Digitizing Specimens in a Small Herbarium: A Viable Workflow for Collections Working with Limited Resources

Authors: Harris, Kari M., and Marsico, Travis D.

Source: Applications in Plant Sciences, 5(4)

Published By: Botanical Society of America

URL: https://doi.org/10.3732/apps.1600125
DIGITIZING SPECIMENS IN A SMALL HERBARIUM: A Viable Workflow for Collections Working with Limited Resources

KARI M. HARRIS² and TRAVIS D. MARSICO²,³

²Department of Biological Sciences, Arkansas State University, P.O. Box 599, State University, Arkansas 72467 USA

• **Premise of the study:** Small herbaria represent a significant portion of herbaria in the United States, but many are not digitizing their collections.

• **Methods:** At the Arkansas State University Herbarium (STAR), we have created a viable workflow to help small herbaria begin the digitization process, including suggestions for publishing data on the Internet. We calculated hourly rates of each phase of the digitization process. We also mapped accessions at the county level to determine geographic strengths in the collection.

• **Results:** All 17,678 accessioned flowering plant specimens at STAR are imaged, databased in Specify, and available electronically on the herbarium’s website. Students imaged the specimens at a mean rate of 145/h. We found differences in databasing rates between the graduate student leading the project (47/h) and undergraduate assistants (25/h). The majority of specimens at STAR were collected within the counties neighboring the institution.

• **Discussion:** With this workflow, we estimate that one person can digitize a 20,000-specimen collection in less than 2.5 yr by working only 10 h/wk. Because STAR is a small herbarium with limited resources, the application of the workflow described should assist curators of similar-sized collections as they contemplate and undertake the digitization process.

**Key words:** biodiversity informatics; digitization workflow; natural history collection; regional collection; small herbarium.

The specimens that comprise many herbaria were collected at a time when plants were collected solely for taxonomic purposes (Chapman, 2005). It is still true that any specimen data used for scientific publications must be traceable back to vouchered sources so that the species’ identities can be verified (Funk et al., 2005). Having access to quality specimens is a requirement for floristic and taxonomic research to advance, and these lines of research are particularly critical for species discovery in our current extinction crisis (Stuessy, 1993). Additionally, herbaria data have emerged as key resources for documenting distributions of biodiversity over time and space (Chapman, 2009; Baird, 2010). The existence of these data, therefore, has important implications for research, education, and public service beyond what was originally envisioned by 19th- and early 20th-century botanists (Funk, 2004; Chapman, 2005). New uses for specimens and their associated data have developed in the past few decades, and technology for linking data virtually through databases has enhanced the utility of these data for answering a variety of scientific questions. For example, changes in land use often result in habitat modification, which can be studied using species occurrences from vouchered herbarium records. Researchers have also used collections data in a variety of other ecological studies. Such studies have used herbarium specimens to track plant viruses over time (Malmstrom et al., 2007), to show that seeds attached to plant specimens are still viable more than 100 yr after collection (Godefroid et al., 2011), and to demonstrate that flowering times are now earlier due to a rise in global temperatures (Hovenden et al., 2008). Effective use of herbarium specimens can assist in detecting and responding quickly to invasive species threats (Baird, 2010). Collections can also be used to study evolutionary change in invasive species as they become established (Marsico et al., 2010).

In the past two decades, there has been a national push to digitize specimen data to make the data more broadly available to the general public and scientific community through Internet access (Owen, 1990; Allen, 1993; Lane, 1996; Network Integrated Biocollections Alliance, 2010; Nelson et al., 2015). The digitizing process consists of predigitization curation, imaging specimens, databasing label and identifying information, and georeferencing locality information (Barkworth and Murrell, 2012; Nelson et al., 2015). Each of these steps can take a considerable amount of time to accomplish, so it is important to note that digitization...
often happens in stages. Any amount of data coming from a collection is useful, and data can be shared at any stage. Many online platforms publish data that are only images, only label data, only locality information, or a combination of the three.

Having specimen data easily accessible and searchable online increases research efficiency (Chapman, 2005). Time previously spent traveling to collections or waiting for specimen loans could instead be spent gathering data. Taxonomists are often able to use digitized collections to identify and annotate specimens. In addition, digitizing specimens reduces handling and potential damage to specimens (Schmull et al., 2005), which is particularly important for rare and special specimens including type specimens.

An online database of accessioned herbarium specimens promotes sharing of information between institutions and fosters biodiversity information networks. Such resources support the development of professionals in the fields of biodiversity informatics, image services, and geographic information systems (GIS). Online data raise awareness of natural history collections and open these rich resources to education and research. Compiling information for new guides, checklists, and other resources used for understanding botanical information is greatly facilitated by online databases.

In the United States, an estimated 800 herbaria are active and house approximately 90 million specimens (Barkworth and Murrell, 2012), with about 78% of the collections associated with academic institutions. Nearly half of all herbaria in the United States can be considered “small” herbaria; that is, nearly half have fewer than 100,000 specimens (Barkworth and Murrell, 2012). In 2012, about 50% of the small herbaria were databasing, about 25% were imaging, and only 15% had portions of their collections available online. These herbaria are spread out across the United States and occur in many areas where there are no large-sized herbarium collections. With so few of these collections available online, there is a significant portion of plant biodiversity data missing from online databases. To represent the known biodiversity of plants in the United States, online databases must include specimens from small herbaria (Boyd, 2008).

There are many reasons small herbaria are not digitizing their collections and making them available online. Many small herbaria face obstacles such as lack of funding, lack of staff, and curators with many responsibilities in addition to the collection (such as teaching, advising students, and research outside the collections). In many instances, curators at smaller institutions are not given any credit toward promotion for their curatorial duties, making prioritizing these efforts even more difficult. Moreover, curators and collections managers who want to digitize may struggle with knowing where to begin and what the options are (iDigBio, 2013).

The Arkansas State University (STAR) Herbarium houses approximately 20,000 specimens and is run by a curator (T.D.M.) with many other academic responsibilities. The herbarium receives no funding for additional staff and has historically had, and continues to have, no budget for operations. Despite this, the STAR Herbarium now has all of its in-state flowering plant collections reorganized, imaged, databased, and available online. Seedless vascular plants and gymnosperms are imaged and will be databased as part of a recently funded project. This paper describes the protocol we used to digitize more than 16,000 flowering plant specimens of the STAR Herbarium collection in 2.5 yr, which may serve as a model for similar small collections with limited resources. In this publication, we share our experiences as a template for others to apply in similar situations. We provide specific material resources and recommendations for those with a limited budget, and we provide calculations of the time it took us to complete each step of our digitization process.

### MATERIALS AND METHODS

A scholarship from the National Science Foundation (NSF) Scholarships in Science, Technology, Engineering, and Mathematics (S-STEM) program provided funding for one graduate student (K.M.H.) and five undergraduate students to gain practical research experience digitizing the flowering plant collection at the STAR Herbarium. Digitizing the herbarium required six steps: (1) organizing all specimens in the cabinets using updated taxonomy and nomenclature and incorporating as many new collections as possible, (2) purchasing and setting up an imaging station, (3) imaging each specimen individually and developing efficient imaging protocols, (4) choosing the database template that best fit our project, (5) entering all label information into the database, and (6) combining all data to make it accessible to the scientific community and public through an online database (Fig. 1).

The equipment we chose was all purchased for US$1500 at the start of the project in 2012. The Dean of the College of Sciences and Mathematics at Arkansas State University (A-State) provided funding for the project. The US$1500 was used to purchase a Nikon D3200 18-megapixel digital single-lens reflex (DSLR) camera (Nikon, Melville, New York, USA) with an 18–55-mm zoom

---

Fig. 1. Arkansas State University (STAR) Herbarium digitization workflow developed and applied in this project.

[http://www.bioone.org/loi/apps](http://www.bioone.org/loi/apps)
images, we set camera settings to the following: ISO 100, Shutter speed 1/200, Aperture F/4.0, White Balance Auto, Exposure Comp. 0, Compression Raw + JPEG (Fine), Metering Mode Multi-pattern. To estimate the imaging rate, we asked students to document the number of specimens imaged and the amount of time they worked. With this information, we calculated imaging rates based on 12,108 specimens out of the total 17,678 that were imaged (~72% of the imaged collection; Table 1).

Databasing was divided into two tasks: keystroking label data into the database and uploading the data sets once they were completed. The Specify 6 software allowed for easy updating of nomenclature as well as georeferencing. In addition, support for this software was considered stable, as Specify and its precursors have had continuous federal funding since 1985 (A. C. Bentley, personal communication, 23 September 2016). Specify does, however, require a significant amount of in-house support to set it up and keep it running. For a curator who does not have access to Information Technology (IT) support, it may be simpler to use an online database like Symbiota to maintain a herbarium database and host images, label data, and georeferencing information online. In Specify we used Darwin Core fields (Darwin Core Task Group, 2009) and populated our taxon tree to family level using Plant Systematics: A Phylogenetic Approach (Judd et al., 2008). Data entry was completed in the Specify WorkBench. The WorkBench is a Specify interface that allows several items to be entered at once in a spreadsheet or list format (Fig. 3). The WorkBench is an easy-to-use platform for those new to data entry or accustomed to using Excel spreadsheets. Data records were entered up to family level in the WorkBench so data were able to sync with the taxon tree upon upload. A data set mapping with appropriate Darwin Core fields was created in the WorkBench. In the WorkBench list view, we were able to put the fields in order according to how they were displayed on the specimen label. This set-up allowed students to easily enter data and was less confusing to those who were less familiar with specimen labels. Specimens were databased by species. The images for each species were uploaded into the WorkBench (Fig. 3) as individual data sets and databased by the same individual. After the data were entered, the graduate student project leader (K.M.H.) checked them before they were uploaded into the main database. The rates at which students verified nomenclature, imaged, and databased
the specimens were recorded. The amount of time to upload the specimens into
the main STAR Herbarium Specify database was also recorded once specimens
were databased by the students. The databasing rates were calculated on a per-
species work interval with start and end times recorded for all specimens of each
species databased. A sample of 11,851 of 16,791 specimens (70%) is used in our
database rate calculations.

The STAR Herbarium Specify database is backed up on a server main-
tained by the A-State IT Department. This server must be accessed by Bitvise
SSH Client each time users log into the A-State Specify database. Students
who use the database are issued log in information for both the A-State server
and Specify. This process is somewhat complicated, but it allows the STAR
Herbarium records to be securely maintained. In addition, the A-State Specify
database and all STAR Herbarium images are backed up on multiple external
hard drives. These hard drives are kept at various locations both on and off
campus.

To make the records publicly available, we have created a STAR Herbarium
website. For this we collaborated with the Department of Computer Science
and initiated the website as a project for computer science students. However,
rather than create our own online database, we chose to use the Specify Web
Portal. We needed the help of an IT expert to create the interface between our
database and images on the WorkBench and a web user interface. It is important
to note that access to an IT professional is essential in the implementation of a

Table 1. Digitization rates by task and student. All calculations are in average specimens per hour.

| Task/Individual                 | No. of recorded work intervals | Specimens/h | SE |
|---------------------------------|-------------------------------|-------------|----|
| Nomenclatural verification (Average for all students)* | 150                           |             |    |
| Imaging (Average for all students working alone) | 57                            | 145         | 6.3|
| Imaging (Average for students working in pairs) | 8                             | 172         | 16.7|
| Databasing:                     |                               |             |    |
| Undergraduate student 1         | 73                            | 26          | 3.2|
| Undergraduate student 2         | 90                            | 27          | 2.9|
| Undergraduate student 3         | 118                           | 21          | 2.0|
| Undergraduate student 4         | 61                            | 26          | 3.3|
| Undergraduate student 5         | 118                           | 26          | 2.4|
| Undergraduate student average   | 460                           | 25          | 1.2|
| Master’s student                | 699                           | 47          | 1.8|
| Uploading*                      |                               | 331         |    |

*For nomenclatural verification and uploading, we only recorded total time and number of specimens, so we calculated an overall mean without a standard error (SE).

Fig. 3. Example of a specimen being databased using Specify WorkBench. The form (left) allows for easy entry of the data displayed from the specimen label image (right).
RESULTS

During a period of 32 months, a total of 16,791 Arkansas-collected angiosperm (flowering plant) specimens were verified for nomenclature, annotated, imaged, and databased. Nomenclatural verifications were completed at an average of 150 specimens per hour (Table 1). This number included specimens for which only nomenclatural confirmation was required with no corrective label added to the specimens. Imaging had similar rates and was completed at the average rate of 145 images per hour with one student working alone (Table 1). Two students working together resulted in a slightly faster rate of 172 images per hour. This rate increase with two students working together is not nearly as efficient as two students working separately. For example, if two students worked together for one hour, they would image 172 specimens on average, but if these two students worked independently for one hour each they would image 290 specimens total, an increase of 69% for the same person-time worked. At our fastest we had one student imaging 250 specimens per hour. At our slowest we had one student imaging fewer than 100 specimens per hour.

We databased the 16,791 specimens from January 2013 through July 2014. Five undergraduate students databasing specimens were able to do so at an average rate of 25 specimens per hour (Table 1). All had very similar databasing rates with a low of 21 per hour on average and a high of 27 per hour. The graduate student project leader was able to database at a rate of 47 specimens per hour, 81% faster than the undergraduate assistants. The project leader uploaded all data sets. This was completed at a rate of over 300 specimens per hour.

Based on these numbers, we have estimated the time for one person to database a 20,000-specimen collection at 1150 hours. If one person was working on a digitization effort for 10 h/wk, such a collection could be verified for nomenclature and annotated in 13 wk, imaged in 13 wk, databased in 83 wk, and uploaded in 6 wk. This adds up to a total of 115 wk or about 2.4 yr to complete a 20,000-specimen collection with just one person working one quarter of full time.

Including additional specimens imaged and databased after August 2014, a total of 17,678 Arkansas angiosperm specimens were digitized at the STAR Herbarium, comprising 154 families, 706 genera, and 1485 species. These specimens represent all 75 Arkansas counties, with Craighead (757), Cleburne (645), Lawrence (585), Randolph (584), and Greene (496) being the most species-rich counties represented at STAR (Fig. 4A). Counties with the most accessioned specimens were Craighead (2513), Greene (1552), Clay (1208), Lawrence (1174), and Randolph (999) (Fig. 4B).

DISCUSSION

Our study provides a specific, implemented workflow by which curators can begin digitizing and making their collections available online for minimal monetary investment (Appendix 2). Through the detailed process outlined, we also hope to alleviate
any concerns or uncertainty curators may have about begin-
ning the digitization process by providing concrete examples of
adequate supplies and personnel time commitments. Through
our effort to digitize the flowering plant specimens from Arkansas
at the STAR Herbarium, we have developed a viable workflow
for those at small institutions with limited support resources
and/or competing time commitments. At the beginning of such
a project, it is difficult to predict all of the obstacles that will
be encountered. Many curators worry that they cannot begin digi-
tizing their collections until the nomenclature has been verified
and the collection has been properly organized (iDigBio digit-
ization workshop, personal communication, July 2014). Begin-
ning with nomenclatural verification will give the curator an
idea of what is in the collection and how well curated it is. More-
over, examining specimens provides important time for the cu-
urator or collection manager to determine the best digitization
workflow for the collection. Annotating a collection can also
take different forms. In the case of the STAR Herbarium, we
only updated nomenclature, without verifying accurate identifi-
cation of the specimens. Adding the step of verifying identifica-
tions would considerably increase the time before digitization
can begin, and this step may not be appropriate if the goal is
to make collection information more easily available to taxonomic
specialists who can verify identifications from online image and
database information. Even through our approach of updating
nomenclature, we invested time that could have been spent im-
ageing and databasing label information. Some people may de-
cide to eliminate any predigitization curation steps from the
workflow. In our case, we used the predigitization curation time
to finalize our imaging station purchases and set up.

Obtaining or gaining access to the appropriate imaging and
databasing supplies can seem cost prohibitive. There are best
practices recommendations available (Nelson et al., 2012,
2015) and specific supply lists from iDigBio (https://www.
idigbio.org/wiki/images/8/86/iDigBioImagingGeneralEquipment
Recommendations1_0.pdf) and the New York Botanical Garden
(http://sweetgum.nybg.org/science/digitization.php) that suggest
a range of adequate to top-of-the-line set-ups for quality imaging
and workflow efficiency. These are excellent resources to ex-
perience, no matter your budget, but some imaging station or
database software options may not be realistic given budgetary
constraints. There are advantages, for example, to a full-frame
DSLR camera, but if there is no budget for that camera, a
cropped sensor camera (for one quarter of the price) will work
very well for most herbarium specimen imaging needs. Mini-
mum imaging requirements are (1) a digital camera with at
least 18-megapixel capacity, (2) a stable light source that min-
imizes shadows, (3) an adjustable mount above the specimens
where the camera can be affixed, (4) a computer, (5) an exter-
nal hard drive, and (6) a color separation guide and ruler to be
placed alongside the specimens. Barcode labels for naming
image files and linking images to database records were not
used in this digitization effort, but we strongly recommend
them to create unique identifiers (see details in Nelson et al.,
2015). The ability to be creative and resourceful in piecing
together imaging station components is important for those
without funding.

Once the imaging station is assembled and photographs are
ready to be taken, access to a reliable workforce is an important
consideration. Small collections can complete imaging within
several weeks from a single dedicated imager who is spending
only 10 h/wk on the imaging effort (see Results). One important
consideration in imaging efficiency is the focus of the imager.

We suspect that the main cause of variation in imaging rates was
the quantity of distractions to the person imaging. For example,
the door to the herbarium was often left open to invite visitors
and demonstrate to all passers-by that the herbarium is an area of
active research. This open-door policy was meant to draw peo-
ple in and help to raise awareness for the herbarium. However,
the adverse effect of the policy seems to have been that visitors
distracted imaging personnel. We observed that when few peo-
ple visited, the student working was able to focus entirely on the
task of imaging, and imaging rates were high. When the person
imaging was observed to be interrupted, imaging efficiency was
lower. In our herbarium, the need to raise awareness and encour-
age people to use the herbarium outweighed the need to com-
plete the imaging task as quickly as possible.

Some features of the STAR Herbarium made the imaging
process efficient. The herbarium consists of a relatively small
room (9.75 × 6.7 m), with 21 cabinets of accessioned collec-
tions. In this space, it does not take much time for a student to
retrieve and replace his/her own specimens. Other models have
suggested that it is faster to have two people imaging at once.
One person prepares the specimens and another captures the
images. At STAR, we found that having two people working
together did not increase efficiency. The time required for one
person to do all the work was not that much more than the time
required for two people to image the same number of specimens.
This was a result of the physical size of the herbarium as well as
the imaging workflow. We worked through the cabinets one pi-
geonhole at a time and took care not to disorganize the speci-
mens. The imaging station was made as efficient as possible by moving
the computer keyboard close to the imaging station. Pressing the
“enter” button on the keyboard captured an image. Then, after
the image was taken, the worker quickly switched the imaged
specimen out for another specimen. Students could move
through folders very quickly this way and still take care not to
damage the specimens. If we had verified nomenclature at the
same time as imaging, we could have possibly reduced risk of
damage to specimens by only removing the specimens from the
cabinets once. Yet, we used the preimaging curation step to fi-
nalize the imaging station plan and obtain all the necessary sup-
plies. Also, it is possible that combining the nomenclatural
review and imaging steps may have actually slowed both of
these steps in the process due to combining separate parts of the
workflow.

Databasing specimens through the Specify WorkBench al-
 lows an easy-to-follow form to be set up. Staff, students, or vol-
unteers can use the WorkBench to transcribe label data directly
from specimens or from the images (Fig. 3). A student can be
trained to database specimens with this form in about one hour.
Another advantage is that utilizing the WorkBench allows speci-
mens to be checked before they are uploaded into the main
database.

At the STAR Herbarium, we observed that the undergraduate
students databased specimens at a rate about half that of the
graduate student project leader. There are many potential rea-
sons for this difference. It is possible that the students were not
very invested in the project, but some of the students seemed
very interested in it. It is possible that the typing speed of the
students played an important factor in the students’ ability to
database. However, the students who could not type very well
maintained a similar rate to those who were efficient typists.
We also considered that better training may have resulted in faster
databasing rates if students better understood the herbarium
labels. Yet, the five undergraduate students were all well trained,
and it did not seem to make a difference whether they had previously taken botany courses or how many years they had been in college. The students came from a variety of backgrounds, and yet all databased at relatively the same rate.

The only obvious difference perceived between the undergraduate students and the graduate student was motivation toward the project. The undergraduates seemed to have been motivated by the time required to spend on databasing, and the graduate student was motivated by the number of specimens that needed to be finished. Based on these observations, one consideration for future digitization projects is to compensate students for their time. At STAR, we did not compensate students in this manner.

Detecting specimens incorrectly entered into the database.

To improve the quality of our datasets, the STAR herbarium implemented a new process, which we call ‘quality control’. This process includes the following steps: specimen identification, checking specimen locality, and verifying specimen location. Specimens that are incorrectly entered into the database can be corrected by updating the species name or taxon name. This process is done manually by the curators of the herbarium. The curators check the specimens for accuracy and update the database accordingly.

The most important aspect of this process is the quality control. This process helps to ensure that the data entered into the database is accurate and complete. It also helps to identify any errors in the data that need to be corrected. This process is an important step in the digitization process and helps to ensure that the data entered into the database is accurate and complete.

The curators of the herbarium check the specimens for accuracy and update the database accordingly. This process is an important step in the digitization process and helps to ensure that the data entered into the database is accurate and complete.
Applications in Plant Sciences 2017 5(4): 1600125
Harris and Marsico—Small herbarium digitization
doi:10.3732/apps.1600125

Appendix 1.  Detailed acknowledgments of collaborators, student participants, and funding sources.

| Collaborator/Student | Role in project |
|----------------------|-----------------|
| Christopher Burkhart, Crystal Davis, Elizabeth Etzkorn, Eddie Hampton, Ashley Hart, Rebecca Kennedy, Devon Loerch, Starlene Loerch, Angeline Morris, Hunter Nunally, Emily Panhorst, Mary Rath, Alexander Worn | arkansas State University students and two student volunteers who contributed by updating nomenclature through specimen annotation, imaging specimens, and databasing label data |
| Drew Prescott | Undergraduate student from University of Arkansas at Monticello who provided advice on imaging set up |
| Alyson Gill, Curtis Steele | Faculty members from Arkansas State University Art Department who assisted with camera settings upon imaging station set up |
| Mary Barkworth, Karen Fawley, Marvin Fawley, John Harris, Tracy Klotz, John Pratte, Thomas Risch, Stan Trauth, iDigBio team, Marsico laboratory students | Individuals who supported and promoted our digitization effort from initiation to publication |
| Joe Burleson | arkansas State University College of Sciences and Mathematics Project/Program Specialist who led the effort to create the virtual herbarium |
| Theresa Miller and Andrew Bentley | Specify software personnel who provided database training and technical support |

http://www.bioone.org/journals/Applications-in-Plant-Sciences on 17 Oct 2020
Terms of Use: https://bioone.org/terms-of-use
Appendix

Workflow for herbarium users considering digitization of their collection.

We recommend the following steps to digitize a herbarium:

1) **Organize** all specimens in the cabinets using updated taxonomy and nomenclature and incorporate as many new collections as possible.

2) **Purchase equipment**: The equipment we chose was all purchased for US$1500. This included a Nikon D3200 18-megapixel digital single-lens reflex (DSLR) camera (Nikon, Melville, New York, USA) with an 18–55-mm zoom lens (US$760), new lights (Bencher Copymate II fluorescent copy lights; Bencher, Antioch, Illinois, USA; US$670) for an existing copy stand (Bencher Copymate II), a Kodak color separation guide (Kodak, Rochester, New York, USA) and grayscale ruler (US$50), and an extra camera battery (Nikon EN-EL 14; US$20). The side fluorescent lights are sufficient, but the camera settings must be carefully manipulated to reduce shadows. The computer used for digitization was already present in the herbarium at the start of the project. We used only open-source software for this project. The Nikon View NX2 software was used for remote capture of images.

3) **Image** each specimen individually and develop efficient imaging protocols. We set our camera settings easily within the software. For optimal lighting, few shadows, and highest quality images, we set camera settings to the following: ISO 100, Shutter speed 1/200, Aperture F/4.0, White Balance Auto, Exposure Comp. 0, Compression Raw + JPEG (Fine), Metering Mode Multi-pattern.

4) **Database**: We used Specify 6 (Specify Software Project, Biodiversity Institute, University of Kansas, Lawrence, Kansas, USA) and primarily uploaded data through the Specify WorkBench. This allowed us to create an easy-to-use form for students to type label data into. The WorkBench allows data to be transcribed in individual lines similar to an Excel spreadsheet, with corresponding images attached to each line. Collections with little or no IT support may consider Symbiota (http://symbiota.org/docs/) as an alternate database platform.

5) **Back up the data**: Keep at least two backups in different locations. We back up our data on a university server as well as an external hard drive. As soon as possible, send data to an online portal such as Symbiota, iDigBio (https://www.idigbio.org/), or the Global Biodiversity Information Facility (GBIF; http://www.gbif.org/).

6) **Combine** all data to make it accessible to the scientific community and public through an online database. We recommend GBIF and iDigBio as potential data repositories.