDGE Activity Reporting (Check-Out)

If your role includes EDGE activity tracking:

- Select the number of EDGE activities
- Choose activity type from dropdowns
- Provide start/end times and number of visitors
- Click **Check Out**
- Comments are optional

---

6. Logging Past Hours

To report hours from previous dates:

- Select **Report Past Hours** from the Action Box
- Choose your task
- Enter the date, start/end time, and mileage

- Click **Save**
- (EDGE activity fields will appear if applicable)

---

7. My Info & Reports

Click **My Info** in the Action Box to:

- View your volunteer history, hours, trainings, and awards
- Print reports for school, tax, or personal use

---

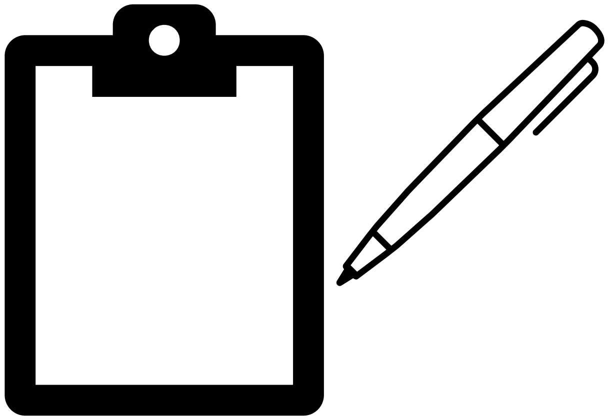
8. Scheduling & Managing Shifts and Enrichments

- Browse and sign up for shifts or enrichment opportunities from your calendar
- Cancel shifts directly from the calendar view
- Use the **Send a Message** option if you need to notify staff about a shift

---

9. Searching for Additional Opportunities

Use the portal's search function to explore and register for additional volunteer roles that match your interests and availability.



EVALUATIONS

First Bundle Mounting Evaluation
Plant Mounting Evaluation Form

Name: ________________________
Role: _________________________
Period of evaluation: ____________
Supervisor: ____________________

Rating scale:
1= Needs improvement
2= fair
3= good
4= very good
5= superior
N/A= not applicable

1.Position & arrangement
____ Specimens are arranged neatly.
____ Key identification parts (flowers & leaves front and back sides) are visible.
____ Excess soil removed.
____ Plant parts are separated and spread out.
____ Specimen is not close to the edge or overcrowded at the corner of the sheet.
Comments: ____
____

2. Label
____ Correctly adhered to sheet based on size of specimen.
____ Glue is not spilling from edges.
____ Label is not wrinkle, crinkled, or buckling.
____ Corner of herbarium paper is not curling up.
____ No dirt smudges on herbarium paper or label.
____ Annotations are adhered above the label in chronological order (old to new).
____ Space is available above the label for future annotation labels.
____ Deteriorated label is in fragment packet and photocopied label is adhered.
Comments: ____
____

3. Fragment Packets

_____ Correct size packet is securely attached to sheet.
_____ Each sheet has a packet.
_____ packets placed in different spots (not always in the same location)
_____ zip-lock bag used for bulky plant parts.
_____ large oversized bulky parts separated from sheet with duplicate label.
Comments: ____
____

4. strapping

_____ Straps are securely attached to sheet.
_____ Straps are snug against the plant.
_____ Straps are clean and free from dirt smudges.
_____ The number of straps is correct for the size of the specimen.
_____ Key identification parts are not covered by straps.
_____ About 7-10 mm of straps extend from each side of fastened plant part.
_____ Straps are attached at right angles from the plant parts.
Comments: ____
____

5. Sewing

_____ Stitches no longer than 1-2 inches
_____ Stitches go over the edge of the leaf.
_____ Used existing holes in leaves.
_____ Knots are on the back side of the sheet.
_____ Knots are covered by backing tape.
_____ Thread is double strands.
_____ Stitches are snug to the plant.
Comments: ____
____

6. Cleanliness

_____ No dirt smudges on label
_____ No dirt smudges or loose dirt on sheet
_____ No dirt smudges on fragment packet
_____ Plant is cleaned of all dirt and debris.
Comments: ____

7. Drop-Tag
____ Date included.
____ Mounter initials included.
____ Sheet number range included.
____ Total number of specimens mounted included.

8. Effectiveness
____ Understands the mission of the museum and the herbarium's role.
____ Exhibits composure and rational handling in difficult situation
____ Exhibits sincere interest, enthusiasm, and eagerness to learn about Botany.
____ Follows through on assigned task.

9. Social aspects
____ Relates well with staff, interns, and fellows.
____ Gets along with other volunteers.
____ Willingness to provide help to visitors.
____ Willing to ask for advice or help from others when in doubt.

10. Responsibility
____ Able to commit to set schedule or time commitment.
____ Enters time into VSYS.
____ Participates in ongoing training.
____ Interested in taking on new roles or responsibilities.
____ Pays attention to detail when necessary.

Comments:____
____
____

Benefits to department from this volunteer's skills, experience and knowledge are:____
____

Overall general performance/score: _________________

Signature of Supervisor: ___________________ Date: ____________
Signature of Volunteer: ____________________ Date: ____________

Six month Mounting Evaluation

Plant Mounting Evaluation Form

Name: ________________________
Role: _________________________
Period of evaluation: ____________
Supervisor: ____________________

Rating scale:
1= Needs improvement
2= fair
3= good
4= very good
5= superior
N/A= not applicable

1.Position & arrangement

____ Specimens are arranged neatly.
____ Key identification parts (flowers & leaves front and back sides) are visible.
____ Excess soil removed.
____ Plant parts are separated and spread out.
____ Specimen is not close to the edge or overcrowded at the corner of the sheet.
Comments: ____

2. Label

____ Correctly adhered to sheet based on size of specimen.
____ Glue is not spilling from edges.
____ Label is not wrinkle, crinkled, or buckling.
____ Corner of herbarium paper is not curling up.
____ No dirt smudges on herbarium paper of label.
____Annotations are adhered above the label in chronological order (old to new).
____ Space is available above the label for future annotation labels.
____ Deteriorated label is in fragment packet and photocopied label is adhered.
Comments: ____
____

3. Fragment Packets

_____ Correct size packet is securely attached to sheet.
_____ Each sheet has a packet.
_____ packets placed in different spots (not always in the same location)
_____ zip-lock bag used for bulky plant parts.
_____ large oversized bulky parts separated from sheet with duplicate label.
Comments: ____
____

4. strapping

_____ Straps are securely attached to sheet.
_____ Straps are snug against the plant.
_____ Straps are clean and free from dirt smudges.
_____ The number of straps is correct for the size of the specimen.
_____ Key identification parts are not covered by straps.
_____ About 7-10 mm of straps extend from each side of fastened plant part.
_____ Straps are attached 0at right angles from the plant parts.
Comments: ____

---

5. Sewing

_____ Stitches no longer than 1-2 inches
_____ Stitches go over the edge of the leaf.
_____ Used existing holes in leaves.
_____ Knots are on the back side of the sheet.
_____ Knots are covered by backing tape.
_____ Thread is double strands.
_____ Stitches are snug to the plant.
Comments: ____
____

6. Cleanliness

_____ No dirt smudges on label
_____ No dirt smudges or loose dirt on sheet.
_____ No dirt smudges on fragment packet.
_____ Plant is cleaned of all dirt and debris.
Comments: ____

7. Drop-Tag

____ Date included.
____ Mounter initials included.
____ Sheet number range included.
____ Total number of specimens mounted included.

8. Effectiveness

____ Understands the mission of the museum and the herbarium's role.
____ Exhibits composure and rational handling in difficult situation
____ Exhibits sincere interest, enthusiasm, and eagerness to learn about Botany.
____ Follows through on assigned task.

9. Social aspects

____ Relates well with staff, interns, and fellows.
____ Gets along with other volunteers.
____ Willingness to provide help to visitors.
____ Willing to ask for advice or help from others when in doubt.

10. Responsibility

____ Able to commit to set schedule or time commitment.
____ Enters time into VSYS.
____ Participates in ongoing training.
____ Interested in taking on new roles or responsibilities.
____ Pays attention to detail when necessary.

Comments:____
____

Benefits to department from this volunteer's skills, experience and knowledge are:____
____
____

Overall general performance/score: ___________________

Signature of Supervisor: ____________________ Date: ______________
Signature of Volunteer: _____________________ Date: ______________

Six Month Volunteer Review Questionnaire

Role: Plant Mounter

Please take a few moments to reflect on your experience so far. Your feedback helps us improve the volunteer experience and ensure you are supported in your role.

1. Do you find the work to be too challenging or too easy?

✎ ____

✎ ____

2. Is there anything that could help streamline the plant mounting process?

✎ ____

✎ ____

3. Are there any tools, resources, or training you feel would be beneficial?

✎ ____

✎ ____

4. If you could change one thing about the plant mounting process, what would it be?

✎ ____

✎ ____

5. Is your current schedule working well for you?

Would you like to adjust your days or times?

☐ Yes – I'd like to make changes

☐ No – My current schedule works well

✎ If yes, please describe: ____

6. Are you interested in exploring other volunteer roles within the department?

☐ Yes

☐ No

✎ If yes, please list any areas of interest: ______________________________

7. How do you feel about your volunteer role?

☐ I look forward to volunteering

☐ I feel obligated to continue because I committed

✎ Please share more about your experience: ___________________________

✎ ____

Additional Comments:

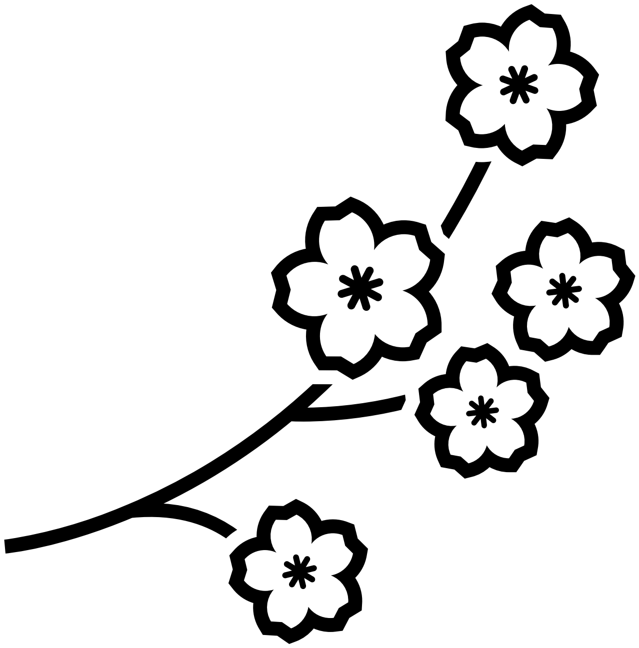
✎ ____

✎ ____

✎ ____

Volunteer Name: _____________________________

Date: ________________



SUPPLEMENTAL INFORMATION

Appendix A.

100 Uses for an Herbarium (Well at Least 72)

By Vicki Funk, US National Herbarium

For the past year or so I have been keeping a list of uses of herbaria. Two recent events have greatly increased that list. First, I published an article titled "The Importance of Herbaria" (Funk 2003) and a number of my colleagues sent in additional uses. Second, I attended a "Workshop to Produce a Decadal Vision for Taxonomy and Natural History Collections" (held in Gainsville, Florida, sponsored by NSF). In preparing for the workshop the list increased to ca. 50 and during the workshop additional uses were mentioned and the current total is 72. Hopefully the list will have 100 after this article is published. This list would not have been possible without the help of many colleagues and I thank them all. If you would like to use this list you can download it on line at the Biological Diversity of the Guianas web site HTTP://www.mnh.si.edu/biodiversity/bdg/ but please send any additions to me so that I can update the site. Herbaria, dried pressed plant specimens and their associated collections data, ancillary collections (e.g., photographs) and library materials, are remarkable and irreplaceable sources of information about plants and the world they inhabit. They provide the comparative material that is essential for studies in taxonomy, systematics, ecology, anatomy, morphology, conservation biology, biodiversity, ethnobotany, and paleobiology, as well as being used for teaching and by the public. They are a veritable gold mine of information and the foundation of comparative biology. According to the updated website of Index Herbariorum (Holmgren & Holmgren, 2003), there are 3240 herbaria in the world. Just in the USA there are more than 60 million specimens in 628 herbaria (Funk and Morin, 2000). At the US National Herbarium (National Museum of Natural History, Smithsonian Institution) there are nearly 5 million specimens, and, just for the record, about 500,000 of the US specimens are in the Compositae. Recent articles have highlighted the problems that are being faced by state and university natural history collections, including herbaria. An article from Nature (Dalton, 2003) and one from BioScience (Gropp, 2003) make it clear that natural history collections are being targeted unfairly in the current budget crises in states and universities. From Los Angeles to Iowa, Nebraska and Virginia, natural history collections are being closed or given away and the staff either re-assigned or fired. All of this has a negative impact on our ability to train systematists (Gropp 2003) and causes much concern over the fate of organismal biology. Hopefully lists such as this one will help those fighting to save their collections from death or dismemberment.

An herbarium can be used to:

Basic Functions & Research

1. discover or confirm the identity of a plant or determine that it is new to science (taxonomy);
2. document the concepts of the specialists who have studied the specimens in the past (taxonomy);
3. provide material for making morphological measurements (taxonomy, systematics);
4. provide locality data for planning field trips (taxonomy, systematics, teaching);
5. provide data for floristic studies (taxonomy);

6. serve as a repository of new collections (taxonomy and systematics);
7. provide data for revisions and monographs (systematics);
8. verify plant Latin names (nomenclature);
9. serve as a secure repository for "type" specimens (taxonomy);
10. provide infrastructure for obtaining loans etc. of research material (taxonomy and systematics);
11. facilitate and promote the exchange of new material among institutions (taxonomy);
12. allow for the documentation of flowering and fruiting times and juvenile forms of plants (taxonomy, systematics, ecology, phenology);
13. provide the basis for an illustration of a plant (taxonomy and general publishing);
14. provide material for DNA analysis (systematics, evolution, genetics);
15. provide information for GIS studies of past and future collecting expeditions (taxonomy, ecology, etc.);
16. house vouchers for photographs that can be used in lectures, web sites, and publications (taxonomy);
17. provide information on rare, extirpated, or extinct species that can no longer be found in nature (taxonomy, conservation biology);
18. provide modern specimens for comparisons with fossils (e.g. classification of leaf patterns; paleobotany);
19. to trace the history of usage of binomials for a given taxon in a given area (local flora); Related Research - Collections are the lynchpin of biological research
20. provide pollen for taxonomic, systematic, and pollination studies as well as allergy studies (taxonomy, systematics, pollination ecology, insect ecology, and medical studies);
21. provide reference samples for the identification of plants eaten by animals (animal ecology);
22. determine native ranges and document which plants grew where through time (invasive species, climate change, habitat destruction, etc.)
23. document what plants grew with what other plants (phytogeography, ecology);
24. provide material for microscopic observations (anatomy and morphology);
25. document the morphology and anatomy of individuals of a particular species in different locations (environmental variation);
26. serve as a repository for voucher specimens (ecology, ethnobotany, environmental impact studies, etc.);
27. provide material for chemical analysis (lead-uptake; pollution documentation; bio-prospecting, for coralline algae - determining past ocean temperatures and chemical concentration);
28. provide information for studies of expeditions and explorers (history of science);
29. provide the label data and field notebooks necessary for accurate data-basing of specimens (biodiversity and conservation biology, biogeography);
30. serve as a reference library for the identification of parts of plants (e.g., seeds) found in archeology digs (paleoethnobotany);
31. provide context for accompanying library and other bibliographic resources (library sciences, general research, taxonomy, etc.);
32. serve as an archive for related material (field notebooks, letters, reprints, etc.);
33. provide information on common names and local uses of plants (anthropology, linguistics, ethnobotany, economic botany);
34. provide insect collections that have been incidentally collected along with the plants (entomology, etc.);
35. serve as a means of locating rare or possibly extinct species via recollecting areas listed on label data (conservation biology, environmental impact statements, endangered species, etc.);
36. provide information on plant predators (e.g., leaf miners, leaf-cutter ants; entomology, ecology);

37. establish the presence and distribution of plant diseases (e.g. anther-smut);
38. track introduction and spread of invasive species (ecology);
39. document C02 change over past 10,000 to 10,000,000 years, a more precise proxy for this than ice core data (climate change);
40. provide information for foliar physiognomy studies of leaf form as it is related to climate change (paleoecology);
41. to document polyploid populations that occur naturally by leaf and epiderml stomatal complex size (phylogeography, paleoecology);
42. to document fungal/vascular plant symbionts;
43. to document biogeography of past plant distributions including regional extinctions (paleobiogeography);
44. document the evolution of major groups of vascular plants (paleobotany);
45. document minor cycles in climate (paleoecology);
46. provide carbon isotope ratios (e.g., Lewis and Clark specimens from 200 years ago have increased C12) (climate change); Education & Training
47. provide material for teaching (botany, taxonomy, field botany, plant communities; ethnobotany; agriculture; dendrology, forestry);
48. promote appreciation of botanical diversity by making specimens available for viewing by students, researchers, and the public.
49. provide internship and job opportunities for undergraduate and graduate students
50. provide opportunities for students and young scientists to meet more established scientists;
51. expose students to systematic research;
52. train local volunteers for specimen handling, scanning, and databasing etc.;
53. run education courses for the public (e.g. local plant families); Outreach
54. serve as an identification center for all kinds of plants parts for many different groups of individuals, e.g., samples for the identification of plants that may be significant to criminal investigations (forensics);
55. serve as an educational tool for the public (garden clubs, school groups, etc.);
56. provide a focal point for botanical interactions of all types (lectures, club meetings, etc.);
57. provide samples for museum and educational exhibits;
58. provide a location for government and state agencies to work on specimens, i.e., USDA, USGS, NFS;
59. provide a home for long-term initiatives (e.g. Smokey Mt. NP ATBI);
60. provide a home for global, regional or local studies;
61. help establish new museums;
62. foster good international relations (e.g. sister institutions, joint field tribs);
63. provide material for the public (e.g. accurate illustrations);
64. provide inspiration for painters;
65. interact with the local people to form volunteer groups for conservation efforts;
66. maintain websites for dispersing specimen information, databases, images, public service information;
67. repatriate data and images from collections to the country where they were collected (international relations);
68. help artists prepare accurate drawings for children's books;
69. provide information on the wild relatives of cultivated plants;
70. facilitate international exchanges of field expeditions;
71. organize photographs of plants associated with voucher collections;
72. help design natural history products for sale in gift shops (e.g. old illustrations for note cards).

At the US National Herbarium, in order to make maximum use of our substantial resources, we have the following goals: additional compacterization of collections to increase storage space, processing of the backlog of unmounted specimens so all material is available, continuing to photograph the type specimens so our most important collections will be available on the web, and data-basing and georeferencing the specimen label information so it can be efficiently used and be made available on line. I am sure other herbaria have similar goals, we must all work together to stress the importance of herbaria and preserve our collections for the future. Indeed the "working together" has already started. A recent NSF sponsored workshop addressed some of the problems that are facing collections and discussed possible solutions. The "Workshop to Produce a Decadal Vision for Taxonomy and Natural History Collections" (held in Gainsville, Florida, organized by Larry Page) involved 61 people from institutions of all sizes. A report will be produced for NSF and a more general public version will also be available. The website for that meeting has some information posted and more will be available in the near future (Page, 2003).

Acknowledgements — This list would not have been possible without the suggestions contributed by many colleagues and I thank them all especially Tom Wendt (TEX), Tom Hollowell (US), David Dilcher (FLAS) and the staff of US.

Literature Cited

Dalton, R. 2003. Natural history collections in crisis as funding is slashed. Nature 423: 575.

Funk, V. A. 2002. The Importance of Herbaria. Plant Science Bulletin 49: 94-95.

Funk, V. A. & N. Morin. 2000. A survey of the herbaria of the southeast United States. SIDA, Misc. 18: 5-52.

Gropp, R. E. 2003. Are university natural science collections going extinct? Bioscience 53: 550. Hollowell, T., V. A. Funk, & C. Kelloff. 1997-2003 (updated every other month). Biological Diversity of the Guianas website http://www.mnh.si.edu/biodiversity/bdg/

Holmgren, P. & N. Holmgren. 1995-2003 (updated monthly). Index Herbariorum (on line) http://www.nybg.org/bsci/ih/ih.html

Page, L. 2003. Workshop to Produce a Decadal Vision for Taxonomy and Natural History Collections web site http://www.flmnh.ufl.edu/taxonomy_workshop/

Vicki Funk, US National Herbarium, Smithsonian Institution MRC166, P.O. Box 37012, Washington DC. 20013-7012 USA; Funk.vicki@nmnh.si.edu http://www.mnh.si.edu/biodiversity/bdg/ 100 Uses for an Herbarium • Page 4 of 4 Division of Botany, The Yale University Herbarium • http://www.peabody.yale.edu

Appendix B.

Journal of Systematics

JSE and Evolution doi: 10.1111/jse.12315

Review

Collections-based science in the 21st Century

Vicki A. Funk*

Department of Botany, MRC-166, National Museum of Natural History, Smithsonian Institution, PO Box 37012, Washington, DC 20013-7012, USA *Author for correspondence. E-mail: funkv@si.edu

Received 9 March 2018; Accepted 27 March 2018; Article first published online 8 May 2018

Abstract Discoveries from collections-based science change the way we perceive ourselves, our environment, and our place in the universe. The 18th Century saw the beginning of formal classification with Linnaeus proposing a system to classify all of life. The 19th Century ushered in the age of exploration as naturalists undertook large-scale collecting expeditions leading to major scientific advances (the founding of Physical Geography, Meteorology, Ecology, Biogeography, and Evolution) and challenging long held beliefs about nature. In the 20th Century collections were central to paradigm shifts, including theories of Continental Drift and Phylogenetic Systematics; Molecular Phylogenetics added testable hypotheses, and computerized specimen records gave rise to the field of Biodiversity. In the first 15 years of the 21st Century we have seen tree-thinking pervade the life sciences, leading to the emergence of Evolutionary Medicine, Evolutionary Ecology, and new Food Safety methods. More advances are on the way: (i) Open access to large amounts of specimen data & images, (ii) Linking of collections and climate data to phylogenies on a global scale, and (iii) Production of vast quantities of genomic data allowing us to address big evolutionary questions. As a result of collections-based science people see themselves not as the center of all things but rather as part of a complex universe. It is essential that we integrate new discoveries with knowledge from the past (e.g., collections) in order to understand this planet we all inhabit. To ensure the health of collections-based science we must come together and plan for the future.

Key words: biogeography, biological-collections, cladistics, classification, collections-based research, evolution, phylogenetics, phylogenomics, systematics, tree-thinking.

Major revolutions in scientific thought have occurred because of collections-based research. But more than that, expeditions, biological collections from around the world, and collections-based science have been at the root of many significant discoveries that fundamentally changed the way we view ourselves, our environment and our place in the universe (Fig. 1).

1 18th Century: Age of Classification

In the 1700's formal classification of organisms was successfully introduced for the first time resulting in two different systems of classification. Carl Linnaeus (1707–1778) proposed the first artificial system of classification for all life on earth (1753). This contrasted with the natural classifications for plants proposed by Michel Adanson (1763) and Antoine Laurent de Jussieu (1789). Linnaeus provided the "species description" and identification keys while Adanson introduced the concept of families and Jussieu set up the hierarchical system (Divisions, Classes, Orders) similar to the one we use today. These efforts changed the way people viewed life on earth: it was no longer random but ordered. Equally important, people could communicate with one another about specific organisms outside the realm of every changing local (common) names.

2 19th Century: Age of Grand Expeditions and Grand Ideas

At the beginning of the 19th century Alexander von **Humboldt** set off on a five-year expedition to Latin America (Andes, Caribbean, Orinoco River Basin, Mexico and USA; 1799–1804; Fig. 2) that started a revolution in scientific investigations and public interest. During his travels, he collected specimens to document the diversity of life, as well as physical features of the landscapes he encountered. He used the knowledge he gathered to support a holistic view of the universe. This privately funded collecting expedition is regarded as having laid the foundation of the sciences of **Physical Geography, Ecology, Biological Geography, and Meteorology**. Humboldt published extensively for both the scientific community and the reading public and his writings and lectures stressed the order in nature and the interconnectedness of all things in the universe (e.g., Humboldt, 1807, 1845; Wulf, 2017). His writings had a big impact on the scientific community, not the least of which was to inspire a generation of young naturalists to

Fig. 1. Some of the biological collections housed at the National Museum of Natural History, Smithsonian Institution, Washington, D.C., USA. [Photos courtesy of NMNH Photo Services; assembled by A. Tangerini (US)].

embark on expeditions around the world that were focused on exploring and collecting. Among comments concerning Humboldt's expeditions and publications:

I have omitted to state. . . the extreme satisfaction I have received from Baron Humboldt's communications. The treasures of information which he possesses are inestimable. . . [Thomas Jefferson, letter, 1804]. Perhaps Jefferson's interest in Humboldt inspired him to send Lewis and Clark into the American West. [Doherr & Baron, continuously updated]

I formerly admired Humboldt, I now almost adore him. . . [Charles Darwin, letter, 1832] [Doherr & Baron, continuously updated]

Among the works…which influenced my future, were Humboldt's Personal Narrative of Travels in South America, *which was, I think, the first book that gave me a desire to visit the tropics.* Wallace in his autobiography *My Life* (1905) [about an event in ca. 1844; Smith & Walklate, 2017]

Charles **Darwin** traveled on the HMS Beagle (1831–1836) a voyage that circumnavigated the globe and stopped mostly in the tropics and the southern hemisphere (Brazil, southern South America, New Zealand, Australia, Cape Town). At the many stops, Darwin took every opportunity to collect animals, fossils and plants. His studies of the flora and fauna, most notably in the Galapagos, led him to develop the Theory of **Evolution** by Natural Selection which has become the underlying assumption of our search to understand the diversity of life (Darwin & Wallace, 1858; Darwin, 1859).

Joseph Dalton **Hooker**'s first expedition traveled to Australia, New Zealand, Auckland Islands, Campbell Island, Kerguelen, Cockburn Island, Falkland Islands, and Fuegia from © Judith Affolter - Fotografie.

Fig. 2. Alexander von Humboldt and Aime Bonpland in a jungle hut in the Amazon (painted by Eduard Ender around 1850 long after Humboldt returned from his expedition). Painting © Archiv der Berlin-Brandenburgischen Akademie der Wissenschaften, Abteilung Sammlungen, Gelehrtengem€alde, P/BON-1053 [Archive of the Berlin-Brandenburg Academy of Sciences]; photograph

1839 to 1843. His publication (1853) based on this expedition resulted in new ideas about the patterns of distribution of the plants and the causes of those patterns. He was the first to publish a method that could be used to compare species lists from his floras and develop ‘‘bands of affinity'' among different locations. He used those bands to speculate that there had once been a continuous southern hemisphere flora "…*spread over a larger and more continuous tract of land than now exists*…" and distinct from that of the Northern hemisphere (Hooker, 1853, page xxi). He made a number of additional field trips over the years including one with Asa Gray to the western United States (Fig. 3). There is little doubt that Hooker's ideas had a profound effect on the scientific community as well as the public, even the entomologist Brundin (1966, page 49) said "*Hooker's suggestion of the former existence of continuous land connections by way of Antarctica has had a powerful effect on the imagination of scientists.*" Hooker is often referred to as the Father of Plant Biogeography."

Alfred Russel **Wallace** did extensive fieldwork, first in the Amazon (1848–1852) and then the Malay Archipelago (1854–1862). A co-proposer of the Theory of **Evolution** (Darwin & Wallace, 1858), he also identified the faunal divide subsequently named Wallace's Line (various early articles but mentioned in Wallace, 1863, well-illustrated in 1876), which separates the Indonesian archipelago into two distinct parts: a western portion in which the animals are largely of Asian origin, and an eastern portion where the fauna are largely of Australiasian origin. He was considered the 19th century's leading expert on the geographical distribution of animal species and is sometimes called the "father of zoological **Biogeography**."

Among the other important explorers of this time period are: Sir Joseph Banks (1768–1771) who traveled on the first voyage of Captain James Cook; Meriwether Lewis and William Clark who were sent by President Thomas Jefferson to the unknown American West (1804–1806); Asa Gray who set up a North American plant collecting network (1830's–1860's); Capt. Charles Wilkes' global expedition (1838–1842) that carried a team of scientists including naturalists, botanists, and a mineralogist; Henry Walter Bates (Amazon 1848–1859); Richard Spruce (Amazon 1849–1864); and others published popular, as well as strictly scientific works, that moved the reading public and scientists in unforeseen directions. Faith in a supreme being was no longer necessary to explain the diversity of life, there was an order to the location and occurrence of plants and animals, and humans and all other life were part of the Kosmos

Fig. 3. Field trip in the Rocky Mountains, La Veta Pass, Colorado, 1877, 9000 feet. Left to right seated: Sir Joseph Dalton Hooker, Professor Asa Gray, Mrs. Strachey, Mrs. Asa Gray, Dr. Robert H. Lambourne, Major-General Richard Strachey and Dr. F.V. Hayden. Mr. James Stenson is standing between Dr. Lambourne and General Strachey. [Photograph reproduced with the kind permission of the Director and the Board of Trustees, Royal Botanic Gardens, Kew]

(sensu Humboldt) and connected to all living and physical things. Most of these individuals deposited large numbers of collections in Museums and herbaria in Europe and North America, wrote extensively about their travels and findings, and interacted frequently with the public. It must have been a heady time for collectionsbased research.

3 20th Century: Age of Synthesis

Many discoveries were made during this century, but there are four collections-based ideas and methods that changed both the way we do science and altered the views of the reading public.

3.1 Continental drift

The idea that the continents moved, relative to one another, was first proposed by the Flemish cartographer and geographer Abraham Ortelius (1527–1598). Ortelius is best known for publishing the first modern atlas (Ortelius, 1570). However, it was not until it was independently proposed and more fully developed, and named ‘‘Continental Drift’’ by Alfred Wegener (1912a, 1912b), that it took hold among some members of the scientific community andthepublic. Initiallythough, Wegener’s theory was rejected by many scientists for lack of a mechanism. A mechanism was published in 1944 (Holmes, 1944) but as late as 1953—just five years before Carey (1958) introduced the theory of plate tectonics—the theory of continental drift was rejected by prominent geologists. In fact, the geoscientific community only accepted the plate tectonic theory after seafloor spreading was validated in the late 1950s and early 1960s, and, as late as the 1970’s there were still prominent holdouts in the scientific community (e.g., Darlington, 1965).

Conversely, many collections-based biologists had long insisted that such connections must have happened. For over a hundred years scientists such as Alexander von Humboldt (1845) and J.D. Hooker (1853) had been proposing various land-connecting options. Other scientists such as botanist Snider-Pellegrini (1859), who studied plant fossils found in coal beds in the US and Europe, and zoologist Carl H. Eigenmann (1909), who studied fish from South America and Africa, were among those who reasoned that some sort of connections had to have taken place (Figs. 4A–4E).

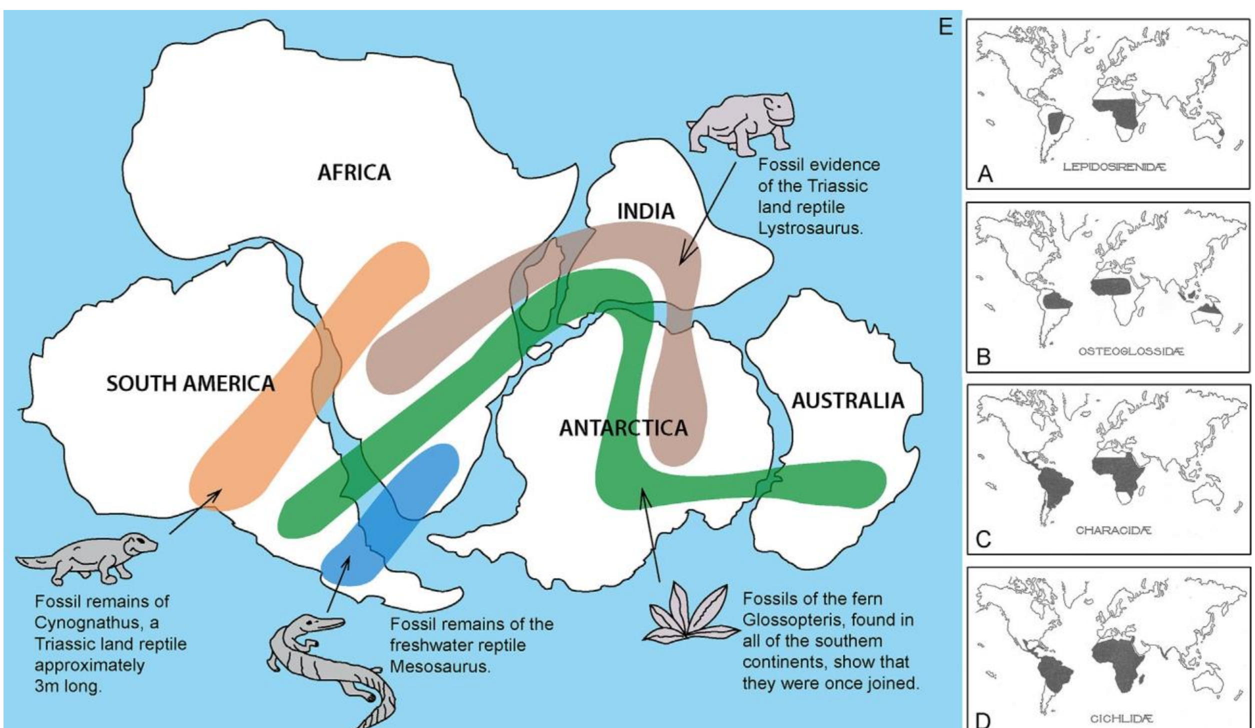


Fig. 4. Continental drift was predicted by collections-based scientists for many years before it was accepted by the geological community largely because there were so many plant and animal distributions that had similar distribution patterns: **A–D,** Fresh water fish family distributions modified from Eigenmann (1909)

showing the linkage between South America and Africa; **E,** Fossil distributions that indicate previous connections among continents. [Continental drift By Osvaldocangaspadilla - Own work, Public Domain, https://commons.wikimedia.org/w/index.php?curid=11310183; map courtesy of the U.S. Geological Survey]

3.2 Phylogenetic systematics (cladistics)

Prior to the arrival of Phylogenetic Systematics (Hennig, 1950, 1966), classification was based on subjective opinions concerning which characters were "important", usually after an extensive study of a group of organisms. Disagreements arose when scientists focused on different characters. What about Phylogenetic Systematics separated it from this traditional process? The core concept was the use of apomorphic (derived) characters to objectively construct relationships, followed by the grouping of taxa into monophyletic groups (groups that contain all taxa that were descended from a common ancestor and included all decedents of that ancestor). The resulting monophyletic groups were used to develop a classification. Finally, the principle of parsimony was applied to all analyses; and although fundamental to science, this principle had not previously been rigorously applied to systematics. All steps in the process had to be transparent and well documented. These concepts, first formalized by Hennig (1950, 1966) and well-illustrated by Brundin (1966), launched a movement that fundamentally changed the way scientists classified and studied organisms. Many of the early promoters of these methods were first introduced to the methods by Gareth Nelson who began his studies on cladistics and biogeography in 1967 (Nelson & Platnick, 1981).This led to many publications, especially in the 1970's and 1980's in *Systematic Zoology* (now *Systematic Biology*), most of which are referenced in edited volumes from the first two meetings of the Hennig Society (Funk & Brooks, 1981; Platnick & Funk, 1983) and ensuing publications of the journal *Cladistics*. The entire process of the efforts to implement the methods of *Phylogenetic Systematics* (Cladistics) was discussed at length in a book by Hull (1988). But did this method change how the reading public viewed themselves? As it became pervasive in text books and general science books, the method made it clear that there was no escape from interested clades of organisms going all the way back to the beginning of life. The early methods, now inextricably linked to the advent of molecular phylogenetics (discussed below), can be found in Wiley et al. (1991).

Some concepts of early phylogenetic studies, such as "parsimony" have been mostly eclipsed by statistical methods such as Maximum likelihood and Bayesian Posterior Probabilities. However, others like monophyly have transformed the classification of life and concepts like the "Progression Rule" (Hennig, 1950, 1966) have gained acceptance as a null hypothesis for testing biogeographic data (Funk & Wagner, 1995; Bell et al., 2015; Shaw & Gillespie, 2016).

3.3 Databasing collections, biodiversity science & niche modeling

The arrival of desktop computers in the early 1980's allowed the development of databases of specimens held in collections. Although the internet was not available at the beginning of the efforts to catalogue collections the datasets could still be shared and combined. The utility of such databases was immediately obvious, and early on, they were adopted by biologists for biodiversity and conservation studies. Arguably, the country leading the way in this development was Australia, where the scientists were supported and encouraged by their government. As a result, data from specimen labels were the basis for a whole new field of research where concepts such as surrogate data (Faith & Walker, 1996), spatial turnover (Ferrier et al., 1999), irreplaceability (Ferrier et al., 2000), reserve networks (Margules et al., 1988), concordance and efficiency of taxon indicators (Moritz et al., 2001), rarity, and complementarity were used for reserve selection (Ferrier, 1997), biological survey design (Ferrier & Smith, 1990), monitoring species decline (Margules & Austin, 1994), strategies to protect biological diversity (Ferrier, 1997), comparative phylogeography and the identification of genetically divergent areas for conservation (Moritz & Faith, 1998), establishing key principles for systematic reserve selection (Pressey et al., 1993), and designating hotspots (Williams et al., 1996).

The data from collections are useful in these and other biodiversity studies because they serve as the only direct evidence of species distributions through time. The development of these concepts and programs helped the public understand that biodiversity had to be studied in order to know how to conserve it and they emphasized the complexity of life on earth. A critical review of the use of information from natural history collections in studies of ecology, evolution, conservation, agriculture and human health contains many additional examples (Graham et al., 2004).

3.4 Molecular phylogenetics

It is common knowledge that collections are an excellent source of material for the extraction of DNA, but they are also important because they provide the vouchers of the DNA sequences, and their presence allows us to check the identification of samples and to gather the data needed to ask questions about character evolution and modes of speciation.

At the end of the 20th Century the small rumblings associated with the use of DNA sequences in systematic studies turned into a major volcanic eruption that rapidly spread over the landscape. The initial methodologies had been around for over a decade but they were slow and expensive. It was the advent of *polymerase chain reaction*, or PCR, that could amplify a single copy or a few copies of a segment of DNA, generating thousands to millions of copies (Mullis et al., 1987; Bartlett & Stirling, 2003) that changed molecular work. Until recently, it was the sequencing of one or several amplified markers, that was the most widely used technique in molecular genetics and evolution. One of the first studies in molecular systematics was published by Jansen and his collaborators. They published a series of papers that upended the classification of the Compositae (Asteraceae), the largest family of flowering plants (e.g., Jansen & Palmer, 1987a, 1987b, 1988; Jansen et al., 1988). They showed that the irregular flowered elements were part of the base of the phylogeny, not highly derived as had been previously accepted. Subsequently, those studies ultimately resulted in major revisions of the family classification (Panero & Funk, 2008; Funk et al., 2009). However, the results of such studies were not always contradictory to traditional classification. For instance, Crandall et al. (1999) and his co-authors published a paper on freshwater crayfishes using the 18S region of the mitochondrial genome and showed that the traditional classification was correct. So, molecular phylogenetics could either support or refute traditional classification, thus illustrating that any classification/taxonomy was a testable hypothesis. The various editions of the book *Molecular Systematics* greatly expanded the use of molecular data (e.g., Hillis & Moritz, 1990; Hillis et al., 1996) and contributed to its rapid application. However, it was the ability of DNA data to turn opinions about character importance and homology into testable hypotheses, and to help answer many of the questions we were unable to answer with morphological data alone, that made it such a success. From classifications to character evolution, everything could be reconsidered using a molecularly-generated tree. Of course, the original investigations were relatively expensive and time consuming, and sampling density was a problem. Often when new taxa were added the conclusions changed and sometimes the prior results were wrong.

Nevertheless, things improved, and by 2000 molecular phylogenetic methods became a part of our tool kit.

The methods of DNA analysis reinvigorated the phylogenetic systematic movement which, when it was based solely on morphology, had become difficult to implement because of homology issues. It also changed the way systematists gathered, analyzed, displayed and interpreted their data. However, in the beginning, there was not much coverage of applied molecular phylogenetics, but subsequently, it had a big effect on the reading public (see below).

4 21st Century, the First 15 Years: An Age of Tree Thinking

In the first 15 years of the 21st century, tree-thinking pervaded the life sciences (e.g., Baum & Smith, 2012) and the public imagination, leading to, among other things, the emergence of Evolutionary Medicine, Evolutionary Ecology, and new treebased Food Safety methods.

4.1 Evolutionary medicine

The explosion of tree thinking has transformed the way medical science operates and tumor identification, origins of viruses, and ethnobotanical bio-prospecting have been affected. Books on Evolutionary Medicine are common and include: *Evolutionary Medicine* (Stearns & Medzhitov, 2015); *Principles of Evolutionary Medicine* (Gluckman et al., 2016); and *Body by Darwin: How Evolution Shapes our Health and Transforms Medicine* (Taylor, 2015). Phylogenies and collections also have been used in the search for origins of diseases, such as smallpox, that once circumnavigated the globe at various intervals, with little understanding of where it originated or how it traveled around. Now we have a much better idea, thanks to molecular phylogenetics (Li et al., 2007). The origin of other diseases such as HIV (Sharp & Hahn, 2011) and Ebola (Gire et al., 2014) have also been tracked using trees. In recent studies on Chagas disease, Pinto et al. (2010) sampled museum specimens of southern plains woodrats and found pathogens similar to those which cause Chagas, signaling that museum collections are also useful in finding the progenitors of diseases. Finally, it is not commonly known, but phylogenetic trees are used to help precidt the likely form(s) of flu virus in an upcoming searon (CDC, 2017).

4.2 Evolutionary ecology

The application of tree thinking to ecology goes by several names such as community phylogenetics, metagenomics, molecular ecology, and phylogeography. The potential for combining phylogenetics with ecology was recognized early, for instance, when Losos (1996) examined some of the potential uses, including community structure. Other uses included taking phylogenetic and biogeographic methods, and applying them at the population level, a field that was named phylogeography (Avise, 2000). Cavender-Bares & Wilczek (2003) discussed using phylogenetics to integrate evolutionary processes in community ecology. Kembel & Hubbell (2006) may have been the first to attempt to gain an understanding of the phylogenetic structure of an ecological community in order to determine the relative importance of different processes structuring that community. They conducted a study on the 50 Ha plot on Barro Colorado Island (BCI), Panama. They specifically sought to use the phylogeny of the trees found in the plot to understand how phylogenetic structure of tree communities varied among spatial scales and habitats. This and other efforts (Webb, 2000) led Kress et al. (2009) to barcode all the tree species in the BCI plot and use those barcodes to produce a more reliable phylogeny than the one produced by Kembel & Hubbell (2006). Barcoding seems to work well on many animal groups, although it is less successful at the species level in plants. Barcoding does seem to work well at the community level in plants and such community phylogenies can be used for evaluating the influence of habitat on community structure. According to Kress et al. (2010; Fig. 5) highly resolved phylogenies derived from DNA barcode sequence data, especially when based on a constraint tree, are useful in comparative analyses of phylogenetic diversity. Conservationists and law enforcement officials are now using these and other barcodes of endangered or economically important species to stem exportation of illegally harvested plants and animals and to identify incidents of illegal logging and fishing (BWP, continuously updated). The combining of data from a variety of fields, such as phylogenetic methods and data from plot studies, can help bridge the gaps between community ecology, evolution and conservation: such efforts have given rise to the field of Metagenomics.

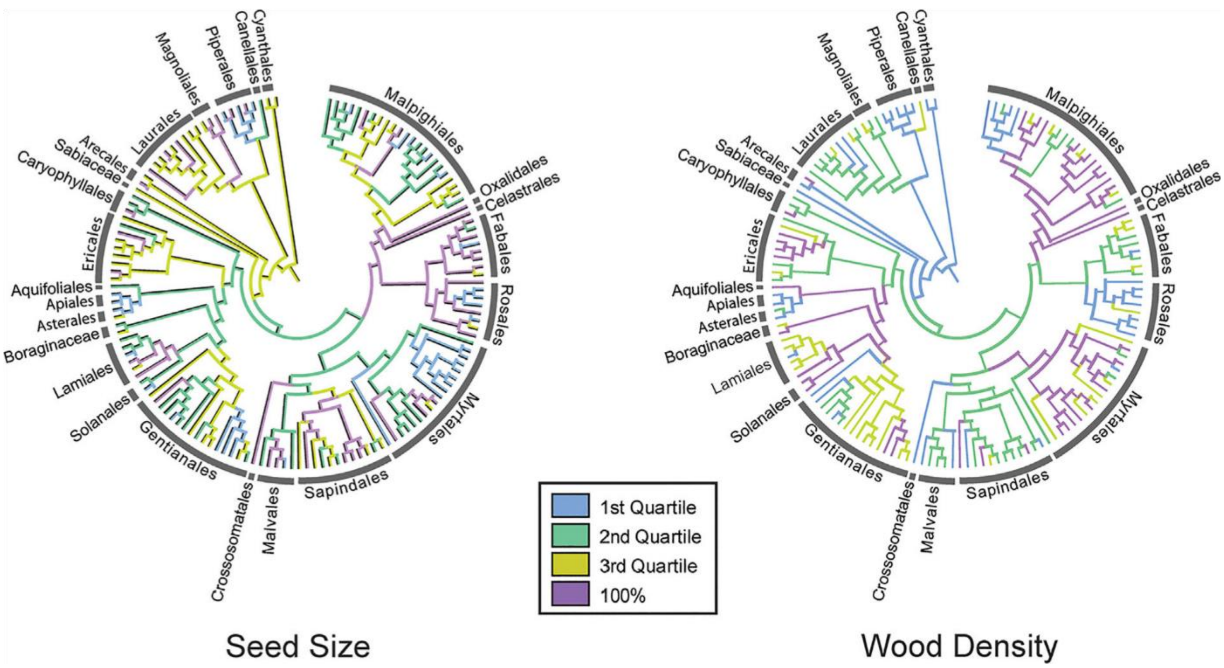


Fig. 5. Community Phylogenies derived from metabarcoding of trees from the Luquillo Forest Dynamics Plot, Puerto Rico (Kress et al., 2015) have information on functional traits (seed size and wood density) mapped onto them in order to elucidate the importance of several community assembly processes (e.g., niche partitioning and competitive hierarchies) in this forest. [Figure courtesy of WJ Kress, US]

In another example, metagenomics seeks to document and monitor the functioning of a particular ecosystem. The coral reef metagenomics project: the *Autonomous Reef Monitoring Structures* Project (ARMS; NOAA, continuously updated; Brainard et al., 2009) places relatively small devices on the sea floor to provide habitat for a variety of organisms. After ARMS are recovered, the organisms are removed. The larger motile organisms are processed via standard voucher-based molecular barcoding techniques. However, the smaller motile and sessile organisms are scraped off, homogenized, and processed via metabarcoding next-generation sequencing techniques. The resulting barcodes are BLASTed against the GenBank collection of DNA sequences, and those that have sequences there in can be identified. The procedure began in 2008 and ARMS have proven to be an excellent platform to document and study the health of coral reef ecosystems and have been employed around the globe. However, for collections-based science they have a definite downside: for all the small mobile and sessile organisms there are no physical voucher specimens or images. That means that when something is sequenced that is not in GenBank we have no idea about its morphology. We know that an organism exists, that it is ‘‘new’’ to barcoding science, where it falls in the tree of life, and what, if anything, it is related to (or at least close to), but we have no idea what it looks like, how it feeds or reproduces, or how it lives and that is a disappointment for those of us interested in the evolution of life.

Tree thinking and specimen data can also be used to track the effects of hybridization and habitat destruction. For instance, Martin et al. (2014, 2018; Fig. 6) published a study using herbarium specimens of common ragweed (*Ambrosia artemisiifolia* L.) collected through time: they recorded the locations and extracted DNA. Ragweed is a native North American plant that is an aggressive global weed that elicits strong allergic reactions. Pollen cores showed that ragweed was uncommon before deforestation. Molecular data from nearly 1000 modern and historical samples showed that sometime prior to deforestation there had been a hybridization event which may have allowed the hybrid to ‘‘take off’’ when deforestation occurred.

Studies such as these that apply tree thinking to ecological and conservation questions have enriched all of the disciplines.

4.3 Human evolution

The application of molecular phylogenetics to modern human evolutionary studies came early in the development of the field (e.g., Excoffier et al., 1992), while more recently new methods have allowed the extraction of DNA from fossils. For instance, Bayesian analyses based on nuclear and mitochondrial DNA data from seven Neandertals and five present day humans as well as bones from three individuals found in a Cave in the Altai Mountains (and subsequently named Denisovans) showed that humans and Neanderthals (H þ N) were sister taxa and that the Denisovans were the sister taxon to H þ N (Sawyer et al., 2015). The study also indicated that the Denisovans existed in the area for quite some time. This study and other phylogenetic analyses increase our knowledge of our human relatives with whom we share a common ancestor. This type of study requires the investigator to have access to humanoid fossil collections from which to sample DNA.

4.4 Tree-based food safety applications

GenomeTrakr: A Pathogen Database was developed by the US Food and Drug Administration. The *GenomeTrakr* network is the first distributed network of laboratories to utilize whole genome sequencing for pathogen identification (Allard et al., 2016, 2018). Only a year ago there were 30 labs and 130 000 sequences, while now there are over 60 labs globally participating by contributing genomes of known pathogens and the number is increasing. Currently, the whole genome sequences of over 150 000 known pathogens (up from

130 000) are available (Fig. 7A), mostly salmonella, *Escherichia coli*, *Shigella* and *Listeria*. When an unknown pathogen is identified in a food source, the sequences of its whole genome can be generated quickly, and, using phylogenetic methods with samples already in the GenomeTrakr system, and the ‘‘unknown’’ pathogen can be matched to the genome of a known pathogen. This system speeds identification of the source of the contamination and reduces illnesses and deaths. Additional software

tools are being developed to speed data analysis, and the FDA is working with the World Health Organization (WHO) and the United Nations' Food and Agriculture Organization (FAO) to make this technology available to developing nations. So, this application of tree-thinking has transformed the way foodborne pathogens are evaluated and decreased the illness and death caused by them (WGS, continuously updated). Soon FDA regulator labs will collect *MetaGenome Trakr* data such as the presence of bacteria in foods like ice cream during preenrichment using "Shotgun Metagenomics" (Ottesen et al., 2016; Fig. 7B).

In other uses of tree based food safety applications, barcoding efforts of medicinally important plants have developed rapidly in the last decade (Kress, 2017) and phylogenetic methods can be used to test the purity of the ingredients in herbal medicines (Zhang et al., 2017).

It is clear that tree-based concepts are now common and have advanced medicine, conservation biology, ecology, and other areas of our lives. All of this knowledge has depended on having a diversity of organisms captured and preserved through time. One cannot help but wonder: *What will happen in collections-based research in the next 80þ years?*

5 21st Century, the Future: An Age of Thinking Big

It seems that during the upcoming years we will be using Big Collaborations to generate Big Data to answer Big Questions. Collections are a gold mine of both information and tissue samples and more advances are on the way with collectionsbased research leading to progress in three main areas: open access to specimen data and images, linking collections data with phylogenies and/or climate data, and phylogenomics.

5.1 Open access to specimen data and images Globally there are ca. 2700 herbaria with a total of approximately 362 million specimens, 132 million (36%) of which are in the 33 largest herbaria (Funk, 2017; also *Index Herbariorum*, IH, Thiers, continuously updated). The same thing is true of zoological collections but there is no overall compendium for animal collections like IH which covers algae, fungi and plants.There is an ongoing effort to establish a global list for all repositories of biological collections (Global Registry of Biodiversity Repositories; GRBio, continuously updated) but it is not fully developed and lacks much of the information for zoological collections that we have for plants.

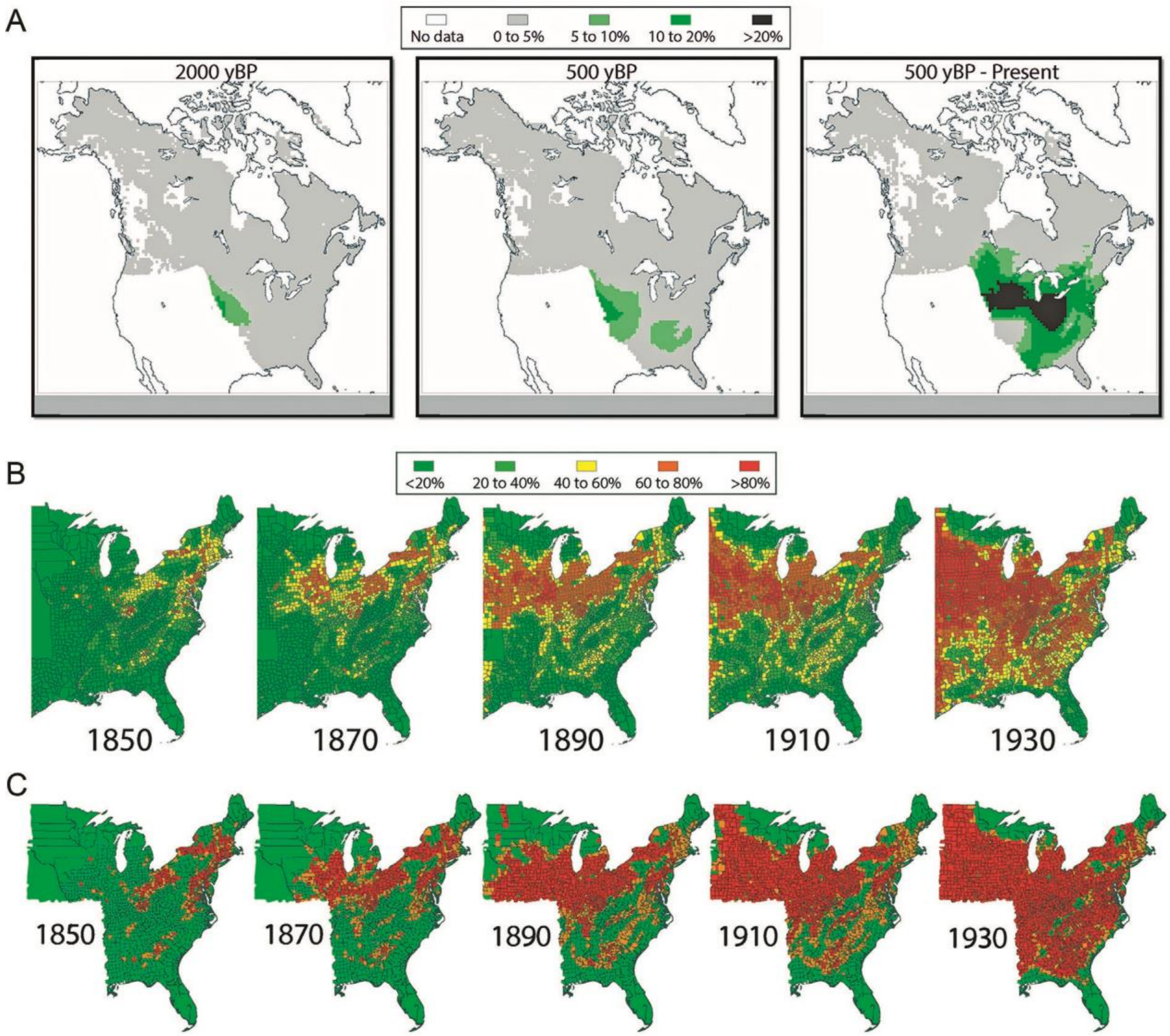


Fig. 6. Visualizations of the ragweed rise from the palynological record. **A,** The long-term palynological record of ragweed abundance. Pixel colors indicate interpolated percentage ragweed pollen at dated sediment core layers. Maps reproduced from World Data Center for Palaeoclimatology's Pollen Viewer service. **B,** Portion of land in farms at historical time points during our study. **C,** The expansion of ragweed populations modeled from data in **A** and **B**. Green counties are below the ragweed horizon (defined by a baseline mean Ambrosia pollen abundance in sediment core records over 1000 years before the colonial period). Orange counties, the ragweed pollen abundance at 5–10X the 1000-year baseline. Red counties, ragweed pollen abundance surpassed 10X the 1000-year baseline. Palynological data sparse or unavailable for uncolored counties. (Martin et al., 2014).

Imagine what would be possible if all specimen data were available to researchers. Their applications include answers to questions such as: What parts of the world need additional collecting expeditions? How many species are rare (known from only 1–5 collections)? How many species have not been collected in the last 50 years and may be extinct? Are there certain areas that have a lot of rarely collected species and are these areas endangered ecosystems? How fast have invasive species moved into new areas? How has community composition changed through time? and many others, could be addressed. In addition, high-resolution images of [Photo courtesy of M. Martin, TRH]

specimens can be subjected to morphometric analyses to better characterize species boundaries, more accurate global biogeographic hypotheses can be investigated, voucher specimens for molecular studies could be more easily accessed (Hollowell & Funk, 2017) and data would be available to open access to the data by non-academics who could contribute images and research (e.g., Calflora, continuously updated). A particularly exciting area is machine learning (Unger et al., 2016) and ‘deep convolutional neural networks’ (CNNs) that can be applied to images of herbarium specimens to identify plants and search for patterns (Schuettpelz et al., 2017). In the Schuettpelz et al. study (2017) the computer was able to ‘‘see’’ things that humans could not. Even on postage stamp size images it could discriminate between two groups of ferns that had no visible differences. This raises the issue of whether it may be possible for taxonomists to learn from computers to better separate groups? Can specimens be rapidly identified to family using CNN’s? When applied to mega datasets across regions could CNN’s be used to look for new plant associations?

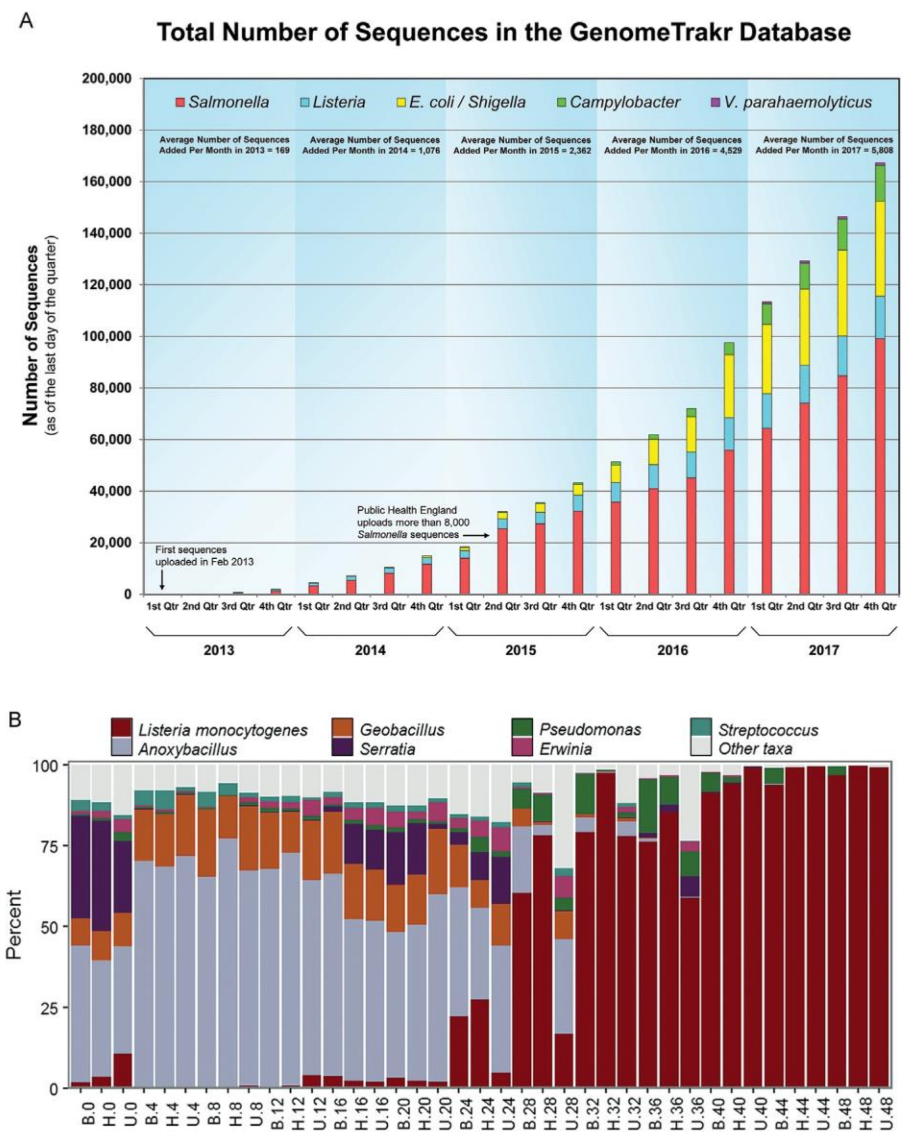


Fig. 7. FDA's *GenomeTrakr: A Pathogen Database* (Allard et al., 2016, 2018): **A,** GenomeTrakr has over 150 000 sequences for foodborne pathogens from 60 national and international labs (Allard et al., 2016, 2018). **B,** Soon FDA regulator labs will collect *MetaGenome Trakr* data such as the presence of bacteria in foods like ice cream during preenrichment using Shotgun metagenomics. Image shows incidence and abundance of *L. monocytogenes* (maroon) and co-enriching bacterial genera at four hour intervals (Ottesen et al., 2016). [Photos courtesy of M Allard and A Ottesen, FDA]

Of course, making data from collections available is not a new idea, individual collection managers started to database in the 1960's on mainframes, and various groups have been working on it at larger scales for years, including the *Global Plants Initiative* (GPI; now GP-JSTOR, continuously updated) and the *Global Biodiversity Information Facility* (GBIF, continuously updated). GPI, funded by the Mellon Foundation, sponsored the imaging of type specimens of plants from herbaria around the world and was instantly popular, now it is indispensable in plant systematic research. The Global Biodiversity Information Facility (GBIF) was established in 2001 and is an open-data research infrastructure aimed at providing access to data about all types of life on Earth. Currently it holds nearly a billion records and involves 1143 institutions. Quality control and coverage issues not withstanding, it is an impressive accomplishment. Many herbaria are actively imaging and data basing their specimens and data are coming on line at a rapid pace. Images of living species are available on some websites, for example: TROPICOS (Missouri Botanical Garden, continuously updated), *West African Photo Guide* (Brunken et al., 2018); *Photo Guide to Southern African Plants* (Jurgens et al., 2018, continuously updated); and€ California Flora (Calflora, continuously updated).

Although there is no central site for images and information on plants or animals, there are regional ones such as the *Atlas of Living Australia* (ALA, continuously updated) which holds label information, images, mapping options and much more. Mostly it covers Australia but it does have some global options. The Integrated Digitized Biocollections program (iDigBio, continuously updated) is the US National Resource for Advancing the Digitization of Biodiversity Collections (ADBC) and is funded by the National Science Foundation. Through ADBC, data and images for millions of biological specimens are being made available in electronic format for the research community and the public. iDigBio is more than just gathering data; it also hosts ideas for research and tools for data analysis and other resources. To be able to ask truly global questions, we need global data. For instance, ecological data can be gathered from labels and used to develop and/or improve niche models to assess the potential future impacts of climate change on species distributions, the spread of invasive species through time can be readily tracked, and images can be scanned for possible misidentified taxa. Can iDigBio and ALA and other efforts be configured to work together, can they be joined with other such efforts to have a truly global portal? Something like these projects on a global level would transform biodiversity science and the public perception of our research. The potential power of regional, national and global databases and imaging projects is obvious but a Central Portal so all resources are available to everyone is critical. It is particularly important that these efforts are making the data and images available to researchers in the countries where the specimens were collected, thereby supporting research in those countries.

5.2 Linking collections data with phylogenies and/or climate data

Big datasets become even more powerful if they are linked together and used to address specific questions. For instance, in a recent publication (Kuzmina et al., 2017) a group of Canadian researchers used leaf tissue from herbarium specimens to produce DNA barcodes for all of the vascular plants of

Canada (BOL, continuously updated). They were very successful sampling 98% of the flora (5076 species). Other large ‘‘data dumps’’ are becoming more common (e.g., Zuniga~ et al., 2017). Linking these efforts is BOLD the barcoding website (BOL, continuously updated). It represents a great resource for research projects that involve metagenomics such as the USGS project (see below) and iDigBio. To make these big data sets maximally useful, they should continue to be expanded to all countries and they must be cross-linked to voucher specimens, images, and GenBank numbers so name changes can be tracked and identifications checked (e.g., Hollowell & Funk, 2017).

An example of what is rapidly becoming possible is an ongoing research project on all species of the Compositae (Asteraceae) in North America (ca. 2500), funded by the Powell Center (USGS). The environment, including climate and topography as well as substrate properties such as geochemistry, texture, water retention, plays a large role in driving the diversity and distribution of species and communities. Interactions include adaptive radiations, key innovations, and parallel evolution to adaptive peaks, and more. Signatures of such processes should be visible in species' morphologies when correlated with environmental data in a phylogenetic context. To date, research identifying larger patterns has not been possible because of a lack of data for all of the environmental, phylogenetic, and phenotypic components. Big Data on all fronts are required to do this at scales beyond the traditional small group studies. The Powell Center project involves the aggregation of hundreds of thousands of species' collecting localities (e.g., GBIF, BISON, iDigBio) cleaned and set up as a framework upon which to integrate spatial environmental and geophysical data (gSSURGO, SoilGrids250m, AdaptWest), and phylogenetics (GenBank, OpenTreeOfLife) to investigate the diversification and distribution of species in response to the environment. This project focuses on what drives speciation and what constitutes extreme environments (R. Edwards, pers. com). Linking this to phenotypic evolution in plants at a broad scale will require the integration of huge morphological matrices (for a few examples see Fig. 8). Other questions that could be answered by these big data projects include: What are the areas that are in greatest need of exploration (by taxon, by ecosystem, or by predicted diversity)? How do regional floras compare with one another? What areas lack adequate sampling of environmental, geochemical, and soil data? and What is driving speciation in North America?

Because biodiversity collections have specimens that cover a time span of hundreds of years, the data harvested from the specimen labels can be used to examine changes in species distributions through time and space and assess the impacts of climate change and habitat destruction. Such studies have shown that plants are flowering earlier and moving as temperatures rise. Other, studies incorporated temperature records and covered large areas (e.g., Calinger et al., 2013). Feeley (2011) used distributional migrations, expansions, and contractions of tropical plant species from dated herbarium records and concluded that possibly 35% may be experiencing dieback due to intolerance of rising temperatures. However, few use them to model past and future distribution records although that is becoming more common. One such project (Still et al., 2015) ‘‘assessed the climate change vulnerability of 34 rare plant taxa from the western United States using two methods: NatureServe's Climate Change Vulnerability Index (CCVI) and one based on Species Distribution Modeling (SDM) using Maxent.’’ Of the eight taxa categorized as Extremely Vulnerable, five showed significant future loss (Still et al., 2015). Diazgranados (2012, 2015) modeled future distributions of the plant subtribe *Espeletiinae* (93–119 species; Asteraceae/ Compositae), iconic plants from the paramo vegetation of the northern Andes, and predicted that up to 80% of the species would experience habitat contraction and 31%–48% would be extinct by 2080. Efforts such as these should increase dramatically as more data become available. The future should bring collections-based studies with broader coverage and more taxa. Conceivably we could model all known organisms at a global level.

Mishler et al. (2014) used *Acacia* in an attempt to understand spatial patterns of biodiversity in Australia. They introduced the terms ‘relative phylogenetic diversity’ and ‘relative phylogenetic endemism’ to incorporate phylogenetic approaches into the studies of biodiversity and conservation planning. These methods were further developed and applied to one of the richest floras in the world: the California flora (Thornhill et al., 2017). The team used 1.39 million data points from herbarium specimens of 5258 species of native California plants, and nine genes to examine relative phylogenetic diversity and phylogenetic endemism. They conducted a categorical analysis of neo- and paleo-endemism (CANAPE). Because the data points were gathered from already existing records in known databases and most of the molecular data were from GenBank (GenBank: 3366 downloaded and 879 new sequences were deposited) this study showed the power of bringing together big data to answer questions that have been of interest for many years.

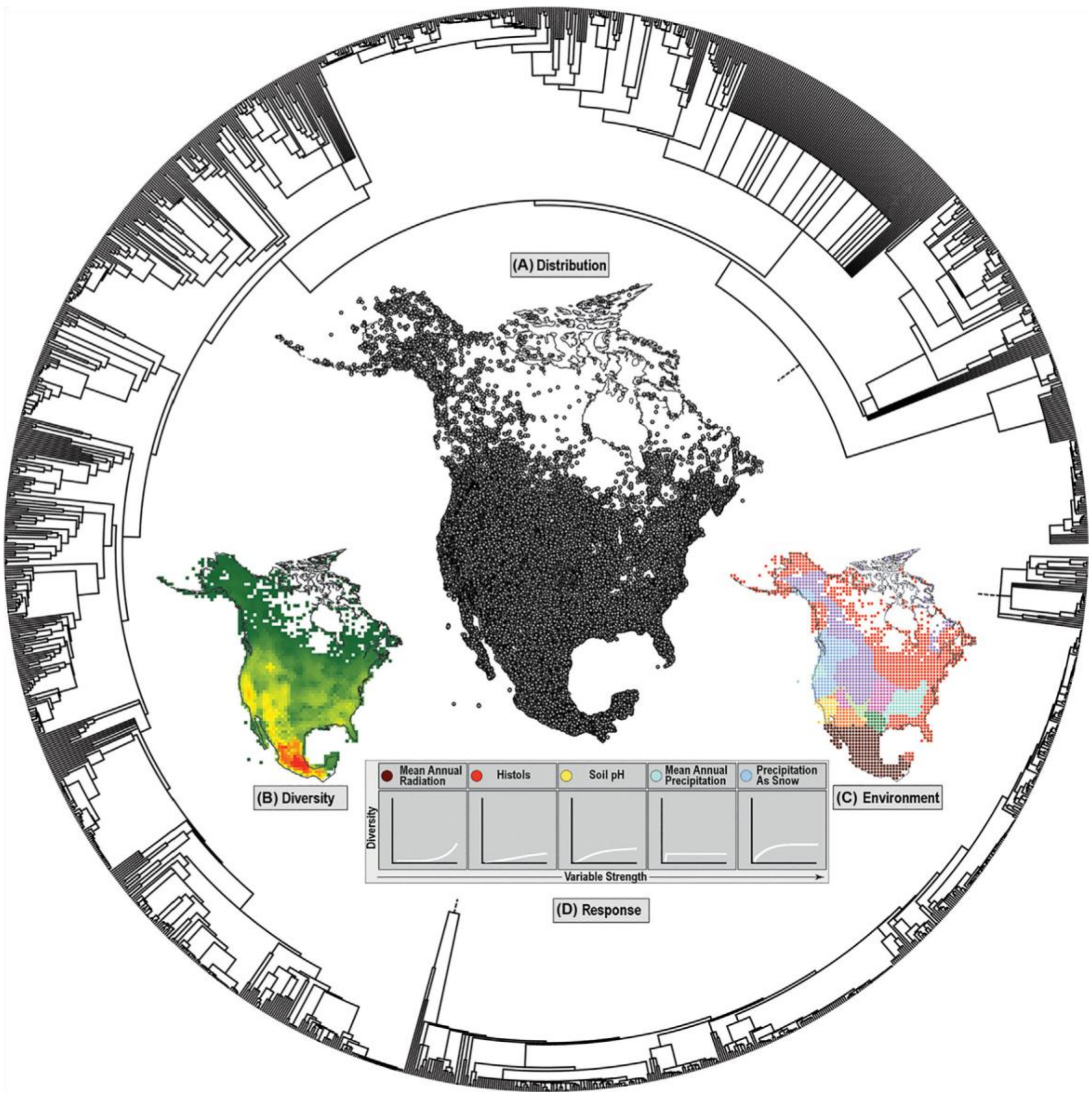


Fig. 8. Using Big Data to answer large-scale questions about the role of the environment in driving species diversity: Locality records for North American radiations of Compositae (Asteraceae) (**A**), are used to calculate diversity metrics (**B**), and are combined with soil, geochemistry, climate, and topological data (**C**), to determine regionally significant environmental variables that correlate with this diversity. How diversity changes across gradients in variable strength can also be modeled (**D**), and placed in a phylogenetic context to explore evolutionary patterns in environmental tolerances. [Figure courtesy of R Edwards, US]

Other issues include: What historic and current environmental factors best explain population structure? What communities and clades are at risk? Will communities retain their integrity (move together)? Can we predict extinctions of taxa at all levels? There are problems with errors in georeferenced points and with Cloud cover impeding data collection from satellites but developments such as automated checking of spectranomics are underway. These methods are already informing our sense of such issues, but as available data grow and are evaluated over larger scales there will be larger and more comprehensive studies.

There are substantial problems with current big data sets: unvouchered or poorly vouchered GenBank records, widespread misidentifications, poor or no geo-coordinates, missing ecological information, cloud cover on satellite photos, etc. For instance, Goodwin et al. (2015) found that: in 4500 specimens of gingers from Africa 58% were misidentified; within 21 000 specimens of Dipterocarps, 29% had different names on the same collection; and of 49 500 *Ipomoea* records in GBIF 59% were incorrect. Cleaning the data is imperative and sometimes much more time consuming than doing the actual research on the data. There are some novel data cleaning algorithms being developed and with online images it should become easier but it is always the responsibility of the researchers to make sure the data they are producing and using are in good condition.

The future will provide more access to big data and should advance all these topics.

5.3 Phylogenomics

Next generation sequencing (NGS) is a DNA sequencing technology that has revolutionized collections-based research: it allows for relatively rapid access to the whole genome of just about any organism. The field of phylogenomics has entered our daily lives by applying phylogenetic methods to the analyses of these new data (e.g., Wen et al., 2015b; Zimmer & Wen, 2015; Mandel et al., 2017). The DNA in herbarium specimens is usually fragmented and although this is a problem for traditional Sanger sequencing, it is not for NGS, which requires that the DNA be sheared. This makes available a vast array of samples spanning the globe and over 250 years of collecting. While the new methods are making it possible to access the DNA of older herbarium specimens (ancient DNA), there is some difficulty in reconstructing genomes. Two key things are changing rapidly: longer reads and more reference genomes and a new machine from

PacBio, a long read instrument that will produce seven times the output. To help with assembly we will have bigger chips with more reads and longer reads and transcriptomes (all the messenger RNA molecules expressed from the genes of an organism) can be done all in one run, so much less assembly is necessary. These advances will give us more data much faster. Beck & Semple (2015) found that in a species rich genus that is notoriously difficult taxonomically (*Solidago* or goldenrod; Compositae) 93 of 95 herbarium specimens (5 to 45 years old) were sequenced successfully using an Illumina platform. The results showed that genotyping by sequencing is broadly applicable to DNAs obtained from herbarium specimens and that pairing genomics with large-scale herbarium sampling is a promising strategy in species rich groups. Also, a study by Van Buren et al. (2015) used whole-genome sequencing and assembly of the grass *Oropetium thomaeum*. Using only single-molecule real-time sequencing, they generated long (>16 kilobases) reads and assembled 99% (244 megabases) of the *Oropetium* genome. This study produced a 'near-complete' draft genome and demonstrates the utility of single-molecule real-time sequencing for assembling highquality plant and other eukaryotic genomes, and serves as a valuable resource for the plant comparative genomics community. It shows the power of the future and what the next-next gen platforms will be able to do: cheap, efficient, single molecule, quasi-real time sequencing. In other words, very long reads of the "raw" DNA can be used to relatively easily and completely assemble complex genomes and sequence across regions that were problematic in the past. The Beck & Semple (2015) and Van Buren et al. (2015) papers show that the future lies within herbarium specimens!

One exciting trend is the developing field of *Intergrative Systematics* where collections-based systematics is combined with extensive field studies, phylogenetics, phylogenomics, detailed morphological studies, biogeographic inferences, and diversification analyses to present a more comprehensive global picture of the taxon. As an example, one can look at recent work by Wen and her collaborators on the small plant family Vitaceae (grape family) which has taken such an approach to their study of the family. The grape team has especially emphasized the training of many young colleagues from different parts of the world, using the family as an example of how this synthetic way of examining taxa works and ultimately providing a training module for systematics and evolution. The last decade of such studies has brought important new discoveries of three of the 17 genera of the family, the oldest fossil record from the late Cretaceous of India, many newly discovered species, and the employment of the family to explore the assembly of the viny plant elements across various biomes around the globe (e.g., Liu et al., 2013, 2016; Dang et al., 2017; Habib et al., 2017, 2018; Lu et al., 2018; Pace et al., 2018; Wen et al., 2018b). It is a model for a holistic treatment of a natural group of organisms that at its core depends on historical and modern collections.

The accessibility of such quantities of genomic data and novel ways of integrating it will allow us to address big evolutionary questions:

What is this? This simple question is still undergoing refinement and redesign. For instance, how do we document species names and concepts in difficult groups: e.g., bluegreen algae (Cyanophyta); deep-sea invertebrates and beetles.

How are microbiomes structured and how did they evolve? Can we use biological collections to pursue those questions? There are many types of microbiomes but some of the most interesting and varied are found in lichens. Lichens are models for symbioses because they comprise more than one taxon and one can reconstruct phylogenetic/phylogenomic inferences from the mycobiont (i.e., the primary fungal partner), the photobiont (green algae, cyanobacteria or both), and the additional bacteria and fungi that are essential components of these complex associations. Dal Forno et al. (pers. comm.; Fig. 9) are investigating lichen microbiomes in different genera and species in *Dictyonema* lichens to determine whether or not microbial patterns found in herbarium samples

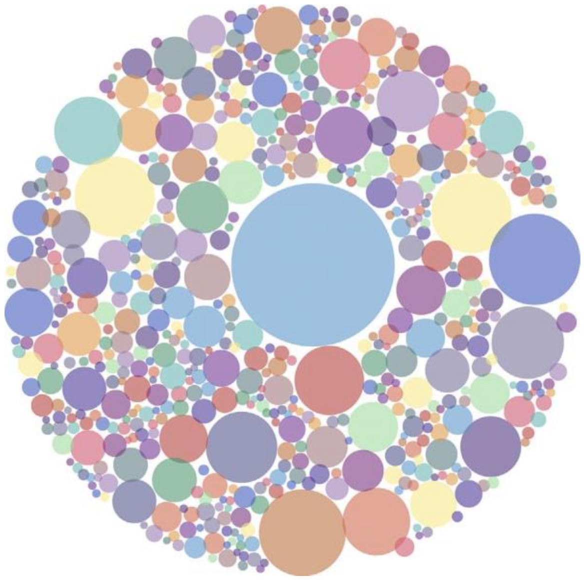


Fig. 9. Microbiomes: An example of the species diversity of bacteria from 697 different samples of many species from a single worldwide clade of basidiolichens (based on 16S rDNA data; analysis in Qiime2). Each circle represents a different OTU, size represents how often a particular OTU occurs. The largest circle is the cyannobacteria photobiont. [unpublished, presented by Dal Forno et al., 2017]

are reflective of specimens recently removed from their natural habitat. Only then are they able to compare these microbiomes to determine if they have changed through time and test different hypotheses to explain these changes. Likewise zoology collections also hold not just specimens of animals but material from microbiomes that are hitchhikers on those specimens. Currently researchers are sequencing 20 phyla of bacteria from a 100 year-old specimen (porcupine skin). Right now, it is not possible to recover whole metagenomes, but it is possible to get 16S metabarcodes to see what organisms are there and then compare that to modern day animals to see how these communities have changed through time (R. Dikow, pers. comm.). Future sequencing efforts from collections surely will bring even more information on microbiomes.

Can we document parental contributions in hybrids (known allopolyploids)? Many plant species, including early lineages of vascular plants, have been found to be allopolyploids. Zimmer and colleagues (pers. comm.) have been able to identify diploid parents of allopolyploids of the lycophyte genus *Isoëtes* L. using next generation sequencing. PacBio sequencing of nuclear markers can provide identification of both parents, while Illumina sequencing of complete plastid genomes can provide the identity of the chloroplast donor (usually the maternal parent). Also, in the course of their studies, they have identified several cryptic species in *Isoëtes*: a tetraploid species originally described from populations in different geographic sites from the endangered type species location are not all comprised of identical diploids.

What is the extent of cryptic speciation? Beheregaray et al. (2017) showed cryptic speciation in the golden perch (Australia) using ddRAD and the indication is that this will be a common result of next generation sequencing methods. It is quite possible that we have vastly underestimated species diversity: something that can be explored using biodiversity collections. [also see Wen et al., 2018a; and comments on *Isoëtes* above]

What is the frequency and impact of whole-genome duplications (WGD)? As more plant genomes become available the existing hypothesis that WGDs result in lineage diversification (Vanneste et al., 2014) can be better evaluated. Recently Tank et al. (2015) tested this idea and found that WGSs may promote increases in diversification but they may not be the sole cause of them. However, new whole genomes are being published regularly and this should allow for a more detailed analysis.

How do genomes change through time and space? (versions of genomes are not currently tracked except those from diseases). Can we establish a new "collection" to track genomes? The Smithsonian Data Science Lab is working to build a Biodiversity Genome Hub that will allow us to preserve genomes with versioning and will also allow us to "host" genomes as part of a Smithsonian Genome Collection that would be open to community annotation and improvement over time as well as the generation of comparative datasets (R. Dikow, pers. comm.).

How do diseases evolve? Collections have been important to understanding how fairly recent diseases have evolved but with NGS they can provide better documentation on older occurrences. For instance, three 1000-year-old mycobacterial genomes from Peruvian human skeletons were used to show that human tuberculosis was introduced post-contact and to implicate sea mammals as the most likely dispersal agent (Bos et al., 2014).

Do epigenetic changes play a role in evolution after all? There is some evidence that epigenetic modifications associated with transposable elements can be inherited, especially in plants (Heard & Martienssen, 2014) but the discussions are ongoing. Comparisons with historical collections and modern specimens would allow sampling for the persistence of these elements, perhaps they are not as transitory as we have thought or perhaps they reoccur over time.

What is the best way to monitor ecosystems? Carew et al. (2017) have successively used NGS on invertebrate collections stored in alcohol at room temperature for up to 12 years and recommend it as a potential technique for rapid and accurate identification. Perhaps collections of mixed samples from monitoring surveys can be analyzed to study change through time. Recently a new method has been introduced (microfluidic PCR-based target enrichment; Gostel et al., 2015) that speeds up and lessens the cost of obtaining hundreds of genes for phylogenomic work. These same methods can be used to speed up barcoding and by allowing many genes to be used, even closely related plant species can be resolved (Gostel et al., 2015; Gostel et al., unpublished data).

There are many things that are possible right now with phylogenomic methods but currently the problems are cost and assembly. Currently, Pac Bio is the best option but it is expensive and has error rates that are high although the error rate and cost are decreasing. Assembly remains a problem, and we need an array of annotated genomes across the tree of life and appropriate samples are lacking. What lies ahead: more reference genomes, new machines with a chip that has millions of wells, single molecule sequencing on a truly large scale. New software will allow us to analyze the character rich data sets with lengths of millions of base pairs. And, new collections are being created for use by the community. The Global Genome Initiative (GGI, continuously updated) at the Smithsonian sponsors the collections of tissue samples (and their vouchers) and stores them in freezers or in liquid nitrogen for future genomic use. GGI is part of the Global Genome Biodiversity Network (GGBN, continuously updated) that lists this and other collections at a single portal. Certainly, with the increase in transcriptome research these collections will be essential to making progress in the future.

As usual, there are concerns: we may be swamped by data and taxa, and large numbers of competing gene trees. How will we sort out the Good from the Bad and the Ugly? How do you present (serve) that much data? What is the best way to balance open access with some level of curation and oversight, how do you have a 2-way flow of information (corrections)? How do you check the accuracy of on line data? How does one best protect the data related to endangered organisms? How do we insure that NGS research is backed up by vouchers? And of course, how do we preserve and increase our collections over the next 250 years?

6 The Way Forward

With all this fascinating research and impactful applications of biological collections, when collections-based research is influencing so many topics from food safety to conservation, one would think that the future of biological collections and the research based on them would be secure. Rather, it is a common occurrence to have collections "orphaned" and while they are usually taken in by larger institutions that have room it removes these collections from the university where they were available for students and citizens that use them. Where will the inspiration for the next generation of collectors and collections-based science originate if biological collections are not housed in universities? How do we create a demand for, and appreciation of, collections-based information? Certainly we need to push question-driven aspects of collections-based research and the use of molecular data to test evolutionary hypotheses, but we must also work to broaden our outreach and promote the results of our research. Perhaps by taking a more active role in Wikipedia and engaging the public in our research efforts would help. Certainly, efforts like "*Plants are Cool Too!*" (Martine, continuously updated) is an informative and entertaining series about plants and it is very popular. Could we develop a series of videos to promote collections-based science? As a community, collections-based researchers must decide what we want to accomplish with biodiversity collections and collections-based research and determine a way forward.

Wen et al. (2015a) began the discussion but overall where do we go from here? From my perspective, all biodiversity collections should be imaged and available to the public. Quality control of data in repositories must be improved, especially needed is the ability of taxonomic experts to make corrections. There should be better linkage among data perhaps at a central portal, such as the proposed Global Biodiversity Cyberbank, as proposed for in Wen et al. (2015a, 2017). Additional types of collections should be brought online (e.g., cleared leaf slides, anatomy slides, pollen images, chromosome count images, published and unpublished illustrations, etc.) and would allow anyone to compare structure globally and to compare between paleobiology and modern collections and interpret what the climate was like at various times in history and the future. Online keys to identify species of all groups would greatly increase the accuracy and number of identifications and make collections more useful to the general public because the keys could contain links to images. Support for expeditions that target areas of interest for many groups of organisms is essential. Open access to all literature, perhaps sponsored by a global company, would be helpful. Lists of all known species and their synonomy should be fully annotated and accessible. We should foster the care of new types of collections (liquid nitrogen preserved tissue, micro-organisms; raw sequences, etc.) to keep all options open for future research. How do we accomplish all these items and more?

Wen et al. (2015a) called for a *World Organization of Systematic Biology*. I suggest we select one or more meetings that many systematists attend (e.g., BioSys, Evolution, Botany-USA, Latin American Botanical Congress, International Botanical Congress, etc.) and schedule a series of symposia on the *Tree* *of Life*. There was a successful one with four sessions at the *Sixth International Congress of Systematic and Evolutionary Biology* (ICSEB) meeting in Patras, Greece (2002) that invited speakers on all major clades of organisms and generated a lot of discussion. Such a series of symposia could be used to attract a large crowd for a discussion on establishing such a society and provide a platform for discussing ideas on how to move forward. A global society could sponsor a survey of collections to judge their health and well-being and make recommendations. The strong leadership of member organizations as well as individual members would be able to take an active role in establishing and maintaining the importance of biological collections and collections-based research.

Acknowledgements

This article reflects my personal views so it is natural that the examples lean heavily on my experiences. That should not be taken as an indication that these are the only examples or even thebestexamples.Manyofthegeneralideasinthispaperwere developed for a presentation at the December 2015 Conference of the *Australasian Systematic Botany Society* in Canberra, Australia. In 2017, they were extensively revised and presented at the*InternationalBotanicalCongress* in Shenzhen, China. Over the last two years the contents have been discussed with many people and I thank all of those who gave of their time and ideas (apologies if I have missed someone; to identify institutions I have used abbreviations from *Index Herbariorum* (Thiers, continuously updated; NY): J. Mauricio Bonifacino (MVFA), Manuela Dal Forno (US), Mauricio Diazgranados (K), Rebecca Dikow (Smithsonian), Robert [Bort] Edwards (US), Morgan Gostel (BRIT, US), Michael Martin (TRH), Sarah Matthews (CANB), Aleks Radosavljevic (CHIC, US), Jun Wen (US), Kenneth Wurdack (US), and Elizabeth Zimmer (US). I appreciate all of the authors who allowed me to use their images and photos; they are cited in the figure legends. Alice Tangerini (US) is thanked for helping me prepare the illustrations. I thank two reviewers who provided helpful comments. Finally, I must thank Jun Wen, the co-Editor-in-Chief for JSE, for her encouragement and Yan Liang for their help and patience.

References

Adanson M. 1763. *Familles naturelles des plantes*. Paris: Vincent.

ALA. Continuously updated. *Atlas of Living Australia*. http://www.ala. org.au [accessed 1 Jan 2018].

Allard MW, Bell R, Ferreira CM, Gonzalez-Escalona N, Hoffmann M, Muruvanda T, Ottesen A, Ramachandran P, Reed E, Sharma S, Stevens E, Timme R, Zheng J, Brown EW. 2018. Genomics of foodborne pathogens for microbial food safety. *Science Direct* 49: 224–229.

Allard MW, Strain E, Melka D, Bunning K, Musser SM, Brown EW, Timme R. 2016. Practical value of food pathogen traceability through building a whole-genome sequencing network and database. *Journal of Clinical Microbiology* 54: 1975–1983.

Avise J. 2000. *Phylogeography: The history and formation of species*. Cambridge: Harvard University.

Bartlett JMS, Stirling D. 2003. A short history of the polymerase chain reaction. In: PCR Protocols. 2nd ed. *Methods in Molecular Biology* 226: 3–6.

Baum DA, Smith SD. 2012. *Tree thinking: An introduction to phylogenetic biology*. New York: W. H. Freeman.

Beck JB, Semple JC. 2015. Next-generation sampling: Pairing genomics with herbarium specimens provides species-level signal in *Solidago* (Asteraceae). *Applications in Plant Sciences* 3: 1500014.

BeheregarayLB,PfeifferLV,AttardCRM, Sandoval-CastilloJ,Domingos FMCB, Faulks LK, Gilligan DM, Unmack PJ. 2017. Genome-wide data delimits multiple climate-determined species ranges in a widespread Australian fish, the golden perch (*Macquaria ambigua*). *Molecular Phylogenetics and Evolution* 111: 65–75.

Bell RC, Drewes RC, Zamundio KR. 2015. Reed frog diversification in the Gulf of Guinea: Overseas dispersal, the progression rule, and in situ speciation. *Evolution* 69: 904–915.

BOL. Continuously updated. *Barcode of Life: Identifying species with DNA barcoding*. http://www.barcodeoflife.org/ [accessed 27 Jan 2018].

Bos KI, Harkins KM, Herbig A, Coscolla M, Weber N, Comas I, Forrest SA, Bryant JM, Harris SR, Schuenemann VJ, Campbell TJ, Majander K, Wilbur K, Guichon RA, Steadma DLW, Cook DC, Niemann S, Behr MA, Zumarraga M, Bastida R, Huson D, Nieselt K, Young D, Parkhill J, Buikstra JE, Gagneux S, Stone AC, Krause J. 2014. Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. *Nature* 514: 494–497.

Brainard R, Moffitt R, Timmers M, Paulay G, Plaisance L, Knowlton N, Caley J, Fohrer F, Charette A, Meyer C, Toonen R, Godwin S, Martin J, Harris L, Geller J, Moews M. 2009. *Autonomous Reef Monitoring Structures (ARMS): A Tool for Monitoring Indices*. Available at http://webistem.com/psi2009/output_directory/cd1/ Data/articles/000442.pdf [accessed 4 Jan 2018].

Brundin L. 1966. Transantarctic relationships and their significance as evidenced by Chironomid Midges. *Kongliga Svenska vetenskapsakademiens handlingar* 11: 1–472.

Brunken U, Schmidt M, Dressler S, Janssen T, Thiombiano A, Zizka G. 2018. *West African plants - A Photo Guide*. www.westafricanplants. senckenberg.de. Forschungsinstitut Senckenberg, Frankfurt/ Main, Germany. [accessed 5 Jan 2018].

BWP. Continuously updated. *Barcode of Wildlife Project*. http://www. barcodeofwildlife.org/ [accessed 29 Jan 2018].

Calflora. Continuously updated. *California flora on line*. http://www. calflora.org/ [accessed 1 Jan 2018].

Calinger KM, Queenborough S, Curtis PS. 2013. Herbarium specimens reveal the footprint of climate change on flowering trends across north-central North American. *Ecology Letters* 16: 103–1044.

Carew ME, Metzeling L, St Clair R, Hoffmann AA. 2017. Detecting invertebrate species in archived collections using next-generation sequencing. *Molecular Ecology* 17: 915–930.

Carey SW. 1958. A tectonic approach to continental drift. In: Carey SW ed. *Continental drift—A Symposium*. Hobart, Australia: Tasmania University. 177–355.

Cavender-Bares J, Wilczek A. 2003. Integrating micro- and macroevolutionary processes in community ecology. *Ecology* 84: 592–597.

CDC. 2017. Influenza Virus Genome Sequencing and Genetic Characterization. Centers for Disease Control and Prevention (CDC). https://www.cdc.gov/flu/professionals/laboratory/geneticcharacterization.htm

Crandall KA, Fetzner JW, Lawler SH, Kinnersley M, Austin CM. 1999. Phylogenetic relationships among the Australian and New Zealand genera of freshwater crayfishes (Decapoda: Parastacidae). *Australian Journal of Zoology* 47: 199–214.

DalForno M, Sikaroodi M, Lawrey JD, Lucking R, Gillevet PM, Grube M.€ 2017. First insights into the microbiome of different morphologies in the *Dictyonema* clade. *Lichen Genomics Workshop II*. University of Graz, Graz, Austria. Available at: https://static.uni-graz.at/fileadmin/ nawi-institute/Botanik/Fritschiana/fritschiana-85/fritschiana-85.pdf Dang VC, Nguyen VH, Dao B-H, Yang W-L, Li F-L, Yang X-K, Wen J, Chen Z-D, Lu L-M. 2017. A new species and new records of *Cyphostemma* (Vitaceae) from China and Vietnam based on morphological and molecular evidence. *Systematic Botany* 42: 449–457.

Darlington PJ. 1965. *Biogeography of the southern end of the world*. Cambridge: Harvard University Press.

Darwin C. 1859. *On the origin of species: By means of natural selection*. London: John Murray. 502.

Darwin C, Wallace AR. 1858. On the tendency of species to form varieties; and on the perpetuation of varieties and species by natural means of selection. *Journal of the Proceedings of the Linnean Soceity, Zoology* 3: 45–62.

Diazgranados M. 2012. *Phylogenetic and biogeographic relationships of frailejones (Espeletiinae, Compositae): An ongoing radiation in the tropical Andes*. ProQuest Dissertations & Theses (PQDT) Open: 213 p. ISBN: 9781267453136. Available at http://pqdtopen.proquest. com/pubnum/3516206.html.

Diazgranados M. 2015. Una mirada biologicá a los paramoś circundantes a la Sabana de Bogota. In: Guhl E eď. *Los paramos circundantes a la Sabana de Bogota*. Jardın Botanico de Bogota. 175–205. http://goo.gl/gDNY1l.

Doherr D, Baron F. Continuously updated. *The Humboldt Digital Library*. http://www.avhumboldt.net/ [accessed 2 January 2018].

Eigenmann C. 1909. *Reports of the Princeton University expeditions to Patagonia, 1896–1899. Vol III, Part III. The fresh water fishes of Patagonia*. Princeton: The University of Princeton. 225–374.

Excoffier L, Smouse PE, Quattro JM. 1992. Analysis of molecular variance inferred from metric distances among DNA haplotypes: Application to Human mitochondrial DNA restriction data. *Genetics* 131: 479–491.

Faith DP, Walker PA. 1996. Environmental diversity: On the bestpossible use of surrogate data for assessing the relative biodiversity of sets of areas. *Biodiversity and Conservation* 5: 399–415.

Feeley KJ. 2011. Distributional migrations, expansions, and contractions of tropical plant species as revealed in dated herbarium records. *Global Change Biology* 18: 1335–1341.

Ferrier S. 1997. Biodiversity data for reserve selection: Making best use of incomplete information. In: Pigram JJ, Sundell RC eds. *National parks and protected areas: Selection, delimitation, and management*. Armidale, Australia: Centre for Water Policy Research. 315–329.

Ferrier S, Gray MR, Cassis GA, Wilkie L. 1999. Spatial turnover in species composition of ground-dwelling arthropods, vertebrates and vascular plants in northeast New South Wales: Implications for selection of forest reserves. In: Ponder W, Lunney D eds. *The other 99%: The conservation and biodiversity of invertebrates*. Mosman: Transactions of the Royal Zoological Society of New South Wales. 68–76.

Ferrier S, Pressey RL, Barrett TW. 2000. A new predictor of the irreplaceability of areas for achieving a conservation goal, its application to real world planning, and a research agenda for further renement. *Biological Conservation* 93: 303–325.

Ferrier S, Smith AP. 1990. Using geographical information systems for biological survey design, analysis and extrapolation. *Australian Biologist* 3: 105–116.

Funk VA. 2017. North American Herbaria and their Tropical Plant collections: What exists, what is available, and what the future may bring. In: Friis I, Balslev H eds. *Tropical Plant Collections: Legacies from the past? Essential tools for the future*? Copenhagen: Royal Danish Academy of Sciences and Letters. 73–96.

Funk VA, Brooks DR eds. 1981. *Advances in Cladistics: Proceedings of the first meeting of the Willi Hennig Society*. New York: New York Botanical Garden.

Funk VA, Susanna A, Stuessy T, Robinson H. 2009. Classification of Compositae. In: Funk VA, Susanna A, Stuessy T, Bayer R eds. *Systematics, evolution, and biogeography of Compositae*. Vienna: IAPT. 171–189.

Funk VA, Wagner WL. 1995. Biogeographic patterns in the Hawaiian Islands. In: Wagner WL, Funk VA eds. *Hawaiian biogeography: Evolution on a hot spot Archipelago*. Washington DC: Smithsonian Institution Press.

GBIF. Continuously updated. *Global Biodiversity Information Facility*. https://www.gbif.org/ [accessed 10 Jan 2018].

GGBN. Continuously updated. *Global Genome Biodiversity Network*. https://ggi.si.edu/ [accessed 20 Jan 2018].

GGI. Continuously updated. *Global Genome Initiative*. https://ggi.si. edu/ [accessed 20 Jan 2018].

Gire SK, Goba A, Andersen KG, Sealfon RSG, Park DJ, Kanneh L, Jalloh S, Momoh M, Fullah M, Dudas G, Wohl S, Moses LM, Yozwiak NL, Winnicki S, Matranga CB, Malboeuf CM, Qu J, Gladden AD, Schaffner SF, Yang X, Jiang P-P, Nekoui M, Colubri A, Coomber MR, Fonnie M, Moigboi A, Gbakie M, Kamara FK, Tucker V, Konuwa E, Saffa S, Sellu J, Jalloh AA, Kovoma A, Koninga J, Mustapha I, Kargbo K, Foday M, Yillah M, Kanneh F, Robert W, Massally JLB, Sinead S, Chapman B, Bochicchio J, Murphy C, Nusbaum C, Young S, Birren BW, Grant DS, Scheiffelin JS, Lander ES, Happi C, Gevao SM, Gnirke A, Rambaut A, Garry RF, Khan SH, Sabeti PC. 2014. Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. *Science* 243:

1369–1372.

Gluckman P, Beedle A, Buklijas T, Low G, Hanson MA. 2016. *Principles of evolutionary medicine*. Oxford: Oxford University Press.

Goodwin ZA, Harris DJ, Filer D, Wood JRI, Scotland RW. 2015.

Widespread mistaken identity in tropical plant collections. *Current Biology* 25: R1066–R1067.

Gostel MR, Coy KA, Weeks A. 2015. Microfluidic PCR-based target enrichment: A case study in two rapid radiations of *Commiphora* (Burseraceae) from Madagascar. *Journal of Systematics and Evolution* 53: 411–431.

GPI. Inactive. *Global Plants Initiative* (see GP-JSTOR).

GP-JSTOR. Continuously updated. *JSTOR Global Plants*. http://plants. jstor.org/ [accessed 4 Jan 2018].

Graham CH, Ferrier S, Huettman F, Moritz C, Peterson AT. 2004. New developments in museum-based informatics and applications in biodiversity analysis. *Trends in Ecology & Evolution* 19: 497–503.

GRBio. Continuously updated. Global Registry of Biodiversity Repositories (GRBio). http://grbio.org/ [accessed 20 February 2018].

Habib S, Dang V-C, Ickert-Bond SM, Zhang J-L, Lu L-M, Wen J, Chen Z-D. 2017. Robust phylogeny of *Tetrastigma* (Vitaceae) based on ten plastid DNA regions: Implications for infrageneric classification and seed character evolution. *Frontiers in Plant Science 8* doi:10.3389/fpls.2017.00590

Habib S, Dang V-C, Ickert-Bond SM, Wen J, Chen Z-D, Lu L-M. 2018. Evolutionary trends in Tetrastigma (Vitaceae): Morphological diversity and taxonomic implications. *Journal of Systematics and Evolution*. doi: 10.1111/jse.12309

Heard E, Martienssen RA. 2014. Transgenerational epigenetic inheritance: Myths and mechanisms. *Cell* 157: 95–109.

Hennig W. 1950. *Grundzuge einer Theorie der phylogenetischen Systematik*. Berlin: Deutscher Zentralverlag.

Hennig W. 1966. *Phylogenetic systematics*. Urbana: University of

Illinois Press.

Hillis DM, Moritz C. 1990. *Molecular systematics*. Sunderland, MA: Sinauer.

Hillis DM, Moritz C, Mable BK. 1996. *Molecular Systematics*, 2nd ed. Sunderland, MA: Sinauer.

Hollowell T, Funk VA. 2017. Increasing research impact by cross-linking NCBI & EMu records. *The Plant Press* 20: 9.

Holmes A. 1944. *Principles of physical geology*. London: Thomas Nelson & Sons.

Hooker JD. 1853. *Flora Antarctica: The botany of the Antarctic voyage*. Vol 3 (New Zealand). London: Reeve.

Hull DL. 1988. *Science as a process: An evolutionary account of the social and conceptual development of science*. Chicago: The University of Chicago Press.

Humboldt A. 1807. *Geographie der Pflanzen in den Tropen-L€andern, ein Naturgem€alde der Anden*. Tubingen, Germany: Cotta.€

Humboldt A. 1845. *Kosmos. Entwurf einer physischen Weltgeschichte.*

Bol I. Stuttgart-Tubingen: Cotta.€ iDigBio. Continuously updated. *Integrated Digitized Biocollections* program. https://www.idigbio.org/ [accessed 28 Dec 2017].

Jansen RK, Palmer JD. 1987a. A chloroplast DNA inversion marks an ancient evolutionary split in the sunflower family (Asteraceae). *Proceedings of the National Academy of Sciences USA* 84:

5818–5822.

Jansen RK, Palmer JD. 1987b. Chloroplast DNA from lettuce and Barnadesia (Asteraceae): Structure, gene localization, and characterization of a large inversion. *Current Genetics* 11: 553–564.

Jansen RK, Palmer JD. 1988. Phylogenetic implications of chloroplast DNA restriction site variation in the Mutisieae (Asteraceae). *American Journal of Botany* 75: 753–766.

Jansen RK, Palmer JD, Michaels HJ. 1988. Investigation of chloroplast DNA variation in the Asteraceae. *Compositae Newsletter* 15: 2–11.

Jurgens N, Strohbach B, Schmiedel U, R€ ugheimer S, Erb E, Wesuls D,€ Schrenk J, Dreber N, Schmidt M, Mayer C, Zizka A, Horn P, Mills A, Etzold S, Schulz A, Beaumont J, Oncken I, Revermann R, Niesler I, Kwembeya E, Deckert J, Kuhlmann M, Reddig C, Miehlich G, Christiaan R, Finckh M, Kruger S, Coetzee M, Fortuin A, Ihlenfeldt H, Le Roux A, Erb P, Groengroeft A, Helme N. 2018, continuously updated. *Photo guide to plants of Southern African*. Hamburg, Germany: BioCentre Klein Flottbek.

Jussieu AL de. 1789. *Genera Plantarum, secundum ordines naturales disposita juxta methodum in Horto Regio Parisiensi exaratam, anno 1774*. Paris: Apud Viduam Herissant, typographum.

Kembel SW, Hubbell SP. 2006. The phylogenetic structure of a neotropical forest tree community. *Ecology* 87: S86–S99.

Kress WJ. 2017. Plant DNA barcodes: Applications today and in the future. *Journal of Systematics and Evolution* 55: 291–307.

Kress WJ, Erickson DL, Jones FA, Swenson NG, Perez R, Sanjur O, Bermingham E. 2009. Plant DNA barcodes and a community phylogeny of a tropical forest dynamics plot in Panama. *Proceedings of the National Academy of Sciences USA* 106:

18621–18626.

Kress WJ, Erickson DL, Swenson NG, Thompson J, Uriarte M, Zimmerman JK. 2010. Advances in the use of DNA barcodes to build a community phylogeny for tropical trees in a Puerto Rican Forest Dynamics Plot. *PLoS ONE* 5: e15409.

Kress JW, Garcia-Robledo C, Uriarte M, Erickson DL. 2015. DNA barcodes for ecology, evolution and conservation. *Trends in Ecology & Evolution* 30: 25–35.

Kuzmina ML, Braukmann TWA, Fazekas AJ, Graham SW, Dewaard SL, Rodrigues A, Bennett BA, Dickinson TA, Saarela JM, Catling PM, Newmaster SG, Percy DM, Fenneman E, Lauron-Moreau A, Ford B,

Gillespie L, Subramanyam R, Whitton J, Jennings L, Metsger D, Warne CP, Brown A, Sears E, Dewaard JR, Zakharov EV, Hebert PDN. 2017. Using herbarium-derived DNAs to assemble a largescale DNA barcode library for the Vascular Plants of Canada. *Applications in Plant Sciences* 5: 1700079.

Li Y, Carroll DS, Gardner SN, Walsh MC, Vitalis EA, Damon IK. 2007. On the origin of smallpox: Correlating variola phylogenics with historical smallpox records. *Proceedings of the National Academy of Sciences USA* 104: 15787–15792.

Linnaeus C. 1753. *Species plantarum*. Stockholm: Laurentii Salvii.

Liu X-Q, Ickert-Bond S, Chen L-Q, Wen J. 2013. Molecular phylogeny of *Cissus* L. of Vitaceae (the grape family) and evolution of its pantropical intercontinental disjunctions. *Molecular Phylogenetics and Evolution* 66: 43–53.

Liu XQ, Ickert-Bond SM, Nie ZL, Zhou Z, Chen LQ, Wen J. 2016.

Phylogeny of the *Ampelocissus-Vitis* clade in Vitaceae supports the New World origin of the grape genus. *Molecular Phylogenetics and Evolution* 95: 217–228.

Losos JB. 1996. Phylogenetic perspectives on community ecology. *Ecology* 77: 1344–1354.

Lu L-M, Cox CJ, Mathews S, Wang W, Wen J, Chen Z-D. 2018. Optimal data partitioning, multispecies coalescent and Bayesian concordance analyses resolve early divergences of the grape family (Vitaceae). *Cladistics* 34: 57–77.

Mandel JR, Barker MS, Bayer RJ, Dikow RB, Gao T-G, Jones KE, Keeley S, Killian N, Ma H, Siniscalchi CM, Susanna A, Thapa R, Watson L, Funk VA. 2017. The Compositae tree of life in the age of phylogenomics. *Journal of Systematics and Evolution* 55: 405–410.

Margules CR, Nicholls AO, Pressey RL. 1988. Selecting networks of reserves to maximize biological diversity. *Biological Conservation* 43: 63–76.

Margules CR, Austin MP. 1994. Biological models for monitoring species decline: The construction and use of data bases. *Philosophical Transactions of the Royal Society of London B: Biological Sciences* 344: 69–75.

Martin MD, Quiroz-Claros E, Brush GS, Zimmer EA. 2018. Herbarium collection-based phylogenetics of the ragweeds (Ambrosia, Asteraceae). *Molecular Phylogenetics and Evolution* 120: 335–341.

Martin MD, Zimmer EA, Olsen MT, Foote AD, Gilbert MTP, Brush GS. 2014. Herbarium specimens reveal a historical shift in phylogeographic structure of common ragweed during native range disturbance. *Molecular Ecology* 23: 1701–1716.

Martine C. Continuously updated. Plants are Cool too! https://www. youtube.com/user/PlantsAreCoolToo/feed [accessed 1 Feb 2018].

Mishler BD, Knerr N, Gonzalez-Orozco CE, Thornhill AH, Laffan SW, Miller JT. 2014. Phylogenetic measures of biodiversity and neo- and paleo endemism in Australian Acacia. *Nature Communications* 5: 4473. doi: 10.1038/ncomms5473.

Moritz C, Faith DP. 1998. Phylogeography and the identification of genetically divergent areas for conservation. *Molecular Ecology* 7: 419–429.

Moritz C, Richardson KS, Ferrier S, Montieth GB, Williams SE, Whiffen T. 2001. Biogeographic concordance and efficiency of taxon indicators for establishing conservation priority for a tropical rainforest biota. *Proceedings of the Royal Society of London, Series B: Biological Sciences* 268: 1875–1881.

Mullis KB, Erlich HA, Arnheim N, Horn GT. 1987. Process for amplifying detecting, and/or-cloning nucleic acid sequences. U.S. Patent 4,683,195.

Nelson G, Platnick N. 1981. *Systematics and biogeography: Cladistics and vicariance*. New York: Columbia University Press.

NOAA Fisheries. Continuously updated. https://www.pifsc.noaa.gov/ cred/survey_methods/arms/overview.php [accessed 5 January 2018].

Ottesen A, Ramachandran P, Reed E, White JR, Hasan N, Poorani S, Ryan G, Jarvis K, Grim C, Daquiqan N, Hanes D, Allard A, Colwell R, Brown E, Chen Y. 2016. Enrichment dynamics of Listeria monocytogenes and the associated microbiome from naturally contaminated ice cream linked to a listeriosis outbreak. *BMC MicroBiology* 16: 275.

Ortelius A. 1570. *Theatrum Orbis Terrarum*. Antwerp: Gilles Coppens de Diest.

Pace MR, Angyalossy V, Acevedo-Rodriguez P, Wen J. 2018. Structure and ontogeny of successive cambia in *Tetrastigma* (Vitaceae), the host plants of Rafflesiaceae. *Journal of Systematics and Evolution* DOI: 10.1111/jse.12303

Panero JL, Funk VA. 2008. The value of sampling anomalous taxa in phylogenetic studies: Major clades of the Asteraceae revealed. *Molecular Phylogenetics and Evolution* 47:

757–782.

Pinto CM, Baxter BD, Hanson JD, Mendez-Harclerode FM, Suchecki JR, Grijalva MJ, Fulhorst CF, Bradley RD. 2010. Using museum collections to detect pathogens. *Emerging Infectious Diseases* 16: 356–357.

Platnick N, Funk VA eds. 1983. *Advances in cladistics: Proceedings of the second meeting of the Willi Hennig Society*. New York: Columbia University Press.

Pressey RL, Humphries CJ, Margules CR, Vaine-Wright RI, Williams PH. 1993. Beyond opportunism: Key principles for systematic reserve selection. *Trends in Ecology and Evolution* 8: 124–128.

Sawyer S, Renaud G, Bence V, Hublin J-J, Gansauge M-T, Shunkov VM, Derevianko AP, Prufer K, Kelso J, P€ €a€abo S. 2015. Nuclear and mitochondrial DNA sequences from two Denisovan individuals. *Proceedings of the National Academy of Sciences USA* 112: 15696–15700.

Schuettpelz E, Frandsen PB, Dikow RB, Brown A, Orli S, Peters M, Metallo A, Funk VA, Dorr L. 2017. Applications of deep convolutional neural networks to digitized natural history collections. *Biodiversity Data Journal*. DOI: 10.3897/BDJ.5.e21139

Sharp PM, Hahn BH. 2011. Origins of HIV and the AIDS pandemic. Cold Spring Harbor Perspectives in Medicine Sept 1(1):a006841. https://doi.org/10.1101/cshperspect.a006841

Shaw KL, Gillespie RG. 2016. Comparative phylogeography of oceanic archipelagos: Hotspots for inferences of evolutionary process. *Proceedings of the National Academy of Science USA* 113: 7986–7993.

Smith CH, Walklate J. 2017. Alfred Russel Wallace Notes 7: Wallace, Bates and John Plant: The Leicester Connection. *The Linnean* 33: 18–24.

Snider-Pellegrini A. 1859. *La Creation et ses mysteres devoiles*. Paris: Franck A & Dentu E.

Stearns SC, Medzhitov R. 2015. *Evolutionary medicine*. Oxford: Oxford University Press.

Still SM, Frances AL, Treher AC, Oliver L. 2015. Using two climate change vulnerability assessment methods to prioritize and manage rare plants: A case study. *Natural Areas Journal* 35(1): 106–121.

Tank DC, Eastman JM, Pennell MW, Soltis PS, Soltis DE, Hinchliff CE, Brown JW, Sessa EB, Harmon LJ. 2015. Nested radiations and the pulse of angiosperm diversification: increased diversification rates often follow whole genome duplications. *New Phytologist* 207: 454–467.

Taylor J. 2015. *Body by Darwin: How evolution shapes our health and transforms medicine*. Chicago: University of Chicago Press.

Thiers B. Continuously updated. *Index Herbariorum: A global directory of public herbaria and associated staff*. New York Botanical Garden's Virtual Herbarium. http://sweetgum.nybg.org/science/ ih/.

Thornhill AH, Baldwin BG, Freyman WA, Nosratinia S, Kling MM, Morueta-Holme N, Madsen TP, Ackerly DD, Mishler BD. 2017. Spatial phylogenetics of the native California flora. *BMC Biology* 15: 96. https://doi.org/10.1186/s12915-017-0435-x

TROPICOS. Continuously updated. *TROPICOS-Missouri Botanical Garden*. http://www.tropicos.org/ [accessed 1 Jan 2018].

Unger J, Merhof D, Renner S. 2016. Computer vision applied to herbarium specimens of German trees: Testing the future utility of the millions of herbarium specimen images for automated identification. *BMC Evolutionary Biology* 16: 248. https://doi.org/ 10.1186/s12862-016-0827-5

Van Buren R, Bryant D, Edger PP, Tang H, Burgess D, Challabathula D, Spittle K, Hall R, Gu J, Lyone E, Freeling M, Bartels D, Hallers BT, Hastie A, Michael TP, Mockler TC. 2015. Single-molecule sequencing of the desiccation-tolerant grass *Oropetium thomaeum*. *Nature* 527: 508–517.

Vanneste K, Baele G, Maere S, Van de Peer Y. 2014. Analysis of 41 plant genomes supports a wave of successful genome duplications in association with the Cretaceous-Paleogene boundary. *Genome Research* 24: 1334–1347.

Wallace AR. 1863. *The geographical distribution of animals*, 2 vols. London: Macmillian.

Wallace AR. 1905. *My life: A record of events and opinions*. London: Chapman & Hall.

Webb CO. 2000. Exploring the phylogenetic structure of ecological communities: An example for rain forest trees. *American*

Naturalist 156: 145–155.

Wegener A. 1912a. Die Herausbildung der Grossformen der Erdrinde (Kontinente und Ozeane), auf geophysikalischer Grundlage. *Petermanns Geographische Mitteilungen* 63: 185–195, 253–256, 305–309. Presented at the annual meeting of the German Geological Society, Frankfurt am Main.

Wegener A. 1912b. Die Entstehung der Kontinente. *Geologische Rundschau* (in German) 3: 276–292.

Wen J, Harris AJ, Ickert-Bond SM, Dikow R, Wurdack K, Zimmer EA. 2017. Developing integrative systematics in the informatics and genomic era, and calling for a global biodiversity cyberbank. *Journal of Systematics and Evolution* 55: 308–321.

Wen J, Harris AJ, Kalburgi Y, Zhang N, Xu Y, Zheng W, Ickert-Bond SM, Johnson G, Zimmer EA. 2018a. Chloroplast phylogenomics of the New World grape species (*Vitis*, Vitaceae). *Journal of Systematics and Evolution* (in press).

Wen J, Ickert-Bond SM, Appelhans MS, Dorr LJ, Funk VA. 2015a. Collections-based systematics: Opportunities and outlook for 2050. *Journal of Systematics and Evolution* 53: 477–488.

Wen J, Liu J-Q, Ge S, Xiang Q-Y (J), Zimmer EA. 2015b. Phylogenomic approaches to deciphering the tree of life. *Journal of Systematics and Evolution* 53: 369–370.

Wen J, Lu L-M, Nie Z-L, Liu X-Q, Zhang N, Ickert-Bond SM, Gerrath JM, Manchester SR, Boggan JK, Chen Z-D. 2018b. A new phylogenetic tribal classification of the grape family (Vitaceae). *Journal of Systematics and Evolution* (in press).

WGS. Continuously updated. FDA-Whole Genome Sequencing Program. https://www.fda.gov/Food/FoodScienceResearch/Whole GenomeSequencingProgramWGS/ucm363134.htm

Wiley EO, Siegel-Causey D, Brooks DR, Funk VA. 1991. *The compeat cladist: A primer of phylogenetic procedures*. Lawrence, Kansas: University of Kansas Special Publication No. 19.

Williams P, Gibbons D, Margules C, Rebelo A, Humphries C, Pressey R. 1996. A comparison of richness hotspots, rarity hotspots, and complementary areas for conserving diversity of British birds. *Conservation Biology* 10: 155–174.

Wulf A. 2017. *The invention of nature: Alexander von Humboldt's New World*. New York: Knopf.

Zhang N, Ramachandran P, Wen J, Duke JA, Metzman H, McLaughlin W, Ottesen AR, Timme RE. Handy SM. 2017. Development of a reference standard library of chloroplast genome sequences, GenomeTrakrCP. *Planta Medica* 83: 1420–1430.

Zimmer EA, Wen J. 2015. Using nuclear gene data for plant phylogenetics: Progress and prospects II. Next-gen approaches. *Journal of Systematics and Evolution* 53: 371–379.

Zuniga JD, Gostel MR, Mulcahy DG, Barker K, Hill A, Sedaghatpour M,~ Vos SQ, Funk VA, Coddington JA. 2017. Data Release: DNA barcodes of plant species collected for the Global Genome Initiative for Gardens Program, National Museum of Natural History, Smithsonian Institution. *Phytokeys* 88: 119–122.