Royal Botanic Gardens
Kew

State of the World's Plants and Fungi

2026

The Critically Endangered blue amaryllis (*Worsleya procera*) grows in seasonally dry, tropical conditions in Brazil.

State of the World’s Plants and Fungi 2026

The Digital Biodiversity Revolution

Cycas revoluta growing in Kew's Agius Evolution Garden, London, UK.

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Introduction: The digital biodiversity revolution

As we mark the tenth anniversary of Kew's *State of the World's* report series, it is worth reflecting on the incredible advances in generating and sharing biodiversity data that have been achieved in this short period of human history. Thanks to the meticulous work of thousands of contributors, over 145 million specimens of plants and fungi have transcended the confines of their storage cupboards and boxes to gain full light on the global digital stage. They are now accessible to anyone, anywhere with an internet connection.

The importance of what has been achieved so far cannot be overstated. This vast, interconnected, global metacollection of digitised specimens is an expanding source of information for understanding the geographical distribution of species in the past, present and future. Linking this biodiversity information with other measurements and models representing key environmental threats, such as climate change, agricultural expansion and deforestation, is enabling us to not only document changes but to take timely action, designing the most effective ways to safeguard biodiversity for the wellbeing of people and all life on Earth.

SUPPORTING SCIENTIFIC ENDEAVOURS

Digitised specimens and the wealth of information associated with them are already helping many scientists to do their jobs better, faster and more collaboratively. These instantly accessible resources are now regularly used by taxonomists to identify and describe new species; by evolutionary biologists to select materials for genomic studies; by conservationists to identify threats to species and assess their risk of extinction; by companies to assess and mitigate the impact of development projects; and by governments to track their progress towards global conservation commitments.

And beyond what digital biological collections are revealing about the species they represent, they are also illuminating elements of human history and behaviour – how previous scientists went about collecting these specimens and how their combined activities contributed to the deep social and economic inequality that characterises our societies today. Who were the people behind botanical and mycological exploration? And how have motivations for, and approaches to, collecting changed over time? These are questions that digitised specimens are helping to address.

In *State of the World's Plants and Fungi 2026*, we report on the latest research using digital specimens, including studies utilising the power of artificial intelligence (AI). The report is based on, and co-released with, a virtual special collection of academic articles entitled 'Harnessing the benefits of specimen digitisation', published in the scientific journals *New Phytologist* and *Plants, People, Planet*. More than 400 experts from 40 countries contributed to this body of work. The summary of their findings presented here is enriched with interviews and covers a wide range of topics, geographies and taxonomic groups. It also touches on how plant and fungal science can best embrace the digital biodiversity revolution in a fair and equitable way.

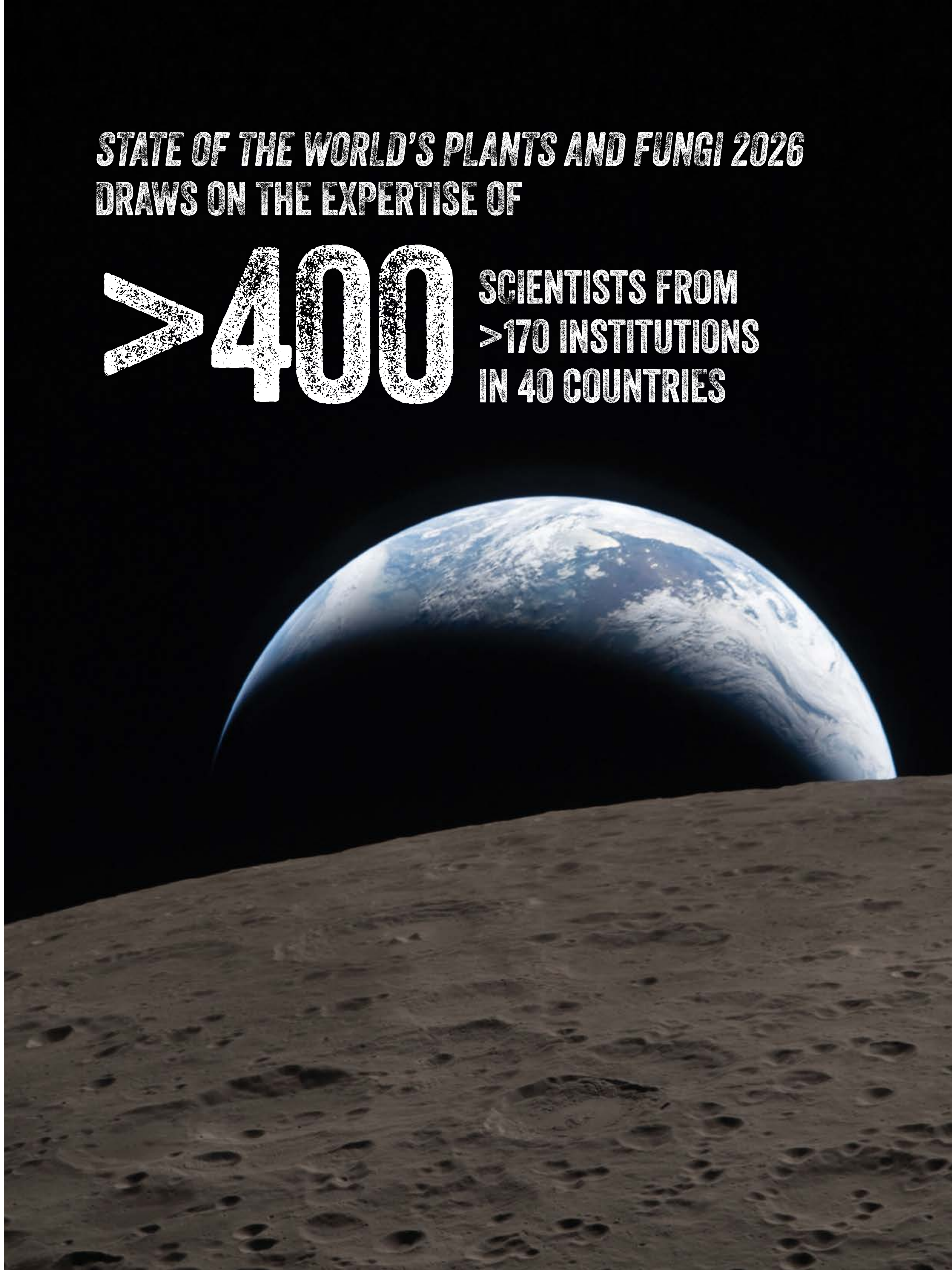
A DIGITAL TRIUMPH

The publication of this report coincides with a major milestone for Kew: the complete digitisation of our Herbarium and Fungarium – together representing one of the world's largest collections of plants and fungi. This effort required the biggest investment in a single scientific project in Kew's 267-year history, with the deployment of over 100 digitisers, curators and other members of staff, along with 42 on-site volunteers and 1,500 remote contributors.

This mass digitisation programme built on the learnings generously shared by several other major collections, such as the herbaria in Leiden (Naturalis), Meise (Meise Botanic Garden), Paris (Muséum national d'Histoire naturelle), Edinburgh (Royal Botanic Garden Edinburgh), Gothenburg (University of Gothenburg), Washington (Smithsonian National Museum of Natural History) and London (Natural History Museum). The resulting digital resources are intended not only to benefit the global community in general but also to support specific data repatriation projects in source countries, exemplified by Kew's partnerships in Brazil, Guinea and Madagascar. Our digitised specimens have already been downloaded by users in more than 140 countries.

Notwithstanding the feats accomplished so far, much work remains to be done. An urgent task is to ensure that the information already digitised is appropriately curated and enriched in a way that meets the full needs of science and conservation. For example, many digitised specimens from Kew and other collections still lack high-resolution geographical coordinates (latitude and longitude). This shortcoming risks precluding detailed analyses of

THIS SIXTH EDITION OF KEW'S *STATE OF THE WORLD'S* SERIES SHOWS HOW DIGITISED SPECIMENS ARE TRANSFORMING PLANT AND FUNGAL SCIENCE.

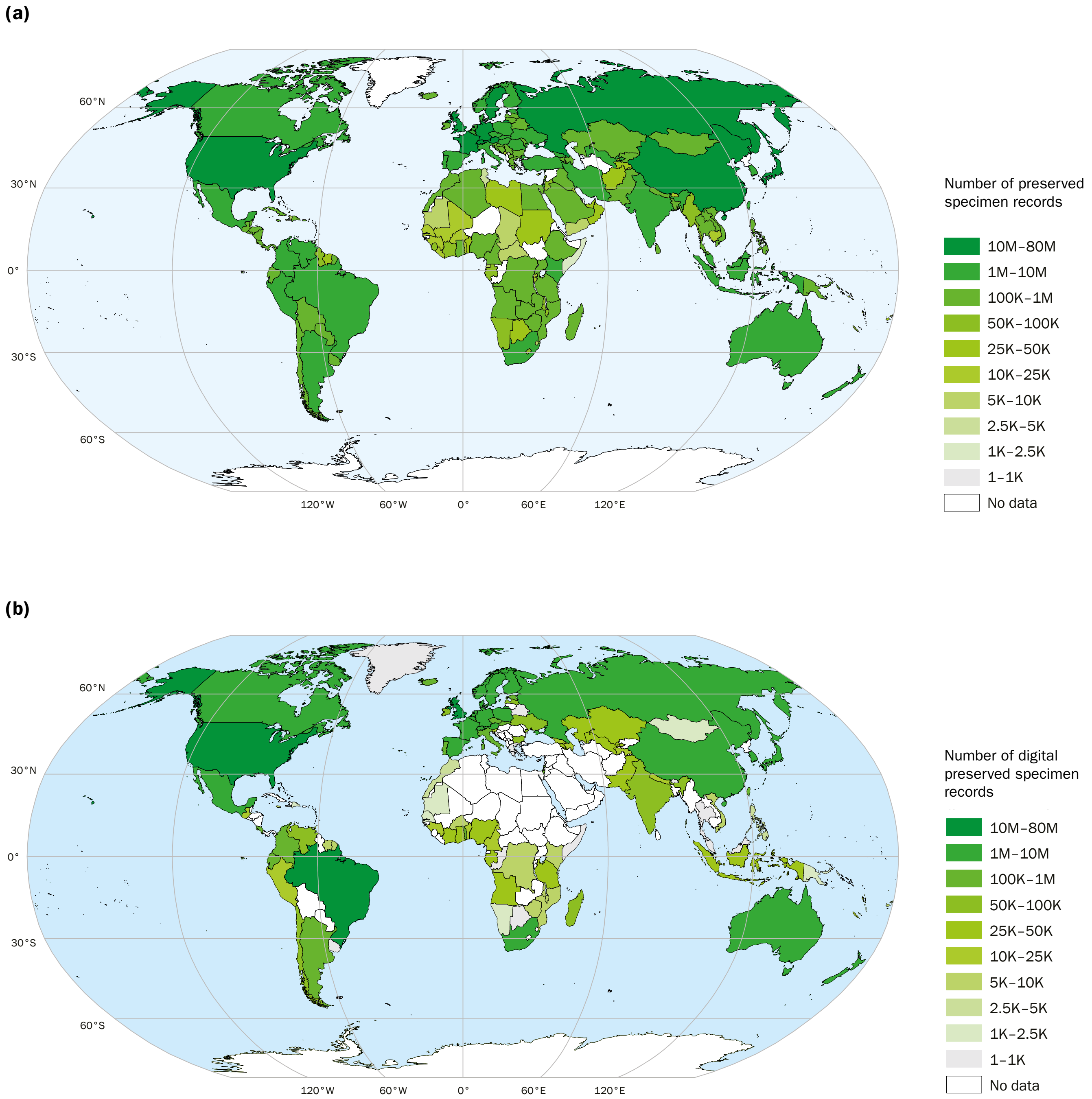


***STATE OF THE WORLD'S PLANTS AND FUNGI 2026* DRAWS ON THE EXPERTISE OF**

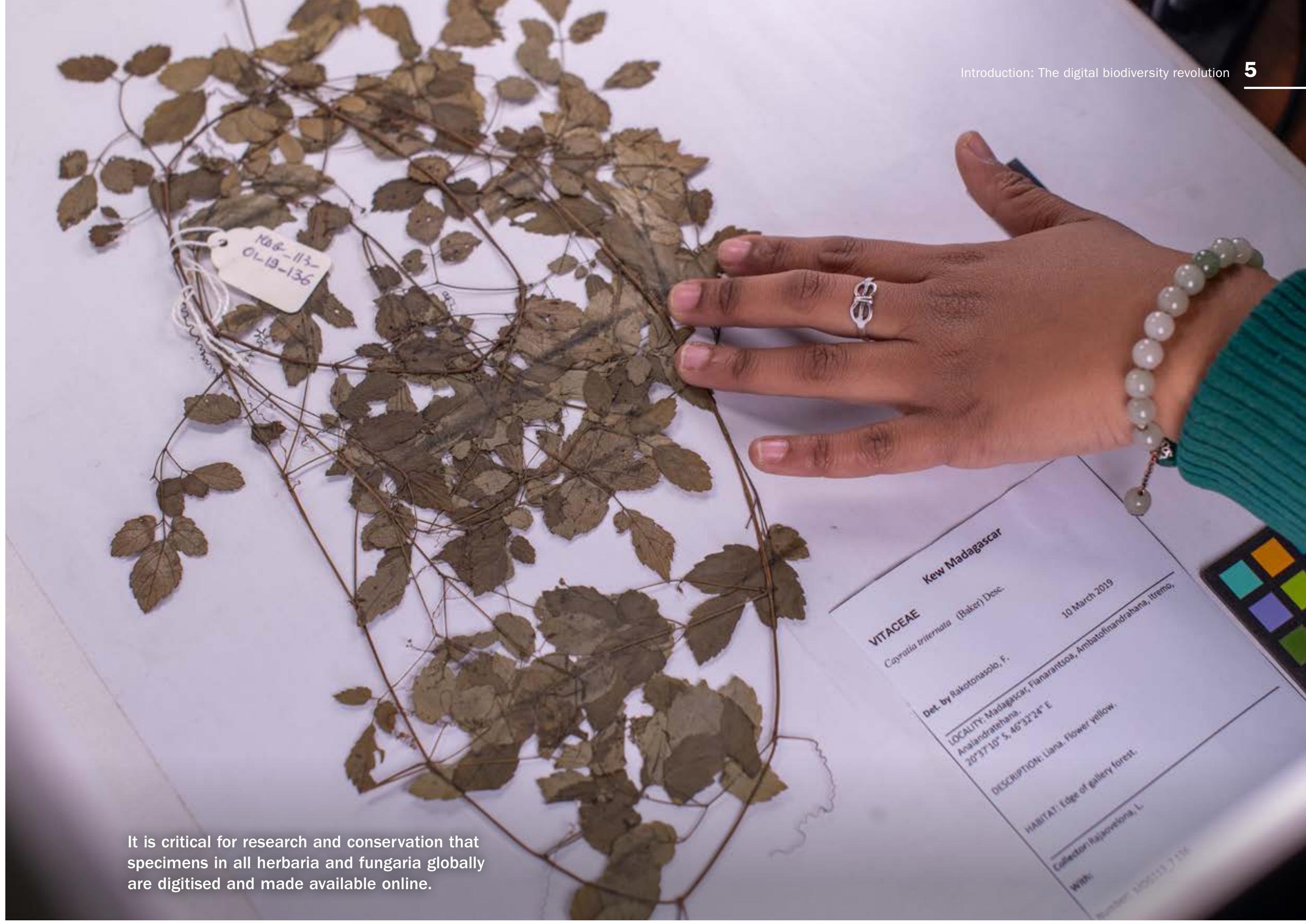
>400 SCIENTISTS FROM >170 INSTITUTIONS IN 40 COUNTRIES

FIGURE 1: The global distribution of preserved plant and fungal specimen records

(a) The distribution of preserved plant and fungal specimens recorded in the global directory Index Herbariorum, mapped by the country or territory holding the specimens. **(b)** The number of digital preserved plant and fungal specimen records mobilised via the Global Biodiversity Information Facility (GBIF), mapped by country or territory of data provider. Not all herbaria are represented in Index Herbariorum and not all countries provide data to GBIF (see Chapter 1 and Chapter 11). Widening the coverage will greatly enhance knowledge of global plant and fungal diversity.



Data from Thiers, B. (2026). *The World's Herbaria 2025: A Summary Report Based on Data from Index Herbariorum;* and from the Global Biodiversity Information Facility (www.gbif.org); both accessed 18 March 2026.



It is critical for research and conservation that specimens in all herbaria and fungaria globally are digitised and made available online.

responses to climate change and the planning of effective conservation interventions. While manually extracting geospatial information from specimen labels is notoriously time-consuming, new methods powered by AI – under expert supervision – could speed up this process.

We must also empower the world's 'silent' collections to speak. These hold important information that has not yet been digitised or included in global databases. There are at least 4,000 active herbaria (covering plants and fungi) worldwide, most of which have digitised relatively few specimens, if any. Unless sufficient resources are urgently allocated to them, we will not be able to meet the goals of the Global Biodiversity Framework, and we will risk losing many species to extinction that we could have safeguarded. If this happens, we will also miss out on many socio-economic benefits, such as new medicines and nature-based solutions to climate change and food security.

We know that investment pays off. In Kew's Today's Flora for Tomorrow project, funded entirely through philanthropy, we have worked with partner organisations in Madagascar to mount and curate 15,000 specimens of plants and fungi at the Tsimbazaza Herbarium, digitise over 37,000 specimens, carry out 780 global extinction risk assessments, and train many students and professionals in the process. It is projects like this that, one by one, are building the global metacollection. We hope that more funders and organisations will be inspired by such efforts and be willing to replicate them, particularly in low-income, highly diverse tropical countries. In doing so, they will be helping to drive forward the digital biodiversity revolution from which all of humanity stands to benefit.

I now invite you to read this report to learn more, and wish you an enlightening and enjoyable journey through the digital biodiversity world.

Alexandre Antonelli
Executive Director of Science,
Royal Botanic Gardens, Kew

THIS VAST, DIGITAL, GLOBAL METACOLLECTION IS AN EXPANDING SOURCE OF INFORMATION FOR UNDERSTANDING BIODIVERSITY.

THE FLORAL AND FUNGAL RENAISSANCE

In this chapter, we learn: how digitised plant and fungal specimens could transform biodiversity science; where specimen collections are being digitised around the world; what 'silent herbaria' are and why they matter; and that accurate curation of physical specimens remains vital in a digital world.

THE WORLD'S LARGEST BIODIVERSITY PORTAL HOSTS DATA ON

>145M

PRESERVED SPECIMENS OF PLANTS AND FUNGI

South Africa is among the pioneers of specimen digitisation.

THE DIGITISATION OF PRESERVED PLANT AND FUNGAL SPECIMENS IS USHERING IN A NEW ERA OF SCIENTIFIC DISCOVERY.

Preserved specimens of plants and fungi may seem an unlikely starting point for a scientific revolution. But these biological artefacts – collected by naturalists down the centuries and stored as dried or otherwise preserved specimens within botanic gardens, museums, universities and other research institutes – contain an untapped wealth of information. Part of continuously expanding, dynamic collections, these specimens retain valuable information on the climates they thrived under when collected, their genetic make-up, the animals they interacted with and the diseases they succumbed to. Meanwhile, their labels show who collected them, when and from where, and how their classifications have been updated over time.

Programmes have been underway since the 1970s to put digital versions of specimens online so that anyone with an internet connection can study them remotely. Today, with artificial intelligence (AI) showing promise for rapidly analysing specimen images and data, it is clear that digitising all the world's preserved biological specimens – to create a virtual global warehouse of time-stamped biodiversity data – could transform understanding of biodiversity loss and climate change, and pave the way to resolving these seemingly intractable crises.

'If all specimens are digitised and available online, then we will be able to make more accurate inferences about biodiversity,' enthuses Daniel Zhigila, a postdoctoral fellow in taxonomy at the Alexander von Humboldt Foundation in Germany. 'Conservation planning will be better informed, and we will feel science is democratised. Researchers will have access to materials, regardless of their location. So, there will be less bias in biodiversity science, and there will be greater accuracy in our predictions, and in our climate-change modelling.'

This dream is moving closer to reality. Many countries have now embraced digitisation – by scanning or photographing specimens, or at least capturing the information from their labels – on small and large scales. Subsequently, organisations have emerged to aggregate the resulting digital specimens into vast online platforms of biodiversity information covering all kingdoms of life. National resources include the USA's Integrated Digitized Biocollections (iDigBio) and the Atlas of Living Australia. There are also portals focused on particular groups of organisms, such as that of the Consortium of Bryophyte Herbaria, covering mosses, liverworts and hornworts, and the Mycology Collections Portal for fungi. The world's largest biodiversity data portal is the Global Biodiversity Information Facility (GBIF), which is amalgamating digital specimen information about all life on Earth and making it freely available online.

When it comes to plants and fungi, the diversity of the former is far better represented in physical – and therefore digital – collections than that of the latter. Although fungal species outnumber plants by at least a factor of five, and possibly closer to ten, plants were collected far more intensively historically. One contributing factor is the elusive nature of fungi, which live within soil, wood and other substrates, often staying invisible until they produce their spore-dispersing structures, such as mushrooms, cups and puffballs. Fungi are also more challenging to preserve and digitise than pressed plant specimens, but the data from their labels denoting their names, locations, habitats, sporing times and other aspects of ecology are easily captured and can themselves reveal patterns and trends on a large scale. Moreover, a new and accelerating wave of fungal study is underway, spurred on by interest in the properties and potential uses of fungi and the ease with which unknown species can be unveiled, for example through analysing the DNA of soils. Mycologists are making great strides, too, in sequencing DNA from preserved specimens – even that of 'endophytic' fungi dwelling within the preserved leaves of plants – and from very old and degraded material (see Chapter 4).

THE INCREASING SCOPE OF COLLECTIONS

When biological specimens were first gathered in reference collections centuries ago, they were primarily used to identify, name and classify organisms – the field of taxonomy. Herbaria (essentially libraries of preserved plants), fungaria (the equivalent for fungi, often integrated into herbaria), and other biological collections became important repositories of 'types', the definitive reference specimens attached to scientific names. Types and related specimens remain crucial for comparing and contrasting the characteristics of species to determine relationships between them and to decide whether a species is new to science (see Chapter 3). Biological collections have also long underpinned the creation of monographs (works describing a particular taxonomic group), checklists (lists of the species found in a delineated area) and Floras (descriptive works on the wild species of a specific region).

As digitisation has made it easier to analyse multiple specimens from different sources, the scale and scope of what is possible has grown. Researchers now routinely use the vast data resources associated with herbarium and fungarium specimens to map shifts in species' distributions over time, assess how the characteristics of plants and fungi are changing in response to climate change, and track population data to quantify extinction risk and inform conservation efforts. With advances in scanning technology allowing accurate 3D image capture, some institutes are now digitising pollen specimens, too, opening up opportunities to look in fine detail at their intricate structures and how they relate to diversity and function (see Box 1, overleaf). Other microscope slide collections, including wood sections, are also being captured.

IF ALL SPECIMENS ARE DIGITISED AND AVAILABLE ONLINE, WE WILL BE ABLE TO MAKE MORE ACCURATE INFERENCES ABOUT BIODIVERSITY.

FORGING A NEW PATH

The move to create digital facsimiles of physical specimens has provided the opportunity to overcome the uneven and often inequitable distribution of preserved natural history resources – particularly plants – resulting from historical patterns of collecting. From the 15th century, European nations expanded by forcibly colonising lands in the Global South, eventually sending administrators, medics and naturalists abroad with instructions to collect and bring back specimens. Early on, they were motivated to take control of lucrative spice trading routes but subsequently sought any species that might be potentially useful as foods, medicines or materials, or that could be horticulturally valuable, so they might outcompete their colonial rivals. With Europe well served by institutions, botanical experts and printing presses from the 17th century onwards, these actions consolidated scientific knowledge in the Global North. So, until work to digitise specimens began, researchers working in the Global South frequently had to either travel to European herbaria to look at specimens from their own nation or request specimens be sent on loan by post.

Brazil, the largest and most biodiverse country of the Global South – with approximately 50,000 known native plant and fungal species – is today a trailblazer in digitally repatriating Brazilian specimens held in foreign herbaria, as well as in digitising its own botanical and mycological collections. Over the past two decades, it has developed an integrated set of online systems, deeply rooted in physical collections, comprising: a collections management system containing specimens from 115 Brazilian herbaria; a 'virtual' herbarium including images of specimens held in Brazil, the USA and Europe; a taxonomic database; and a digital cataloguing tool for Brazilian protected areas (see Figure 1). Its success in creating these interlinked products is underpinned by the collaborations it has forged between bioinformaticians skilled in applying computer science to manage and analyse biological data, and taxonomists with expertise in naming, describing and classifying living organisms. The bioinformaticians have been able to build and hone platforms well matched to the needs of the end-users, and the taxonomists have populated this bespoke resource with knowledge extricated from specimens accumulated over four centuries.

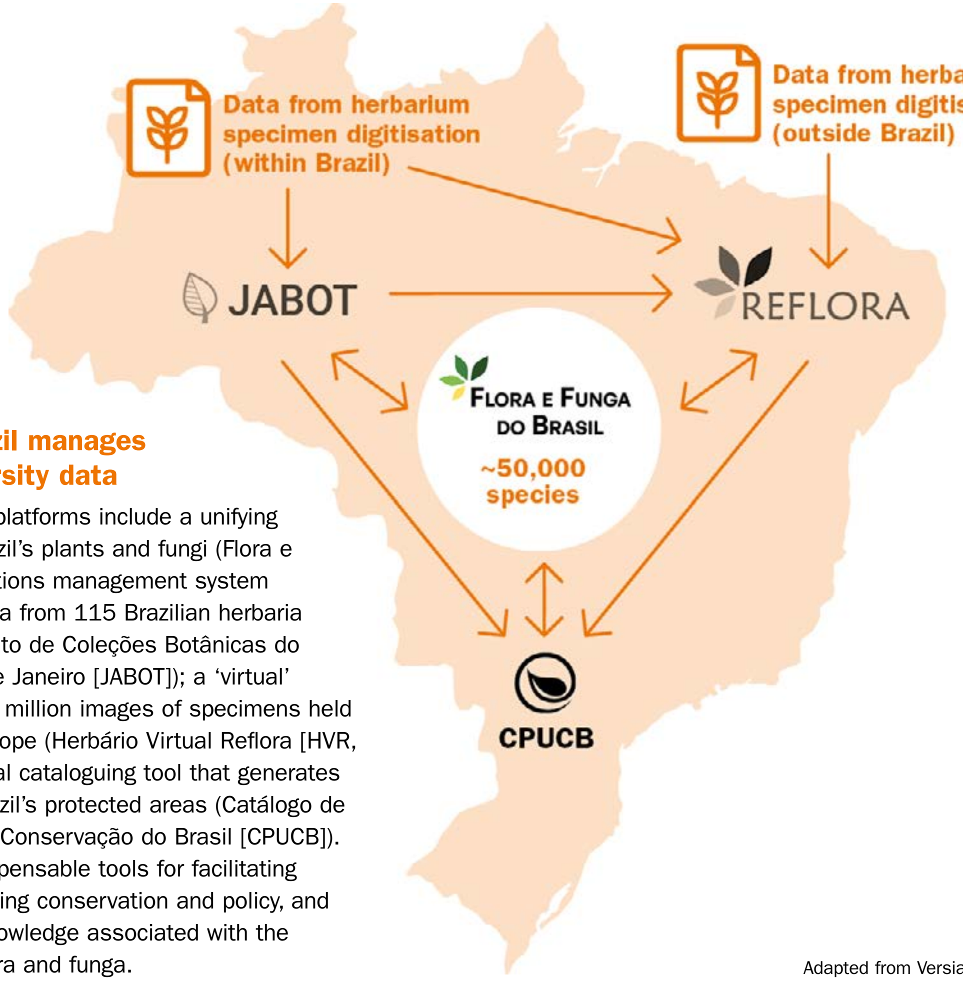
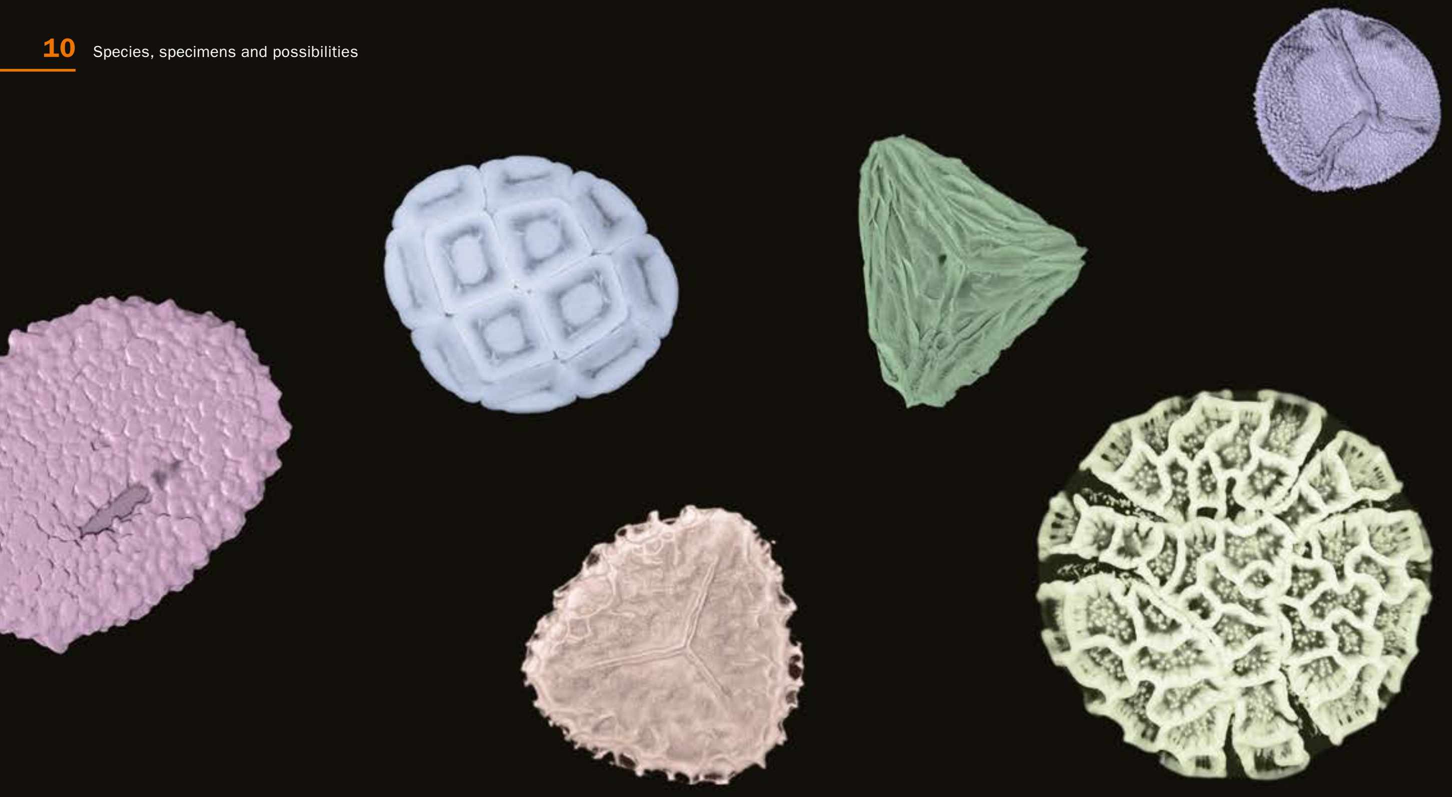


FIGURE 1: How Brazil manages its digitised biodiversity data

Brazil's integrated online platforms include a unifying directory of names of Brazil's plants and fungi (Flora e Funga do Brasil); a collections management system aggregating specimen data from 115 Brazilian herbaria (Sistema de Gerenciamento de Coleções Botânicas do Jardim Botânico do Rio de Janeiro [JABOT]); a 'virtual' herbarium with nearly five million images of specimens held in Brazil, the USA and Europe (Herbário Virtual Reflora [HVR, or REFLORA]); and a digital cataloguing tool that generates lists of the species in Brazil's protected areas (Catálogo de Plantas das Unidades de Conservação do Brasil [CPUCB]). These have become indispensable tools for facilitating scientific research, informing conservation and policy, and sharing resources and knowledge associated with the country's megadiverse flora and funga.

Adapted from Versiane et al. (2025)



BOX 1: Bringing tropical pollen into the light

What makes someone decide to digitise 35,000 microscope slides of pollen grains? In the case of palynologist (pollen expert) Carlos Jaramillo, currently leading such a project at the Smithsonian Tropical Research Institute (STRI) in Panama, it came down to money. He valued the effort involved in amassing the collection – from botanists identifying and collecting plants in the field, to herbarium curators assessing specimen taxonomy, and palynologists obtaining pollen from plants' anthers and creating microscope slides – at USD 40 million. Not digitising the slides would make it virtually impossible for people to use the collection, which was locked away in several cabinets at the Institute, where it was deteriorating. And this would mean that the resources put into compiling the collection would have been largely wasted.

Jaramillo had also been forced to spend two years in Europe during the Covid-19 pandemic, during which time he had seen advanced microscope technology in use in medical institutes in Montpellier, France. He wondered whether computer-controlled microscopes could scan the fine resolution of 3D pollen grains in the same way as they could digitally recreate cancer cells. It turned out they could. He decided to digitise the STRI pollen collections – in total spanning more than 18,000 living and 150 fossil species – using three kinds of imaging: brightfield, differential interference contrast (both optical microscopy techniques) and confocal microscopy (which uses lasers to capture many layers and create 3D images from them).

The team comprised 50 palynologists working in rotation – 'to stop them going crazy!' says Jaramillo. For each of the extant taxa (a taxon is a unit of classification, such as species or genus), they imaged 20 pollen grains with the brightfield and differential interference contrast but only five grains with the confocal imaging, as the latter took much longer. They also digitised 50 grains for each of the most abundant fossil taxa. The collections had to be curated during the process, as many names had changed since the specimens were originally collected; the largest of these, the Graham Pollen Collection of 23,000 slides, had been initiated in 1954. In total, these dedicated experts photographed 800,000 pollen grains, over 2.5 years, with the imaging process meticulously planned and honed, as 'every additional second added up to three months' work when replicated across the collection,' says Jaramillo.

In 2019, volunteers – including farmers in North Dakota seeking to while away the time when snowed in during winter – had helped to transcribe the information on the index cards associated with the slides. The next step will be for Jaramillo and his team to work out the best way for people to access the digital pollen collection, including via data aggregators such as the Global Biodiversity Information Facility. With the entire collection amounting to 50 terabytes of data, this may involve providing low-resolution images with links to download high-resolution versions for slides of interest.

The final task will be to use artificial intelligence to classify unknown pollen grains, using the new digital pollen library as training data. This work will be undertaken with the Smithsonian Office of Digital Innovation and external partners such as the University of Illinois, a pioneer of this approach. Once the project is complete, the collection will be available for use. Potential applications include evolutionary and ecological studies, forensic investigations, and research on honey, allergies and CO_2 sequestration. The project provides a blueprint for undertaking similar digitisation efforts across the world, yielding further benefits. In time, the collection could generate returns that greatly exceed its original USD 40 million valuation.

DEDICATED EXPERTS PHOTOGRAPHED 800,000 POLLEN GRAINS OVER 2.5 YEARS.

DIGITISING SOME OF THE SMALLER, LOCAL COLLECTIONS HAS REVEALED SPECIES NEW TO SCIENCE THAT WERE ENTIRELY ABSENT FROM LARGER COLLECTIONS.

'Not only have these resources highlighted where gaps in collections exist, such as in the Amazon rainforest, but digitising some of the smaller, local collections has revealed species new to science that were entirely absent from larger collections,' explains Paula Leitman, Reflora Coordination Assistant at Rio de Janeiro Botanical Garden.

Another biodiverse country, South Africa – with more than 20,000 native plant species – is also a pioneer of digitising herbarium collections. The southern part of the country contains the exceptionally biodiverse Cape Floral Kingdom, where more than 9,000 plant species occur in an area of just 90,000 km^2. As far back as 1970, the country's Botanical Research Institute (now the South African National Biodiversity Institute, SANBI) developed a database to capture herbarium specimen label information. Then, in 1998, SANBI initiated the six-year Southern African Botanical Diversity Network project, aimed at developing a circle of professional botanists within each of the region's ten countries. Among other tasks, the network digitally transcribed 450,000 herbarium specimen labels. In South Africa today, SANBI manages three of the nation's biggest herbaria, including the National Herbarium of South Africa in Pretoria, which holds 1.2 million specimens. Meanwhile, the Natural Science Collections Facility – a network of institutions including SANBI and many other natural history organisations – is enhancing existing specimen collection databases and making them openly available online.

'We have numerous herbaria in South Africa, including many small private collections which may have unique specimens,' says Hester M. Steyn, Senior Scientist at SANBI. 'It's very difficult to say definitively what the state of digitisation is across all of them. For the SANBI herbaria, I would say the proportion of specimen labels transcribed would be around 70% to 80%. And currently there's a project to digitise the images of specimens in the National Herbarium, but that's a long-term project that will take a while. The situation is likely to vary among the smaller herbaria; even if their labels or specimens have been digitised, they might be on databases that are not accessible.'

AN EXPANDING RESOURCE

The aggregator GBIF is among organisations striving to widen access to digital specimen data as they become available. A network of around 2,700 public and private organisations contribute to GBIF, which receives data from plant, fungal, animal and microbial specimens and makes these accessible and searchable through a single portal. At the time this report went to press in May 2026, GBIF held over 145 million plant and fungal specimen records, of which 70 million had known coordinates. The facility is constantly expanding; all 7.4 million herbarium and fungarium specimens held at Kew have now been uploaded (excluding those with restrictions), with Rio de Janeiro Botanical Garden and SANBI also among many ongoing contributors. However, while major scientific institutions around the world are key to driving global digitisation progress, it is critical that specimens from less well-resourced herbaria and countries are also included in GBIF (and similar data aggregators), to present as accurate a record of past and present biodiversity as possible, and for biodiversity research to be truly inclusive. As increasingly larger numbers of scientists embrace using such resources in biodiversity studies, understanding where gaps and biases currently exist so that research findings can be tempered accordingly will be vital (see Box 2, overleaf).

QUESTIONING THE DATA

In 2024, the question of how to understand the extent and quality of data on GBIF was preoccupying Daniel Zhigila during his postdoctoral fellowship at the Harvard University Herbaria in Massachusetts, USA. He and his colleagues had discussed a paper that had concluded that South America harbours a greater diversity of flowering plants than Africa. The study had relied on data from GBIF and GenBank (a genetic sequence database). Zhigila and colleagues wondered if the perceived difference between the two continents might be influenced by the scarcity of data from Africa and decided to investigate.

They felt Nigeria would provide a good case study, as when Zhigila had been deciding what to study after his undergraduate degree there, he had opted for plant taxonomy after learning there was not a single plant taxonomist in the whole of north-eastern Nigeria. The team took three approaches. The first was to assess the extent to which Nigerian herbaria were connected to global biodiversity research networks. The second was to investigate how much of the herbarium data from Nigeria had been mobilised online through digitisation. And the third was to assess how conclusions made about the distribution of biodiversity might differ when using specimens from in-country herbaria versus those held in herbaria outside Nigeria.

The starting point was to consult Index Herbariorum (IH) – a global directory of the world's herbaria and their staff, through which taxonomists connect and exchange specimens. The scientists learned that of 801 herbaria registered since 2016 (from which point herbaria had been able to self-register), 326 (41%) were located in the Global South, with the majority being in South-East Asia or South America. Only 6% were in Africa. When they conducted an independent survey of herbaria in Nigeria, they found that 73% of these facilities were not even listed in IH. Not only that, but more than 90% of herbaria in the country were not yet digitised. This essentially rendered them 'silent', greatly hindering their ability to contribute to the global discourse on biodiversity (see Figure 2a).

Nigeria is highly biodiverse, with around 8,000 native plant species. Between 1861 and 1960, the country was under British rule, and it suffered a similar fate to other colonised nations in that many of its plant specimens were taken out of the country. However, over the past 25 years, the number of herbaria in Nigeria has increased at a rate exceeding the global average. The researchers found that although 20% of in-country herbarium specimens had been digitised, only 7% were accessible through global aggregators such as GBIF. They also found that 97% of all digitised specimens collected in Nigeria since 2000 were stewarded by local herbaria and provided greater spatial and more recent temporal diversity than external collections, both within each year and across recent decades. For example, when they mapped the distribution of the medicinal plant *Cnestis ferruginea* using in-country versus out-of-country specimens held on GBIF, they found the inferred distribution of the species using only specimens held in herbaria outside Nigeria encompassed just 20% of the area predicted when using the in-country data (see Figure 2b and 2c).

'The most important finding from this work, to me, is that biodiversity science is hampered when these kinds of silent herbaria are not included in biodiversity studies,' says Zhigila. 'There could be incorrect inferences made about the global distribution of plants.'

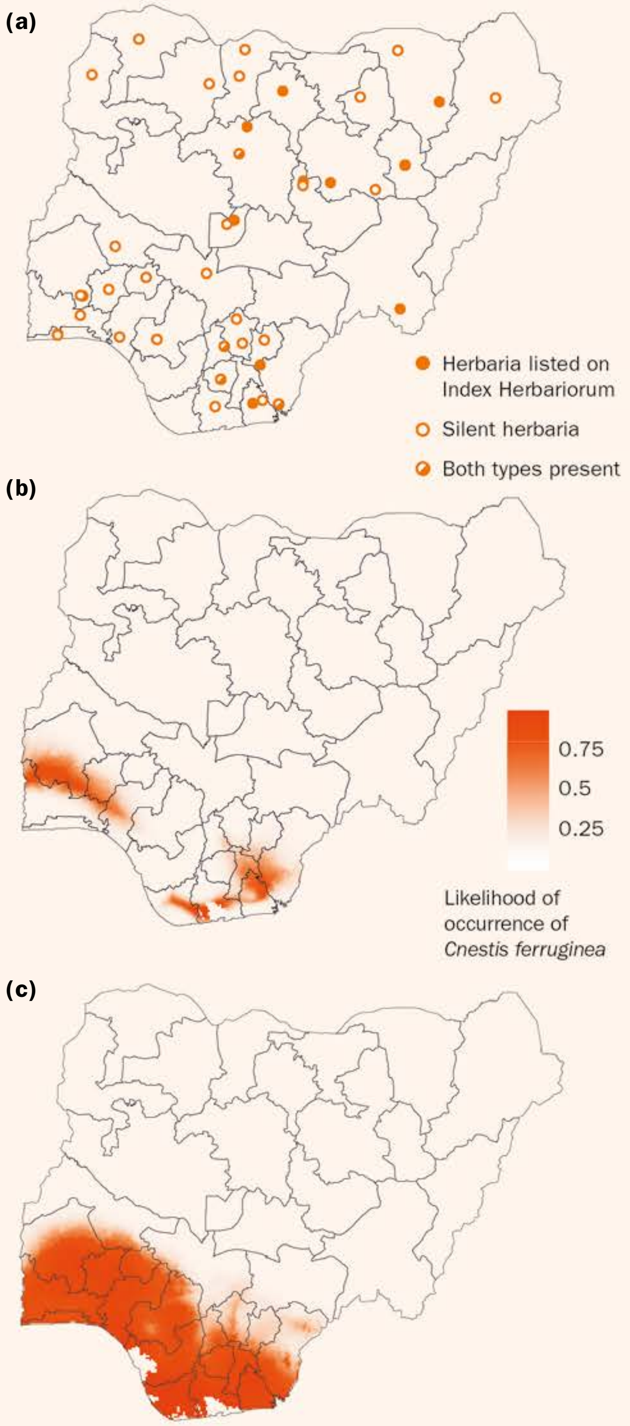
ENSURING ACCURACY IN DIGITAL ANALYSES

Aside from IH being valuable in connecting herbaria and taxonomists globally, it is also used by scientists researching herbaria. So, the more facilities it includes, the greater the accuracy of knowledge about both herbaria and the progress being made towards the goal of universal specimen digitisation. With the value of digital herbarium specimens largely dependent on the accuracy and accessibility of the data captured from the physical specimens, one study sought to see how curation practices – such as acquiring, identifying and updating the taxonomy of specimens, as well as maintaining and digitising collections – differed among different-sized herbaria. The lead author, Celia Aceae, was at the time studying for a master's degree in the Biodiversity and Taxonomy of Plants, jointly run by the University of Edinburgh and the Royal Botanic Garden Edinburgh. During her studies, she had read a review of tropical plant collections led by her colleague Zoë Goodwin, which concluded that more than half of herbarium specimens were likely to have incorrect names and that nearly one third of duplicate specimens (those collected from the same plant, or another individual presumed to be of the same species, at the same time) had different names in different herbaria.

Wanting to better understand just how herbaria curated the data associated with their specimens, Aceae decided to conduct a survey of herbaria listed in IH. Those that responded (representing 3,500 herbaria) were widely spread, but there were few or no responses from China and many African countries. Aceae and her co-authors categorised the herbaria by size on the basis of how many specimens they contained: small (100–100,000); medium (100,001–1,000,000); and large (1,000,001–8,000,000).

FIGURE 2: Nigeria's silent herbaria

(a) The large number of unfilled circles on this map shows the extent of Nigeria's 'silent' herbaria – those that are unknown to or underused by the global botanical community but that hold important biodiversity data. Silent herbaria steward approximately 70% of the 560,000 specimens housed in the country. Drawing conclusions about Nigeria's biodiversity without including all available specimen data has the potential to skew research results. For example, **(b)** shows the inferred distribution of the medicinally important and frequently collected species *Cnestis ferruginea* using only records of specimens held in herbaria outside Nigeria, while **(c)** maps the distribution of the same species using only in-country specimens, showing a far more widespread distribution.



Adapted from Zhigila et al. (2025)

Costa Rica hosts a large diversity of fungi, including (clockwise from top left) the genera *Aseroe*, *Rigidoporus*, *Phyllachora* and *Leotia*.

BOX 2: Getting the measure of Costa Rica's fungi

Despite their ecological importance, tropical fungi are severely underrepresented in global databases and research. A team of researchers in Costa RIca, a megadiverse tropical country, sought to fill in some of the gaps. By comparing digitised records of fungal specimens collected in the country with species that had been reported in published literature, they increased the number of known species in Costa Rica by almost 20% (from 5,676 to 6,789 species), as well as revealing other important aspects of tropical fungal biodiversity.

'Tropical countries like Costa Rica harbour extraordinary fungal diversity, yet much of it remains poorly documented,' says lead author of the study Melissa Mardones, Curator of the Fungal Collection at Herbarium USJ of the University of Costa Rica, where she is also a professor. 'Digitised collections allow us to uncover patterns of biodiversity that would otherwise remain hidden.'

Mardones and colleagues collated 78,333 online and physical records spanning 170 years, with 83% obtained from two major collections in Costa Rica and 17% from 38 external sources. The dataset included all major fungal groups and contained 2,862 recorded species. Using standard methods to estimate total fungal diversity based on the ratios of plants and arthropods to fungi, and DNA studies, the expected species diversity in the country ranged from 6,911 to 40,373. This meant the collections represented at most 41% of the estimated total species diversity in the country, or as little as 7%. It highlighted just how much more there is to learn – as is the case for fungi globally.

Costa Rica hosts diverse ecosystems bordering both the Pacific and Atlantic coasts. Distribution mapping revealed species richness to be highest in forests in tropical lowlands and on cooler, moist mountainsides. Meanwhile, comparing climatic variables with patterns of mushroom emergence suggested that precipitation had a key influence on the timing of fungal reproduction. Despite gaps and biases in the source collections, the study was able to develop a critical baseline of historical and ecological data, which will be invaluable for future research and conservation.

Over 50% of *Camellia* specimens analysed during a master's project had incorrect or outdated names.

The responses confirmed what her studies had led her to suspect: that the practices and standards used in curating plant specimens, the tools and approaches employed for identifying unknown plants, and digitisation efforts varied wildly between herbaria of different sizes.

For example, only 53% of large, 27% of medium and 45% of small herbaria reported following a single institutional protocol when curating. Moreover, the majority of herbaria said they only became aware of new taxonomic publications when actively searching. Large herbaria relied on networks of curators, researchers and taxonomists to hear of updates, while small and medium-sized facilities were more likely to perform regular literature searches, and rely on word of mouth and social media. Changes in taxonomy are captured in World Flora Online and Kew's Plants of the World Online, but 49% of curators globally used neither resource. Some respondents reported drawing heavily on the Facebook group *Herbarium Junkies.* Around half of surveyed herbaria said staff spent time identifying 'indeterminate' specimens of uncertain taxonomy. They used methods ranging from using taxonomic keys to systematically narrow down potential species, to applying their own knowledge or searching for named duplicates held elsewhere.

Regarding digitisation, the study found that half of herbaria were partially digitised but only 18% were fully digitised. While a fifth of small herbaria had entirely digitised their collections, they also had the largest number that were not accessible to the public. Of herbaria with digitised collections, large herbaria were more likely to share some or all of their data with aggregators. GBIF was found to be a popular portal for sharing data; some other services used were iDigBio, Symbiota (software for managing and mobilising digital biodiversity data), *species*Link (a Brazilian-led online biodiversity information system), Herbário Virtual Reflora, JSTOR Global Plants (the world's largest online database of high-resolution digitised plant type specimens) and the Atlas of Living Australia. In some cases, cost influenced decisions around how and with which aggregators herbaria shared their data. There was clearly a move towards digitisation, but institutions were at different stages, and the curation of the underlying physical specimens was equally inconsistent.

'When I was carrying out my master's project on curation methods of *Camellia*,' says Aceae, 'I found that over 50% of the specimens that I analysed using molecular methods had incorrect or outdated names – similar to Goodwin and colleagues' results. If our collections have incorrect names and then those all get digitised, we're essentially spreading misinformation. And that's particularly important right now, because we're starting to use AI learning tools and automated specimen identification.'

There is no doubt that AI has unprecedented potential for helping scientists to trawl through datasets, extract data with particular characteristics and find patterns within those data. Similar automated functionality is already enabling us to translate texts, receive comprehensive answers to internet queries and navigate our way around unknown places. However, where AI is trained on an existing dataset, it relies heavily on the accuracy of the data with which it is provided. Attention must therefore be given to both curation and digitisation practices, to ensure that data captured within herbaria are accurate, consistent and updated as new scientific information becomes available. And to be useful to all, these data must be made available through aggregators, and also kept up to date.

Neither must the human element be neglected as researchers navigate using these new tools. The ratio of taxonomists and curators to the number of specimens globally is critically low, with large and small institutions alike often having too few resources to meet their curation needs. Overlooking specialists' perspectives and expertise would undermine AI's ability to transform our understanding of biodiversity. Support must be particularly directed towards nations with lesser capabilities, or facing greater challenges, to ensure they are not left behind. One possibility, proposed by botanists from southern Africa and the Western Indian Ocean Islands, is that better-resourced herbaria twin with less-well-supported institutions. Only if the coming scientific revolution is expansive and inclusive can the inequality rooted in taxonomy's past be eradicated, and the potential of digitised plant and fungal data be fully realised.

This chapter is based on the following publications in our special collection:

Aceae, C.C., et al. (2025). Assessing current curation, identification and digitisation practices in herbaria: Results from a global survey. *Plants, People, Planet.* DOI: https://doi.org/10.1002/ppp3.70083

Jaramillo, C., et al. (2025). Digitizing collections to unlock the full potential of palynology: A case study with the Smithsonian palynology collection. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70073

Klopper, R.R., et al. (2025). Digitisation of herbarium specimens to the benefit of research: An African perspective focusing on South Africa and Western Indian Ocean Island states. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70117

Mardones, M., Carranza-Velázquez, J., Rojas, C. (2026). Exploring Costa Rica's fungal trends: Insights from digitized specimens. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70203

Versiane, A.F.A., et al. (2025). Synergistic efforts in specimen digitisation, curation and cataloguing of Brazil's megadiverse flora and funga. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70021

Zhigila, D.A., et al. (2025). Biodiversity science is improved when silent herbaria speak. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70091

IF OUR COLLECTIONS HAVE INCORRECT NAMES AND THEN THOSE ALL GET DIGITISED, WE'RE ESSENTIALLY SPREADING MISINFORMATION.

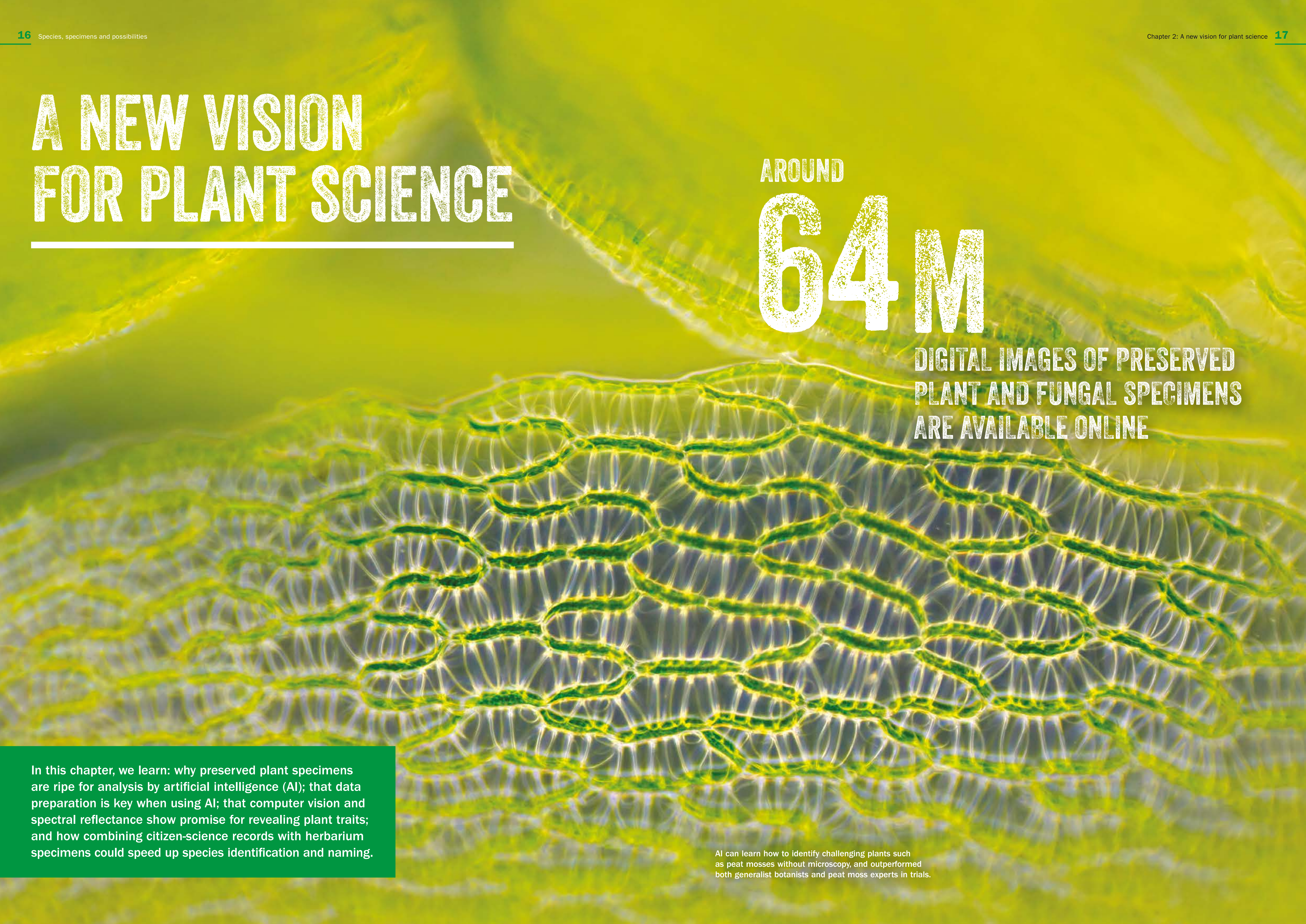
A NEW VISION FOR PLANT SCIENCE

AROUND

64 M

DIGITAL IMAGES OF PRESERVED PLANT AND FUNGAL SPECIMENS ARE AVAILABLE ONLINE

In this chapter, we learn: why preserved plant specimens are ripe for analysis by artificial intelligence (AI); that data preparation is key when using AI; that computer vision and spectral reflectance show promise for revealing plant traits; and how combining citizen-science records with herbarium specimens could speed up species identification and naming.



AI can learn how to identify challenging plants such as peat mosses without microscopy, and outperformed both generalist botanists and peat moss experts in trials.

THE GROWING VIRTUAL HERBARIUM AND NEW IMAGING METHODS ARE FACILITATING THE USE OF ARTIFICIAL INTELLIGENCE TO BETTER UNDERSTAND BIODIVERSITY.

Artificial intelligence (AI) – spanning technologies that can detect patterns, act logically and generate content – is the new frontier for analysing herbarium collections. The ‘computer vision’ branch of AI is enabling rapid data capture from digital plant specimens on everything from leaf shape to the presence or absence of flowers. And ‘machine learning’ techniques, which give computers the ability to find patterns in large datasets, are helping scientists to make sense of vast amounts of complex information. Although fewer than 16% of the estimated 406 million herbarium specimens worldwide have been digitally scanned or photographed, this subset of images is enabling plant scientists to experiment with using AI to identify species, detect damaged specimens, measure plant parts, decipher label text and record whether plants were flowering or fruiting when collected (see Figure 1). Together, these pioneering investigations are paving a new path for plant science in the digital age.

SEEING SPECIMENS WITH NEW EYES

Computer vision is simply the processing of visual information by computers. It can, for example, recognise letters and symbols within images. Since the first practical modern AI-based computer-vision system (which could read handwritten numbers on cheques) was developed in the 1990s, AI has become a ubiquitous technology. Many tasks in botanical research can be accomplished using computer vision, with applications ranging from mapping plant distributions to investigating trends in past plant collecting.

‘Digital herbarium specimens are great objects for computer-vision analysis because the people digitising them have gone to great trouble to make sure that everything is as consistent as possible,’ explains Damon Little, Curator of Bioinformatics at New York Botanical Garden, USA. ‘They’ll have put colour calibration cards and rulers on every specimen, so you have a very good idea of the colour and size range, which helps immensely. Also, the process of identifying specimens usually involves one or more professionals, so the labels of well-curated groups tend to have a high level of accuracy. This is important for those specimens used as training data.’

‘However,’ warns Michael Tessler, Assistant Professor at Medgar Evers College at City University of New York (CUNY), ‘if you work with one herbarium, you often get a much more robust kind of internal calibration. When you start to look across herbaria, it becomes much more challenging but is often worth the effort.’

A review by Little and Tessler based on their own work shows in detail how computer vision is being implemented within plant science. Computer vision tasks typically involve either classification, regression or translation. Classification determines what something is, from a list of predefined categories. It could identify a species or recognise a certain feature, such as a flower, for example. Regression gives a directly interpretable number, such as leaf length or a count of the total number of flowers – any number that you can calculate normally or measure directly. And translation converts something from one mode to another. For example, it might convert French to English, or take a text request for views of a tree and provide a set of images. It can isolate areas of interest from an image, such as labels or a particular kind of plant material, and can calculate the proportion of an image taken up by an object of interest, such as leaves.

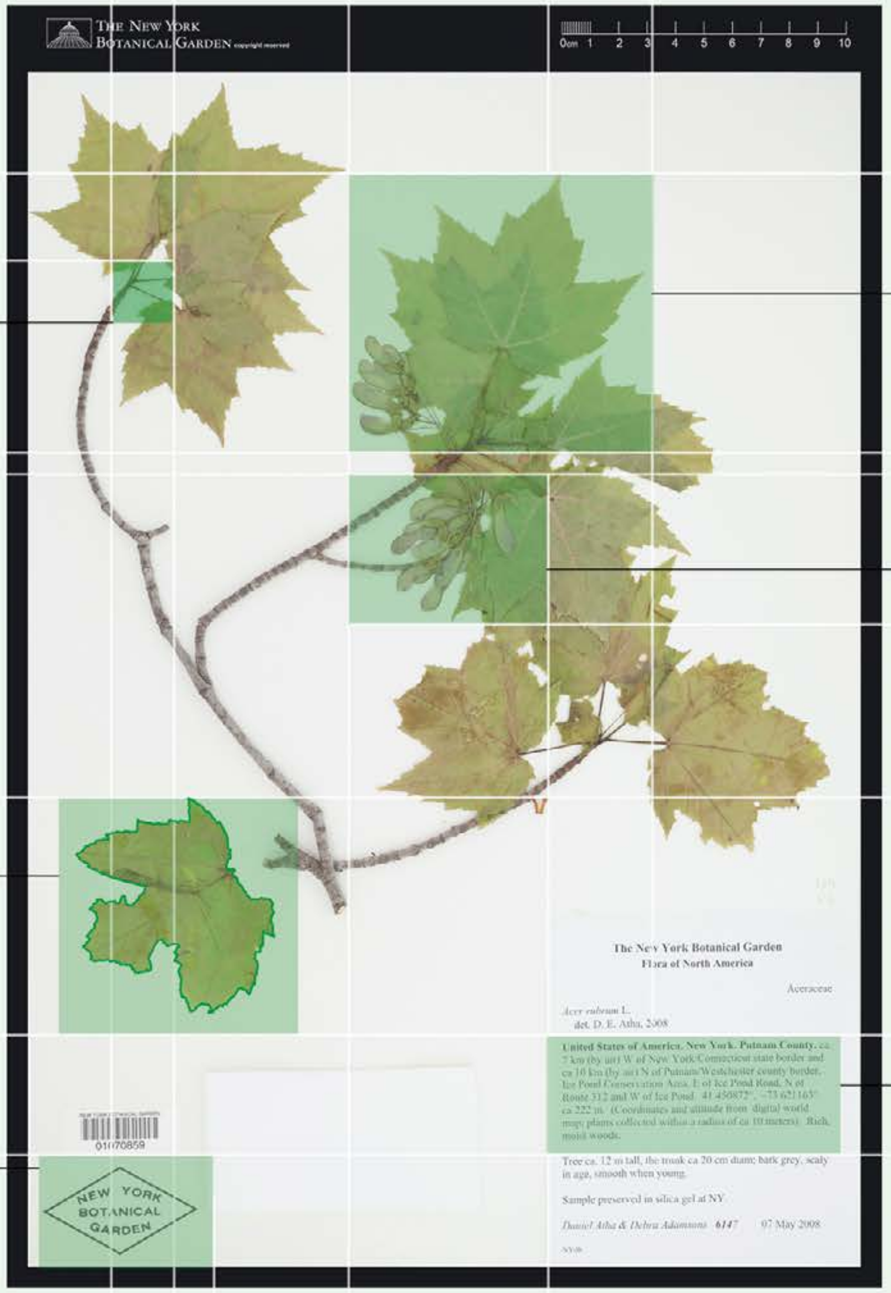
Plant scientists can use AI to address all kinds of hypotheses, such as whether certain characteristics are useful for distinguishing between species, or whether climate change is causing shifts in distribution and flowering times (see Chapter 6). But before a set of digital herbarium specimens can be used to address such questions, some preparation is needed. This might involve: cleaning the data to remove images that are not relevant or are of insufficient quality; pre-processing images to remove or mask unwanted elements such as barcodes or institutional logos; partitioning the dataset to form subsets for training, validation and testing; and identifying and mitigating biases inherent in the data. The next step is to establish suitable workflows that tell the technology how to process the data. And, finally, comes the critical process of choosing an appropriate AI model and training it to make predictions. An important consideration influencing this choice is loss selection; put simply, this is a measure of how much information is lost between input and output.

In their review, Little and Tessler provide hints and tips for navigating all of these steps, drawing on their own experiences of using machine learning to analyse maples (*Acer* species) and peat mosses (*Sphagnum* species). They chose maples to exemplify ‘typical’ specimens that are mounted on herbarium sheets and often display stems, leaves and flowers or fruits (see Figure 1). They selected peat mosses to represent more challenging cases for identification; these mosses are often displayed in unseparated clumps and require microscopes to distinguish the key features. One important point the researchers make in the review is the need to ensure AI learns from the desired plant material and not from irrelevant features. For example, an AI model could pick up on the manila mounting paper frequently used in French herbaria – rather than the plant itself – to identify species as being from France and former French territories. They also report that trying different model architectures and training strategies is important because the outcomes are unpredictable and the best results sometimes come from combining different approaches.

‘Getting started with AI work can be daunting,’ admits Tessler. ‘Most botanists do not currently have the computer science background or the requisite mathematical knowledge to be able to code AI models and training routines, although this is changing for some of the new generation coming through. Accordingly, they should consider developing collaborations in which they produce the datasets and co-design the experimental protocols with a specialist who can code and train the AI models.’

FIGURE 1: What computer vision can tell us about a maple specimen

Computer vision – a type of artificial intelligence that processes visual information – can extract many types of information from digitised images of preserved plants. It can narrow down or determine the species’ identity, measure key features such as leaf size or stem length, record whether the plant was in flower or fruit at the time of collection and count the reproductive structures present. It can also extract data from the label, such as the time and place of collection and the name of the collector. The end results are underpinned by processing tasks, such as masking irrelevant information and segmenting the image to distinguish key features. For example, segmentation is used to determine which parts of the image represent leaves, flowers and fruits, or to separate out the shape of a single leaf that is overlapping with others so that measurements can be taken.



MEASURING

Taking measurements from the image, such as leaf stalk length, fruit width or leaf area

SEGMENTATION

Determining which parts of the image are leaves, fruits, stems etc.

MASKING

Hiding non-relevant features, such as logos or blobs of glue

IDENTIFYING TAXA

Using features of the specimen image to identify the species – in this case *Acer rubrum*

COUNTING

Providing counts of different features present, such as the number of flowers or fruits

READING ANNOTATIONS

Extracting the collection location or other information from the label

Adapted from Tessler & Little (2025)

Scanning a plant specimen to produce a digital image.

A NOVEL TOOLSET FOR PLANT SCIENTISTS

Some help is at hand for plant scientists starting out with AI, in the form of ready-made computer-vision tools. Among these is 'Herbariograph', which Little was involved in developing. This multi-layered machine-learning tool can simplify the process of filtering a dataset of images for use in particular AI applications, allocating them to one of 17 categories – such as live plant, animal, colour illustration or microscope slide. When trained, validated and tested on 208,896 images, the Herbariograph model performed well at differentiating among the categories. It therefore shows promise as a tool that researchers can use to categorise large numbers of images and then focus on the subset most appropriate for addressing their hypotheses.

'For AI to work at any real level, you need images to be comparable,' says Little. 'So, they need to all be of pressed specimens at the same scale with more or less the same sort of lighting, rather than something completely different, such as an illustration of the specimen. But herbaria digitise all sorts of things. Many are pressed plant specimens, but they may also include items made from plants, such as a basket made from the fibre of a particular palm species. All of those are valuable specimens and images. But the Herbariograph project was born out of the frustration of seeing these data and wanting to make it better. I thought if we made an AI model that was good at sorting through all the different kinds of specimens that are out there, we could not only improve the quality of our dataset but make a tool that other people could use as well.'

Researchers are experimenting, too, with building computer-vision tools to help scientists extract data on plant traits – characteristics such as leaf size or flowering time – from digital herbarium specimens. For example, one team has built a tool to automatically predict leaf mass per area (LMA). LMA is of particular interest to scientists as it can be used to position species on the 'worldwide leaf economics spectrum'. This ecological continuum is a measure of how species balance the cost of producing leaves with the benefits that those leaves provide, and can be used to study the interactions between plant traits and their environment, including climate. At one end of the spectrum is the strategy of 'slow return', where species have leaves with high LMA that are costly to produce but give better protection against environmental stressors and last longer, such as those of the great laurel (*Rhododendron maximum*). At the other end is the strategy of 'fast return', where species have leaves with low LMA that are low-cost, fast-growing and short-lived, such as those of the American blue vervain (*Verbena hastata*). The relationship between these traits and climate has been explored extensively, but there are still gaps in trait knowledge, particularly for tropical taxa, and this hampers the ability to understand general global patterns.

'My colleagues and I have just been trying to expand the breadth of the traits that we can get from digitised images,' says William Weaver, Postdoctoral Fellow at the Michigan Institute for Data and AI in Society at the University of Michigan, USA. 'Leaf mass per area is one of the most important ones, since it's involved in all sorts of different fields in botany, and particularly because it allows you to compare living and fossil taxa a little bit better. So that's what we started exploring, asking: With computer vision and machine-learning tools, can we start to build a more comprehensive global leaf mass per area dataset? And, if we can, what can we do with that?'

Generally, the thicker the petiole – the stalk that attaches a leaf to the stem of a plant – the heavier the leaf it supports, so this relationship can be used to predict LMA for herbarium specimens, where mass cannot be measured due to the processes involved in treating, drying and pressing the leaves. Weaver and colleagues used a computer-vision tool to automate the measurement of petiole width and leaf area from thousands of digitised woody flowering plant specimens in order to predict LMA. After filtering out specimens with inaccurate coordinates and missing data, they ended up with measurements of 22,549 leaves from 5,665 digitised specimens representing 1,670 species from 245 families. Manual petiole measurements taken from a subset of 1,755 specimens correlated well with the automated results. The error associated with the automated measurement of the digitised specimens was actually lower than the general error associated with using petiole width in the proxy equation to predict LMA.

'With so many herbarium specimens existing, the fact that we can get comparable results to manual measuring in an automated batch is exciting,' says Weaver. 'And if most of the error comes from the proxy, that makes me ask if we should be revisiting those proxies. And I think the answer is yes. With continued refinement, these tools have the potential to revolutionise how we extract and analyse plant trait data globally.'

Using the AI-generated dataset, the team explored the geographical origin of specimens, relationships between the predicted LMA and climate, and the effect of incorporating phylogenetic information – which reveals the evolutionary relationships between species. Eight biomes were represented in the dataset, with specimens from temperate conifer forests tending to have lower LMA and those from deserts and dry shrublands exhibiting higher LMA. This replicated known patterns. When they examined the relationships between predicted LMA and each of latitude, temperature, precipitation, temperature seasonality and solar radiation, they found that mean annual temperature (MAT) and solar radiation appeared to have the largest effects on LMA. Lower LMA was expected in environments with high MAT and low solar radiation, typical of tropical, subtropical and temperate broadleaf rainforests with persistent cloud cover. A link to latitude also emerged, with plants nearer the equator tending to have lower LMA values.

Overall, the work demonstrated the clear potential for using machine learning to quantify, categorise and rank plant functional traits using digitised herbarium specimens. Importantly, many of the species analysed were absent from the largest and most widely used open dataset of functional traits – the TRY Plant Trait Database. Measurements from digital images of dried, pressed specimens are not directly comparable with those from unpressed leaves, so would need to be considered separately if incorporated into TRY, but their addition to the database could still be a powerful way to address the gaps in the coverage of global biodiversity data.

CAPTURING DATA ACROSS THE SPECTRUM

Alongside traditional digitisation of herbarium specimens, which produces visual, 2D red-green-blue images suited to human viewing and computer vision, a new means of digital data capture is emerging that also lends itself to analysis by machine learning. This is reflectance spectroscopy, which essentially measures the pattern of how light interacts with and bounces off a surface (see Figure 2, overleaf).

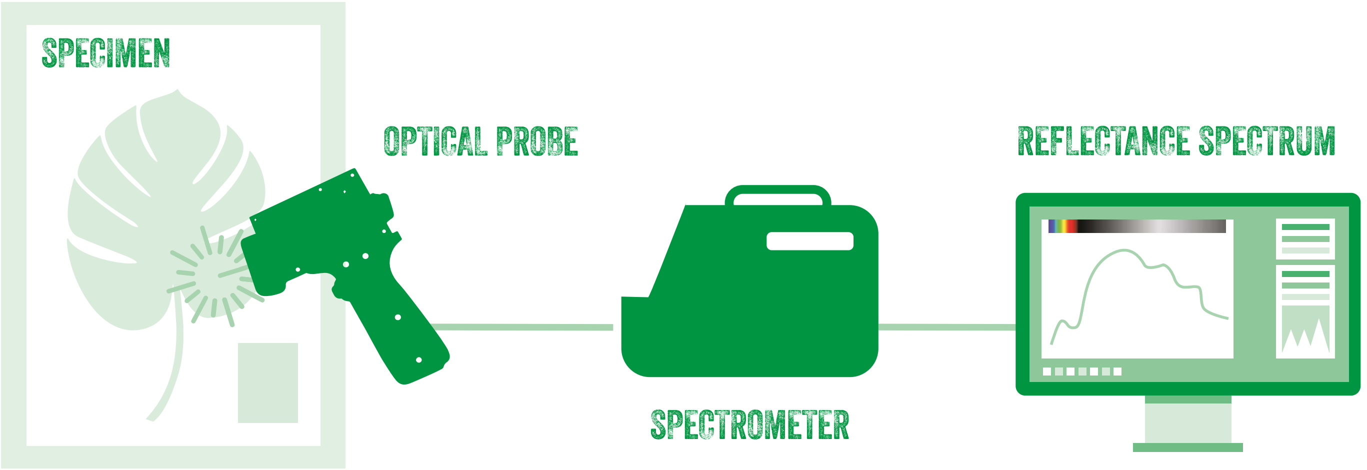
'Photons that bounce back to your eyes in the visible range allow you to see all of the colour, but those with longer near-infrared or short-wave infrared wavelengths also contain information on plant structure, chemistry and many other aspects of plant morphology,' explains Jeannine Cavender-Bares, Director of the Harvard University Herbaria, Massachusetts, USA. 'Using traditional and machine-learning models, reflectance spectra can be used to predict a suite of plant functional traits and to differentiate among species and broader plant groups. It works well on fresh leaves, but when you remove the water, absorption features are revealed that are otherwise masked. You can sometimes get better information from dried leaf tissue, and that's why it works well in herbarium specimens.'

This was among the findings of a study undertaken by Cavender-Bares and colleagues to test the potential for obtaining trait data by applying reflectance spectroscopy to herbarium specimens. Previous studies had already demonstrated that this approach could be used on both fresh

THESE TOOLS HAVE THE POTENTIAL TO REVOLUTIONISE HOW WE EXTRACT AND ANALYSE PLANT TRAIT DATA GLOBALLY.

FIGURE 2: How reflectance spectroscopy works using plant material

Reflectance spectroscopy is a non-destructive analytical technique that measures the light reflected from a surface across various wavelengths. When used on a physical herbarium specimen, it produces a profile that can reveal the species' identity, as well as key characteristics, such as a leaf's structure and biochemistry.



leaves and recently pressed ones, but the jury was still out on whether it would work for older preserved specimens. Herbarium specimens tend to have been subjected to a much broader array of collection and preservation protocols – often with minimal documentation – and stored for considerably longer periods. The additional processing and degradation they undergo means they have more variable tissue. The researchers decided to use a framework established for pressed leaves to investigate whether reflectance spectroscopy could also be applied to herbarium specimens to predict leaf traits and identify species.

The team studied 24 species of trees, shrubs and herbs from North American broadleaf forests and one Australian tree species with high LMA values, to broaden the sampling. They measured reflectance spectra for each specimen, along with leaf weight, area and thickness, and built models to predict LMA and identify the specimens to genus and species level from the measured spectra. They found that LMA models built from herbarium specimen spectra performed equally as well as those built from the spectra of recently pressed leaves. The herbarium-based genus and species identification models performed reasonably well but were less accurate than when using recently pressed leaves. This was likely due to the tissue in the older herbarium specimens – collected up to 179 years ago – being more degraded than that of recently pressed leaves, which were three years old at most. Certain preservation techniques, such as being treated with alcohol and having glue applied to fix them to paper, could have also influenced the results. Although the models based on herbarium specimens were not quite as accurate as those from recently pressed leaves, the availability of large numbers of herbarium specimens means that the technique shows promise for filling global gaps in trait data.

Currently, the TRY Plant Trait Database contains data taken primarily from living plants. Applying reflectance spectroscopy to pressed plants and herbarium specimens offers the potential to generate a huge dataset of plant functional traits, such as LMA and nitrogen concentration, for a whole set of species that are not yet in the database. 'It will allow us to model variation in plant communities based on all of this functional trait information,' says Cavender-Bares. 'It will also allow us to model trait evolution back in time over the world's plants and therefore model the evolutionary history of plant functions across the world's taxa in ways we've never been able to do before. Reflectance spectra will also help us to differentiate species and other taxa. Essentially, it's a new source of information that will allow us to identify and better understand the diversity of life on Earth.'

CAPITALISING ON NEW DATA STREAMS

Finding ways to automatically identify species has long been a goal within plant science. Both computer vision and reflectance spectroscopy have the potential to discriminate between species (see Box 1), but the relative effectiveness of each had not previously been studied in collections. A project that sought to do so compared the identification capabilities of Pl@ntNet, a platform employing computer vision to identify and inventory plant species – mostly using citizen-science photographs of live species but also used with herbarium

> IDENTIFYING HERBARIUM SPECIMENS COULD BECOME SIMPLER AND FASTER THANKS TO AI TOOLS.

The genera *Ziziphus* (pictured) and *Bulbostylis* were used to test an AI identification pipeline.

BOX 1: Automated pipelines to speed up plant science

Identifying herbarium specimens could become simpler and faster thanks to a new pipeline designed to help scientists and herbarium curators generate datasets for training artificial intelligence (AI) models. The pipeline uses specimen images alongside data provided in the DarwinCore format – a freely available, community-developed biodiversity data standard that enables the sharing of data using a common terminology. DarwinCore has, for example, made it possible to integrate hundreds of millions of specimen records and observations into the Global Biodiversity Information Facility (GBIF).

The international team that developed the pipeline tested it using species from two contrasting and distantly related flowering plant families: the sedges (Cyperaceae) and buckthorns (Rhamnaceae). They sampled herbarium specimens available on GBIF and used them to train and compare models at the genus level for the two families, and at the species level within the sedge genus *Bulbostylis* and the buckthorn genus *Ziziphus*. The models performed well in identifying specimens to genus level, with the best model settling on the correct identification in 75% of cases for the sedges and 72% of cases for the buckthorns. Species-level identification was equally accurate for *Ziziphus* (72%) but less accurate for *Bulbostylis* (63%). The accuracy rose to around 90% or more in all models when the results were evaluated based on the correct identification being within the top five of the most probable genera or species.

Although the approach enables the automated identification of herbarium specimens, it incorporates an element of expert verification to enhance the quality of the data used to train the model. Its potential applications include identifying and locating misidentified specimens and finding taxa that may be new to science.

Another new automated pipeline could speed up the extraction of valuable information from herbarium specimens. It was developed by scientists at the Missouri Botanical Garden using the generative AI programme ChatGPT to recognise and transcribe label data. The pipeline achieved a high level of accuracy during tests, and its implementation resulted in time and money being saved when compared with traditional methods. The scientists suggested other institutions should consider similar approaches, arguing that the 'perfect should not be the enemy of the good' when adopting automated pipelines. Even with less than 100% accuracy, important information such as the collection location is usually captured when using such pipelines, or can easily be inferred, especially if only varying by one or two letters.

The pipeline combines optical character recognition (OCR) with the large language model power of ChatGPT to output a spreadsheet formatted for upload to an institutional database. It can also be set to recognise the language of the OCR-derived text and translate it into English, widening its application and usefulness.

Peach (*Prunus persica*) blossoming along the Great Wall of China.

BOX 2: Using artificial intelligence to help identify Chinese species

Thousands of preserved specimens in herbaria around the world are awaiting identification and are therefore in curatorial limbo. In some cases, there is no one with time to fulfil the task; in others, available staff do not have the necessary expertise. Artificial intelligence (AI) has the potential to help identify such indeterminate species, and tools are starting to be developed with that goal in mind.

One freely accessible AI model has been built to help identify China's vascular plants (those with specialised vessels for transporting water and nutrients – the majority of land plants), drawing on the 6.5 million specimens of known species digitised across the country's herbaria to date. The model was trained on more than two million images representing 21,589 species, 3,144 genera and 309 families. At the species level, this covers more than half of China's vascular plant diversity and 98.6% of the Chinese specimens so far digitised.

The model was tested with 244,749 expert-identified specimens, and it correctly identified species with an accuracy of 67.3%. This rose to 86.5% at genus level and 91.7% at family level. However, when used to identify Chinese specimens held in and digitised by Kew's Herbarium, the model achieved only 24.5% accuracy at the species level, 55.7% at the genus level and 67.1% at the family level (considering only the species in the training dataset). This may reflect different mounting and photographing processes. It highlights the potential inadequacies of AI approaches when faced with the results of varied digitisation and curation practices and the need for greater levels of standardisation globally.

Ultimately, the hope is that the new model, alongside a related tool with identified photographs of 20,000 live vascular species common in China, can help to reduce the backlog of unidentified specimens in herbaria hosting collections from China and adjacent countries.

specimens – with those of leaf reflectance spectra. Pl@ntNet, which leverages red-green-blue images, was known to work particularly well on plants exhibiting reproductive structures, such as flowers and fruits. The team chose to focus on stone oaks in the genus *Lithocarpus* for the study, as species in this diverse genus were known to be difficult to identify in the absence of reproductive features and because specimens were frequently collected in vegetative form – with just stems, leaves and roots. When the two approaches were applied to the exact same set of herbarium specimen images, the scientists found that the *Lithocarpus* specimens were accurately identified to species level from relatively small spectral datasets. Despite not incorporating reproductive features, which are frequently present in Pl@ntNet images, spectral reflectance from leaves was only 14% less accurate at identifying species.

'I think there's an opportunity for synergies between these two automated identification methods that could help us highlight or streamline how curatorial attention is provided to specimens and collections,' says Barbara Neto-Bradley, who undertook the work as part of a PhD for the University of Cambridge, UK, and Harvard University, USA. 'There were a couple of specimens that we looked at where both models agreed with each other on an ID that differed from the herbarium label. To me, that suggests that there are specimens in herbaria that are sitting under the wrong label, or that at least warrant someone having another glance to double-check that they're not what the two models agreed on. So, I think there are opportunities to leverage this work, not just for the indeterminate specimens, but even for the named specimens that maybe no one's looked at in 20 or 30 years.'

SETTING HIGH STANDARDS

The findings of all the projects outlined here are evidence that herbarium specimens are a vast source of untapped information that computer vision, reflectance spectroscopy and machine learning are poised to help unlock. In these early days, attention must be paid to data standards and technical specifications, to ensure that this treasure trove of plant data can be used effectively to enhance understanding of biodiversity (see Box 2). The International Herbarium Spectral Digitization Working Group is setting a good example in this regard, by initiating a global collaborative programme that is outlining key issues ahead of establishing protocols, standards and best practices, and proposing next steps. The hope is to smooth the path to data aggregation and to ensure fair and equitable use. Taking careful steps at this new frontier of plant science will serve to bridge the gap between experimenting with these unparalleled technologies and applying them to solve pressing real-world environmental challenges.

This chapter is based on the following publications in our special collection:

Arno, J., et al. (2025). A pipeline to compile expert-verified datasets of digitised herbarium specimens for automated plant identification to accelerate taxonomy. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70149

Austin, M.W., et al. (2025). Using large language models to automate herbarium specimen transcription: A case study at the Missouri Botanical Garden. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70128

Ávila, F.A., et al. (2025). *Herbariograph*: a deep-learning tool to classify specimen images. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70447

Cavender-Bares, J., et al. (2025). Next-generation specimen digitization: capturing reflectance spectra from the world's herbaria for modeling plant biology across time, space, and taxa. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70645

Little, D.P., et al. (2025). AI for difficult herbarium specimens: identification of peat mosses (subgenus *Sphagnum*) without dissection. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70461

Neto-Bradley, B.M., et al. (2025). Using reflectance spectra and Pl@ntNet to identify herbarium specimens: a case study with *Lithocarpus*. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70258

Tessler, M., Little, D.P. (2025). On herbarium specimen images and artificial intelligence. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70312

Vasconcelos, T., et al. (2025). Automated extraction of leaf mass per area from digitized herbarium specimens. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70292

White, D.M., et al. (2025). Seeing herbaria in a new light: leaf reflectance spectroscopy unlocks trait and classification modeling in plant biodiversity collections. *New Phytologist*. https://doi.org/10.1111/nph.70357

Xie, G., et al. (2025). AI-based identification of Chinese vascular plants from herbarium specimens: a tool for all herbaria with Chinese holdings. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70443

THE HOPE IS TO SMOOTH THE PATH TO DATA AGGREGATION AND TO ENSURE FAIR AND EQUITABLE USE.

WHERE TRADITIONAL TAXONOMY MEETS DIGITAL TECH

In this chapter, we learn: that digital photos and digitised specimens are helping to pinpoint new plant and fungal species; how scientists are still finding towering trees that are entirely unknown to science; that only 205,000 of an estimated 2.5 million fungal species have been scientifically named; and why it took 92 years to name a palm.

>4,600

NEW SPECIES OF PLANTS AND

>7,800

NEW SPECIES OF FUNGI WERE SCIENTIFICALLY NAMED IN 2024 AND 2025

Telipogon cruentilabrum, a new species of orchid from the cloud forests of Ecuador

Aphelandra almanegra

Dendrobium eruciforme

The new plant species scientifically named in 2024 and 2025 range from the miniature to the mighty (clockwise from top left):

Aphelandra almanegra, a new species of shrub from Colombia, is related to the zebra plant (*A. squarrosa*) from Brazil, a popular houseplant.

Dendrobium eruciforme, a new orchid species from West Papua, Indonesia, is one of the smallest species of its genus. It is threatened by logging of its forest habitat for pineapple and cassava plantations.

Adonidia zibabaoa, from the Philippines, is known as *Amuring* in the local Waray-Bisaya language. A beautiful, red-fruited palm, it is already sought after by palm enthusiasts for cultivating.

Plagiosiphon intermedium is the first species to be added to the *Plagiosiphon* genus in 80 years. It is known only from Ngovayang, an area of exceptional plant diversity in Cameroon.

Eugenia venteri is believed to be pollinated, and have its seeds dispersed, by giant ground rats that are found in its native home of New Guinea.

Mediocalcar gemma-coronae is one of five spectacular orchids named as new to science from Indonesia in 2024.

The snowdrop *Galanthus subalpinus* was being cultivated in the UK but did not match any formally known species. Scientists traced its origin to the subalpine grasslands of Mount Korab in northern Macedonia and Kosovo, and named it as new to science.

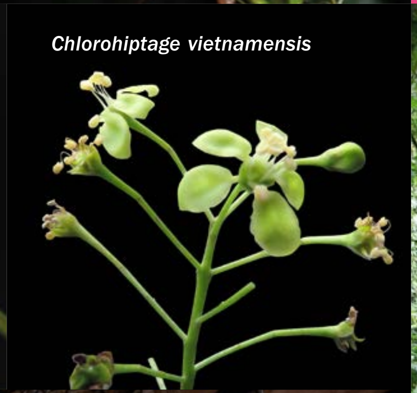
Aphelandra calciferi, collected in a moist tropical forest in Peru, shows potential as an ornamental plant due to its striking flame-like flowers.

Found only in Vietnam, *Chlorohiptage vietnamensis* is not only an entirely new species of liana, but also a new genus. It is already under threat, however, due to cement quarry excavation in its habitat.

Galanthus subalpinus

Aphelandra calciferi

Mediocalcar gemma-coronae



Chlorohiptage vietnamensis

Plagiosiphon intermedium

Adonidia zibabaoa

Eugenia venteri

NAMING ALL THE WORLD'S PLANTS AND FUNGI IS AN ONGOING CHALLENGE, BUT DIGITAL SPECIMENS, DATA AND NEW MACHINE-LEARNING TOOLS MAY HELP SPEED UP THE PROCESS.

In the world's remaining wild areas are thousands of species that have yet to be officially described and named. Scientists estimate that at least 100,000 plant species and more than two million fungal species are currently unknown to science, any one of which could yield a valuable food, medicine or material. With three-quarters of these unknown species already likely to be at risk of extinction, the race is on to find and classify them. However, the global shortage of expert taxonomists is likely to be limiting progress in this regard. The annual rate at which new plant species are named has remained constant at 2,500 or so for decades. For fungi, it is higher, recently rising to around 4,000 per year, but given the vast number of unknown species, this is barely scratching the surface. With ongoing threats to ecosystems worldwide, the pace needs to increase. Could digitised specimens, coupled with the capacity for machine-learning technology to recognise shapes and reflectance patterns, help to overcome this bottleneck in biodiversity science?

Although plant and fungal scientists are experimenting with artificial intelligence (AI), the world is a long way off developing a machine for using in the field to accurately identify known species or determine whether something is new to science. For plants, such a machine would have to be trained to accurately recognise all species that already have scientific names, requiring multiple images of live and preserved specimens of each. These are simply not available for rarer plants. To identify fungi, it would need to tap into a combination of images and DNA sequences that are also not universally available. Plus, a significant injection of cash would be needed to cover the costs of the imaging and sequencing, and to develop appropriate algorithms – at a time when competition for research funding is fierce.

That is not to say that digital specimens and new technologies have no role to play in identifying species. Indeed, the digitisation of herbarium and fungarium specimens and the profusion of digital photographs of live plants and fungi now available through apps such as iNaturalist, along with the ability to disseminate images and information through social networks, are already helping taxonomists to identify, describe and name new species.

For example, Martin Cheek, Senior Research Leader and head of Kew's Africa team, recently encountered a new species while looking through specimens on the Global Biodiversity Information Facility (GBIF) digital specimen portal. He had conducted a search for digitised herbarium specimens of all the species within the genus *Afrothismia* – which he thought he knew inside out – when up came a plant he had never seen before. After acquiring the physical specimen from the herbarium that had uploaded the image to GBIF, Cheek realised that the plant had never been described and named. And digital photos are helping Cheek's team to narrow down the identity of another specimen – a plant likely to be in the genus *Sabicea* that was collected during work to survey peat swamp forests in the Republic of the Congo. The photos, sent to Cheek from the original collector, indicate that this, too, could be a species new to science.

For plants, though, there is no doubt that physical – rather than digital – herbarium specimens are still the mainstay of species identification. Indeed, plant taxonomy is largely conducted via a process that has changed little since the herbarium sheet was invented in the 16th century. This was when Luca Ghini, botany professor at the newly established University in Bologna, found that when plants were pressed, dried and mounted on paper, they could be kept as a record and studied long after they died. He taught his methods for preserving plants in this way to his students, and, as other herbaria became established in universities – in Florence, Montpellier, Paris, Oxford and beyond – the practice spread across Europe. Today, as then, the process of naming a species as new to science usually begins when a plant specimen is collected in the wild and preserved on a herbarium sheet. If the specimen is suspected of being a species new to science – and the resources are available to investigate the plant further – then a journey of botanical detective work gets underway.

'If you have an unfamiliar specimen you think is from a genus you know very well, you can be pretty sure from the outset that it's going to be a species new to science,' explains Cheek. 'But it's still worth double checking it is actually from that genus, because it's very easy to think you've found an astounding new species, with totally weird characteristics, and then it turns out not to be in the genus you think it is. Once this is confirmed, you would check the specimen against all the information available for the known species in that genus, to be certain it really was new. And for an unfamiliar species encountered in the wild – rather than as an already-mounted specimen – you'd be sure to make a really good collection of specimens, take photographs and gather all the information about it that you might possibly need for publishing a species as new to science.'

NEW SPECIES LARGE AND SMALL

During 2024 and 2025, Kew scientists published a total of 262 new species of plants and 70 of fungi in collaboration with partners, contributing to the global tallies of 4,687 and 7,851, respectively. The plants range from the diminutive, creeping caterpillar orchid (*Dendrobium eruciforme*), one of six new orchid species from Indonesia, New Guinea and Maluku, to *Plagiosiphon intermedium*, a 34-m-high tree from a rainforest in Cameroon. Another newly named tree, from Manus Island, Papua New Guinea, is *Eugenia venteri*, which stands 18 m high and bears fruit tasting of banana and guava. And alongside them in the latest line-up of plants new to science are two species in the genus *Aphelandra*. The first is the scarlet-blossomed fire demon flower of Peru, given the scientific name of *Aphelandra calciferi* after Calcifer, the fire demon in the cult 2004 Hayao Miyazaki film *Howl's Moving Castle*, and the second is a new species of deciduous shrub with spectacular pink flowers, *A. almanegra*, named after its distinctive black heartwood.

The newly named fungi are no less fascinating. One of the most unusual is *Purpureocillium atlanticum*, a 'zombie' fungus that parasitises trapdoor spiders in Brazil's Atlantic rainforest. It takes over a spider's body, covering it in soft, cotton-white mycelium. A purple fungal fruiting body up to 2 cm long then emerges from the corpse, passes through the nest's trapdoor hole, and releases its spores above the ground to continue the cycle. Other new macrofungi include three species in the genus *Russula*, several toothy toadstools in the genus *Phellodon* and a new fungus in the 'pea stone' genus *Pisolithus*. Not all fungi have visible mushrooms or similar spore-bearing structures, however, making them harder to spot. Among these are fungal endophytes, which spend their lives inside living plants. A newly named example is *Magnaporthiopsis stipae*, which was isolated from the roots of a grass, *Stipa sareptana*, growing in Inner Mongolia, China. A high proportion of the fungi that scientists have yet to describe are anticipated to be species like this that are not easily detected by the human eye.

'Fungal taxonomy remains one of science's most exhilarating frontiers of discovery, even though it may also be the most daunting one we face,' says Irina Druzhinina, Kew's Senior Research Leader in Fungal Diversity and Systematics. 'From giant bracket fungi growing on tree trunks to microscopic filaments in the soil, Kew scientists estimate there could be between two and three million species of fungi globally, of which only just over 205,000 have been named so far. So, the challenge is immense but so is the wonder and privilege of uncovering new branches on the tree of life.'

A TIME-CONSUMING PROFESSION

The process of naming a species as new to science can be very slow. For the ghost palm of Borneo (*Plectocomiopsis hantu*), which was named in 2024, it took a whopping 92 years from a specimen being filed in a herbarium to the palm being scientifically described and named (see Box 1, overleaf). At a time when deforestation, urban development and climate change are driving up extinction rates, delays in naming species are a major concern.

This is where AI, backed up by expert verification, could come into its own. After all, as Chapter 2 has shown, multiple pipelines and algorithms are being developed, aimed at helping plant scientists to identify species within particular taxonomic groups, highlight misidentifications among herbarium specimens, or identify specimens from defined regions. And work is ongoing to build a genomic reference database for fungal identification (see Chapter 4), which could underpin future analyses with new technologies.

What seems likely in the short term is that machine learning will yield tools to further support traditional taxonomy, rather than superseding it, in much the same way as DNA sequencing technology has done.

DNA barcoding is a genetic sequencing technique focusing on areas of DNA that are shared across many organisms but variable enough to tell them apart. It was initially hailed as a technology that could be used ubiquitously to rapidly identify large numbers of species without needing an expert taxonomist. The idea was that samples could simply be sent to a laboratory, barcoded and then matched against known reference sequences to identify the species present, leaving taxonomists to get on with the business of describing and naming the unknown species. In reality, the costs and logistics of applying barcoding technology have led to it being used selectively within certain groups of plants and fungi, rather than comprehensively. For example, taxonomists used it to untangle the relationships between members of the morning glory (Convolvulaceae) family. It has also proved helpful in resolving cryptic species – where what appears to be one species is actually two or more very similar ones. This was the case for the new species of *Phellodon* tooth fungi mentioned above.

One of the main issues with barcoding is that to use it for identification, you need to already have a reference database of all the potential species you might find, which takes time to build. The technique can still be used if the reference sequences are not available, but it will simply yield information on the number of entities present and the relationships between them. It is routinely employed to quantify fungi in soil samples in this way, by simultaneously sequencing all microorganisms present. Although not quite living up to the initial hype, the technology has undoubtedly become a useful tool – and AI has similar power to help taxonomists do their job faster and better within the coming decades.

'I think the potential for AI is enormous, but it is still currently potential,' says Cheek. 'It would be very useful to be able to name stuff reliably more rapidly. You'd still need taxonomists to check those names were accurate and that there were no mistakes. But with less time spent on identifying the more common 90% of species, we'd have more time to get on and describe the unknown species and to do things to conserve the threatened species.'

For more information on plant and fungal species, see:
Plants of the World Online (powo.science.kew.org) and Species Fungorum (speciesfungorum.org)

See page 100 for the full list of references for the new species featured in this chapter.

> THE CHALLENGE IS IMMENSE BUT SO IS THE WONDER AND PRIVILEGE OF UNCOVERING NEW BRANCHES ON THE TREE OF LIFE.


Magnaporthiopsis stipae


Pisolithus madagascariensis

The new fungal species scientifically named in 2024 and 2025 exhibit an interesting array of characteristics (clockwise from top left):

Magnaporthiopsis stipae is one of 24 species, 11 genera and one family published as new to science in a study of a group of fungi that mostly live in the tissues of other organisms. Some do so without harming their host, while others can cause disease.

Pisolithus madagascariensis is newly described from Madagascar. The genus name means 'pea stone' and is a reference to its spore-filled sacs, which are embedded in a gel-like substance.

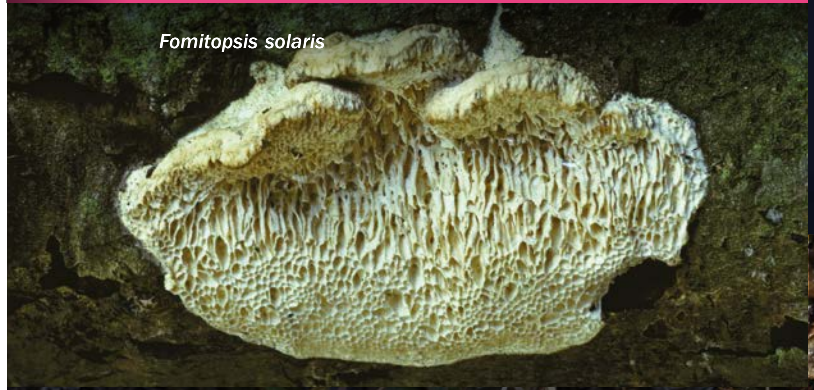
Purpureocillium atlanticum was found in Brazil's Atlantic Forest, its purple stalk erupting from a trapdoor spider that it had infected and consumed.

Phellodon frondosoniger has an inky black cap and bears its spores on long tooth-like structures. It was among four species identified as new to science after extensive analysis and DNA sequencing of *Phellodon* species across Europe.

Russula neopascua was described from the High Rockies in Colorado and Montana, USA. *Russula* species are mycorrhizal fungi that have brittle gills, and stalks that resemble the flesh of apples.

Fomitopsis solaris is a small, white bracket fungus that grows on the dead wood of willows (*Salix* species) and conifers. Its distribution spans the UK, a swathe of mainland Europe from Sweden to France, plus Argentina, Canada and Israel.


Purpureocillium atlanticum

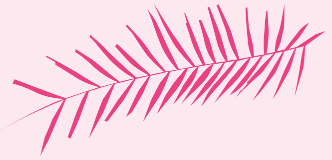

Fomitopsis solaris

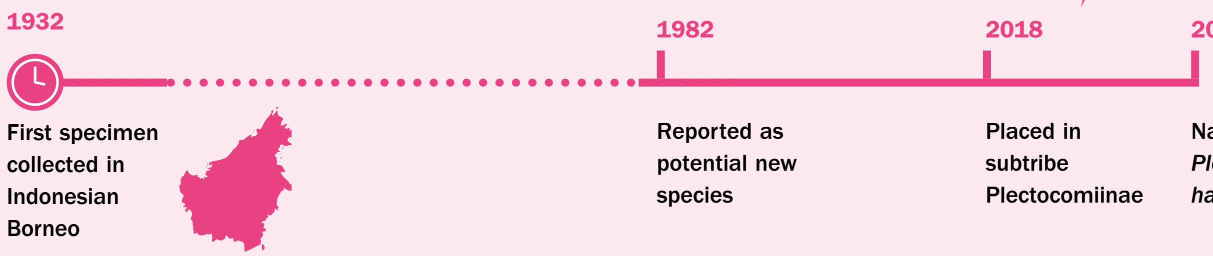

Phellodon frondosoniger


Russula neopascua

Plectocomiopsis hantu in its rainforest habitat in Indonesian Borneo.

BOX 1: Ninety-two years to name a ghost





1932 First specimen collected in Indonesian Borneo

1982 Reported as potential new species

2018 Placed in subtribe Plectocomiinae

2024 Named ***Plectocomiopsis hantu***

In 1932, a striking specimen of climbing rattan palm was collected in Indonesian Borneo. It stood out because its fronds were glossy green on top and chalky white underneath. Its collector, recorded as being ‘A. Beck’, deposited the specimen in the country’s Forest Research Institute, in Bogor.

Fifty years later, John Dransfield, at the time Head of Palm Research at Kew, reported the specimen as a potential new species of *Plectocomiopsis*, while reassessing the genus. He noted that its unique leaf colouration set it apart from all other species of the genus. However, because the specimen had no flowers or fruits – usually needed to describe species as new to science – he decided not to formally name the species until more material became available.

More years passed until, in 2018, an expedition to Malaysian Borneo including Kew botanists Benedikt Kuhnhäuser and William Baker, and local guides Sirukit anak Dubod, Mugu anak Sanggap, Dellie anak Medie and Medie anak Aloh, came across the same unusual rattan species. Yet again, no reproductive parts were present and so the collections they made comprised only stems and leaves.

Back at Kew’s Jodrell Laboratory, Kuhnhäuser’s phylogenomic research placed the specimen firmly in the subtribe Plectocomiinae, but its affinities with the three closely related genera *Plectocomiopsis*, *Plectocomia* and *Myrialepis* remained unclear. Dransfield helped to locate additional specimens of the same species that had been collected in 1993, 1995 and 2001. These were also without flowers or fruits, but DNA sequencing confirmed them to be the same species.

In 2024, the Kew palm team took the decision to officially name the species as new to science so that researchers could refer to it more easily while they tried to find out more about it. They placed it in the genus *Plectocomiopsis* based on the specimens and data available, as it appeared to have the closest affinity with this genus. They chose the species epithet *hantu*, meaning ghost in Indonesian, to reflect both the palm’s elusive nature and its white leaflet undersides.

Plectocomiopsis hantu was already known to locals in Borneo – who called it *wi mukoup* or *wee mukup* – but having a scientific name now means it can be included in conservation and management plans. This is critical because the plant is known only from three rainforest locations. The hope is that, before long, the species will be found in flower and fruit to allow its full characterisation, and that new methods will become available to reveal the exact position of this elusive palm on the plant tree of life.

The unusual colouration of the palm’s leaves helped to single it out as a new species.

MAKING THE MOST OF MUSHROOM MUSEOMICS

A mycologist in Kew's Fungarium carefully prepares a specimen to sample for DNA extraction.

SCIENTISTS HAVE SEQUENCED THE WHOLE GENOME OF A 180-YEAR-OLD FUNGAL SPECIMEN

In this chapter, we learn: that scientists have cracked how to sequence the genomes of preserved fungi; why short-read sequencing is effective when sampling older fungal specimens; that different fungal groups yield different amounts of DNA; and how widescale sequencing of historical specimens is set to benefit us all.

WHOLE-GENOME SEQUENCING OF HISTORICAL FUNGAL SPECIMENS IS UNDERWAY, OPENING A PATHWAY FOR NEW MYCOLOGICAL STUDIES.

Unlike plants, which largely undertake their life cycles in plain sight, most fungi live hidden lives. Some grow from spores into long filaments called hyphae, which can branch and form vast subterranean networks known as mycelia. Only when they develop mushrooms or other reproductive structures to release their spores do these fungi reveal their presence in the world. As a result of their elusive nature and the fact that a staggering 2.5 million species of fungi are estimated to exist, more than 90% remain unknown to science. Even known species still hold many secrets, but preserved specimens could help to unlock them.

In a pioneering study, Kew's mycologists and collaborators have methodically tested different ways to extract, sequence and assemble DNA from fungarium specimens and found it possible to produce high-quality genomes from fungi collected more than a century ago. This advance could not only shed light on their evolutionary history, confirming or questioning existing classifications and uncovering novel species, but also reveal the roles they play in ecosystems and any useful compounds they contain (see Figure 1).

'I was leading the fungal component of the Plant and Fungal Trees of Life project here at Kew, which aimed to sequence the DNA of every genus of fungus to explore their evolutionary relationships,' explains Ester Gaya, Senior Research Leader in Mycology. 'Instead of going all over the world trying to collect fungi that were missing from this tree of life, we thought we would make use of our preserved specimen collections. We also wanted to generate molecular data for our prized 'type' specimens, as these are the definitive physical reference material on which scientific names are based.

Gaya and colleagues began assembling a target list of preserved specimens to sequence from among Kew's 1-million-strong Fungarium collection, which holds more than 50,000 species. Using the digitised specimen records, they aimed to gather samples of varying ages from across the fungal tree of life and different parts of the world (see Figure 2, overleaf). For the most species-rich groups – the mushroom-forming Basidiomycota and cup-forming Ascomycota – specimens were sampled from all continents. Where available, the scientists included type specimens, and they prioritised fungi of uncertain taxonomy, altogether compiling a set of 2,104 specimens that had been collected between 1770 and 2023. The eclectic mix ranged from the lion's mane or bearded tooth fungus (*Hericium erinaceus*), used in traditional Chinese medicine and popular in food supplements, to octopus stinkhorn (*Clathrus archeri*), the putrid smell of which attracts insects to disseminate its spores, and the truffle-like *Hysterangium nephriticum*, which plays a vital role in forest health.

GLEANING DATA FROM FUNGAL FRAGMENTS

The team used a technique called short-read sequencing to generate whole-genome sequences for the fungarium specimens. A major benefit of this technique is that it is cost-effective for large numbers of samples and can be used successfully on degraded specimens where the DNA has become fragmented over time. The first stage of the process involves extracting DNA from a specimen and then breaking it apart. The resulting small fragments are then tagged at each end to enable processing, forming a 'library'. Next, these fragments are sequenced simultaneously, generating millions of randomly ordered 'reads' (short strings of DNA sequences). In the final phase, using a computational process similar to solving a vast, complex puzzle, the overlaps between the sequences of these millions of reads are used to reassemble the specimen's whole genome.

Initially, the team focused on the first part of the process, seeking to understand how the method used to extract DNA might influence the yield obtained and subsequent sequencing success. They tested six methods, including one aimed specifically at extracting ancient DNA and others commonly reported in scientific literature as effective for fungi and plants. To sample each selected fungarium specimen, the mycologists took a 1–2 mm piece of tissue from the layer of spore-bearing cells – the hymenium – carefully avoiding any attached soil, bark or other substrates that might contain other fungal species and contaminate the sample. Fungal cultures and freshly collected fungi were also included in the study so that the researchers could compare the results from recent and historical specimens. In total, they carried out 2,524 DNA extractions.

Ahead of genome sequencing, to confirm the DNA they had extracted was from the target species or genus, the team attempted to barcode as many of the specimens as possible, focusing on the less-degraded material. For this, they used the internal transcribed spacer (ITS) region, which is the most commonly used region for identifying fungi and has two sections that are variable enough to distinguish species in a quick and easy process. Large databases of such DNA barcodes already exist, which the team drew on to make sure their DNA samples matched the specimen and had not been contaminated. Because this technique requires the ITS region of DNA to be intact, however, it is less effective for older specimens. Nonetheless, the team was able to generate barcodes for 771 specimens, 319 of which were not included in existing databases.

FUNGAL SPECIES HOLD MANY SECRETS THAT PRESERVED SPECIMENS COULD HELP TO UNLOCK.

For the whole-genome sequencing, the next step involved constructing libraries for a selection of specimens – chosen based on the yield of DNA extracted and the level of fragmentation exhibited. 'With short-read sequencing, you sequence shorter fragments of DNA,' explains Kew Research Fellow Torda Varga, who played a key role in designing the methodologies applied during the project and analysing the data. 'The sequencing machine is optimised to read DNA fragments that are 600–800 base pairs long, with base pairs being the 'letters' that code the genetic information. So, if need be, you shear the DNA to the correct-sized lengths – but we skipped this process in many instances due to the historical DNA already being fragmented. Then you tag these by attaching extra molecules to make them compatible with the chemical reaction in the sequencing machine and to sort sequenced reads into associated libraries.'

Of the 442 specimen libraries, 392 were deemed to be sufficiently robust to send for whole-genome sequencing. Then, back at Kew, Varga constructed an automated assembly pipeline, combining various bioinformatic tools to enable the vast amount of output data to be managed and assembled. The pipeline was able to produce 16 alternative genome assemblies for each library. 'Because we had so many different species, with different genomic structures, one tool would not necessarily work for all of them,' says Varga. 'That's why we put together this automated pipeline. At the end, once the process was complete, we could work with the best assembly for each specimen.'

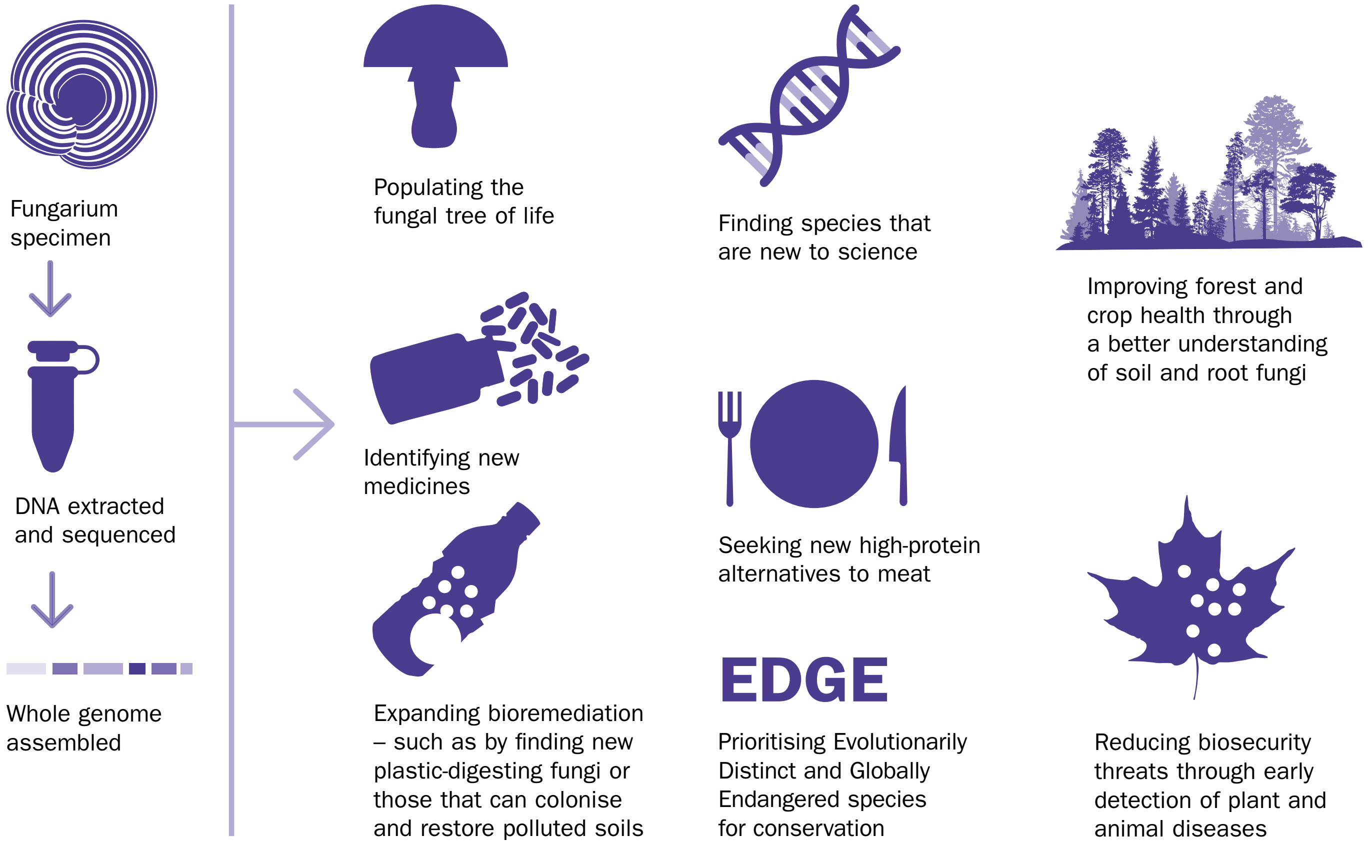
To keep the analyses simple, the researchers focused on 220 non-lichen species (lichens are more complex, being a mixture of a fungus and algae or cyanobacteria). The team employed various established ways to assess the quality of genome assemblies. When using the best assembly for each sequenced specimen, 159 of the 220 specimen assemblies attained a quality comparable to genome assemblies from fresh cultures. Pleasingly, high-quality assemblies were obtained for many of the oldest specimens in the study, including 23 type specimens. For example, the assembly of the 180-year-old type of the false truffle *Hysterangium nephriticum* resulted in a high-quality 63-million-base-pair genome, despite its age. The team found that the assembly quality could be increased by sequencing more reads per library.

IDENTIFYING WHAT INFLUENCES DNA YIELD

Sequencing success relies on a minimum concentration of DNA being present. To explore what – if any – factors might affect the total amount of DNA extracted, the team looked at the effect that the input sample weight, specimen age, taxonomy (specifically, which high-level group of fungi the species belonged to), extraction protocol and climate (of the geographic region of collection) had on DNA yield.

FIGURE 1: Understanding fungal genomes will bring many benefits

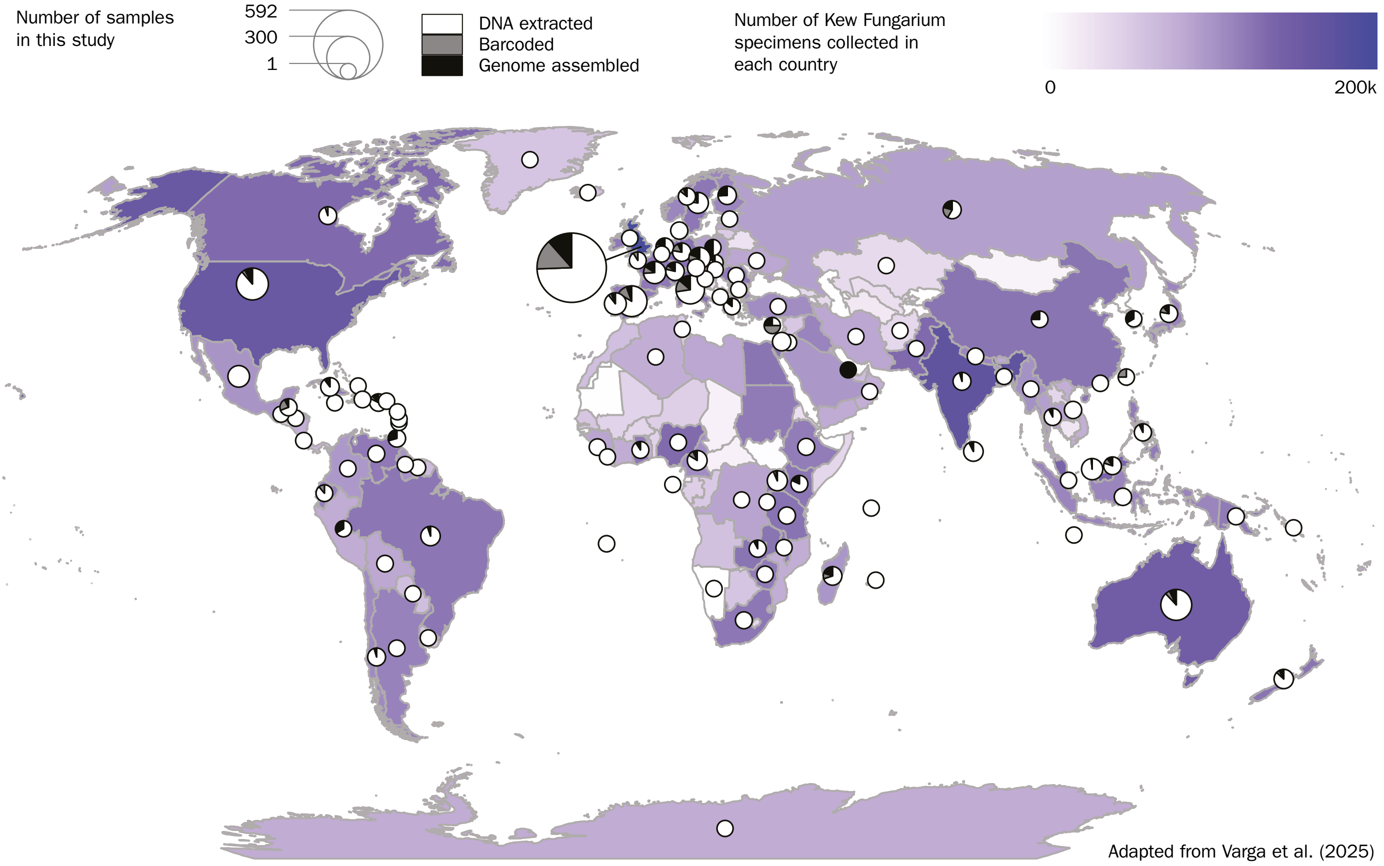
The new findings on how best to sequence the whole genomes of preserved fungal specimens will drive innovation and facilitate wide-ranging research and applications.



Great care must be taken during DNA sequencing not to contaminate samples.

FIGURE 2: Specimen collection locations and sampling information

The map shows the source countries of all 2,104 specimens used by the study team, as well as of the one million accessions in Kew's Fungarium as a whole. The size of each pie chart reflects the number of specimens from that country used in the study, and the pie segments show the proportions of those that: only had their DNA extracted; were barcoded after extraction but didn't progress to sequencing for technical reasons; or had their full genomes assembled.



Adapted from Varga et al. (2025)

This revealed that taxonomy and the extraction method used had the biggest effects on the total yield, followed by specimen age and climate. Interestingly, there was only a weak positive correlation between the dry weight of the fungal tissue used and the amount of DNA extracted, meaning that future DNA studies can be successful with minimal amounts of destructive sampling.

When it came to taxonomy, the team observed the greatest total DNA yields in the Pezizomycetes, followed by the Agaricomycetes, relative to the low-yielding Dothideomycetes. The effect was significant but less pronounced for the Eurotiomycetes, Lecanoromycetes and Pucciniomycetes, while no effect at all was observed in the Sordariomycetes. These results echoed the findings of earlier studies that had also found a link between taxonomy and the success rate of molecular work.

Regarding extraction protocols, the scientists found that a buffer-based protocol using a chemical called N-phenacylthiazolium bromide (PTB) produced a higher total DNA yield than the commercially available kits. This concurred with the findings of other studies that had found PTB buffer-based approaches to be effective for extracting the short fragments associated with historical specimens. Another buffer-based approach, using cetyltrimethylammonium bromide (known as CTAB) also performed better than the commercially available kits.

Climate and the age of the specimen had the smallest relative influence on the total DNA yield. The climate in which each specimen had been collected was assigned to one of five climate zones: equatorial, arid, warm temperate, snow, and polar. Total DNA yield increased from arid to warm temperate to snow zones, relative to specimens collected from the equatorial zone; there were insufficient specimens to assess the polar zone. The adaptive traits that species had evolved to deal with their environments, the different methods used to preserve specimens, and the varying times at which they had been collected were not independent of climate, making it hard for the team to isolate specific causes for this pattern. One explanation could be that a colder climate had helped to preserve DNA at the point of collection in the field, while high temperatures and humidity in tropical climates might have accelerated the rate at which DNA had degraded, reducing its quality.

REVELATIONS FROM FUNGAL GENOMES

To date, most sequencing for taxonomic and evolutionary studies has been carried out on particular regions of the genome, primarily to identify species and develop fungal evolutionary trees. However, to understand more about how fungi function and to identify genes involved in the biosynthesis of complex molecules, mycologists ideally need to examine the entire genome. Biosynthesis is of particular interest as it underpins: the production of life-saving medicines, such as antibiotics and statins; fermentation for food and drink products; the production of biofuels; and the generation of vital industrial enzymes that help to degrade environmental pollutants.

Around the world are collections of fungal specimens covering a broad geographic range and, in some cases, extending back centuries. By showing how large numbers of high-quality genomes can be produced from historical material using customised DNA extraction protocols and assembly methods, Kew has paved the way for an explosion of whole-genome sequencing of historical specimens. Moreover, the genome assemblies that the project yielded could help mycologists to design other fungarium sequencing research in the future. Thanks to the success of this study, work is already underway in the UK to carry out whole-genome sequencing for a much wider study set of fungal specimens. This collaborative, large-scale, short-read sequencing project is drawing on not only Kew's collections but also those of the Natural History Museum in London and the Royal Botanic Garden Edinburgh. The aim is to sequence 7,000 type specimens in total, including both fungi and lichens, by 2028. The hope is that sequencing the whole genomes of these important specimens will greatly advance fungal science and its applications.

'Currently, a lot of people are undertaking environmental DNA sequencing, where they take, for example, a soil sample and obtain DNA sequences of everything in it,' explains Gaya. 'We'll be able to put names on some of the unknown elements from the environmental sequencing by providing reference genomes to identify them against. We're going to give fungal science a stronger evolutionary foundation.'

Most specimens in Kew's Fungarium have 'not even been sequenced at barcode level, let alone the whole genome,' continues Gaya, 'and around 70% of the species are not currently represented in public fungal sequence repositories.' The new undertaking will vastly expand the data available to scientists, facilitating population genomic studies – where the complete DNA of many individual fungi from the same species is analysed. This will help mycologists begin to understand the genetic variation within fungal species, how they have evolved and adapted to local conditions, and how traits such as drug resistance have spread. As the most effective ways to extract, sequence and assemble DNA are further honed, and these protocols applied to other preserved collections, the secret lives of fungi will finally come into view.

This chapter is based on the following publication in our special collection:

Varga, T., et al. (2025). Whole genome sequencing of historical specimens from the world's largest fungal collection yields high-quality assemblies. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70472

THIS WORK HAS PAVED THE WAY FOR AN EXPLOSION OF WHOLE-GENOME SEQUENCING OF HISTORICAL SPECIMENS.

READING THE PAST AND FORECASTING THE FUTURE

SPECIMEN RECORDS SPANNING

4 CENTURIES

CAN PROVIDE DEEP INSIGHTS

In this chapter, we learn: why native tomatoes are under threat from an introduced species in the Galápagos Islands; how herbarium specimens can help to track the expansion of non-native species; that hybridisation can result in 'extinction by mating'; and how studying DNA from preserved specimens can tell us about biodiversity's past and future.

The Galápagos Islands have long attracted scientists to study their unique species.

DIGITISED HERBARIUM SPECIMENS AND THEIR GENOMES CAN REVEAL NEW INSIGHTS INTO THE EVOLUTION, DISTRIBUTION AND DIVERSITY OF SPECIES.

The increasing availability of digitised herbarium specimens has made it easier to map how plant species and populations have shifted over time. And genomic data have enhanced understanding of the diversity and evolutionary history of species. Now, scientists are finding that the combination of the two can be an even more powerful tool. Specifically, the analysis of herbarium specimens can extend the timescale and geographic extent across which genetic inferences about species can be made. In the Galápagos Islands, this approach is helping to unravel the evolutionary history of two native and one introduced tomato species, and to determine what effect the newcomer from the mainland might have on its wild island cousins.

'We wanted to find out what we could understand about the ecological and evolutionary timescales of these three really interesting species, using historical records rather than making somewhat indirect inferences from genomic data and from population genetic models,' explains Leonie Moyle, Professor of Biology at Indiana University in the USA, who led the study. 'We found it's a really nice complementary approach to using high-tech genetic analyses – by taking advantage of this absolutely beautiful, diverse and deep historical record from the Islands.'

Administratively part of Ecuador but lying 960 km west of the mainland, this volcanic archipelago has long fascinated plant collectors. The earliest known herbarium specimens were collected there by the Scottish surgeon Archibald Menzies in 1795. Naturalist Charles Darwin subsequently gathered and preserved numerous specimens when he stopped off in the Galápagos in 1835 on the *HMS Beagle* expedition. And other significant collections were made by the Hopkins–Stanford scientific collecting trip of 1898–99 and the California Academy of Sciences First Expedition of 1905–06.

The 13 major islands (>10 km^2) and numerous smaller islands, islets and rocks of the Galápagos host more than 600 native vascular plant species (those with specialised vessels for transporting water and nutrients – the majority of global land plants). Of these, 30% are endemic (found only in the Galápagos). Islands act as laboratories of evolution because newly arrived species adapt to the environmental forces around them, without influx from the wider gene pool of their parent population. This drives differentiation and the formation of new species. However, it also makes island species vulnerable to change, as they cannot easily escape threats and have less genetic diversity to respond to new and unexpected pressures.

PLANTS UNDER PRESSURE

Permanent human settlements became established on the Galápagos from 1832, with the population expanding greatly during the 1980s. Today, four of the islands are permanently inhabited. These are Isabela, Santa Cruz, San Cristobal and Floreana. Over the past century, there have been huge changes in the Galápagos, including: the introduction (and later deliberate eradication from some islands) of non-native animals such as goats, pigs and donkeys; the increase in human residents to more than 30,000 today, along with an associated rise in agriculture; the quadrupling of tourist numbers since 2000 to 270,000 in 2019; the introduction of invasive plants; and climate change. These major waves of human disturbance have put wild species under great pressure.

The two native tomatoes researched by Moyle and colleagues are among the species affected by human activity. Both endemic to the Galápagos, *Solanum cheesmaniae* and *S. galapagense* are today under threat from the introduced tomato *S. pimpinellifolium*. The latter is native to mainland Ecuador and Peru but now also grows wild on the Islands. All three species are herbaceous perennials that live for up to a decade but differ in their leaf shapes, bushiness, hairiness, scent and habitat. Field observations indicate that *S. galapagense* favours exposed coastal and arid locations (even growing on bare volcanic rock), while *S. cheesmaniae* is more frequently found in arid or transitional habitats, often with other perennial plants. *Solanum pimpinellifolium,* meanwhile, establishes itself in disturbed ground, including roadsides.

'The two endemics have a lot of traits that are unique to the islands,' says Moyle. 'Our inferences from genomic data suggest that the ancestor of these two species arrived in the Galápagos within the last half million years. So, there's been a single colonisation and then a diversification into two morphologically and ecologically different species. They have lots of interesting individual traits that differentiate them from each other, but the thing they have in common is their unique orange fruit colour. In contrast, the non-native *S. pimpinellifolium* has red fruits, but since its introduction, some of its populations have started to evolve orange fruit as well.'

ISLANDS ACT AS LABORATORIES OF EVOLUTION BECAUSE NEWLY ARRIVED SPECIES ADAPT TO THE ENVIRONMENTAL FORCES AROUND THEM, WITHOUT INFLUX FROM THE WIDER GENE POOL OF THEIR PARENT POPULATION.

Specimen of *Solanum cheesmaniae* collected by Charles Darwin in the Galápagos Islands on the 19th-century *Beagle* expedition. Note, the labels show previous names for this species, reflecting changing understanding of plant taxonomy.

Box 1: Tracking the expansion of non-native species in the tallgrass prairies of Missouri, USA

The silent, creeping spread of non-native species is not unique to the Galápagos Islands but threatens biodiversity in many countries. Without long-term and widespread data, it can be hard to know what impact these newcomers are having on native species. For example, while the history of how North America's tallgrass prairie was transformed by agriculture, wildfire suppression and the removal of large, native herbivores is well documented, much less is known about how non-native species have affected native ones across broad scales in this threatened ecosystem.

Herbarium specimens are helping to change this. A study that harnessed more than 65,000 digitised herbarium specimens across 522 species used a demonstrated relationship between the relative abundance of species in the field and in herbarium collections to show how the composition of the tallgrass prairie flora had changed since the 1890s across three ecoregions of Missouri, USA. This work revealed that in the Interior Plain and Interior Highlands, the relative abundance of non-natives was more likely to have increased. In contrast, species in the Atlantic Plain that had changed in abundance were more likely to have decreased – regardless of whether they were natives or non-natives.

This research highlights the potential for specimen-based studies to provide quick overviews of how non-native species have affected native assemblages across broad areas. This could be helpful for guiding more precise, fine-scale investigations of ecosystem composition shifts over time to support more targeted and effective conservation actions. Further studies could include genetic analysis of species that are having the largest impact, alongside detailed field surveys of contemporary populations, to track their source and spread.

The Missouri Prairie Foundation's Schuette Prairie, a 40-acre unploughed, old-growth prairie in Polk County.

IT'S A REALLY NICE COMPLEMENTARY APPROACH TO USING HIGH-TECH GENETIC ANALYSES – BY TAKING ADVANTAGE OF THIS DIVERSE AND DEEP HISTORICAL RECORD FROM THE ISLANDS.

Using field assessments and genomic data, Moyle and colleagues had previously shown that hybridisation between the endemic and invasive species was causing the change in colour. Hybridisation between introduced and native species is problematic as it can result in the non-native gene pool diluting and eventually replacing the native one in a form of 'extinction by mating'. Understanding where and how the hybridisation is happening is therefore important for safeguarding the native species. However, because contemporary samples of the three species were limited, the scientists had found it difficult to pinpoint, using genomic methods, exactly when *S. pimpinellifolium* had arrived and its subsequent interactions with *S. cheesmaniae* and *S. galapagense*. This had prompted them to see if digitised herbarium specimens might be able to shed more light on the problem.

SEEKING HELP FROM HISTORY

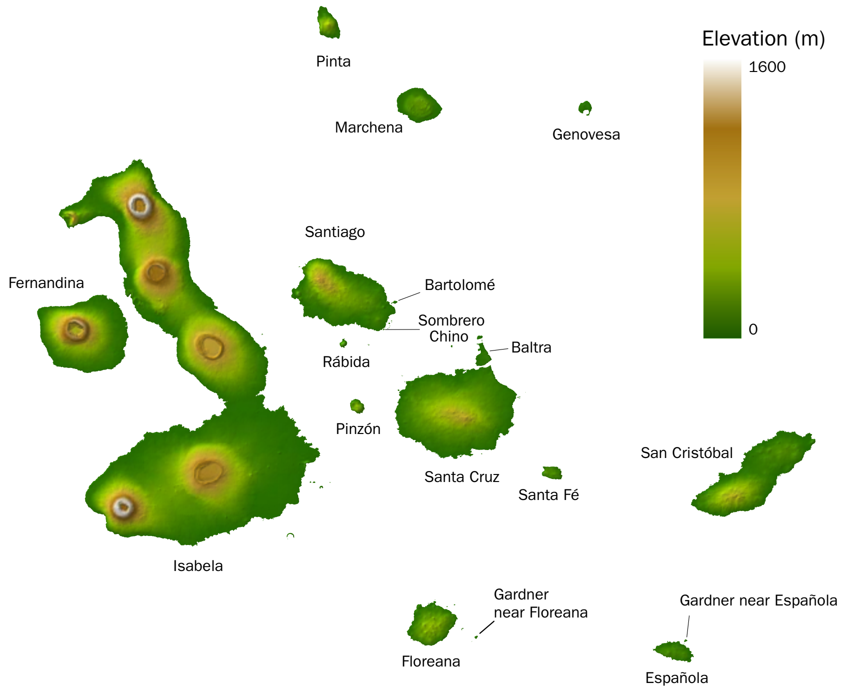
The team aggregated digitised herbarium and other collection records, spanning four centuries from 1795 to 2021. After a series of cross-checks, they arrived at a dataset of 410 unique historical records, including specimens from 18 herbaria, as well as geolocation and associated data from germplasm collections held at the C.M. Rick Tomato Genetics Resource Center at the University of California Davis site, USA, and field occurrence records from the Charles Darwin Research Station on Santa Cruz Island. The dataset also included contemporary collection records made by the scientists during field surveys between 2018 and 2021. In total, there were 169 records of *S. cheesmaniae,* 144 of *S. galapagense* and 82 of *S. pimpinellifolium*. In addition, there were 15 records for proposed or confirmed hybrids (*S. cheesmaniae* × *S. pimpinellifolium*).

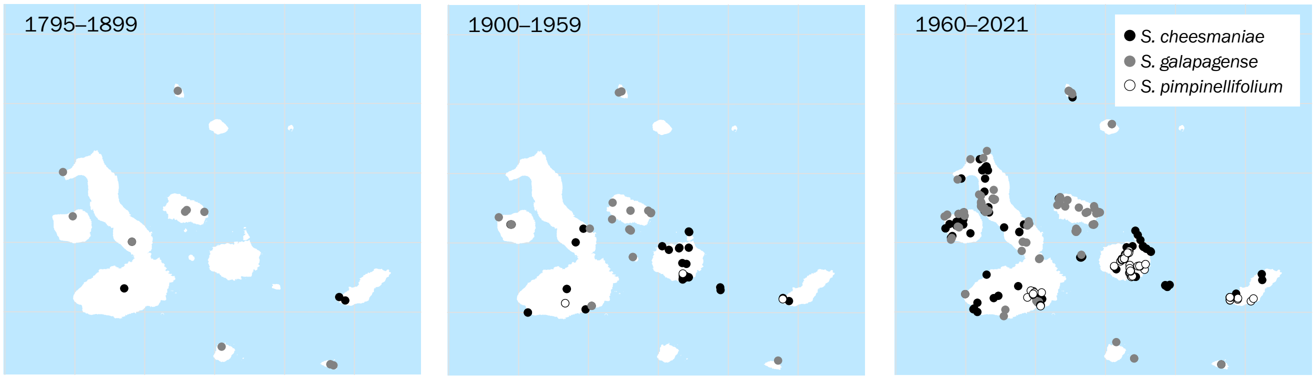
The scientists used this dataset, along with geographical and climate data, to find out more about the three species' past and current distributions, and to investigate factors influencing where they might grow in future. First, they mapped the distributions of records of the species from across the archipelago. This revealed that *S. cheesmaniae* had only ever been found on islands greater than 18 km^2, that *S. galapagense* had been collected both on large and much smaller islands, and that *S. pimpinellifolium* had historically only been recorded on three islands, all of which were inhabited (see Figure 1).

Next, they layered the specimen occurrences with climate information. The Galápagos have three main climate zones:

Figure 1: Charting the spread of a non-native tomato in the Galápagos

The map on the right shows the major islands of the Galápagos. *Solanum pimpinellifolium* is a non-native tomato species that is spreading across the islands and into the habitats of the native tomatoes *S. cheesmaniae* and *S. galapagense*. The former is particularly at risk, as its habitat preferences and projected distribution are similar to those of the non-native species, with which it hybridises. For example, *S. cheesmaniae* has only ever been found on islands that are larger than 18 km^2 – which have higher elevations providing moist conditions – and three of those are the populated islands on which *S. pimpinellifolium* has become established. The maps below show how the distribution of field collection records for the three species has changed over time.





Adapted from Kutza, Hert & Moyle (2025)

Improved techniques for extracting and sequencing the DNA of herbarium specimens have opened up new areas of research.

Box 2: Specimen DNA provides windows into the past and future

Recent advances have made it feasible to extract and analyse DNA from even very old preserved specimens, offering new opportunities to look at changes in plant and fungal diversity and evolutionary dynamics. So, what can we learn from mobilising the vast amount of genetic data within the world's herbaria?

Genetic variation and population resilience are connected, so monitoring genetic change is important for biodiversity and conservation studies, particularly in the context of a changing environment. As the Galápagos tomatoes work shows, herbarium specimens can extend the timescale over which change can be monitored by allowing scientists to look back into the genetic past of a species, generating otherwise absent baseline data. DNA from historical collections can therefore reveal changes in genetic metrics over timescales of decades or more, which is more informative than simply examining current values.

One way to investigate these changes is to aggregate specimens collected from the same location and time period to recreate historical populations that can be compared with contemporary samples. Mobilising these data digitally and then sampling the physical specimens can bring new insights across a range of topics. For example, such comparisons can reveal changes in genetic variation preceding and following extinctions, helping us to understand more about the signals, causes and wider consequences of such events. Past reductions in diversity and the loss of unique genetic variation might have affected the resilience of a population or species, making extinction more likely, and this information could be useful for conservation planning.

Herbarium specimens also provide an opportunity to investigate adaptive responses to global change. Identifying the genes that contribute to adaptation is vital to understanding how past populations have responded to environmental pressures and how current populations may respond to future changes. For example, historical potato (*Solanum tuberosum*) specimens enabled researchers to investigate the genes involved in the species' adaptation to shorter growing seasons and longer days following its introduction into Europe from South America in the 16th century. Being able to scan across genomes for signatures of natural selection, and compare historical and contemporary diversity, can also highlight genes and corresponding characteristics that are not commonly measured but that might be important indicators of adaptation.

Herbarium specimens show potential for predicting future adaptive responses, too, particularly in relation to climate. This involves combining digitised specimen data with genetic and climate data to identify genes or gene families that may be involved in adaptation to climate, and then projecting into the future using climate models to predict whether a population will be adapted or maladapted to the new conditions. While this method is typically used to predict genetic change in the future, herbarium collections could offer an opportunity to validate the method by testing predictions about the genetic composition of past populations.

With so many applications and so many species to use as test subjects, it is clear that collating the data from specimen-based genetic studies across the globe will create an invaluable resource. Over time, this could yield insights that go far beyond those of the individual studies.

arid lowlands, a transition zone at intermediate elevations, and humid highlands that only occur on higher-elevation islands. By looking at where the conditions favoured by each species existed elsewhere around the islands, the scientists came up with a set of projected locations that could potentially support them in future. The projected distribution for *S. galapagense* spanned the arid zones across the archipelago and extended up into the transition zone on most islands. *S. cheesmaniae*'s forecast distribution coincided substantially with that of *S. galapagense* but also encompassed humid ecosystems.

The non-native *S. pimpinellifolium* was projected to be more prevalent on larger islands with higher-elevation climate zones, coinciding with humid highland ecosystems. Its projected niche overlap was consistently greater with *S. cheesmaniae* than *S. galapagense* and encompassed some areas in the transition zone where *S. pimpinellifolium* and *S. cheesmaniae* already both occur and are hybridising. Precipitation appeared to have a strong controlling influence on island specimens of *S. pimpinellifolium*. Meanwhile the current and projected locations of *S. cheesmaniae* were mostly on the largest islands with high-elevation humid habitats, suggesting an inability to tolerate the persistent aridity, periodic severe droughts and lack of soils characteristic of the small, low-elevation islands.

UNDERSTANDING IMPACTS

The main drivers of change in the Galápagos are climate change, local population growth, unsustainable tourism and invasive species. *Solanum cheesmaniae*, living as it does on larger, higher islands, including those with a substantial human presence, is thus at particular risk in future. During fieldwork on three of the main islands in 2018–2019, Moyle and colleagues had not been able to relocate more than 80% of the *S. cheesmaniae* and *S. galapagense* populations recorded prior to 2003. The new study showed that the projected areas with greatest future exposure to environmental threats coincided substantially with the historical distribution and projected suitable habitat of *S. cheesmaniae.* As well as these general threats, the species faced specific pressure from its contact with *S. pimpinellifolium*, through direct competition and hybridisation.

'The projection forward is important because it identifies that *S. cheesmaniae* is much more vulnerable to future contact with the invasive species than the other endemic species,' says Moyle. 'It tells us something about the likely locations of future populations of the invasive on the islands unless restrictions to prevent it moving within and between islands are maintained.'

Understanding more about the dynamics of *S. pimpinellifolium* could help to define exactly how much of a threat it is and guide actions to minimise its negative impacts. Moyle and colleagues had previously inferred from genomic data that most individuals of *S. pimpinellifolium* on the islands were descended from a single introduction from central Ecuador, but genetic ancestry pointed to at least two other independent introductions, one each from Ecuador and Peru. The new study revealed that the oldest unambiguous specimen of *S. pimpinellifolium* had been collected in 1985 but that older specimens also exist – dating back to 1956 and 1905 – for which the identity is currently contested. In future, extracting DNA from these additional physical specimens could prove whether they, too, are *S. pimpinellifolium* and, hopefully, confirm how many times the invasive has been introduced and when, and reveal its path to becoming established. This could help to indicate how – and how fast – it may spread from any additional introductions in future, unless preventative measures are put in place.

'If we can actually trace the familial relationships among each of these different invasive individuals, we will be able to say whether there has just been one introduction or more than one,' says Moyle. 'We will be able to ask: Where did each specimen come from? Did they all come from the centre of Ecuador, which is where we know most of the invasive ones are currently from? Or did they come from Peru? There's lots of actual genealogical data that you can then map, because you can sample the DNA of these things. That's why herbarium specimens themselves are sort of magic. They have human historical dimensions, and then they have evolutionary historical dimensions from the DNA itself.'

This chapter is based on the following papers in our special collection:

Austin, M.W., et al. (2025). Herbarium specimens reveal regional patterns of tallgrass prairie invasion and changing species abundance across 130 years. *New Phytologist.* DOI: https://doi.org/10.1111/nph.70632

Eckert, L., et al. (2025). Using herbarium collections to study genetic responses to global change. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70454

Kutza, A.D., Hert, Z.L., Moyle, L.C. (2025). Endemic and invasion dynamics of wild tomato species on the Galápagos Islands, across two centuries of collection records. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70321

THE PROJECTION FORWARD SHOWS *SOLANUM CHEESMANIAE* IS MORE VULNERABLE THAN *S. GALAPAGENSE* TO FUTURE CONTACT WITH THE INVASIVE SPECIES.

KEEPING A WEATHER EYE ON PLANTS

DIGITISED SPECIMENS ARE HELPING TO FILL KNOWLEDGE GAPS IN UNDERSTUDIED AREAS

In this chapter, we learn: that flowering seasons are getting longer in some places and shorter in others; how the Arctic is experiencing ‘shrubification’; why species are converging at mid elevations on mountains; and that specimen collectors may need to change their focus to benefit climate studies.

A new checklist of Greenland’s plants is among research outputs that are contributing new knowledge on Arctic biodiversity.

PHENOLOGY – THE STUDY OF SEASONAL AND CYCLICAL EVENTS IN SPECIES' LIFE CYCLES AND HOW THEY ARE INFLUENCED BY THEIR ENVIRONMENT AND CLIMATE – IS MAKING ADVANCES, THANKS TO DIGITAL HERBARIUM SPECIMENS.

Societies have long observed the life cycles of plants to inform optimal times for hunting, gathering, sowing, harvesting and celebrating. Written records of cherry tree flowering in Asia date back more than a thousand years, while a two-centuries-long record of seasonal cues – such as trees coming into leaf and snowdrops emerging – began in the UK in the early 18th century. In recent decades, phenology has become established as an effective way to track the impacts of climate change. But living plants are not the only source of seasonal information. Herbarium specimens are usually annotated with their time and place of collection, thereby capturing the life-stage of the plant at that point. Today, digitised specimens and AI-based technologies are facilitating phenological studies that are larger in scale, reach further back in time or include understudied regions, as well as enabling scientists to pose novel ecological questions related to climate change.

The use of herbarium specimens in phenology began in earnest in the late 20th century, and the first comprehensive paper demonstrating their application to studying climate change was published in 2004. Based on flowering times in the Arnold Arboretum of Harvard University, USA, the study showed it was possible to combine both preserved and living specimens to examine flowering times over long periods. With very little digitised material available at the time, the work had only focused on this single location and had involved pulling specimens from cabinets and shelves.

'Now, with more and more digitised specimens accessible online, we can draw information from many different herbaria at the same time,' says Natalie Iwanycki Ahlstrand, Assistant Professor and Curator at the Natural History Museum of Denmark. 'And we're benefiting from tools such as machine learning that are allowing us to automate data collection from digital images in ways that were unthinkable, even ten years ago. So, the study of phenology using specimens is really burgeoning.'

FACILITATING LARGE-SCALE STUDIES

The power of machine learning to analyse vast numbers of herbarium specimens at speed enabled scientists to publish the first comprehensive phenological study at the global scale in 2025. Scientists in Norway trained a model to classify images based on the presence or absence of flowers and then applied it to eight million preserved specimens collected worldwide, representing 200,000 species. They found that the timing of flowering had shifted across the course of a century, with trends differing between ecoregions. The data revealed both advances and delays in flowering date (median shift of 2.5 days per decade in either direction), as well as shortened and lengthened flowering seasons (1.4 days per decade). Low-latitude regions (the tropics) had higher-magnitude shifts in flowering phenology than high-latitude regions, with strong trends towards both earlier and later flowering times (see Figure 1). Other studies have frequently recorded temperature and daylight hours as the key drivers of phenology, but this may reflect a northern-hemisphere bias. The global analysis suggested that the greater magnitude of shifts in tropical ecoregions could represent changes in the timing or reliability of precipitation, and that phenological shifts were more complex than simple responses to temperature.

'High-latitude phenology – or vegetation responses – are largely linked to temperature, but there's also the limitation of the photoperiod, or day length,' says James Speed, Professor of Plant Ecology at the Norwegian University of Science and Technology, who led the work. 'That isn't changing, so it's a constraint on how much phenology can shift at high latitudes, because it can't go any earlier. On the other side of the coin, down at the low latitudes, the climatic limitation may not be temperature but precipitation patterns, which can be more variable than seasonal changes in temperature. At high latitudes, we might have a bad summer or a good summer, but we know we're getting a summer of some sort. In more arid regions, the wet season might come early, it might come late, or it just might not happen. So, I think the pattern we're seeing is a function of the variability in precipitation seasonality compared to temperature seasonality.'

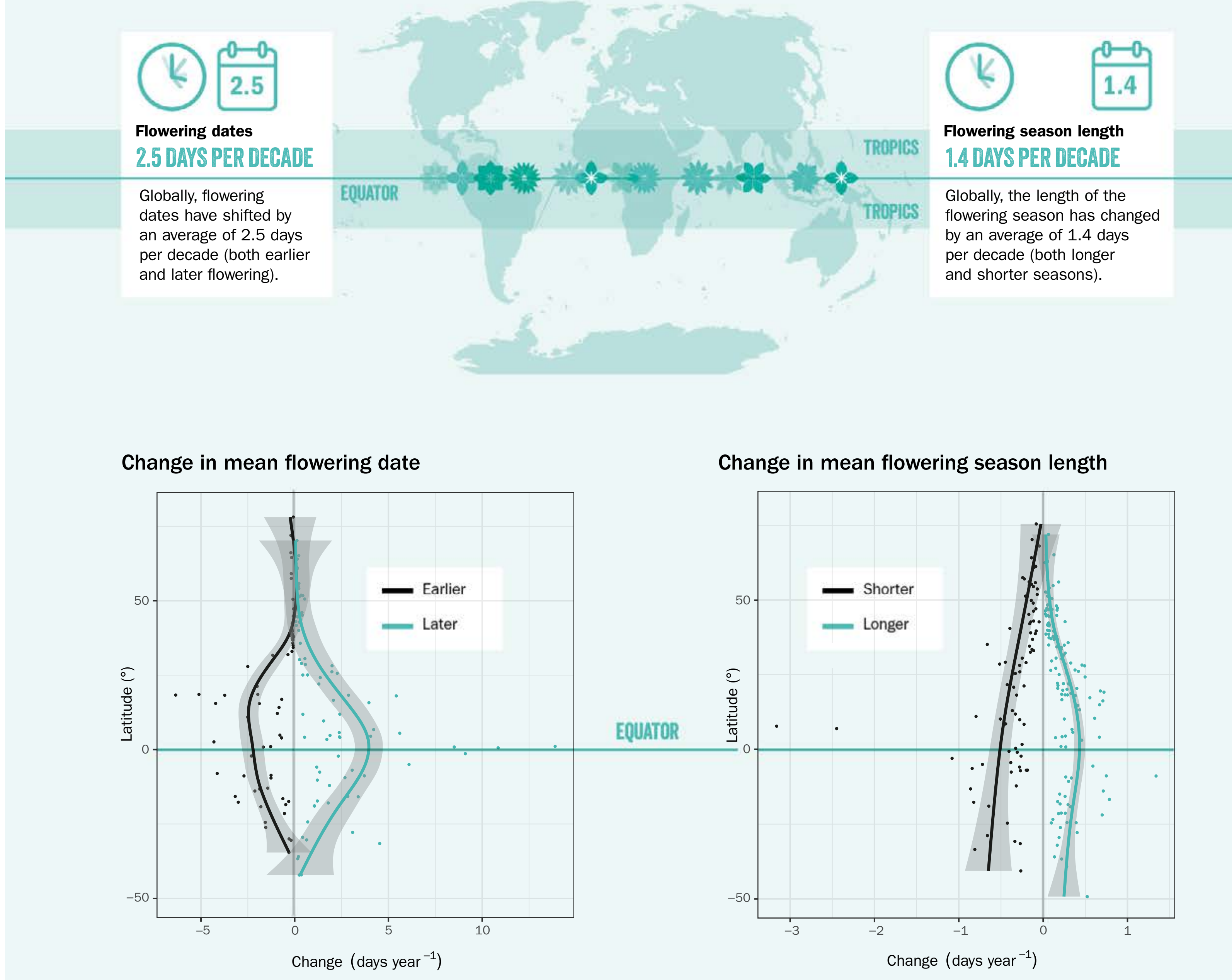
FILLING GAPS FROM UNDERSTUDIED AREAS

Digitised herbarium specimens have also facilitated new work in the tropics and Arctic – areas understudied by phenology experts, in part due to the logistical challenges they present for conducting field research. One study of tropical phenology focused on the Western Ghats mountain chain, a Global Biodiversity Hotspot and UNESCO World Heritage Site in India that has experienced a significant rise in mean annual temperature and a marked decrease in mean annual precipitation over the past 70 years. The study found that the common and commercially important kindal tree (*Terminalia paniculata*) was flowering and fruiting at less predictable times than in the past.

The scientists studied preserved specimens of the tree gathered from 19 regional herbaria. Specifically, they applied a modified version of the Augspurger flowering synchronicity index – a metric widely used in ecology to measure the degree of overlap in flowering times among individuals in a population – to examine flowering trends between the 1950s and the 1990s. The index has a scale of zero to one, with zero showing no overlap and one exhibiting perfect synchronicity. The value for the 1950s was 0.79, dropping to 0.59 for the 1980s and further to 0.47 for the 1990s, indicating a reduction in flowering overlap over time. Within the Western Ghats, the kindal tree is important for maintaining forest diversity through its bee, fly and butterfly

FIGURE 1: Global changes in flowering patterns over the last century

An analysis of eight million digitised herbarium specimens undertaken using AI showed that flowering times and the length of the flowering season have shifted significantly over the last century. The changes were more variable in tropical regions (low latitudes), with flowering shifting earlier in some regions and later in others. The length of the flowering season was also more variable at low latitudes. The study showed that in tropical Africa, the main trend was for the length of the flowering season to have decreased over the last century, while in Australia and Central and South America, the length of the season increased. Trends also varied over time. For example, in Africa, flowering season length increased overall before 1970 and decreased after this point, alongside rapid warming of the climate.



Flowering dates
2.5 DAYS PER DECADE
Globally, flowering dates have shifted by an average of 2.5 days per decade (both earlier and later flowering).

Flowering season length
1.4 DAYS PER DECADE
Globally, the length of the flowering season has changed by an average of 1.4 days per decade (both longer and shorter seasons).

Adapted from Williamson et al. (2025)

VARIABILITY IN FLOWERING SHIFTS IS GREATEST IN THE TROPICS, OCCURING EARLIER IN SOME REGIONS AND LATER IN OTHERS.

pollinators. A concern, therefore, is that as climate change progresses, the life cycles of these interdependent species could fall out of sync.

'We couldn't find a clear cause for the trend among climate, latitude or elevation but we think that it might be because there are many microclimates in the Western Ghats,' says Sivagnanam Chandrasekaran, Professor in the Department of Plant Science at India's Madurai Kamaraj University. 'But it is important because our observations suggest that three of the most common *Terminalia* species – *T. paniculata, T. arjuna* and *T. bellirica* – flower in a relay system. When one stops flowering, the next starts. So, increased asynchronicity in *T. paniculata* could lead to overlapping of the flowering of the three species – and the reproductive fitness of these species could come down as a result. More studies using herbarium specimens are needed to analyse the community-level responses of these and many different species, to reflect the larger-scale influence of climate change on tropical ecosystems.'

Similar efforts are being made to fill knowledge gaps in the understudied Arctic. One project has made strides towards developing a single, curated digital checklist for the flora of Greenland, opening new doors for large-scale studies of Arctic plant diversity. Another examined 17,000 digitised herbarium specimens of 97 plant species collected across the Canadian Arctic to determine whether flowering times there had shifted over the past century, and if so, by how much. The latter project found that flowering times were generally changing but that the change was not consistent across species. At one extreme, the flowering time of Richardson's willow (*Salix lanata* subsp. *richardsonii* [= *S. richardsonii*]) had shifted later by 2.25 days per decade since 1900. At the other, that of the dwarf hawksbeard (*Askellia pygmaea* var. *pygmae* [= *Crepis nana*]) had shifted earlier by 3.85 days per decade since 1915. Overall, flowering times were found to be converging, shortening the tundra flowering season – with later-flowering species shifting their flowering times to a greater degree than earlier-flowering species. The results of the study concurred with those of an International Tundra Experiment synthesis based on 25 years of field monitoring.

'What I suspect may be partially behind the convergence of Arctic flowering times is that temperatures at the end of the growing season as winter approaches are rising more than those at the beginning of the growing season in the springtime,' says Zoe Panchen, Assistant Professor of Plant Biology at Acadia University, Nova Scotia, Canada. 'If you're an Arctic plant that's sensitive to temperature, then your flowering will shift more if you flower at the end of the season, than if you flower at the beginning of the season. This has implications for the ecosystem. In the Arctic, the growing season is so short that if you flower at the end of the season, there's a high chance you won't produce viable seed or your seed won't mature because the temperature is cold and it has already started snowing. But if those species are now flowering earlier and temperatures are warmer, then there's more chance the seeds will be viable. Therefore, their reproductive success will go up and we might see them become more dominant in plant communities.'

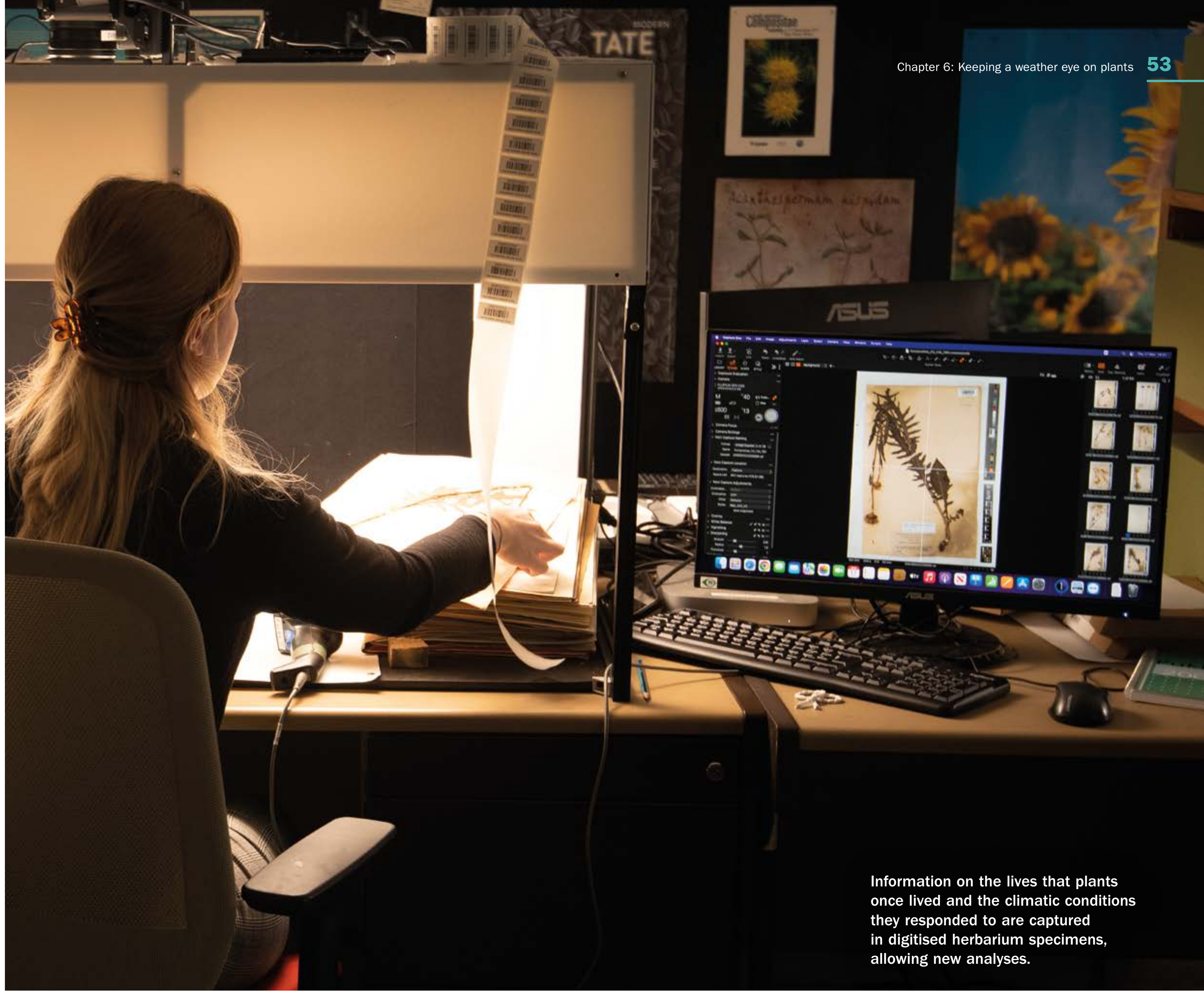
UNDERSTANDING ECOLOGICAL SHIFTS

Digital herbarium specimens are also providing opportunities for scientists to try new approaches to answering ecological questions. In another Arctic study, researchers sought to better understand the drivers behind an observed increase in the dominance of some shrub species – termed 'shrubification'. Arctic shrubs live for many decades and have annual growth rings within their stems that vary in width from year to year depending on local climate fluctuations and other factors, such as herbivory. These rings can be used to study how the shrubs perform over time and as a climate proxy for reconstructing historical conditions. Herbarium collections of Arctic plants span the long time-intervals needed for such studies, but cutting stems from specimens to examine growth rings is destructive and therefore undesirable for rare or historical specimens. The researchers of the new study took a novel approach by applying the proxy of annual stem growth to herbarium specimens, and measuring multiple years of elongation on digital images.

Using 482 digitised specimens, they quantified incremental growth chronologies from the stems of four ecologically diverse species of willow (*Salix* species) collected over 160 years in Greenland. They then used this dataset to investigate how annual stem growth had changed over time and to examine whether the observed growth was related to the summer temperature of the growing year.

The analyses revealed that the growth of only one species – *S. herbacea* – had changed significantly over time, indicating that some species may be stable over the long term, even under climate change. Another species – *S. glauca* – was the only one to show a positive relationship with mean July temperature. This is an upright willow, a growth form previously shown to be more sensitive than others to climate. In keeping with other studies that had used more conventional annual growth ring techniques, the findings indicated that species-specific factors, local conditions and microhabitats had played an important role in influencing growth. The work serves as a template for investigating the incremental past growth of other shrubs across the Arctic biome, and highlights the potential for other ecological and trait-based studies using non-destructive assessments of digital herbarium collections.

OVERALL, FLOWERING TIMES WERE FOUND TO BE CONVERGING, SHORTENING THE TUNDRA FLOWERING SEASON.



Information on the lives that plants once lived and the climatic conditions they responded to are captured in digitised herbarium specimens, allowing new analyses.

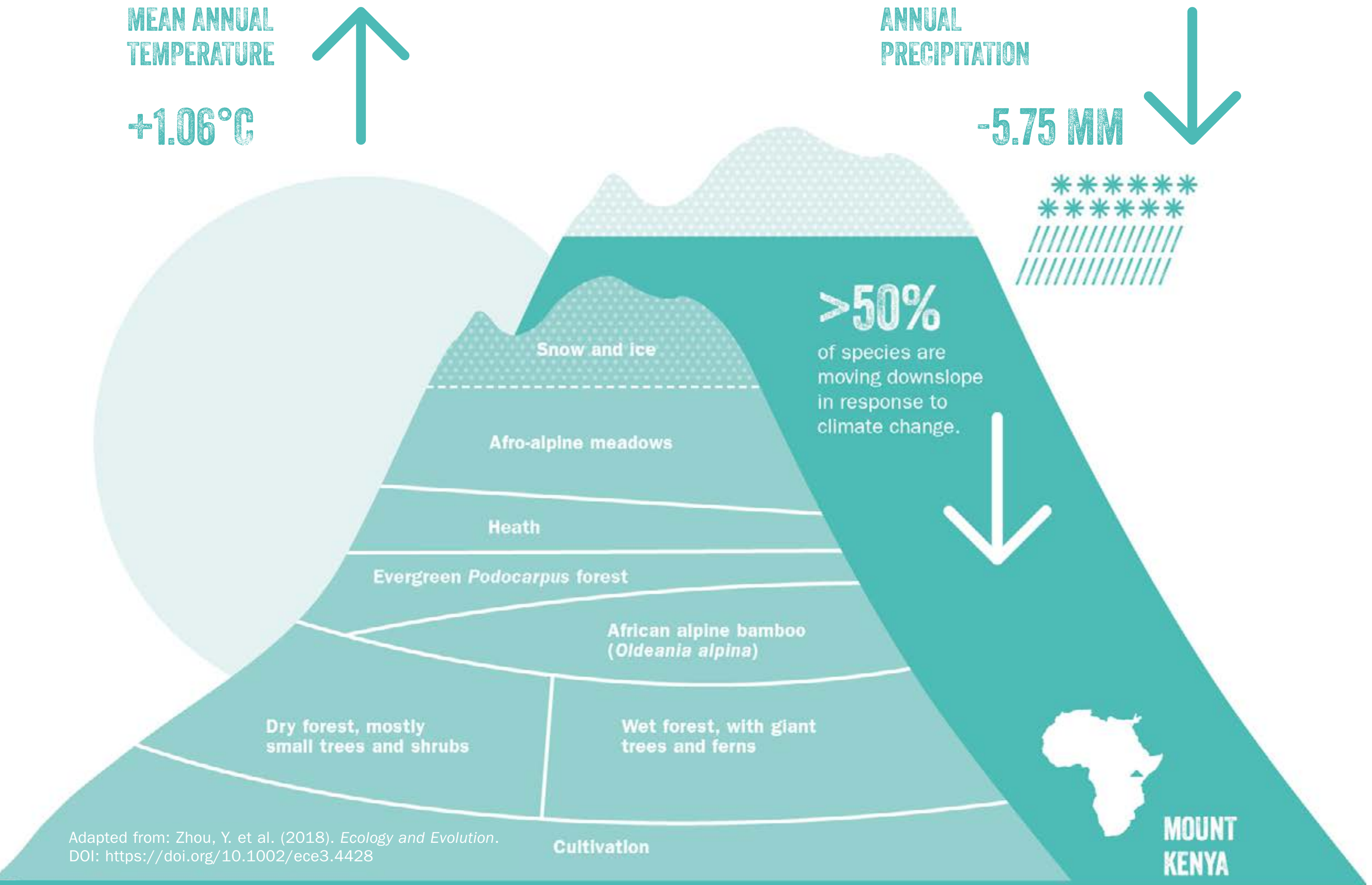
A YEAR IN THE LIFE

Another novel approach, this time developed in the USA, was used to examine the effect of climate on the reproductive characteristics of 14 *Streptanthus* species (some also known under the name *Caulanthus*). Part of the cabbage family (Brassicaceae), the lineage arose in the deserts of south-western North America and diversified to form new species as it spread westwards and northwards. Today, the species inhabit open, bare, rocky or sandy ground and span desert to mountain habitats but largely grow under mediterranean climate conditions of hot, dry summers and mild, wet winters.

The species examined were all annuals (a term for plants that complete their life cycle from germination to death within one year), in this case germinating in the autumn (fall) and completing their reproductive cycle in early to mid summer. The scientists sought to reconstruct the conditions that the plants had experienced while growing – their 'lived climate' – and examine how this might have affected reproduction. They characterised the conditions of precipitation, temperature and water deficit that the plants had been subjected to from germination to the time of collection, and they gathered data on their reproductive stage and performance. The latter process involved counting how many buds, flowers and fruits were present on up to 200 herbarium specimen images per species, spanning 1898 to 2016.

The team estimated the length of time a specimen had been growing from its likely germination date. Based on previous studies showing the amount of precipitation sufficient to trigger germination, the researchers assumed plants had germinated during the first weather event in the previous autumn or winter where 25 mm of rain had fallen over one or more consecutive days. The team found that, overall, the onset and amount of precipitation predicted the timing of reproductive events in the plants' lifetimes better than other variables. This contrasted with previous large-scale analyses that had identified temperature as the more important factor.

'Precipitation was more important than temperature for these species, and that's generally true for many other mediterranean and water-limited systems,' says Sharon Strauss, Distinguished Professor Emerita in Evolution and Ecology at UC Davis College of Biological Sciences. 'In mediterranean climates, rainfall is so seasonal. Because water comes in a short period of time, plants have to take complete advantage of it, and they have adapted to respond



Adapted from: Zhou, Y. et al. (2018). *Ecology and Evolution*.
DOI: https://doi.org/10.1002/ece3.4428

BOX 1: Upland plants shift downslope on Mount Kenya

A study of herbarium records of plants from the tropical extinct volcano Mount Kenya has found that more than half of species are moving downslope in response to climate change. This contrasts with trends observed on many mountains – including in Hawaii, Europe and China – that have generally found more species to be moving upslope. For example, a study of 29 mountains in China found that while the elevational range of species was contracting, there was a greater movement of lower-range limits upwards than of upper-range limits downwards, primarily driven by temperature change. The scientists working on the Mount Kenya study, who found the opposite to be the case – despite a similar overall pattern of contraction – believe that a greater reduction in precipitation at high elevations may be driving the anomalous trend.

Undertaken by scientists at institutions in China and France, the study involved gathering and digitising all plant specimens that had been collected on Mount Kenya. These were held in the East African Herbarium within the National Museums of Kenya in Nairobi and 18 other herbaria worldwide. After a process of checking and cleaning the data, a dataset of 6,131 occurrences – representing 1,095 species of seed plants collected between 1907 and 2016 – was obtained. This was split into two datasets consisting of specimens collected during 1907–1974 and 1975–2016, with 1974 chosen as the dividing year because it marked the start of a shift after which the local temperature systematically remained above historical baseline conditions.

The researchers screened and identified 139 plant species with sufficient specimens from both time periods. Comparing the distribution of species occurrences between these two time periods revealed that 77 species had moved downslope from higher elevations and 62 had shifted upslope from lower elevations. Of the species that had moved upslope, 53.2% were lowland species, and of those that had moved downslope, 72.7% were upland species. With a mean annual temperature rise of 1.06°C having affected the Mount Kenya region during the 1975–2016 period (similar across both upland and lowland regions), the scientists surmised that temperature may have driven some species upslope after 1974 but that precipitation had had a greater influence in causing more species to shift downslope.

'It surprised me, as we generally think that with climate change, species move upslope to reach cooler temperatures,' says Yadong Zhou, Professor of Botany at Nanchang University, China, and senior author of the study. 'We believe that on Mount Kenya, the upland plants cannot survive the dry conditions, so species are migrating to the middle elevations.'

to cues, such as how fast the soil is drying out and the day length. These have shaped their evolution in terms of their phenology and how they fruit. When it comes to predicting how they'll respond to future climatic conditions, these cues around precipitation are really important – particularly given we're getting patterns of more variable rainfall in the fall now, which is when a lot of these plants are growing.'

DIRECTING FUTURE EFFORTS

The new approaches and methods facilitated by digital herbarium specimens, and novel technologies for analysing them, are highlighting where phenological and other climate-response research should be directed in future. First and foremost, scientists are calling for the continued collection of herbarium specimens, so that preserved plants can be used to record responses to ongoing climate change (see Box 1). While collections from understudied areas are vital to filling data gaps and overcoming the bias of past studies, those from well-studied floristic regions also remain important. These will facilitate in-depth investigations of long-term trends, show how individual species are responding to change, and reveal the patterns in those responses at multiple scales and through time.

Collection protocols already exist on how researchers should gather, press, dry, freeze (to eliminate pests), mount and label herbarium specimens. However, some researchers are requesting additional protocols specifically to support phenology, particularly for herbaceous plants. These include: gathering specimens at later fruiting stages to capture full reproductive cycles; collecting individuals at random within populations to cover the variation in specimen traits; and encouraging community – or citizen – scientists to take and share pictures of plants at all stages of their life cycles to complement herbarium specimens (see Chapter 11).

There is great potential to enhance the scope of research by using herbarium specimens and community science alongside data from observatory networks and remote sensing. This would enable researchers to combine the historical, single-point-in-time, species-level data captured in herbarium specimens with the continent-wide, inter-annual changes recorded in satellite images, the long-term data on individuals' complete phenological cycles gathered by observation networks, and the high-resolution specimen data from broad geographic areas provided by community science. The fact that, to date, studies have tended to rely largely on one data source may reflect a lack of data harmonisation between sources, making integrating them difficult. Along with using common terminology and notation, various approaches that already exist for harmonising ecological data could also be applied to phenological data.

In the past two decades, the use of herbarium specimens has helped to transform phenological research from a niche activity into a cornerstone of climate-change biology. In the decades to come, continued use of machine learning, new collections, accelerated digitisation of herbarium specimens, and increased data interoperability will help climate research span space, time and species like never before – yielding ever-deeper insights into how biodiversity is responding to planetary change.

This chapter is based on the following papers in our special collection:

Ahlstrand, N.I., et al. (2025). Herbarium specimens reveal drivers of Arctic shrub growth. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70285

Ahlstrand, N.I., et al. (2025). The promise of digital herbarium specimens in large-scale phenology research. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70178

Amador, L.G., et al. (2025). Bridging data silos to holistically model plant macrophenology. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70249

Bontrager, M., et al. (2025). Specimen-tailored 'lived' climate reveals precipitation onset and amount best predict specimen phenology, but only weakly predict estimated reproduction across a clade. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70338

Fu, Z., et al. (2024). Climate change drives plant diversity attrition at the summit of Mount Kenya. *New Phytologist*. DOI: https://doi.org/10.1111/nph.20344

Karthikeyan, A., et al. (2025). Flowering out of sync: Climate change alters the reproductive phenology of *Terminalia paniculata* in the Western Ghats of India. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70022

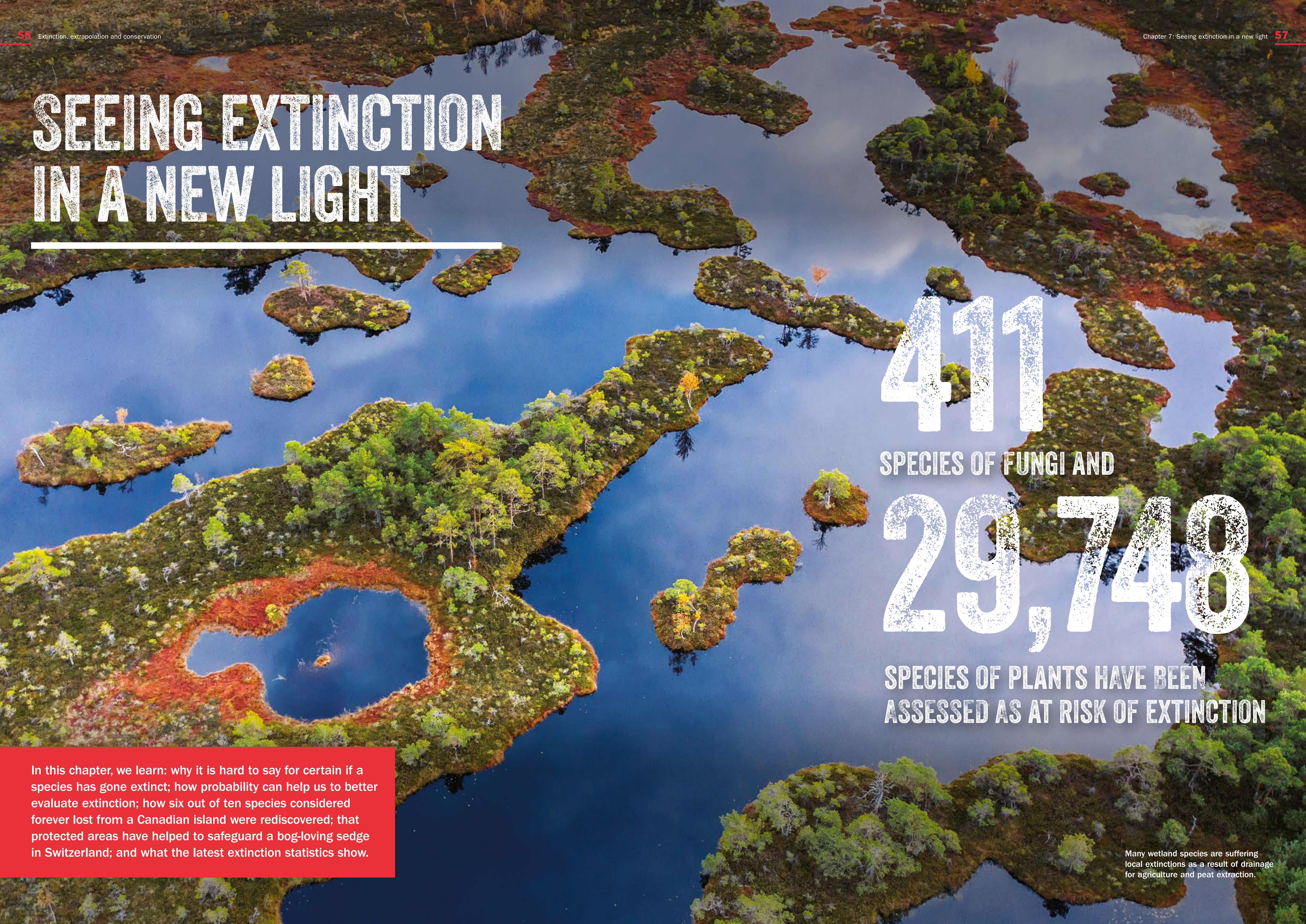
Panchen, Z.A., et al. (2025). Digitised herbarium specimen data reveal a climate change-related trend to an earlier, shorter Canadian Arctic flowering season, and phylogenetic signal in Arctic flowering times. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70386

Whitley, B.S., et al. (2025). Harmonising digitised herbarium data to enhance biodiversity knowledge: Major steps towards an updated checklist for the flora of Greenland. *Plants, People, Planet.* DOI: https://doi.org/10.1002/ppp3.70044

Williamson, D.R., et al. (2025). Long-term trends in global flowering phenology. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70139

Zu, K., et al. (2025). Changes in species' elevational range limits and range sizes uncovered by herbarium specimens. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70664

THERE IS GREAT POTENTIAL TO ENHANCE THE SCOPE OF RESEARCH BY COMBINING HERBARIUM SPECIMENS WITH OTHER DATA SOURCES.



SEEING EXTINCTION IN A NEW LIGHT

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SPECIES OF FUNGI AND

29,748

SPECIES OF PLANTS HAVE BEEN ASSESSED AS AT RISK OF EXTINCTION

In this chapter, we learn: why it is hard to say for certain if a species has gone extinct; how probability can help us to better evaluate extinction; how six out of ten species considered forever lost from a Canadian island were rediscovered; that protected areas have helped to safeguard a bog-loving sedge in Switzerland; and what the latest extinction statistics show.

Many wetland species are suffering local extinctions as a result of drainage for agriculture and peat extraction.

NEW WAYS TO QUANTIFY GLOBAL AND LOCAL EXTINCTIONS COULD ENHANCE UNDERSTANDING OF PLANT DIVERSITY LOSS.

It seems like a black and white issue: a species either has at least one living individual, or it is extinct. But life and death in nature are not that straightforward to categorise. With habitats often remote and hard to access, it can be difficult to know whether any given plant species (among around 400,000 that are known to science) is rare or has completely died out. This is further complicated by the fact that some 100,000 or more plant species are estimated to remain undocumented, many of which could go extinct before being described and named. If we are to understand and halt biodiversity loss, we need to understand plant extinction better. But how?

At the start of the decade, this question was vexing Aelys Humphreys, who at the time was coming to the end of her tenure as a postdoctoral researcher at Kew. She had led a global analysis of plant extinctions and rediscoveries, which had prompted people to actively look for some of the species listed as extinct. As a result, some were rediscovered (see Box 1). From a conservation point of view, this was fantastic news, but it risked giving the impression that scientists were wrong about the scale of the extinction crisis, and highlighted the difficulties of proving the absence of a species. Humphreys felt there must be a more nuanced way of representing extinction.

'The evidence underlying reports of plant extinctions is not always very easy for non-experts to see and understand,' she explains. 'An expert on a particular plant may declare it extinct, having seen it during frequent visits to its last known spot on a mountain ridge during their career, and then suddenly no longer finding it. Or there's a species that's only ever been known from one patch of forest and this has been replaced by a motorway or a city. So, the habitat has gone and therefore the assumption is that so has the species. It bothered me that extinction was usually reported as either/or – a species is either extinct or it isn't – which can be incredibly hard to prove.'

This approach was certainly at odds with other fields of science, where providing a measure of confidence in, or uncertainty of, a particular finding was routine. For example, the assessment reports on climate change published by the Intergovernmental Panel on Climate Change since 1991 used a scale for denoting the probability of a specific finding (from virtually certain to exceptionally unlikely) and a confidence scale (from very low to very high) based on the quality and consistency of evidence and scientific agreement. When Humphreys and her colleague Diana Fisher, Associate Professor at the University of Queensland, Australia, looked into the idea of applying a measure of probability to extinction, they found that many scientists, particularly those studying birds and mammals, were already doing so. In fact, mathematical models for quantifying the chance of a species being extinct had existed for 30 years.

'I realised that although these methods had not been widely applied to plant species, there was a framework that already existed for doing this,' says Humphreys, who is now Associate Professor at Stockholm University. 'The types of information these mathematical approaches need are things like when and where species have been seen – and not been seen. So, if a species has been documented at certain points through time but then has suddenly not been observed any more, this information could be used to calculate the probability that it is either extinct, or simply undetected or not looked for. And this is exactly the type of information that you can get from herbarium specimen data.'

Humphreys and Fisher, along with Kew's Executive Director of Science Alexandre Antonelli and other colleagues, set out to explore how scientists might harness data from digitised herbarium specimens to infer recent and ongoing plant extinctions. They started by formally acknowledging that due to incomplete, biased or inconclusive data and the challenge of proving absence, it is often difficult to establish the occurrence, severity, time or place of biodiversity loss. They defined this as the 'unknown loss of biodiversity', calling this gap in knowledge the Katuš shortfall. (Katuš means to 'go away' or 'depart' in Yaghan, one of the Indigenous languages of Tierra del Fuego, whose last native speaker died in 2022.) Broader than the term 'dark extinction', which refers to species becoming extinct before being formally described scientifically, it also includes the unrecorded loss of known species, as well as encompassing the unrecorded loss of other aspects of biodiversity, such as lineages, genes, functions and even ecosystems.

'We know that most plant species are rare and narrowly distributed, and that biodiverse ecosystems around the world – from natural grasslands to forests and wetlands – have been replaced by agricultural land and urban developments,' says Antonelli. 'Yet, fewer than a thousand plant species are documented as having gone extinct in recent centuries. That doesn't add up. But demonstrating the gap that probably exists between actual and documented extinctions requires a robust statistical approach.'

The team were interested in how the data from herbarium collections might be used to reduce the Katuš shortfall. They first looked for documented examples of such data being used for extinction-risk assessments, such as those set out by the International Union for Conservation of Nature (IUCN). IUCN assessments use well-defined criteria to assign species to categories reflecting their risk of extinction, such as Critically Endangered or Near Threatened. As part of their review, the team found that digitised herbarium specimens were regularly being used for this purpose, and that the need to speed up such assessments had led to statistical and machine-learning methods being developed. They also found that DNA sequence data from herbarium specimens were being used for detecting the genetic signatures of diversity declines, rarity and invasiveness.

The data being used to infer global extinction risk were primarily species' names, along with the collection dates and locations – gathered from labels or deduced from travel journals or survey records. The review team realised it would be possible to calculate extinction probabilities using similar information, which could be enhanced with other available data, such as on land-use and habitat changes, to improve the accuracy of the analyses. For example, if a species was only known from a single wetland site that had been drained for development five years earlier, the probability of extinction would be high.

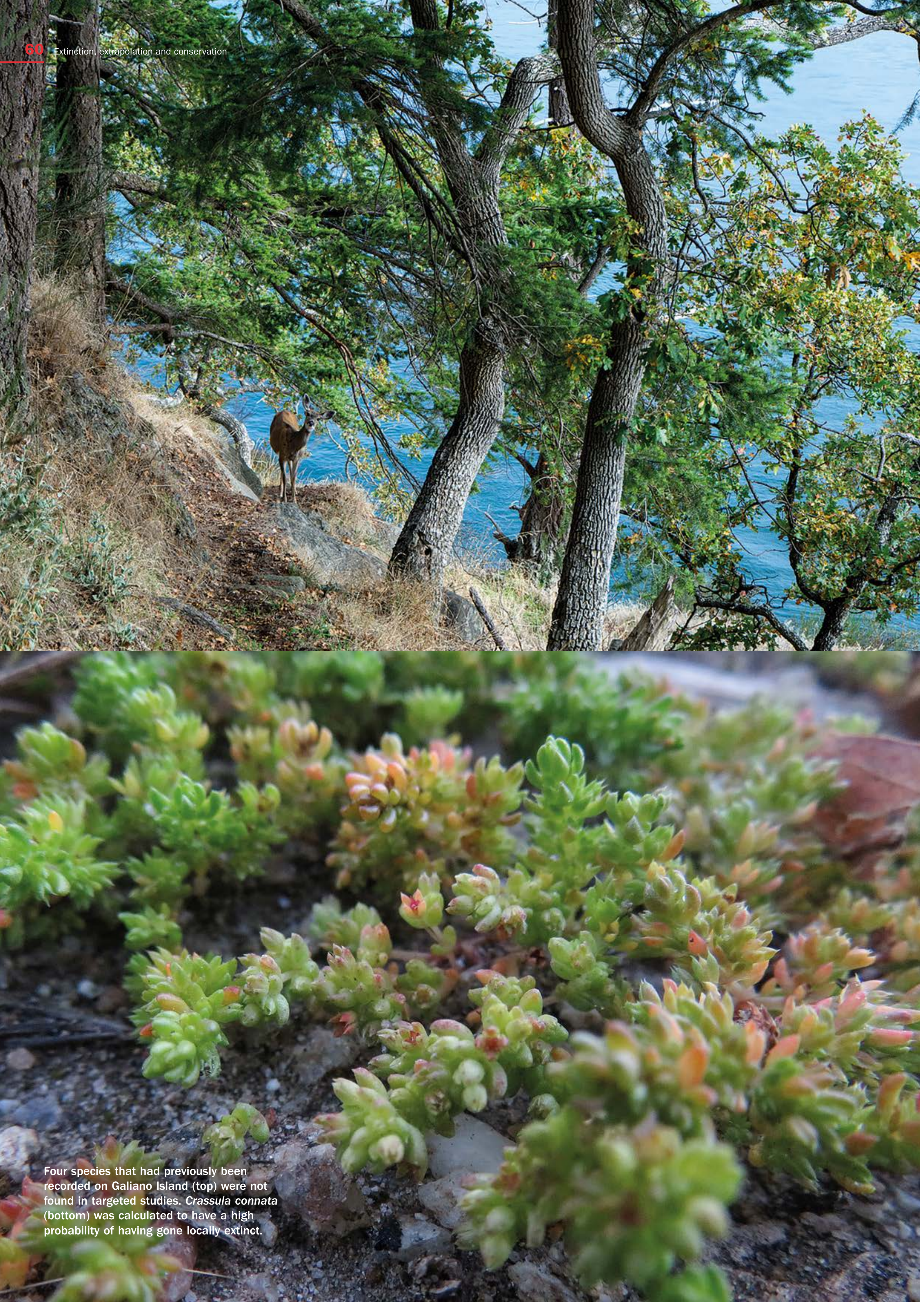
The team looked for existing models for estimating the probability of individual species having gone extinct. They found one type that was based on the distribution of sightings over time, and another concerned with species' characteristics, threats and distributions. Ten specimens – sometimes fewer – were sufficient for the models to be used. While such models had been applied to over a hundred species of animals, only three plant species categorised as globally Extinct had probabilities associated with their status. Currently, just one species classified as Extinct on the IUCN Red List of Threatened Species has the probability that it is indeed extinct included in its assessment. This is the Everglades orchid (*Govenia floridana*) that was endemic to the Everglades National Park in Florida, USA, and for which extinction probability estimates were made using herbarium specimens, documented surveys and collector notes.

The IUCN began recommending the inclusion of estimated extinction probabilities in Red List assessments as far back as 2019. Humphreys and her colleagues are hopeful that the vast resource of digitised herbarium specimens and the power of artificial intelligence will now be leveraged to accelerate this

THE EVIDENCE UNDERLYING REPORTS OF PLANT EXTINCTIONS IS NOT ALWAYS VERY EASY FOR NON-EXPERTS TO SEE AND UNDERSTAND.

BOX 1: 'Extinct' Chilean blue crocus rediscovered

Species that have been declared extinct are sometimes rediscovered. The Chilean blue crocus (*Tecophilaea cyanocrocus*), was found in 2001 near Santiago, Chile, after decades of not being seen (other than in cultivation). Because it is difficult to know for certain whether a plant is extinct or not, scientists are increasingly using digitised specimen data and other information sources to model the probability that species no longer exist in the wild, giving a more accurate picture of biodiversity loss.



Four species that had previously been recorded on Galiano Island (top) were not found in targeted studies. *Crassula connata* (bottom) was calculated to have a high probability of having gone locally extinct.

process for plants. This will not only improve understanding of recent and ongoing extinctions by increasing the accuracy of national and global Red Lists but can also help to reduce the Katuš shortfall – as scientists strive to address the ongoing biodiversity crisis.

CALCULATING AN ISLAND'S LOCAL LOSSES

Global extinction is essentially the sum of many local extinction events. With this in mind, one international research team has developed a framework for Galiano Island in British Columbia to detect local extinction events, in line with IUCN extinction criteria. The IUCN defines a species as 'presumed Extinct, when exhaustive surveys in known and/or expected habitat, at appropriate times (diurnal, seasonal, annual), throughout its historical range, have failed to record an individual'. To build the framework, which could also be applied elsewhere, the team combined historical collection data from the 60 km^2 island with five years of recent community observations.

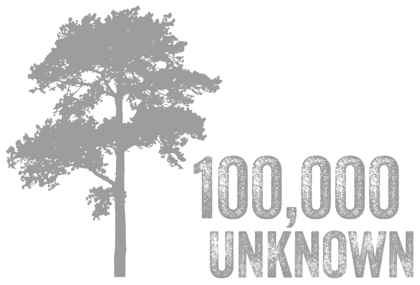
'When it comes to IUCN population assessments for species at risk, it's very common to have insufficient data, and often you're drawing on proxy variables or making calls that are somewhat qualitative in order to make those assessments,' says Andrew Simon, co-founder of the Institute for Multidisciplinary Ecological Research in the Salish Sea, who led the Galiano study with Quentin Cronk, Professor of Botany at the University of British Columbia. 'The framework we have created is quite useful, as it has enabled us to be much more rigorous in our approach. So, I think that this work fills a major gap, and that there are implications far beyond just this model system and the small island that we've been working on.'

The Galiano study was rooted in Simon's passion for harnessing the power of community science to create biodiversity inventories. Six years before working on the framework, he had consolidated all the data he could find on the historical biodiversity of the island, from herbarium specimens, technical reports and species lists. He then launched a project to engage the wider community in documenting the island's biodiversity using iNaturalist (an app for recording and sharing species observations). This work generated a comprehensive baseline of vascular plant diversity on the island. It confirmed the presence of 432 of the 607 historically reported species but left 175 (29%) unaccounted for. Of these, 74 species had not been reported for more than 20 years prior to 2020.

Simon and his colleagues decided to focus on a selection of these species, choosing those that: were native; had herbarium specimens demonstrating past local occurrences; and exhibited conspicuous flowers or petal-like features (which were less likely to have been overlooked in the recent searches). They chose ten from this list, for which 24 people undertook systematic surveys over an additional four years. Six of the target species were redetected. For the others, which all occupied narrow niches in woodland habitat, the team set about inferring extinction probabilities. This involved constructing generalised habitat grid maps, with 30 m × 30 m cells, of the habitats that were favoured by the species. These areas were then split into two, with 'historical' habitat reflecting where observations of the species had been made and 'potential' habitat referring to areas of suitable habitat with no previous observations.

Using a robust statistical approach, the team inferred local extinction (also termed extirpation) probabilities based on 'strict' and 'relaxed' interpretations of the IUCN criterion for the Extinct category. The strict interpretation demanded that adequate search effort had been made in both historical and potential habitat areas, whereas the relaxed interpretation was based on historical habitat alone. Under the strict interpretation, the local extinction probabilities for two species, *Crassula connata* and *Primula pauciflora*, were calculated to be 89.1% and 83.7%, respectively. Under the relaxed interpretation, this rose to more than 95% for both. Probabilities could not be calculated with high confidence for the other two species, *Meconella oregana* and *Plagiobothrys tenellus*, due to challenges in defining the extent of historical habitat patches. The six species that were redetected, meanwhile, became conservation priorities.

Around 400,000 plant species have been scientifically named.



Some 100,000 or more plant species are unknown to science.

Fewer than 1,000 plant species are documented as having gone extinct, but the true scale of biodiversity loss has likely been underestimated.

‘I realised that we saw some patterns in those plants that we redetected,’ says Simon. ‘They are habitat specialists, and they have what appear to be fairly restricted distributions. That information matters when it comes to, for example, identifying priority areas for biodiversity. If you detect a particular species after so much exhaustive effort but they’re only occurring sparsely, that means they are marginal, right? They are still at risk of extirpation, and so extra measures can be taken for habitat conservation. We want to make the case that this methodology can be applied not just to infer likely extinction events, but also to ideally prevent extinction from happening. Not only that, but continued search efforts can be tracked iteratively over time, helping to guide efforts to redetect species and update estimates of local extinction probabilities.’

This study also highlighted the importance of the living knowledge of local naturalists. The late Harvey Janszen, whose deep familiarity with Galiano Island’s flora helped to define the historical habitat patches and guide this research, was particularly instrumental. His passing is a reminder that human knowledge of biodiversity is itself vulnerable to loss.

UNDERSTANDING PRESSURES ON WETLAND PLANT POPULATIONS

In Switzerland, scientists have similarly used specimens and surveys to assess extinction among local populations of the perennial hare’s-tail cotton sedge (*Eriophorum vaginatum*, also known as hare’s-tail cotton grass). This time, the end goal was to predict the probability that contemporary populations would go extinct. The researchers collated and added geographical coordinates to more than 700 digitised specimens from nine Swiss herbaria, then revisited 197 locations where the species had been collected between 1803 and 1949. This revealed where previous populations had been extirpated or had survived. They combined this information with records for mean annual temperature and precipitation, along with 20 other environmental variables. This enabled them to model the environmental niche of the species and examine the extent to which climate change and other environmental shifts might have contributed to the observed local extinctions. They then used the model to predict impacts on contemporary populations and identify those at risk from ongoing environmental pressures.

‘We used the local extinction data, based on our visits to sites where specimens had been collected in the past, to identify the environmental pressures that are associated with these extinctions,’ explains biologist Gabriel Ulrich, who led the research while working at the Institute of Integrative Biology at the Federal Institute of Technology (ETH) Zurich. ‘We then used the relevant environmental variables to predict the extinction probability locally. So, this can be interpreted as a risk estimate. Therefore, this approach has the potential to not only identify the relevant pressures, but also to identify where they are acting on the existing populations.’

The tussock-forming hare’s-tail cotton sedge is native to acidic wetlands throughout the subarctic and temperate northern hemisphere, where it can live for a hundred years. In Switzerland, it thrives in peat bogs at elevations of up to 2,600 m above sea level. Below 2,000 m, it often occurs in raised bogs. A sharp decline in bogs over the past two centuries, primarily caused by drainage for farming and the extraction of peat for fuel, has led to the species being classified under IUCN criteria as Near Threatened at the national level in Switzerland. Drainage ditches have been particularly detrimental, changing the water table and chemical properties of the soil. Nutrients flowing into bogs from farming have exacerbated the problem, leading to more nutrient-demanding trees and shrubs colonising the habitat and making it less favourable for the cotton sedge and other shade-intolerant peat bog specialists.

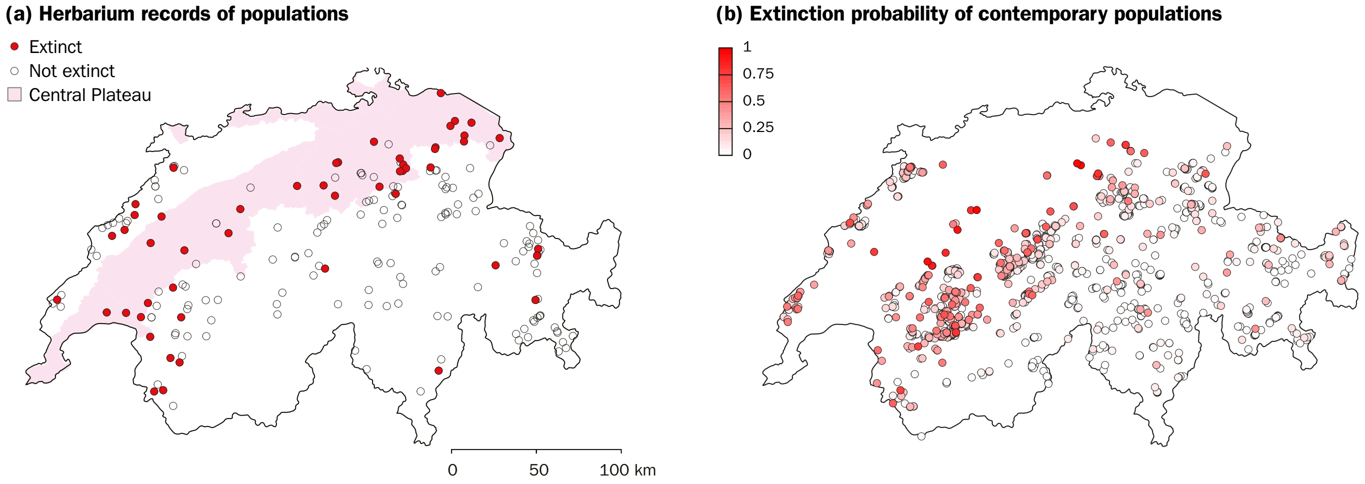
The study found that the hare’s-tail cotton sedge was no longer present at 52 of the 197 revisited locations – an overall loss of 26.4%. This was lower than anticipated, given that 80%–90% of the peat bog habitat had disappeared since 1700. However, it was possible that some populations had persisted while being greatly reduced in size. The losses were highest in the Swiss Central Plateau, where 28 out of 41 (68.3%) of the populations had been extirpated (see Figure 1), compared to the country’s five other biogeographical regions, where only 24 out of 156 (15.4%) of the populations had become extinct. Reassuringly, the scientists found that a significantly lower proportion of extinctions had occurred in protected areas (in 1987, the Rothenthurm Initiative had enshrined moorland protection in Switzerland’s constitution). However, more than half (54.8%) of revisited locations were outside of protected areas and are therefore facing the additional risk of future disturbance from human activities.

Increased nutrient levels and soil pH, as well as planted trees or crops, were identified as predictors of increased extinction probability for hare’s-tail cotton sedge populations in Switzerland. The presence of wetland, wetland-like, and shrubland habitats were, in contrast, predictors of reduced extinction probability. The positive link to shrublands was a little surprising, as such areas can be associated with the invasion of nutrient-favouring species; however, natural shrublands also grow around the edges of bogs. The climate study, meanwhile, indicated that most of the extinct populations experienced warmer, drier conditions than those that had survived, and that climate change was therefore likely to increase the extinction risk of certain populations in the future.

UNDERSTANDING HOW AND WHY POPULATIONS OR SPECIES GO EXTINCT AT THE LOCAL LEVEL HELPS US TO IDENTIFY MEASURES TO PROTECT THEM.

FIGURE 1: Using patterns of local extinction to predict how contemporary populations might fare

(a) Researchers used herbarium specimens to map populations of the hare’s-tail cotton sedge (*Eriophorum vaginatum*) in Switzerland and then visited these sites to determine whether the species was still present there or had gone locally extinct. The sedge had disappeared from 52 of the 197 revisited sites, with 68% of the extinctions occurring in the densely populated and heavily farmed Swiss Central Plateau. **(b)** The researchers combined the information on local extinctions with data on temperature, precipitation and other environmental variables to estimate the probability of contemporary populations also going extinct. They predicted that future extinctions of the species would be highest in the Central Plateau, with medium to high levels of extinction probable in additional areas in western Switzerland.



Adapted from Ulrich et al. (2025)

THE STUDY FOUND THAT THE HARE’S-TAIL COTTON SEDGE WAS NO LONGER PRESENT AT 52 OF 197 REVISITED LOCATIONS – AN OVERALL LOSS OF 26.4%.

Overall, the study predicted extinction to be more likely than survival for 3.2% of the contemporary hare’s-tail cotton sedge populations in Switzerland, mostly in the Central Plateau but also in the Jura Mountains and northwestern Swiss Alps. As a result, the scientists recommended that protection and restoration efforts should prioritise these regions. The fact that fewer extinctions were observed in protected areas highlighted the importance of habitat protection in mitigating population extinctions and species decline; the team therefore also called for the extension of protected areas to cover more raised bog habitat. They suggested that specific nature conservation management measures for the hare’s-tail cotton sedge could, at the same time, benefit other species associated with wetlands in Switzerland.

The projects undertaken in Switzerland and Galiano Island confirm that assigning probabilities to extinction events and extinction risk has real value for understanding biodiversity and enhancing conservation efforts. Illuminating many small extinctions at the local level – and potentially covering multiple species within an area – can help to enhance understanding of extinction at larger scales. ‘Global biodiversity loss is ultimately the sum of many small local-scale processes,’ says Ulrich. ‘So, to get a good global picture, we need many of these local puzzle pieces. Understanding how and why populations or species go extinct at the local level helps us to identify measures to protect them, and the insight gained from local studies can often be generalised, applied elsewhere and scaled up – which helps to develop solutions that work at much broader scales.’

This chapter is based on the following publications in our special collection:

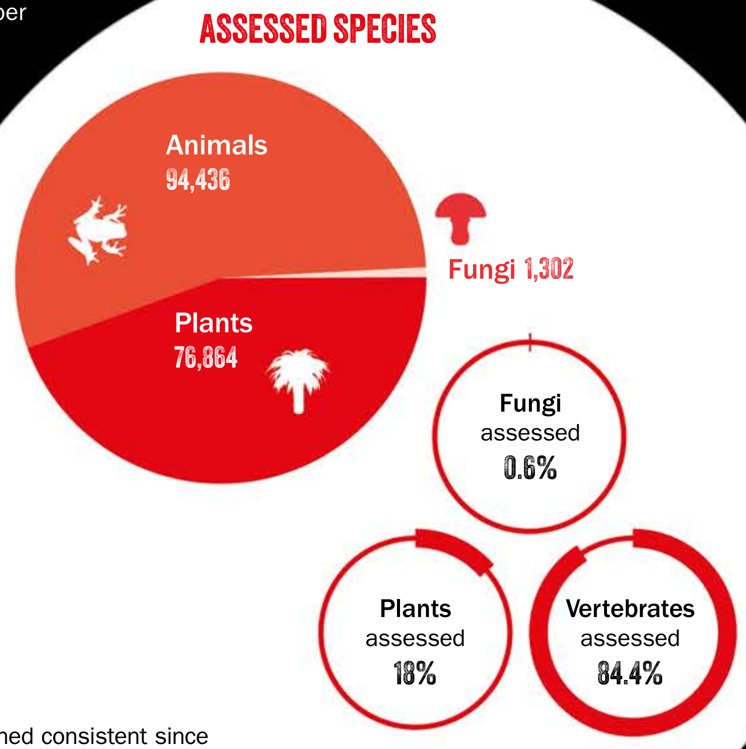
Humphreys, A.M., et al. (2025). Harnessing the benefits of herbarium specimen digitisation for inferring recent and ongoing plant extinctions. *New Phytologist*. DOI: https://doi.org/10.1111/nph.70552

Simon, A.D.F., et al. (2025). Detecting extirpation: A localized approach to a global problem. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70130

Ulrich, G.F., et al. (2025). Herbarium digitisation sheds light on historical distribution and drivers of population extinction of a peat bog specialist. *Plants, People, Planet.* DOI: https://doi.org/10.1002/ppp3.70046

WHAT WE KNOW ABOUT EXTINCTION RISK

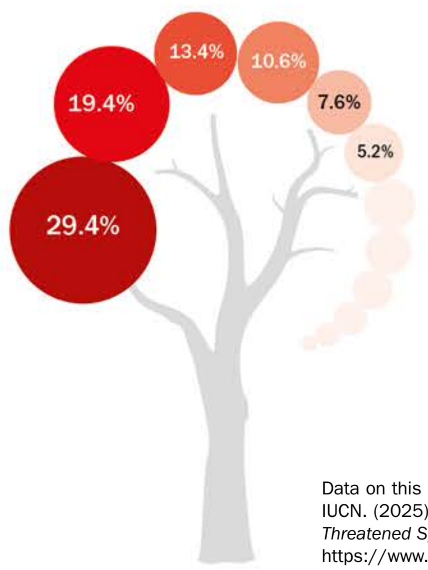
The International Union for Conservation of Nature's Red List of Threatened Species is a free online resource of extinction risk assessments, which assign organisms to threat categories based on their risk of going globally extinct. The total number of plant species assessed is 76,864, and with an average of 6,100 new assessments per year over the last five years, it is fast approaching the number for animals (94,436). However, this represents only around 18% of all plant species known to science – itself a moving target as many new species are described each year (see Chapter 3). Fungi, meanwhile, pose numerous challenges for Red List assessors, due to substantial data gaps and difficulties defining even basic concepts, such as what constitutes a single individual or a population. However, a concerted effort by the fungal conservation community over the last decade has led to the number of fungal assessments passing the 1,000 milestone.



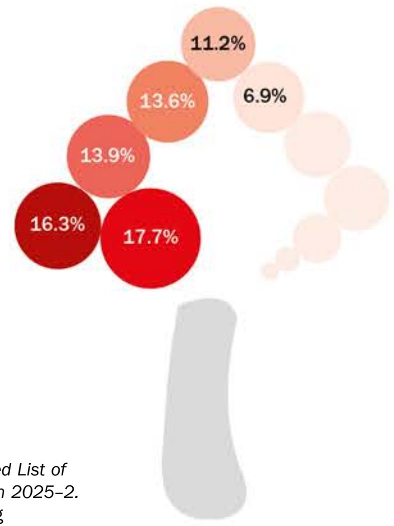
Why species are at risk

The dominant threats to plants and fungi globally have remained consistent since previously reported in *State of the World's Plants and Fungi 2020*, with the top four being 'Agriculture and aquaculture', 'Biological resource use', 'Residential and commercial development' and 'Natural system modifications'. The main change is that 'Biological resource use' is now the top threat listed in fungal extinction risk assessments. This is largely due to recent assessments of fungi threatened by logging and other wood-harvesting activities. Climate change is less frequently listed as a threat, but this probably reflects a lack of conclusive evidence at species level, and it is likely to be more frequently identified as a major threat in the coming years.

Plants



Fungi



- Agriculture and aquaculture
- Biological resource use
- Residential and commercial development
- Natural system modifications
- Invasive and other problematic species
- Climate change and severe weather

Data on this spread from IUCN. (2025). *The IUCN Red List of Threatened Species. Version 2025–2.* https://www.iucnredlist.org

2 IN 5 PLANTS ARE ESTIMATED TO BE THREATENED WITH EXTINCTION

How many species are at risk?

Number of species in six of the nine IUCN Red List categories (excluding Extinct, Extinct in the Wild and Not Evaluated) and the corresponding percentages.

Plants

Critically Endangered (CR)
6,445 (8%)

Endangered (EN)
12,707 (17%)

Vulnerable (VU)
10,596 (14%)

Near Threatened (NT)
4,880 (6%)

Least Concern (LC)
35,732 (47%)

Data Deficient (DD)
6,317 (8%)

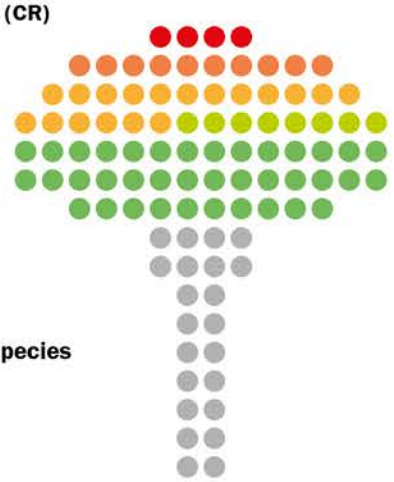
Threatened plant species
29,748

Fungi

Critically Endangered (CR)
48 (4%)

Endangered (EN)
129 (10%)

Vulnerable (VU)
234 (18%)



Near Threatened (NT)
110 (8%)

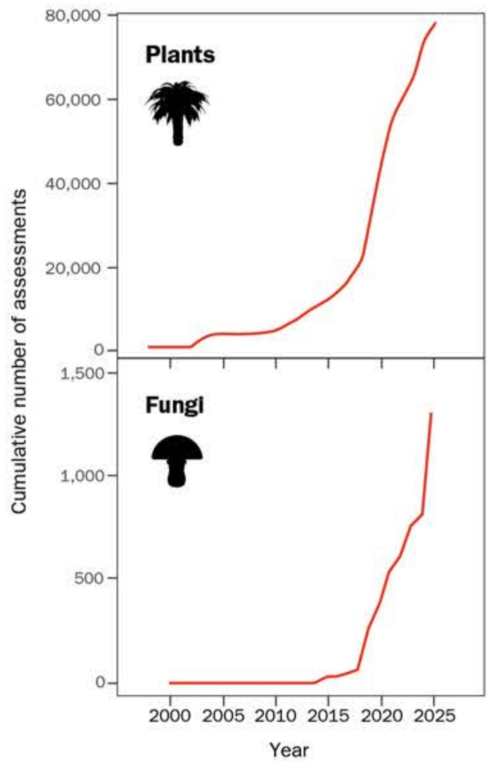
Least Concern (LC)
491 (38%)

Data Deficient (DD)
290 (22%)

Threatened fungal species
411

29,748 PLANT SPECIES +411 FUNGAL SPECIES HAVE BEEN ASSESSED AS AT RISK OF EXTINCTION

Number of extinction risk assessments



BRINGING EVOLUTION INTO CONSERVATION

Not all species are equal in evolutionary terms. Some are isolated on the tree of life, having few or no close relatives and often being the last representatives of ancient lineages, while others have diverged recently and have many close relatives. The Evolutionarily Distinct and Globally Endangered (EDGE) approach combines information from the tree of life with extinction risk data obtained from IUCN Red List assessments (or estimated when Red List data are not available). Scientists use this information to identify EDGE species – those that are threatened and represent a large amount of unique evolutionary history – and to estimate what proportion of the entire tree of life is at risk of extinction. The EDGE approach has been applied widely to plants and a pilot study to test its application to fungi showed that more extinction risk assessments are needed to accelerate progress.

EDGE

EVOLUTIONARILY
DISTINCT AND
GLOBALLY ENDANGERED

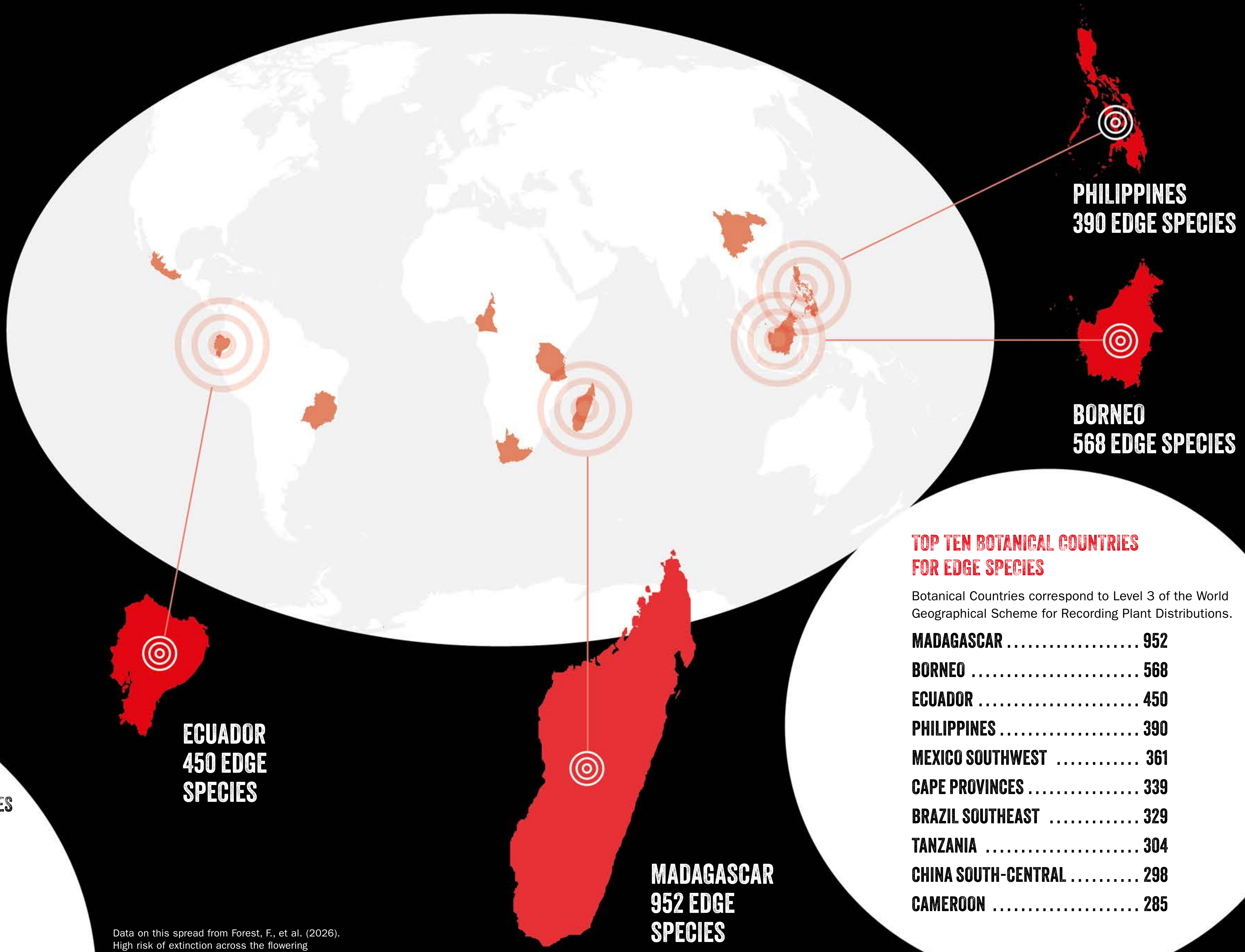
Plant families with the highest number of EDGE species

Araceae (arum family)	893
Myrtaceae (myrtle family)	714
Fabaceae (legume family)	555
Orchidaceae (orchid family)	546
Annonaceae (custard apple family)	393

PROPORTION OF THE TREE OF LIFE THREATENED

ANGIOSPERMS	GYMNOSPERMS	JAWED VERTEBRATES
21.2%	14.4%	13%

GLOBALLY, 3% OF ANGIOSPERMS (FLOWERING PLANTS) AND 26% OF GYMNOSPERMS (CONIFERS AND THEIR CLOSE RELATIVES) ARE EDGE SPECIES.



TOP TEN BOTANICAL COUNTRIES FOR EDGE SPECIES

Botanical Countries correspond to Level 3 of the World Geographical Scheme for Recording Plant Distributions.

MADAGASCAR	952
BORNEO	568
ECUADOR	450
PHILIPPINES	390
MEXICO SOUTHWEST	361
CAPE PROVINCES	339
BRAZIL SOUTHEAST	329
TANZANIA	304
CHINA SOUTH-CENTRAL	298
CAMEROON	285

Data on this spread from Forest, F., et al. (2026). High risk of extinction across the flowering plant tree of life. *Science* 392: 655-659. DOI: https://doi.org/10.1126/science.adz0773

SAFEGUARDING NATURE WITH ACCURATE DATA

DIGITISED HERBARIUM SPECIMENS CAN SUPPORT CONSERVATION IN MYRIAD WAYS

In this chapter, we learn: that Latin America is highly biodiverse but faces many threats; why knowing how evolutionarily distinct a species is can help guide conservation efforts; how herbarium specimens are boosting knowledge of protected areas in Honduras; and what seed-collection data can tell us about genetic diversity.

A study of ferns in the protected areas of Honduras has highlighted how herbarium data can improve conservation planning.

DIGITAL SPECIMENS CAN SUPPORT CONSERVATION IN DIVERSE WAYS, FROM SAFEGUARDING THREATENED SPECIES TO HELPING TO RESTORE HABITATS.

Latin America is a biodiversity superpower, likely hosting more than a third of the world's species. Extending from Mexico southwards and including the Caribbean, the region is home to more than 118,000 vascular plant species (those with specialised vessels for transporting water and nutrients – the majority of land plants). Moreover, around 750 more are named as new to science every year. Icons among its native plant species are the rubber tree (*Hevea brasiliensis*), on which today's USD 50 billion global industry was founded; more than 50 showy orchids of the *Cattleya* genus; and the world's largest cactus, the Mexican giant cardón (*Pachycereus pringlei*). The numbers for fungi are as yet unknown but likely to be extremely high, too (see Chapter 1). This vast expanse of exceptional biodiversity is critical to the health of the planet, helping to regulate the global climate, lock carbon away from the atmosphere and maintain ecological stability.

The region's ecosystems are highly threatened, however, by agricultural expansion and intensification, logging, overexploitation, illegal mining and climate change. With more than 650 million people living in Latin America and high levels of poverty in many countries, allocating funds to protecting and conserving natural resources is a challenge. This is where digitised specimens are proving valuable, as studies in Brazil and Honduras reveal. In Brazil, scientists have used digitised collections to pinpoint which threatened species most warrant conserving and to document biodiversity loss caused by development. And in Honduras, digitised specimens are helping to bolster incomplete species lists from protected areas, supporting more efficient management.

MAPPING BIODIVERSITY LOSS

When many important floral lineages face extinction, what do you save? This is a question troubling Brazil, where many biodiverse areas are threatened by agriculture, development, tourism and climate change. The genus *Cambessedesia* is in particularly dire straits, with 23 of its 24 species categorised as threatened with extinction. To identify species and geographic areas that would benefit the most from conservation actions, scientists sourced digitised herbarium specimens from two Brazilian platforms: the National Institute of Science and Technology's Virtual Herbarium of Flora and Fungi (via *species*Link) and Reflora (see Chapter 1).

The researchers used the specimens to assess the conservation status of each *Cambessedesia* species under International Union for Conservation of Nature criteria. They mapped the loss of these species' habitats over the past ten years and gave each a score for how evolutionarily distinct and globally endangered (EDGE) it was. EDGE scores provide a measure not just of how threatened a species is, but also how much unique evolutionary history it represents (see Chapter 7). Use of EDGE enabled the scientists to prioritise conservation action in two areas of Brazil rich in *Cambessedesia* species that have experienced severe habitat loss and are facing ongoing threats: the *campo rupestre* (rocky fields) – a hyper-diverse ancient montane ecosystem – and the Cerrado, a vast tropical savanna.

'This work highlights how digital herbarium collections are transforming conservation science in Brazil,' says Juliana Rando, a professor at the country's Federal University of Western Bahia. 'They are allowing us to rapidly assess the risk to species and prioritise action in highly diverse and threatened ecosystems.'

Another study in Brazil used herbarium records to document ongoing biodiversity loss caused by railway development to the Cerrado and two other particularly species-rich and threatened regions: the Caatinga and the Atlantic Forest in north-eastern Brazil. Work to build the Brazilian West–East Integration Railway has been underway since 2011, aimed at improving goods transport. By overlaying herbarium records and vegetation-loss maps from locations within the railway's area of influence, scientists showed that 13 species of high conservation priority had lost more than 10% of their distribution area between 2002 and 2021. They concluded that the railway construction posed a particular risk to threatened species within the Cerrado and called for sustainable practices that protect biodiversity while supporting economic development.

BETTER-INFORMED CONSERVATION

Digitised herbarium specimens can be equally useful in the context of protected areas. Scientists studying Honduran ferns and lycophytes (clubmosses, spikemosses and quillworts) used these resources to show a mismatch between species listed from protected areas and those recorded from herbarium specimens. Of 660 species reported across protected-area management plans and herbarium records, 66 species were unique to the management plans, while 216 species were found only in herbarium records for the same areas. Conversely, almost a third of species noted in management plans were not confirmed by specimens in herbaria. While it was possible that some species represented by herbarium specimens might no longer be present in the landscapes examined, the findings suggested that combining specimen and survey data could help to ensure biodiversity is accurately recorded and appropriately safeguarded.

THIS WORK HIGHLIGHTS HOW DIGITAL HERBARIUM COLLECTIONS ARE TRANSFORMING CONSERVATION SCIENCE IN BRAZIL.

***Cambessedesia regnelliana*, an Endangered species from a highly threatened and evolutionarily distinct genus endemic to Brazil.**

DIGITISED SPECIMENS ARE HELPING TO BOLSTER INCOMPLETE SPECIES LISTS FROM PROTECTED AREAS, SUPPORTING MORE EFFICIENT MANAGEMENT.

'Previously, in collaboration with local botanists, we had mapped all the herbarium material available in-country and internationally for ferns for the whole of Honduras,' explains Sven Batke, Associate Head of Research and Knowledge at Edge Hill University, UK. 'We later decided to see how many of the country's protected areas had ferns listed in their management plans – and found some species that we'd never seen in Honduras, including some species that only grow in South-East Asia. We realised that the herbarium data were telling us a different story from the management plans. They should really be the same – the herbarium records should inform the management plans, and, in the other direction, the herbarium records should be used to validate the survey observations.'

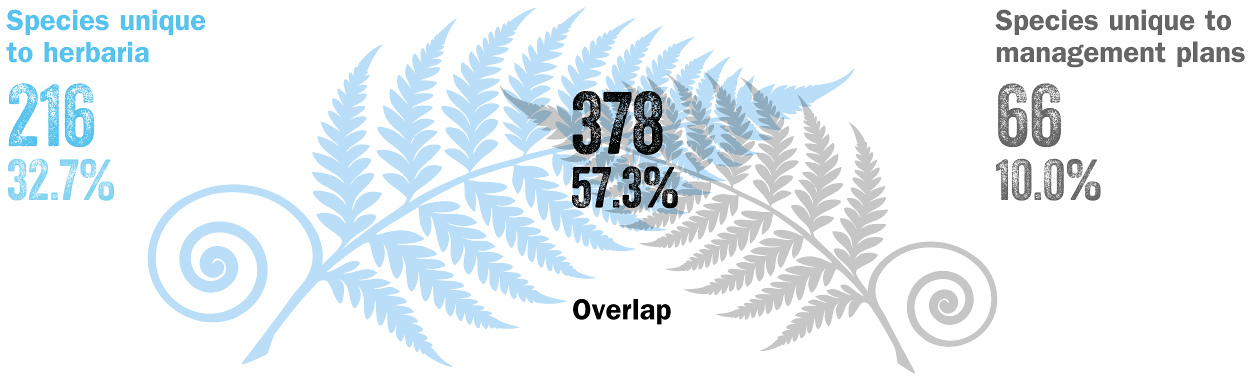
The rich habitats of Honduras encompass high-elevation cloud forests, lowland tropical rainforests, pine-oak forests, wetlands and coastal mangrove ecosystems. There are 91 major protected areas with differing designations that include National Park (protecting large-scale ecosystems and scenic, environmental and cultural heritage) and Biological Reserve (highly biodiverse, often with strict controls on access). Managed by the Instituto de Conservación Forestal (ICF; Forest Conservation Institute) and the Sistema Nacional de Áreas Protegidas de Honduras (SINAPH; National System of Protected Areas of Honduras), these areas serve to protect, conserve and manage biodiversity and ecosystem services.

When Batke and colleagues realised that Honduras's most valued natural places might not be accurately catalogued – making managing them a challenge – they set about systematically studying the management plans of all protected areas to see how ferns and lycophytes were represented. Honduras is home to 713 of the world's estimated 13,000 species within these groups. Of the protected areas, only 54 (59%) had management plans that the researchers could access. The team classified these into four types of plans according to the information they contained on ferns and lycophytes: with appendices containing species lists; mentioning ferns and lycophytes but lacking comprehensive species lists; without species data but citing relevant external scientific or grey literature; and having no species-related information.

Excluding the protected areas without any species data, a total of 36 (40%) could be investigated in detail. Compiling all available management-plan data from these areas yielded 1,481 fern and lycophyte records; the team then checked and updated the scientific names as necessary. This reduced the database to 1,233 records. Among them were 92 records from 30 species not recognised in the latest authoritative inventory (checklist) of Honduran ferns and lycophytes. And of these species, 18 were potential new records for Honduras but were lacking valid herbarium records.

FIGURE 1: How herbarium records are boosting knowledge of plant diversity in Honduran protected areas

A study of the ferns and lycophytes in Honduras's protected areas revealed an overlap of just 57.3% between species recorded from herbarium specimens and those noted in management plans. Herbarium records covered 90% of the total species, including 216 that were only reported from this source. Management plans covered just 67.3%, with 66 species not represented among herbarium specimens. These findings show that incorporating herbarium records when producing species lists for protected areas could more accurately capture the composition of fern and lycophyte communities, supporting more effective management and conservation.



Data from Batke et al. (2025)

Next, the researchers turned their attention to the herbarium data on ferns and lycophytes, gathering records from herbaria within Honduras and abroad, for the protected areas themselves as well as other locations in the country. These were sourced from the digital inventory of herbarium data that Batke and colleagues had previously compiled. The resulting dataset included 17,539 spatially referenced specimens from 39 global herbaria. The team used it to undertake various spatial analyses, primarily seeking to determine the difference between species data obtained from protected-area management reports and those from herbarium records.

COMPARING DISPARATE DATA SOURCES

The representation in herbaria of ferns and lycophytes from the 36 protected areas differed according to designation. National Parks had the highest number of species with herbarium specimens, followed by Biological Reserves. Encouragingly, several protected area categories that had little or no associated information on fern species in their management plans were represented in herbarium records. These included *zonas productoras de agua* – high-altitude watersheds on which Honduras relies for its water supply. When the team plotted the numbers of species recorded from protected areas from the two data sources, the overlap between those reported in management plans and those recorded in herbarium specimens was less than 60% (see Figure 1). In other words, two fifths of the ferns and lycophytes known from protected areas in this biodiverse and environmentally important country were absent from management plans and only recorded from herbarium specimens.

'It was a shock that they didn't match up to such a large degree, because usually when writing a management plan, most people start by getting in touch with a herbarium or at least looking online to see what's already out there,' explains Geraldine Reid, Lead Curator at the World Museum, National Museums of Liverpool, UK, who worked with Batke on the study. 'These plans had obviously been written from scratch from a fairly superficial field survey; crucially much of the species diversity of the spore-bearing plants, which are key parts of the ecosystems in these areas, had not been taken into consideration.'

As well as pinpointing the large discrepancy in what management plans and herbaria suggested was growing in Honduras's protected areas, the study revealed that management plans accounted for only 15–30% of the species representation within individual fern families noted from protected areas. Exceptions were Marsileaceae, Schizaeaceae and Woodsiaceae, where species were either equally represented or covered better by management plans than records from herbaria. Notably, there were no herbarium records of Woodsiaceae collected from any of the protected areas. This surprised the researchers, as 143 herbarium records of Woodsiaceae had been reported from outside protected areas in Honduras.

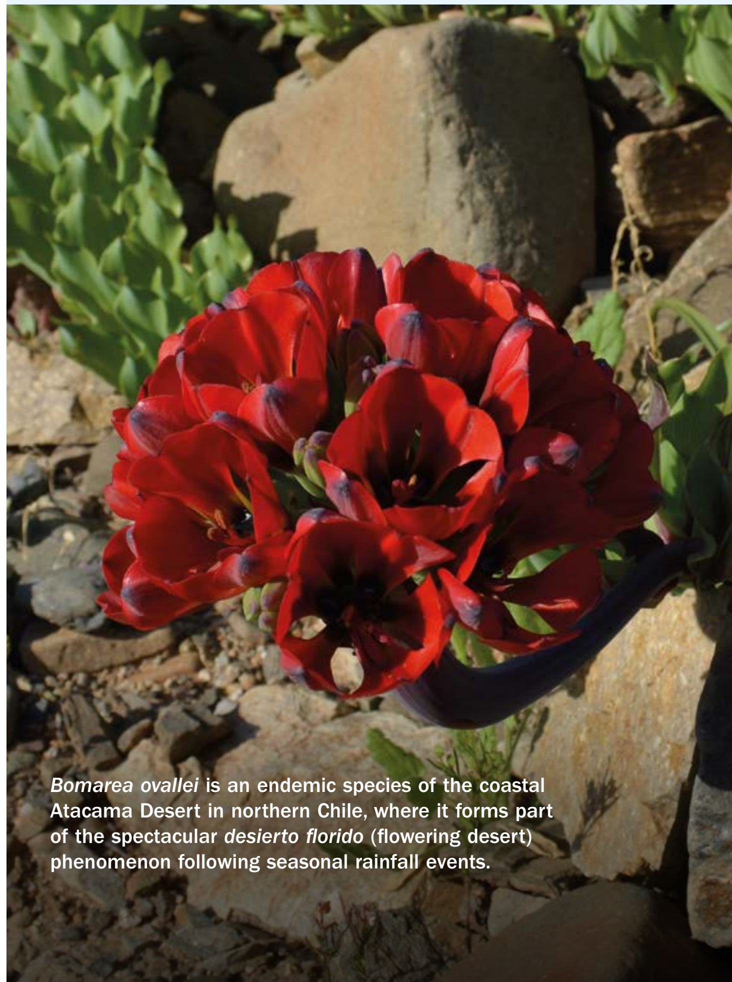
HONDURAS HOSTS 713 SPECIES OF FERNS AND LYCOPHYTES.

Box 1: Building an accurate biodiversity catalogue for research and conservation

Local expertise and global resources make for a powerful combination, as a project in Chile reveals. A team of scientists integrated over 120,000 digitised plant specimens (representing more than 3,900 species) from two Chilean herbaria to establish a standardised, expert-curated national inventory and monitoring system. The specimen records were made available through the Herbario Digital online portal, laying the foundations for further digitisation of Chilean herbarium collections and widened global access to data on Chilean plant diversity.

To evaluate the coverage and resolution of this new resource, the scientists compared the local inventory with Chilean records from the global online Catalogue of Life, which revealed discrepancies in species richness across several families. This highlighted the important role that local experts play in understanding and updating the taxonomy of species in their own countries. In response, the researchers integrated their locally curated plant list with the global catalogue to create a preliminary, updatable and potentially collaborative national inventory of Chilean biodiversity.

The new combined catalogue revealed that Chile is home to almost 20,000 known species of animals, plants and fungi, with land plants representing more than a third. The hope is that specialists in different aspects of Chilean biodiversity can progressively enrich the catalogue, to provide essential data for biodiversity research, conservation and policymaking.



Bomarea ovallei is an endemic species of the coastal Atacama Desert in northern Chile, where it forms part of the spectacular *desierto florido* (flowering desert) phenomenon following seasonal rainfall events.

Kew's Millennium Seed Bank holds nearly 2.5 billion seeds from over 40,000 species, which are a rich source of data.

Box 2: Using seed-bank data to understand genetic diversity

The conservation of species in their natural habitats – termed *in situ* conservation – is complemented by the storage of living plants, seeds, spores and other propagules in dedicated facilities outside their natural habitats – known as *ex situ* conservation. Seed banks are vitally important *ex situ* collections, particularly for capturing the genetic diversity of rare, threatened, endemic and useful species. As well as being an insurance policy against extinction, they can be used to restore degraded or lost habitats. And they can help to make agriculture more resilient to climate change by contributing useful traits, such as drought-resistance, that are conserved in the seeds of wild relatives of crop species. However, the full potential of seed banks is not presently being realised because scientists have limited understanding of the genetic diversity that exists within seed collections from individual species.

Gathering genetic data about seed collections through DNA sequencing is time-consuming and expensive, and also depletes the collections. Researchers at Kew and the Morton Arboretum, Illinois, USA, examined the information collected alongside seed samples to see if it might reveal anything about the genetic diversity of the collections. The team, led by Roberta Gargiulo, Research Leader in Conservation Genetics at Kew, observed that analysing digitised data, such as the location of sampling sites, estimated population size and number of mother plants from which seeds were collected, could predict the genetic diversity captured within collections for which genetic data were unavailable.

The scientists identified several challenges associated with relying solely on digital information, however. These included data gaps related to information not being recorded in the field or for certain categories of species (such as those with recalcitrant seeds that cannot be stored using regular drying and banking processes – which includes up to half of tropical tree species) and poor data processing and standardisation. Also, they found that databases were generally not linked, making it difficult to connect field-collection data with information on germination, nursery propagation and planting. Having interconnected databases could help to trace the proportion of seeds and genetic diversity lost at each stage of use and inform seed sourcing prior to restoration efforts.

Currently, most databases of seedbank digital information are not publicly available. An exception is ENSCOBASE, produced by the European Native Seed Conservation Network, which has been used for research within Europe, as well as to assess progress towards conservation targets. Moreover, Kew's SeedPOD (Seed Portal for Online Data) will be available online in late 2026. The first open-access database of global wild-origin seed collections, it will make available field, processing, seed-quality and test data. Digitising images and incorporating new automated technologies into studies could stimulate further innovative work in this field in future, underpinning vital conservation and restoration projects.

The analysis further revealed that species assemblages derived from herbarium data differed from those associated with management plans. Importantly, representation of different families was substantially broader when using herbarium records than when relying solely on management-plan species lists. Several protected areas exhibited little similarity in community structure when comparing herbarium data with management-plan data. This indicated that, taxonomically, protected-area management plans were not adequately representing the composition of fern and lycophyte communities. And they were likely to be failing to capture the true extent of other plant biodiversity, too.

One potential reason behind the mismatch is the structure of conservation funding in Honduras. SINAPH operates under a co-management legal framework between the government and NGOs or similar associations. The operating costs of these organisations are covered mostly by small grants and the management of tourism activities, with limited intervention by the state. 'These tourism activities are focused on landscapes and charismatic fauna such as birds, butterflies, reptiles and so on, so funds are centred around ecological characteristics, not really plant diversity,' explains Honduran conservation management expert Johan David Reyes Chávez, a PhD candidate at University College Cork in Ireland, who was also involved in the study. 'And this is not a problem endemic to Honduras.'

NURTURING NATURE WITH JOINED-UP DATA

The significant disparities between herbaria and management plans in representing species and assemblages of ferns and lycophytes have important implications for conserving biodiversity in Honduras. Both sources hold valuable information, and understanding the relative contribution each makes to the total known diversity in protected areas paves the way for improvements to be made. Batke and colleagues suggested that a starting point would be to enhance data integration within protected-area management frameworks. They reasoned that by enhancing collaboration between herbarium and management authorities, and ensuring surveyors of protected areas also deposit plant specimens in herbaria, the overall quality and reliability of biodiversity data could be significantly improved. And doing so would provide opportunities for creating and updating comprehensive checklists of species to underpin effective conservation strategies.

With this intention in mind, the study team developed a strategy for integrating herbarium data into protected-area management in Honduras. They proposed several processes, including: efforts to understand and verify data that already exist and to identify gaps in those data; digitisation programmes to make herbarium records more widely available, as well as analysis to understand biases in the available collections; and the development of a strategy, grounded in scientific evidence, outlining conservation priorities and plans for fulfilling them. There would also need to be monitoring and feedback to determine whether the process was working and, if not, to improve it.

'Basically, it gives managers an evidence base for prioritising areas that are botanically important but currently under-protected,' says Reyes Chávez. 'At the country scale, we aim to use fully integrated herbarium datasets – for all plants – to redefine Key Biodiversity Areas in future work in collaboration with the government. We need to use our limited resources in a smart way in Honduras, and the next steps of data integration will give conservation practitioners an even deeper understanding of plant diversity for conservation purposes.'

The study, and those in Brazil, show that digitised herbarium specimens can be applied in diverse ways to support conservation – from prioritising the species that will safeguard evolutionary history, to identifying those most at risk from development and ensuring that the biodiversity within protected areas is clearly understood and effectively managed. Many countries in Latin America are characterised by high levels of plant and fungal biodiversity, stretched resources, and looming threats to biodiversity from development aimed at boosting national and regional economies. Combining the innovative use of digital herbarium specimens, international partnerships that direct resources to stretched institutions, and expert local knowledge could help the region to retain its biodiversity superpower status into the future.

This chapter is based on the following publications in our special collection:

Batke, S.P., et al. (2025). The importance of integrating herbarium records into conservation plans: a case study on Honduran ferns and lycophytes. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70013

Gargiulo, R., et al. (2025). The potential of seedbank digital information in plant conservation. *Plants, People, Planet*, DOI: https://doi.org/10.1002/ppp3.70017

Rocha, A.L.S., et al. (2025). Balancing tracks and trees: Assessing railroad impact on Brazilian biodiversity. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70153

Scheidegger, N.B., et al. (2025). Assessing the evolutionary distinctiveness of a highly threatened plant group: The urgency to preserve a unique lineage of evolution in Brazil. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70088

Segovia, R.A., et al. (2025). Digitising biological collections to advance National Species Inventories: A case study from the flora of Chile. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70089

THE STRATEGY GIVES MANAGERS AN EVIDENCE BASE FOR PRIORITISING AREAS THAT ARE BOTANICALLY IMPORTANT BUT CURRENTLY UNDER-PROTECTED.

A COLLECTIVE ACHIEVEMENT

Plant collecting helped to boost the wellbeing of British soldiers during WWI.

UK COLLECTIONS HOLD AT LEAST

6,700

PLANT SPECIMENS COLLECTED DURING WWI BY SERVICE PERSONNEL

In this chapter, we learn: that many soldiers collected plants while serving in World War I; how historical collector networks contributed to fungaria on two continents; that individual specimen collectors have more in common than you might think; and why specimens collected on a 19th-century Arctic expedition are only now coming to light.

DIGITISED PLANT AND FUNGAL SPECIMENS ARE HELPING TO REWRITE SOCIAL HISTORY BY HIGHLIGHTING THE CONTRIBUTIONS TO SCIENCE MADE BY UNSUNG COLLECTORS.

It is not only biodiversity science that stands to benefit from digitised specimens. New research suggests that using them to turn the spotlight on specimen collectors can enlighten social science and history, too. Three separate studies that mined specimen labels for information on collectors and their practices were surprisingly revelatory. The first showed that many British soldiers collected plants while fighting in World War I (WWI). The second revealed how women-led networks helped to expand collections of fungi in the UK and New Zealand during the 20th century. And the third found that many individual collectors have adopted parallel sampling habits down the years, paving the way for a better understanding of bias in natural history collections. Together, they demonstrate that connecting biological accessions with related texts, photos and artefacts to form ‘extended specimens’ can be particularly valuable for piecing together the contributions of forgotten plant and fungal collectors.

‘It’s this blend of history and science that we were trying to get across in our work,’ explains James Wearn, Strategic Operations Manager for Science at Kew. James worked with Christopher Kreuzer, Quality Assurance Officer on Kew’s Digitisation Project, to research the prevalence of, and motivations for, plant collecting during WWI. ‘In historical research, we often talk about how the research adds to, or changes, the narrative,’ continues Wearn. ‘And in scientific research, we often talk about testing hypotheses. They’re not mutually exclusive but until recently there had been little published analytical research on the botanical aspects of the First World War. So, we’re breaking new ground with this research. These collections are not just scientifically useful; they are tangible pieces of our heritage from a turbulent time.’

Digitisation programmes in the UK – at Kew, London’s Natural History Museum (NHM) and the Royal Botanic Garden Edinburgh – were already underway when Wearn and Kreuzer, who are also historians, began their study. This meant it was quite straightforward for them to search online for specimens dated to the war years of 1914–18, and home in on those collected from battle areas. Then, in an example of the power of using varied information sources, a tweet about wartime plant collections at the NHM prompted Kreuzer to visit the museum’s archives in person. This revealed the presence of letters and other documents that pointed him in the direction of additional as-yet-undigitised wartime collections at the NHM.

At the outset of the project, around 2,100 plant specimens collected during WWI by service personnel were known to exist in the UK. By combining an analysis of digitised and physical plant specimen collections with published and unpublished archival records, Wearn and Kreuzer identified more than 4,600 additional specimens collected by at least 30 previously unknown or not-well-documented WWI collectors (see Figure 1). These soldiers had ranks from major general to private, and many had little or no experience in collecting specimens. The researchers anticipate that the total number of WWI specimens collected by service personnel, from sites around the world, will continue to increase with further UK digitisation. Currently untapped collections on mainland Europe could yield additional specimens, too.

‘Many people are familiar with remembrance flowers, principally poppies, and, in France, the cornflower,’ says Wearn. ‘But when it comes to actual collecting of plants during wartime, even academics and enthusiasts aren’t really aware of anything beyond the sporadic pressing of flowers within letters sent home from the front, or flowers picked from gardens and sent as symbols of love and home life to the servicemen. What we’ve been doing is uncovering mass collection events in the theatre of war.’

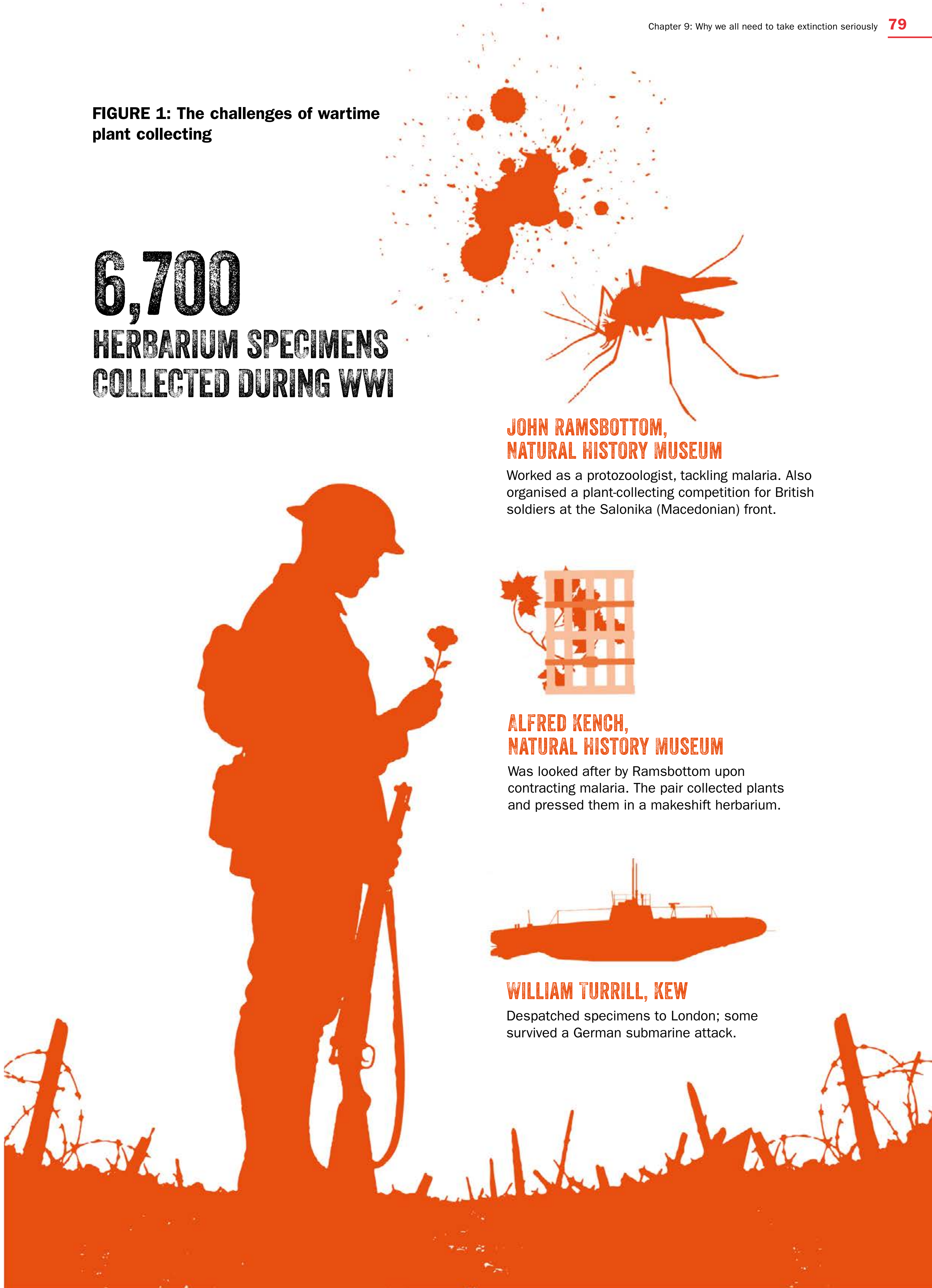
The research identified the Salonika (Macedonian) front as a particular focus of plant collecting during the conflict. While some independent botanising took place, major collection efforts tended to be coordinated by individuals allied to scientific institutions – including the NHM and Kew – but acting on their own initiative rather than through institutional direction. For example, in 1918 the NHM botanist and mycologist John Ramsbottom organised a plant-collecting competition for privates and non-commissioned officers of the British Salonika Force (BSF) while he was serving as a protozoologist – concerned with treating parasite-borne diseases, such as malaria. Ramsbottom advertised the competition in the general routine orders issued to all troops and explained how to collect plants in the *Balkan News* newspaper produced for the BSF. Researching the collection, about which little was published following the war, not only revealed its extent – as many as 4,000 specimens – but also unearthed stories about life for the collectors at the front.

‘There’s a collector called Alfred Kench, who worked with Ramsbottom at the NHM, who is completely unknown,’ says Kreuzer. ‘But in a letter he wrote to the pair’s departmental head at the museum, he talked about how Ramsbottom looked after him in the war. Kench had come down with malaria and Ramsbottom made sure he got assigned to his section. They set up a mini herbarium in a tent, where they had presses and were drying the plants. They had a really efficient operation going there.’

The study also shed light on the wartime contributions of Kew botanist William Turrill, as well as the difficulties of sending specimens to London in one piece during wartime.

> THESE COLLECTIONS ARE NOT JUST SCIENTIFICALLY USEFUL; THEY ARE TANGIBLE PIECES OF OUR HERITAGE FROM A TURBULENT TIME.

FIGURE 1: The challenges of wartime plant collecting



6,700 HERBARIUM SPECIMENS COLLECTED DURING WWI

JOHN RAMSBOTTOM, NATURAL HISTORY MUSEUM

Worked as a protozoologist, tackling malaria. Also organised a plant-collecting competition for British soldiers at the Salonika (Macedonian) front.

ALFRED KENCH, NATURAL HISTORY MUSEUM

Was looked after by Ramsbottom upon contracting malaria. The pair collected plants and pressed them in a makeshift herbarium.

WILLIAM TURRILL, KEW

Despatched specimens to London; some survived a German submarine attack.

Turrill, who served with the Royal Army Medical Corps on the Salonika front, was responsible for collecting 550 of the wartime specimens in Kew's Herbarium. *The Journal of the Kew Guild* published insights from servicemen's letters to Kew during the war, and the organisation's archive holds a sheet, dated 1918, noting that one of the parcels of specimens sent back to Kew by Turrill had been lost due to water damage. Meanwhile, the labels of three of the specimens that Turrill collected record: 'specimen packet, submerged, German submarine'. Kreuzer believes that the labels and the journal account likely refer to the same incident.

JOINING LINKS IN THE PAST

Kreuzer's detective work with other colleagues has helped to reveal the hidden contributions of networks of collectors, many of them women, who gathered fungal specimens for mycologist Greta Stevenson in the 20th century. Stevenson is best known for a five-part series she wrote for *Kew Bulletin* on gilled mushroom fungi (Agaricales) of New Zealand, in which she described more than 100 species that were new to science. But she also wrote and illustrated several educational books, including on ferns, bacteria, fungi and viruses. Stevenson studied botany in Dunedin, New Zealand, and plant pathology in London, UK, attaining her doctorate in 1938. She worked in both countries for extended periods of time as a research scientist and teacher.

During her life, Stevenson amassed 3,000 fungal specimens, which were collected in New Zealand and divided between two fungaria. The first comprised fungi collected between 1948 and 1958, which Stevenson brought to Kew in 1959. The second was compiled in the 1970s and early 1980s, where it today forms part of the New Zealand Fungarium (Te Kohinga Hekaheka o Aotearoa). Examining these collections, and texts and artefacts associated with them, yielded information on Stevenson's collector networks that had previously been obscured by the separation of the two fungaria. Studying them together helped Kreuzer and his colleagues to quantify the contributions of these previously hidden individuals to 20th-century science.

'If you'd tried to do this work 15 or 20 years ago, you could have done it but you would have had to fly to New Zealand and physically go through the fungarium there and also at Kew,' explains Nathan Smith, Head of Plant and Earth Science at the National Museum of Wales (Amgueddfa Cymru) and a Kew Honorary Research Fellow, who was involved in the study. 'And there are lots that you might have missed because the collections contain information that might not be recorded in written work and vice versa. Kew's Fungarium has a million specimens – it's massive – so you'd probably have missed something. Having digital specimens allows for a far more comprehensive approach.'

One insight provided by studying the two collections is how the involvement of women changed over time. The most prolific collectors for the first fungarium were women (with many having new species named after them), while those for the second fungarium were men. It is possible that this reflects a wider societal or disciplinary trend. For example, it tallies with the decline in female presidencies of the British Mycological Society from nine between its founding in 1896 and 1950, to only four between 1951 and the end of the 20th century.

Key characteristics of Stevenson's collector networks that emerged from the study were their transient nature, and links to relationships, time and place. For both fungaria, Stevenson was the main collector, contributing 810 specimens (53%) to the first collection and 653 (45%) to the second. Stevenson, often known by her married name of Cone, had initially lived with her husband and young family in Wellington, New Zealand. After the pair separated in 1951, Stevenson had moved frequently, her collector networks reflecting this peripatetic lifestyle. The researchers were able to group 22 other people, who had collected more than five specimens each for the first fungarium, into four clusters linked to Stevenson's bases of: Wellington (1946–53); Dunedin (1953); Wellington (1958); and Nelson (1954–58).

'She is clearly treated with respect and gets her work published, but she doesn't tend to stay in one place and get a permanent role,' says Smith. 'She almost represents a very modern researcher in that regard. She is always active as a mycologist but is always on the outside. When we tell the histories of institutions, we often talk about the people who are there for 30 or 40 years. Greta Stevenson is not one of those people. She's here and there, she's in, she's out. And on top of that she's going between two hemispheres – she's in New Zealand, she's in the UK.'

In 1959, Stevenson returned to the UK, where she worked at Kew on the fungal specimens she had brought with her. The institution supported her in publishing new species from the collection, which she did in collaboration – across the two hemispheres – with her New-Zealand-based mentee and fellow mycologist Marie Taylor. In the UK, Stevenson focused on fungal taxonomy and nitrogen fixation, as well as teaching and writing, before returning to Wellington in 1970, leaving her fungal collection at Kew. The researchers noted that 31 people from Stevenson's later period in New Zealand had collected more than seven specimens apiece for her second fungarium. These could be clustered according to their connections with Wellington Botanical Society; Victoria University, Wellington (VUW – where Stevenson worked for ten years as an unpaid research officer); and 'other'.

Family, including children, and work colleagues featured strongly among Stevenson's collectors. Her enthusiasm for both fungi and exploring New Zealand's wild places rubbed off on the people around her, making it easy for her to inspire them to collect. And when Stevenson was in the UK, Marie Taylor took up the mantle of encouraging collectors in New Zealand. In a 1949 article Stevenson wrote for the *Wellington*

STEVENSON AMASSED 3,000 FUNGAL SPECIMENS IN TWO FUNGARIA – IN THE UK AND NEW ZEALAND.

Mycologist Greta Stevenson (below), who motivated a network of collectors to compile two major fungaria; illustrations she drew for her article in *Kew Bulletin* (left); William Turrill (bottom left), who worked at Kew's Herbarium before and after WWI and collected plants while serving on the Salonika front; and a specimen of *Linaria simplex* grown at Kew from seed collected by Turrill on the front in 1917 (Specimen barcode, not shown: K004511127).

A specimen collected during the Greely Expedition of 1881–84 (left) and the six men who survived the expedition (right). Greely is seated bottom right.

BOX 1: Piecing together specimen journeys

Launched in 1881, the Greely Expedition sought to establish a meteorological research station at Lady Franklin Bay, Ellesmere Island, in far north-eastern Canada. It contributed to the First International Polar Year (1882–83), an international effort to coordinate polar expeditions, observations and research. None of the 25 members was formally trained in botany, with natural history specimens considered to be ‘elective observations’. The failure of planned resupply ships to reach the expedition forced the crew to retreat south and by the time rescue came in 1884, only seven of the men remained alive. Another died soon after. Any specimens that had been collected were forgotten about amid tales of mismanagement and cannibalism.

One hundred and forty years later, researchers encountered 49 specimens collected during the expedition in the Carnegie Museum of Natural History herbarium, in Pittsburgh, USA. Wondering how they had come to be there, they turned to the Global Biodiversity Information Facility portal to see if they could find out more. Their search revealed a total of 223 digitised specimens from the voyage, physically located in 11 herbaria around the world. Of these, the majority were vascular plants (those with specialised vessels for transporting water and nutrients – the majority of land plants), spanning 20 families, 44 genera and 99 species, subspecies or varieties. But there was also one moss specimen and four fungi. Of the fungi, three were type specimens (the definitive reference specimens for species names), highlighting that the expedition had uncovered species new to science.

The specimen labels named four collectors, the most prolific of which were expedition leader Adolphus W. Greely (48% of the collections) and meteorologist David C. Ralston (43%). As there were no records of Ralston having made any botanical observations, it is possible that Greely also collected those specimens, but that Ralston (who eventually succumbed to starvation) carried them as the men retreated. Either way, they ended up among his personal effects. A set of 69 book-bound specimens collected by Greely – which coincidentally also ended up in Pittsburgh – contained a handwritten inscription to his daughter Rose on her 17th birthday. ‘Certain I am that these plants from the high white north will ever be valued as gathered and saved by her loving father in 1881–1884.’ It serves as a reminder that the expedition members were people, with hopes, dreams and families.

As with the other studies outlined in this chapter, this research highlighted the benefits of combining specimens with other information sources and artefacts. Greely noted in the official expedition report that the collection of mosses and lichens was exceptionally ‘large and important, and its necessary abandonment is greatly to be regretted’. Meanwhile, a 1923 record from the *Carnegie Museum Annual Report* hinted that more specimens could yet show up: ‘From Mrs Myrtle Walkinshaw-Shupe was obtained a set of about 200 specimens of plants, collected by Sergeant David C. Ralston, in the vicinity of Lady Franklin Bay, Greenland, during the Greeley [sic] Arctic expedition in 1881–1883.’ Currently, the whereabouts of these specimens remains a mystery.

‘We often think of specimens as strictly scientific objects, but they also have histories,’ says Mason Heberling, Associate Curator of Botany at the Carnegie Museum of Natural History in Pittsburgh. ‘Our project highlights the value of digitisation, not only of natural history collections but also of books and newspaper articles, to reconnect specimens scattered around the world and tell their stories.’

Botanical Society Bulletin, she explains the joy to be had from collecting: ‘ … anyone may find a quite new fungus in a place which has been well searched many times before [so] fungus hunting offers rewards and excitement entirely different from ordinary plant collecting, and in New Zealand it is especially so, for little has been done in this field.’

COMMON COLLECTING GROUND

It is easy to think that disparate people living in different places and having varied levels of expertise and discrete motivations for collecting would exhibit vastly different approaches to what they collect and how. But a study of one million digitised specimens collected in the north-eastern USA by some 10,000 collectors revealed that the opposite is true. Surprisingly, the researchers identified six norms that were common to the practices of all the collectors. These were that they tended to collect: many different species rather than multiple specimens of the same species; an average of ten specimens per collecting site during their lifetime; from the same locations as other collectors; during the peak growing season in spring and summer, when climates were more favourable and plant growth was generally higher; species from smaller genera and families; and particular species that were conspicuous outside the peak growing season.

‘We wanted to try to figure out how differences in the ways that individual people viewed the world and collected specimens have influenced how biodiversity science is done today,’ explains Ryan Schmidt-Knapik, a PhD candidate in Organismic and Evolutionary Biology at Harvard University Herbaria, USA.

Schmidt-Knapik and colleagues downloaded more than two million digitised herbarium specimens of plants from the north-eastern USA (Connecticut, Maine, Massachusetts, New Hampshire, New Jersey, New York, Pennsylvania, Rhode Island and Vermont) available on the Global Biodiversity Information Facility online portal. These were physically housed in 237 herbaria around the world. After various checks and filters, their curated dataset contained just over 1.3 million georeferenced records (those with geographical coordinates). From this, the team identified 9,247 people who had collected plant specimens in the region – from minor collectors who gathered only a few plants to one, Robert L. Schaeffer, who amassed an astonishing 50,287 specimens.

Many prolific collectors were trained botanists. However, others had professions outside the natural sciences – including medical doctors, lawyers and judges – reflecting a strong trend for hobbyist collecting. Botanical clubs or societies – including Philadelphia Botanical Club, Torrey Botanical Society (founded as Torrey Botanical Club, the oldest botanical society in the Americas) and New England Botanical Society – were important for mobilising collectors. Clusters of collections around colleges indicated that students were likely among the most influential specimen contributors in locations throughout the region.

The team determined that the six collector practices had led to particular biases within collections. For example, personal preferences for different plant groups among the collectors had led to a wide taxonomic coverage, while their habit of collecting species from smaller, easier-to-identify genera and families left the large, complex genera and families underrepresented. Meanwhile, the practice of collecting species that were conspicuous outside the peak growing season of May to September resulted in these being overrepresented. These findings can guide researchers seeking to better account for biases in future collections-based research. This could potentially extend to developing models that incorporate statistical tools to address collections biases from the outset.

‘When we understand how collecting practices shape the biodiversity record, both the strengths and the blind spots, we can build better models of plant diversity, and collect with intention to avoid biases going forward,’ says Charles Davis, Professor of Organismic and Evolutionary Biology and Curator of Vascular Plants at Harvard University Herbaria.

HONOURING THE UNSUNG

The studies outlined here show that turning the spotlight on collectors – rather than solely focusing on plants – can illuminate the past in new ways (see Box 1), uncover narratives of people previously hidden from biological histories and join up the dots between collaborators to show a larger picture. They suggest, too, that sometimes focusing on people can inform science, such as by identifying biases rooted in predictable human behaviour. Perhaps most importantly though, they make clear that the collective contributions of many unsung people, taking small actions in different places, often only during short periods of their lives, have added considerable value to modern scientific understanding.

In Schmidt-Knapik’s words, ‘I was honestly blown away with how much of an impact the “collective of everyone” had – especially the people who collected fewer than 20 specimens,’ he says. ‘We think about these collections, these resources, as having been created by a few, prominent and extremely prolific collectors, but herbaria and fungaria would be far less valuable without the efforts of everyone else.’

This chapter is based on the following publications in our special collection:

Heberling, J.M., Wright, J.P. (2025). Digitization connects scattered specimens and enables new historical research: Plants from the Lady Franklin Bay Expedition (1881–1884). *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70063

Kreuzer, C., Ridley, G.S., Smith, N.E.C. (2026). Digitisation as archival intermediary: Quantifying and qualifying Greta B. Stevenson’s mycological collector networks. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70173

Kreuzer, C., Wearn, J.A. (2025). How digitisation of herbaria reveals the botanical legacy of the First World War. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70028

Schmidt, R.J., et al. (2025). The collector practices that shape spatial, temporal, and taxonomic bias in herbaria. *New Phytologist.* DOI: https://doi.org/10.1111/nph.70297

HERALDING THE RISE OF LOCAL PLANT SCIENCE

THE TIDE IS TURNING ON

>400

YEARS OF INEQUALITY IN PLANT SCIENCE

In this chapter, we learn: why ‘holotypes’ are highly prized specimens; that many specimens collected in the Global South now reside in the Global North; how countries are increasingly retaining specimens collected within their borders; and that collaboration has been key to digitising specimens from the Western Indian Ocean islands.

In the past, many plant specimens taken from habitats in Central and South America ended up in North America and Europe.

LOCAL PLANT SCIENCE IS OVERCOMING ITS COLONIAL PAST, WHICH SAW COLLECTORS AND INSTITUTIONS TAKE VAST NUMBERS OF SPECIMENS FAR FROM THEIR COUNTRIES OF ORIGIN.

'Holotypes' are celebrities within collections. As the original type specimens on which the names of species are based, they are fundamental references for scientific and historical research. In the 18th and 19th centuries, colonial powers in the Global North collected many plant specimens from the Global South that they retained and later designated as holotypes. Without access to these key resources – at least, not without travelling abroad or requesting a time-consuming loan – researchers in the Global South were thereafter put at a disadvantage. Today, however, the situation is changing. New research using digital specimens from the Global Biodiversity Information Facility (GBIF) shows that holotypes are increasingly designated and held closer to the locations from where the original plant material was collected, particularly within Africa, Asia and Latin America. The findings suggest that local scientific infrastructure and capacity are growing and biodiversity governance is shifting in a positive direction – but that more must be done to address the inequities of the past.

'We started to work with GBIF 20 years ago,' explains Dominik Tomaszewski, Curator of the Herbarium at the Institute of Dendrology of the Polish Academy of Sciences. 'The Institute was involved from the outset in programmes to digitise natural history collections in Poland. We were aware of the potential of digitisation and of the importance of making collections publicly accessible. We have one of the biggest collections of brambles [*Rubus* species] in Europe and digitised our holotype specimens first. We noticed that other researchers began using these digital specimens, highlighting the research potential. I love GBIF and I discovered that there are a lot of holotypes there. We wanted to learn more about how they were distributed around the world, so we started studying them in detail.'

Tomaszewski and his colleagues used a dataset of 119,361 holotype records of vascular plants from 528 herbaria in 88 countries, collected between 1800 and 2023. Vascular plants are those with specialised tissues for conducting water and nutrients, and make up the vast majority of plant species on Earth. GBIF provided data on the holotypes themselves, including the herbarium in which each was stored, and the place and time of collection. Index Herbariorum (IH – the global directory of herbaria) yielded the coordinates and country of each herbarium, and the date it was founded. The two sets of data were merged and any entries deemed to be uncertain or inaccurate omitted. Both the collection sites and herbaria were then classified by region into: Africa; Asia; Australasia (Australia and New Zealand); Central and South America (including Mexico and the Caribbean); North America; Europe; and Oceania.

The team first looked at how specimen collection sites and associated herbaria were spread across the world, finding that neither was distributed evenly. Tropical regions had a greater abundance of collection sites, reflecting their rich biodiversity. The herbaria holding those holotypes, meanwhile, were most numerous in Central and South America (215), Europe (106) and North America (104), followed by Asia (62), Africa (21), Australasia (16) and Oceania (4). The team noted that within all regions, a few herbaria housed a far greater number of specimens than the others. Older, larger herbaria tended to house more holotypes, with younger facilities hosting fewer of these prized specimens. Examining founding dates of herbaria showed that, in general, they were younger in Asia and in Central and South America, and older in North America and Europe. In all calculations, the researchers were mindful that, despite being the largest publicly available data portal of its kind, GBIF was a long way from representing all holotype specimens and would have inherent biases (see Chapters 1 and 9).

PROVIDERS AND EXTRACTORS

Comparing where specimens had been collected with the herbaria now housing them revealed there were net 'providers' and net 'extractors' of plant material that became holotypes, as well as regions that, in general, retained their specimens. Some net providers had experienced a severe loss of these critical biodiversity-documenting resources. The case was particularly stark for Africa and Asia, for which 98% and 93% of holotypes, respectively, were shown to be held in herbaria outside those regions. Of the African holotypes, 92% were located in European herbaria, and 6% in North America. Madagascar was particularly well represented among these holotypes, which may reflect recent digitisation programmes focused on inventorying Madagascar's biodiversity (see Box 1). In a similar situation to that of Africa, 70% of holotypes collected in Asia resided in Europe, and 23% in North America. And despite the proximity of Australia and New Zealand to Oceania, almost 80% of holotypes designated from plant material collected in Oceania were hosted in Europe and North America (see Figure 1, overleaf).

IMAGINE THAT YOU WANT TO STUDY PLANTS FROM YOUR OWN COUNTRY, BUT ALL YOUR HOLOTYPES ARE DISTRIBUTED IN DIFFERENT COUNTRIES HUNDREDS OR THOUSANDS OF MILES AWAY.

Digitisation and capacity-strengthening programmes are helping to ensure Malagasy scientists can access and use plant and fungal specimens to understand and conserve Madagascar's rich biodiversity.

BOX 1: Collaboration drives digitisation of specimens from the Western Indian Ocean islands

Herbaria on the Western Indian Ocean islands (WIOI) of Madagascar, Mauritius, Mayotte, La Réunion, the Comoros and the Seychelles together house 468,000 specimens. Each island has at least one herbarium, but development of these local resources has been relatively recent (apart from for Mauritius, which gained its first herbarium in 1830). In common with many Global South countries, the WIOI's earliest botanical collections were mostly taken and stored in European herbaria. However, thanks to fruitful partnerships over three decades, specimen digitisation is helping to make plant science more equitable.

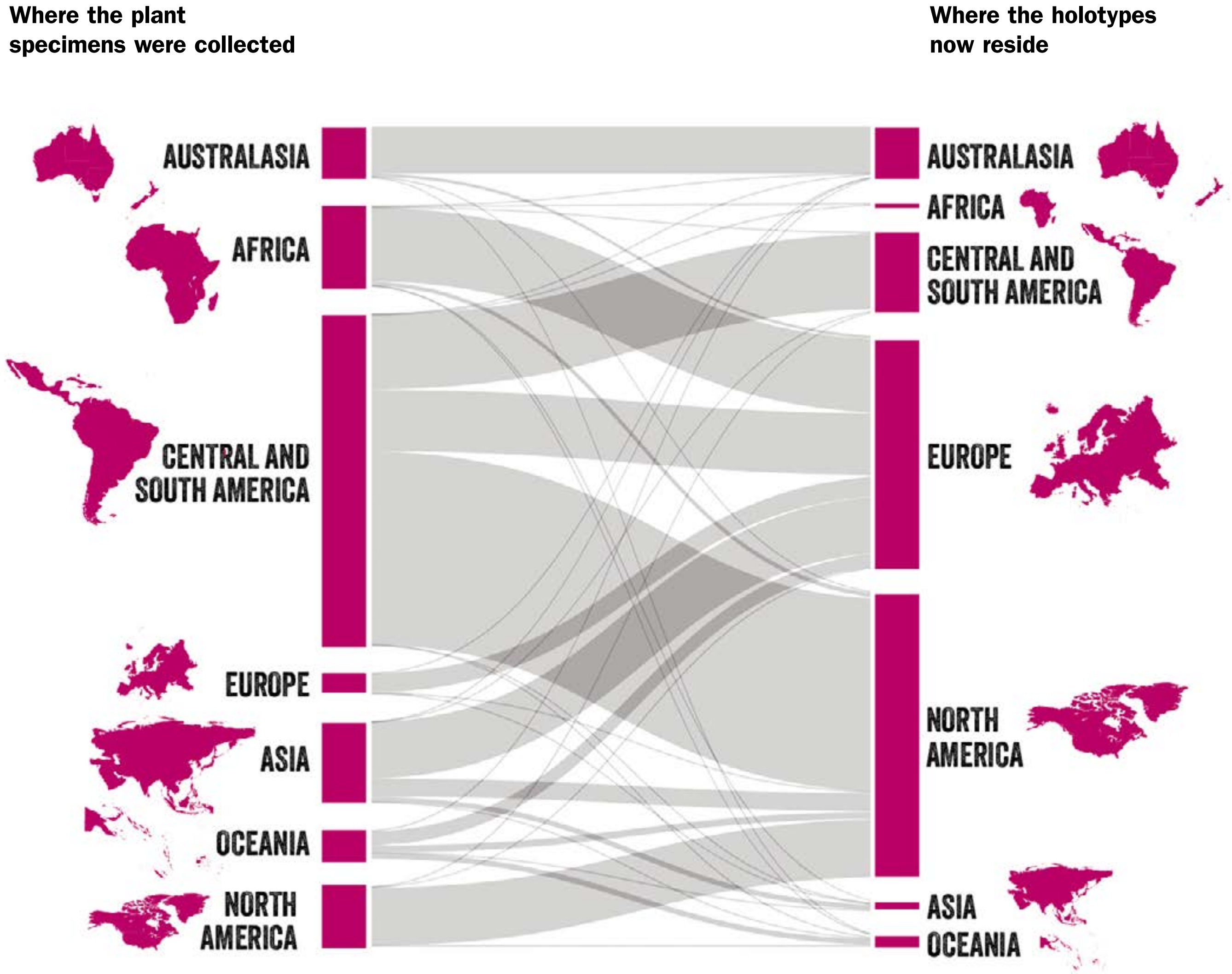
The first programme, which started in 1992 with northern-hemisphere partners, saw more than 160,000 specimen data records from Madagascar digitised and made available online. Madagascar has the richest biodiversity of all WIOI countries, with around 13,000 native plant species, just over 80% of which are endemic – unique to the island. Since 2022, the ongoing Today's Flora for Tomorrow project has digitised 37,000 specimens from Madagascar (around 10% of the national collection), in a project led by Kew with local partners. All of the Madagascar herbarium specimens held by Kew have also been digitised and made available through the Global Biodiversity Information Facility.

In the 2000s, local digitisation programmes began in Mauritius, La Réunion and the Seychelles. And between 2015 and 2018, the Indian Ocean Commission implemented a programme that led to a network being established for sharing information on Floras and collections in WIOI, as well as Tanzania and Kenya. Further support from South Africa and the UK enabled an orchid-digitisation pilot project to be set up, which led to new species descriptions and distribution records being published, as well as a small field guide in French. The project connected isolated partners and fostered mutual support, which, in turn, helped to secure additional funding for digitisation across ten WIOI herbaria under the 2022–2026 Varuna biodiversity programme.

'These larger programmes are enabling the different herbaria to start this kind of digitisation project,' says Cláudia Baider, Herbarium Officer at the Mauritius Herbarium. 'For example, I had been digitising the data labels here in Mauritius, but I couldn't image the specimens because there was no funding available for a camera. Since we received a camera in 2018, we have been able to image the specimens – all flowering plants and ferns have been imaged so far. This is why for all these small herbaria, this external funding is vital.'

Figure 1: How holotype specimens have flowed across the globe since 1800

A study of 119,361 holotype records from 528 herbaria in 88 countries shows how some regions have been net ‘providers’ of specimens, while others have been net ‘extractors’. As providers, Africa, Asia, Oceania, and Central and South America have lost 98%, 93%, 78% and 77%, respectively, of the specimens that later became holotypes to external collections, primarily in Europe and North America. The extractor regions of Europe and North America have, meanwhile, tended to keep holotypes originating in their own regions – each retaining 99%. Australasia has similarly retained 92% of its holotypes. These trends are rooted in colonial practices; today, the distance between the collection site and herbaria for holotypes is decreasing due to the increase in local herbaria, more equitable collaborations, and changes in national laws and international governance.



Adapted from Tomaszewski et al. (2025)

MANY GLOBAL NORTH COUNTRIES EXTRACTED FOREIGN BIOLOGICAL RESOURCES FOR THEIR OWN GAIN BACK HOME, HINDERING INVESTMENT IN LOCAL COLLECTIONS AND FACILITIES.

The concept of the herbarium developed first in Europe, so many of the largest and oldest collections still reside there today.

‘Imagine that you want to study plants from your own country, but all your holotypes are distributed in different countries hundreds or thousands of miles away,’ says Tomaszewski. ‘If you really want to study a plant in depth, you need to have access to the primary material. Digitisation can be helpful but sometimes you have to consult the physical specimen, not only an image. For example, it is difficult to study micromorphology, which is my field, without accessing physical material. You can’t study the minuscule structures like trichomes [hairs] on the leaf and stem surfaces, as they are invisible even in the best images from digitisation.’

The situation for Central and South America was particularly complex. The dataset contained 60,956 holotypes from the region, with the USA being the largest recipient, hosting 59%. It held holotypes from many countries, with specimens from Mexico, Colombia and Peru featuring strongly in its collections. The second-largest recipient was Brazil, hosting 14% of Central and South American holotypes, almost all of which were collected in Brazil. Next were Germany and the UK, with 5% and 4%, respectively. Notably, 60% of the holotypes collected in Brazil were housed in herbaria within that country. In fact, only a few countries were found to have retained more holotype material collected in their own territories, namely: USA (99%), New Zealand (93%), Australia (92%) and Spain (86%).

THE LONG SHADOW OF EMPIRE

The history of how herbaria developed over time had undoubtedly influenced the observed patterns of provision, extraction and retention. The two main net extractors of plant material that later became holotypes – Europe and North America – had collected and retained specimens from both home and foreign sites since their inception. This was not surprising – since the earliest herbaria were founded in Europe as far back as the 16th century, taxonomic practice subsequently evolved from there, and collecting was extended overseas as European empire-building and exploitation gathered pace. Some holotype material from North America collected in the first half of the 19th century had ended up in Europe; thereafter, though, this became rare, corresponding to the development of botanical institutes in North America. In Australasia, collected material was initially taken primarily to British herbaria (reflecting former British control of both Australia and New Zealand) but after the end of World War II, almost all holotype specimens collected in the region had remained there.

Disparities in the distribution of herbaria and research infrastructure have their roots in the colonial period, when many Global North countries extracted foreign biological resources for their own gain back home, hindering investment in local collections and facilities. However, the number of herbaria around the world has increased greatly since those times, and there have been explicit efforts over the years by Global North countries to address the problematic uneven and unfair distribution of specimens. As far back as the early 20th century, for example, London’s Natural History Museum distributed duplicate reference specimens to the countries

Investing in plant science in under-resourced locations, such as Montserrat, can underpin more effective environmental management.

BOX 2: Caribbean study highlights need for investment and training in biodiverse but under-resourced parts of the world

Conserving plants effectively around the world calls for the benefits of digital data to be shared equally. However, a project that analysed biodiversity specimens and citation data from the British Overseas Territories of Montserrat and the Cayman Islands found that despite digitisation making specimen data more accessible, research using such data was still dominated by institutions in the Global North.

The authors used data from the Global Biodiversity Information Facility and Wikidata to examine who had collected specimens from the islands, how they were used and by whom. They found that physical specimens were largely housed in the Global North and were initially mostly used for taxonomy and biogeography studies by their collectors. Following digitisation, specimens were used to investigate a broader range of topics but – with the exception of sizeable use from Brazil and China – were still largely being employed by researchers in the Global North.

The authors concluded that strengthening the capacity for conservation in biodiverse but under-resourced regions called for investment in training, infrastructure and equitable partnerships. As part of ongoing work on Montserrat in collaboration with local partners, a herbarium has been set up in Montserrat National Trust (MNT) Botanical Gardens. The project exemplifies how training in specimen preparation, digitisation and conservation can strengthen skills within environmental organisations and government departments.

of origin, including important historical specimens collected by the naturalists Joseph Banks and Daniel Solander that were sent back to Australia.

SHIFTING DYNAMICS OF PLANT SCIENCE

In the holotype study, among the initial providers of specimens, a sharp increase was observed in recent years in the proportion of holotypes remaining within their regions. This may reflect an increase in investment in botanical collections and research infrastructure. The trend was so marked in regions of the Global South that they could no longer be considered to be net providers of holotypes, with the process most advanced in Central and South America. This represents a crucial development for researchers in the region. When holotype collections remain in their countries of origin, local researchers can readily access them to conduct taxonomic work. And documenting plants in this way is even more important in biodiverse areas given the current extinction crisis affecting the planet.

The observed patterns led the research team to hypothesise that, over time, newer herbaria in the Global South had increased their collecting activities. This trend likely led to a growing proportion of collections – and therefore any newly designated holotypes – being deposited in local scientific institutions rather than being taken to herbaria in the Global North. The team tested their theory by grouping plant collection dates into 25-year periods and then analysing how distances between collection points and receiving herbaria had changed over time. This work revealed that for the first quarter of the 19th century, the average distance between collection site and herbarium was 8,995 km. However, by the equivalent period at the start of the 21st century, it had decreased to 2,654 km. A clear shift in the distribution of holotype specimens over time was ongoing, from global to more localised patterns, reflecting increased storage, curation and research capacity in the Global South.

Changes to national laws and international governance have likely contributed to the observed trends. The Nagoya Protocol, an international agreement under the Convention on Biological Diversity (CBD) now ratified by 142 countries (Parties), is implemented through national law and provides a legal framework for the fair and equitable sharing of benefits derived from the use of genetic resources, including traditional knowledge associated with plants and fungi. The Protocol suggests Parties put in place national legislation setting out how users obtain consent and agree terms of use before accessing resources from other countries. Some nations – such as Australia, New Zealand, Brazil and Indonesia – have even more stringent regulations aimed at protecting genetic resources, while others (including some that have ratified the Protocol) have no national laws governing access and benefit-sharing.

'The CBD and its Nagoya Protocol represent a global effort to make things more equitable,' explains Tomaszewski. 'Countries such as Brazil and Indonesia have laws that say newly described species – and specimens, because, of course, they are connected – are considered heritage. And that this is something that should be kept within the country because it belongs to the nation.'

The study shows that ambitions to make plant science more equitable are being fulfilled, but that more needs to be done. The team's use of digital specimens, for example, highlights both the value of, and need for more, digitisation programmes. These are needed to address challenges uncovered by the project (and also highlighted in Chapter 1), including the underrepresentation of many countries in global portals such as GBIF, and considerable biases. Further investment in herbaria is needed, along with improved digitisation (see Boxes 1 and 2).

'I feel that it is so important now for science to gather the so-called dark data from within our specimen cabinets and show it to the world, and the only way we know how to do it is through digitisation,' says Tomaszewski. 'I want to see a virtual mega-herbarium. I like the idea of creating one big, interconnected resource without any restrictions, so any researcher could see all the specimens from each herbarium around the world.'

This chapter is based on the following publications in our special collection:

Groom, Q., et al. (2025). Capacity building needed to reap the benefits of access to biodiversity collections. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70029

Klopper, R.R., et al. (2025). Digitisation of herbarium specimens to the benefit of research: An African perspective focusing on South Africa and Western Indian Ocean Island states. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70117

Tomaszewski, D., et al. (2025). Tracing holotype trajectories: Mapping the movement of the most valuable herbarium specimens. *Plants, People, Planet*. DOI: https://doi.org/10.1002/ppp3.70071

A CLEAR SHIFT IN THE DISTRIBUTION OF HOLOTYPE SPECIMENS OVER TIME WAS ONGOING, FROM GLOBAL TO MORE LOCALISED PATTERNS.

EMBRACING THE DIGITAL FUTURE

If employed wisely, specimen digitisation and new technologies have the potential to open up new research areas, make plant and fungal science more equitable, and speed up progress towards understanding and conserving biodiversity.

ONLY 36% OF THE WORLD'S

406M

PLANT AND FUNGAL SPECIMENS ARE ON THE LARGEST ONLINE BIODIVERSITY PORTAL

In this chapter, we learn: that artificial intelligence is poised to transform biodiversity science; why Indigenous communities must co-curate ethnobotanical data; how 'extended specimens' will underpin future interdisciplinary research; and that amid global digitisation programmes, physical specimens remain vital for biodiversity science.

AT A TIME WHEN THE BIODIVERSITY AND CLIMATE CRISES LOOM LARGE, DIGITISATION AND ARTIFICIAL INTELLIGENCE OFFER NEW PROMISE FOR PLANT AND FUNGAL RESEARCH.

It is an exciting time for biodiversity science. As this report shows, digitisation and new technologies are mobilising data from specimens collected over centuries and held in herbaria and fungaria around the world, making them more widely available than ever before. Scientists embracing these new opportunities are demonstrating potential applications that span diverse fields, from taxonomy and phenology to history and sociology. There is real hope that a comprehensive, virtual, accessible and inclusive global repository of specimen data is within reach, and that coupling this fundamental resource with the power of artificial intelligence (AI) could truly transform humanity's ability to address the current environmental crises.

BUILDING ON FIRM FOOTINGS

Any repository, real or virtual, must stand on strong foundations. For a global, interconnected metacollection of digitised specimen data, this means, first and foremost, that the physical specimens must have an accurate name. As Chapter 1 highlights, this is not always so. Taxonomy is constantly evolving as new information comes to light, making it difficult for those curators with limited resources to know when species names and classifications have been authoritatively updated. In the survey on curation led by Celia Aceae and reported on in the chapter, 85.3% of respondents indicated that they would find it useful to subscribe to a network that provided regular news of such updates and which offered a searchable database for publications related to classification changes. Spreading the word about existing networks could be one easy win to support robust curation practices. For plants, this might be achieved by disseminating information generated by the World Flora Online project's taxonomic expert networks (TENs), for example. Implementing the 2024 Disentis Roadmap, which seeks to liberate and link together data from scientific publications and make them available online, could also help.

'Biodiversity research relies on well-curated collections,' says Alan Paton, Director of Scientific Collections at Kew. 'Openly accessible digital collections allow new possibilities for improving the quality of collection data and how physical specimens are curated. With new tools, researchers based anywhere can remotely check identifications, compare duplicate specimens held in different institutions, share updates between collections, and connect specimen records to citations in literature describing particular species.'

As highlighted in Chapter 2, the computer vision field of AI is showing huge promise for analysing digital images of herbarium specimens, with the potential to apply automated recognition more widely for identification, as well as for measuring plant traits such as leaf mass per area and growth increments. But this requires specimens and images, along with the data extracted from them, to be comparable across facilities. Paton and colleagues have drawn up a series of recommendations to institutions holding herbarium collections. Among them, they call for collections managers to adopt rigorous, community-agreed data standards, such as Darwin Core, and support open-access platforms, such as the Global Biodiversity Information Facility (GBIF), either directly or through regional coalitions. Putting in place standards and protocols now will help to avoid duplication of effort and will serve plant and fungal science well in the long term.

The same applies to digitisation beyond visual, red-green-blue imaging. As also discussed in Chapter 2, reflectance spectroscopy has the potential to provide additional digital perspectives of herbarium specimens by profiling the light reflected across various wavelengths from the surfaces of the preserved plants. The International Herbarium Spectral Digitization Working Group, comprising 31 individuals from 25 institutions, is already working to establish standards for reflectance spectroscopy. Specifically, it is seeking to ensure that research delivers spectral data that are consistent, high quality and reproducible.

Bulky specimens – from large seeds to fruits and many fungi – are not stored as flattened, easily scannable specimens, but their label data can still be captured digitally and analysed, and DNA sequencing and other techniques used to unlock additional information about them. In this regard, the methodologies outlined in Chapter 4 to sequence whole genomes from preserved fungal specimens – even century-old ones – will open up vast amounts of data to mycologists. These will enable them to better understand the evolution of, and genetic variation within, fungal species, as well as to identify the useful compounds they contain and the biosynthetic pathways used to produce them. The potential applications for humanity span food production, medicine, waste treatment and more.

MANAGING DIGITAL DATA WISELY

Just as herbaria and fungaria require appropriate specimen cataloguing systems to enable researchers to use them effectively, so collections of digital equivalents call for well-designed and durable systems of virtual organisation. Here, Brazil's successes, rooted in the collaborative efforts of bioinformaticians and taxonomists (see Chapter 1), can serve as a blueprint for other countries. While there is still work to be done – as would be expected in the most biodiverse country in the world – Brazil has shown how it is possible to create an integrated online collections-management system, underpinned by robust classification and naming, that facilitates the accurate curation of virtual specimens and the creation of species checklists. And the process of developing such systems can help to highlight gaps in collections and even reveal species new to science.

Brazil is also pioneering a way forward for equitably incorporating Indigenous knowledge into virtual herbaria, through its programme to digitise Rio de Janeiro Botanical Garden's Ethnobotanical Collection (see Box 1). This is highly important given that the first major study exploring

Box 1: Finding fair ways to connect tradition and technology

A project to digitise the Ethnobotanical Collection at the Rio de Janeiro Botanical Garden is now complete. This collection of preserved plant specimens from the Atlantic Forest and Amazon encompasses valuable biocultural details, including how Indigenous Peoples and local communities refer to, use and manage plants and fungi. Available online through the Global Biodiversity Information Facility, the resource will enable new generations to reconnect with their heritage, support the traceability of traditional knowledge and help to inform future conservation policies.

The physical collection comprises raw and processed plant products that range from fibres, ornaments and instruments, to necklaces, baskets, construction materials, brooms, household utensils and more. Brazil has 305 ethnic groups, along with 165,000 'quilombolas' (descendants of Africans who escaped slavery) and several other traditional communities. A curation and management system for the collection will be incorporated into Brazil's existing JABOT platform (see Chapter 1). The focus will be on intercultural understanding, the importance of linking knowledge-holders to objects, and the educational relevance of the collection's items.

More than a million herbarium specimens around the world may contain ethnobotanical information, ranging from common plant names to cultural uses and local management practices. This was the finding of an international collaboration of biocultural collections managers and researchers from Brazil, Canada, France, Jamaica, Mexico, the UK and the USA. The study reported that considerable variation currently exists in how ethnobotanical data are recorded across different herbaria, with biocultural data on specimens frequently overlooked. The hope is to use the findings to foster dialogue and guide best practices among global herbaria to locate, acknowledge and responsibly steward this information, together with source communities.

'Collections are not just scientific resources,' says Ina Vandebroek, Professor of Ethnobotany at the University of the West Indies, Jamaica, and an author of the study. 'They are repositories of living cultural heritage, and the communities whose traditional knowledge they hold must have a voice in how the associated data are kept and used.'

Vandebroek and colleagues highlighted the pressing need to continue digitisation efforts while also respecting communities' sovereignty over data and adopting effective data-governance principles prioritising equitable access and benefit-sharing. These might include controlled-access systems for culturally sensitive information, specific vocabularies linking cultural and academic knowledge, and mechanisms for repatriating materials to source countries, as well as for rematriation – an Indigenous-led process of restoring sacred relationships between Indigenous Peoples and their ancestral lands, including associated cultural artefacts.

The researchers concluded that future efforts should prioritise co-curating specimen-label data with source communities to ensure that names, provenance and uses are accurately attributed, and that decision-making around the collections – which can be complex – is undertaken as a collaborative endeavour. Initiatives such as Biocultural and Traditional Knowledge Labels (digital tools co-designed with Indigenous communities to manage, identify and govern intellectual property, cultural heritage and biodiversity data) and Collections Care Notices (visual identifiers developed to guide institutions and repositories on how to provide proper cultural care and stewardship of collections) should be used to ensure Indigenous and local communities can assert ownership of their knowledge.

'More than a technical milestone, the digitisation of biocultural collections is important for associating, recognising and valuing the holders of knowledge linked to the belongings of Indigenous Peoples and traditional communities,' says Viviane Fonseca, Researcher and Curator of the Ethnobotanical Collection at the Rio de Janeiro Botanical Garden. 'By recognising these communities as true guardians of biocultural diversity, we can foster meaningful intercultural dialogues and ensure the traceability and protection of their traditional knowledge.'

This bag, made from the fibres of the piassava palm (*Attalea funifera*), is one of many biocultural items in the Ethnobotanical Collection at the Rio de Janeiro Botanical Garden, Brazil.

perspectives on biodiversity digitisation – particularly of herbarium specimens – identified the potential exclusion of Indigenous Peoples' knowledge as the primary risk involved. Björn-Ola Linnér, Professor of Environmental Change at Linköping University, Sweden, who led the study, examined biodiversity reports, conducted surveys and interviewed participants in international biodiversity negotiations. Encouragingly, Linnér and colleagues reported broad support for biodiversity digitisation across a wide range of countries of all income levels, particularly for its value in enhancing monitoring, forecasting impacts, combatting environmental crimes, improving accessibility to data and facilitating evidence-based decision-making. However, they highlighted the need for governance frameworks covering responsible innovation, digital literacy and equitable benefit-sharing with Indigenous knowledge-holders.

Currently, a complex and overlapping set of regulations, obligations and responsibilities govern how institutions manage digitised data. Legal frameworks exist, but as technologies including AI and approaches to digitisation continue to evolve, institutions must be active, forward-looking and agile to respond, and they should consider both the current and potential future uses of the data they are generating. Where policy frameworks lack legal certainty or precise regulatory pathways, digital collections managers may need to think carefully about potential risks. For example, in the absence of any guidelines, it might be prudent for them to consider whether sharing a digital specimen record may be detrimental in any way. The principles of CARE (Collective benefit, Authority to control, Responsibility, Ethics) and FAIR (Findable, Accessible, Interoperable, Reusable), published between 2016 and 2020, provide guidance for navigating such challenges. However, their implementation is not always straightforward, and many institutions may have insufficient resources to do so. When negotiating data ownership, a collaborative and interdisciplinary approach, and the use of emerging digital tools such as Biocultural Labels (see Box 1), can help.

AMBITIONS FOR THE REVOLUTION

The last decade has seen extensive digitisation of botanical collections by institutions. The number of specimens accessible through GBIF has risen dramatically during this time to encompass more than 144 million specimens of preserved plants and fungi. However, based on an estimate using Index Herbariorum (IH) that the world's herbaria hold more than 406 million specimens, the specimens shared through GBIF currently represent only around 35% of the estimated total – with plants contributing around 32% and fungi 3%. Moreover, as Chapter 1 has shown, many herbaria and fungaria may be 'silent' and missing from IH. This would make the percentages lower still. Small herbaria in megadiverse countries may hold specimens that could be key to making accurate assessments of biodiversity and extinction risk. It is therefore imperative that efforts are made to include all collections in digitisation programmes – to reduce inherent global biases and engender more robust research, policymaking and conservation. If not managed well, digitisation could reproduce historical inequities at digital speed. Forging partnership between well-resourced herbaria and those constrained by limited staff, funds or facilities can help to carry everyone into the digital future (see Chapter 1 and Chapter 10).

While building a virtual repository of all the world's digitised specimen data is a worthy goal in itself, the ultimate objective is to also link entries to other complementary data, forming 'extended specimens'. This would see specimens connected in the digital universe to multiple types of data, from genetic to ecological and historical (see Figure 1), and in wide-ranging formats, spanning newspaper cuttings, videos and databases. A 'born digital' approach – in which a digital record of a biological specimen is created at the point of collection – is also gaining ground and has the potential to facilitate rapid biodiversity research.

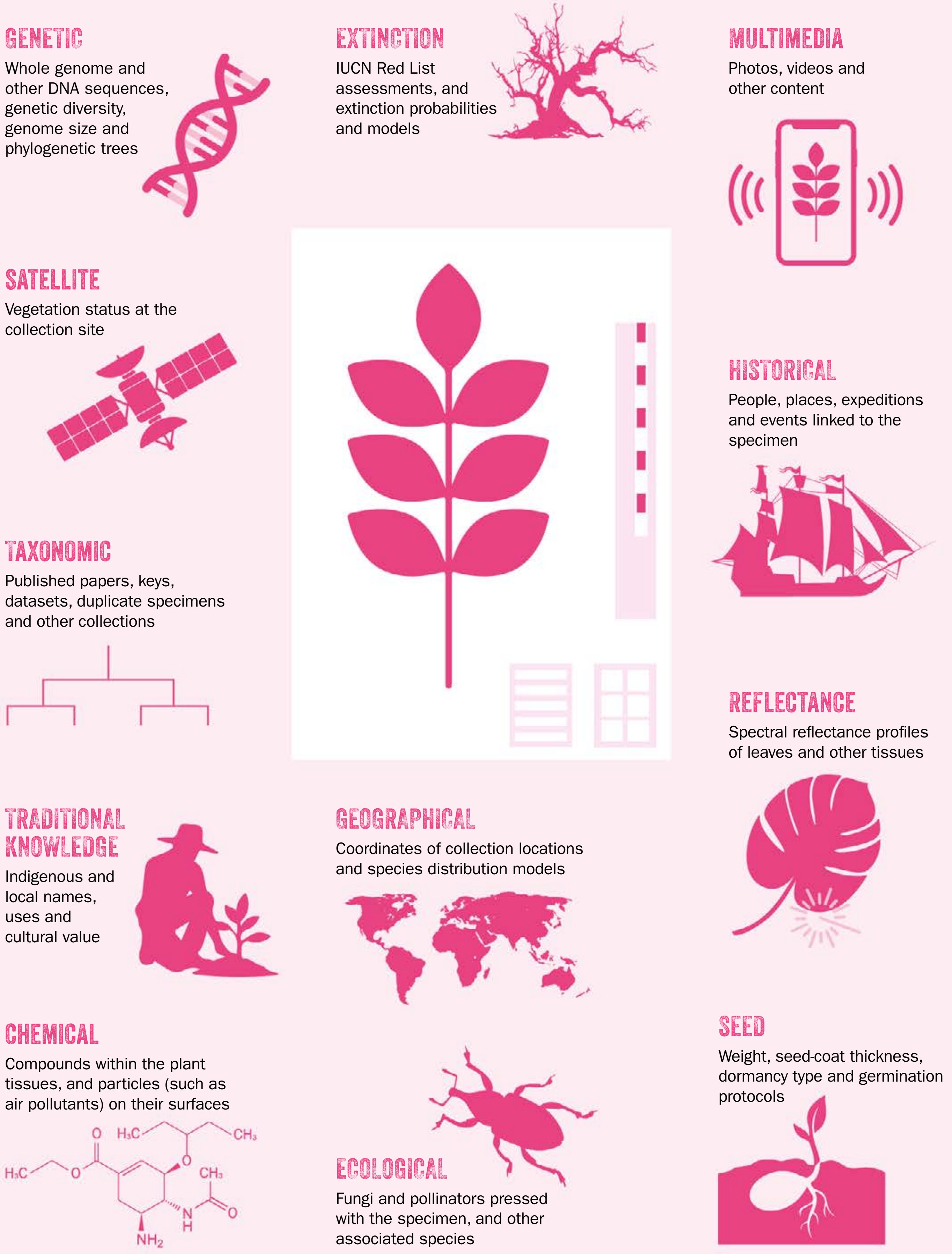
For mapping biodiversity and monitoring how the climate is affecting species, there are opportunities to mine additional data sources – from remote-sensing images captured by satellites, to photographs of living specimens taken by researchers and citizen scientists and posted on apps such as iNaturalist. The number of observation records is much greater than the number of herbarium and fungarium specimens globally and so represents a huge resource, although the varying quality of those data necessitates close scrutiny. Observations that have been verified by multiple users, termed 'research grade' in iNaturalist, represent a valuable subset that can inform scientific studies but must still be used with caution.

Work led by Rebecca Wilcox, Research Scientist at the California Academy of Sciences, which compared and contrasted the efficacy of specimen-based and citizen-observation approaches for assessing biodiversity, found that diversity was recorded as being higher when these data sources were combined. Meanwhile, a study led by Yingbo Yang, a postdoctoral researcher at Aarhus University, Denmark, found that integrating local digital specimen datasets with data sourced from GBIF improved understanding of the distributions and climatic preferences of introduced plant species – with implications for predicting future spread and ecological impacts. These findings tally with research reported in Chapter 1 and Chapter 8 that

> IT IS IMPERATIVE TO INCLUDE ALL COLLECTIONS IN DIGITISATION PROGRAMMES – TO REDUCE GLOBAL BIASES AND ENGENDER MORE ROBUST RESEARCH, POLICYMAKING AND CONSERVATION.

FIGURE 1: Examples of the types of data that can be linked to form an 'extended specimen'

The extended specimen concept elevates physical biological specimens from isolated objects to anchor points in a dynamic digital space, connecting diverse sources of information (depicted for a herbarium specimen below).



Plant and fungal scientists must not only continue to expand collection digitisation programmes but also consider how best to continue collecting physical specimens in future.

found combining disparate datasets bolstered biodiversity data. Another study, in South Africa, led by Ross Stewart, formerly affiliated with the University of Johannesburg and now a postdoctoral researcher at the University of Guelph, Canada, showed that machine learning can help to leverage the vast wealth of existing citizen-science data to map large-scale shifts in plant phenology, such as the timing of flowering or the length of the growing season.

Looking ahead, it is important that plant and fungal scientists focus not only on expanding digitisation programmes and capitalising on digital observations, but also consider how to build on physical specimen collections. Having a greater understanding of biases in existing collections can facilitate the targeted collection of specimens to fill data gaps, for example. And continued experimentation with AI can indicate whether new protocols and standards are needed to ensure specimens collected in future meet research needs. For phenology, for example, it may be pertinent to collect samples repeatedly from the same spot, which past collectors often did not do (see Chapter 6 and Chapter 9).

And when it comes to past collectors, we must not neglect the many unsung people – from Indigenous communities and women, to serving soldiers, students and others – who have contributed specimens and knowledge to biological collections over the centuries. As Chapter 9 shows, plant and fungal specimens can be a rich source of data on past collection practices, particularly when linked to journals, newspapers, books and photos. And this can extend the uses of plant and fungal specimens beyond science to encompass studies on social science and history. Collectors and communities – past, present and future – deserve to have their stories told. After all, without their efforts, the world's herbaria and fungaria would not exist. And it is these irreplaceable collections of specimens – each representing a moment in time, place and ecology – that are underpinning the rapidly evolving digital revolution in biodiversity science.

This chapter is based on the following publications in our special collection:

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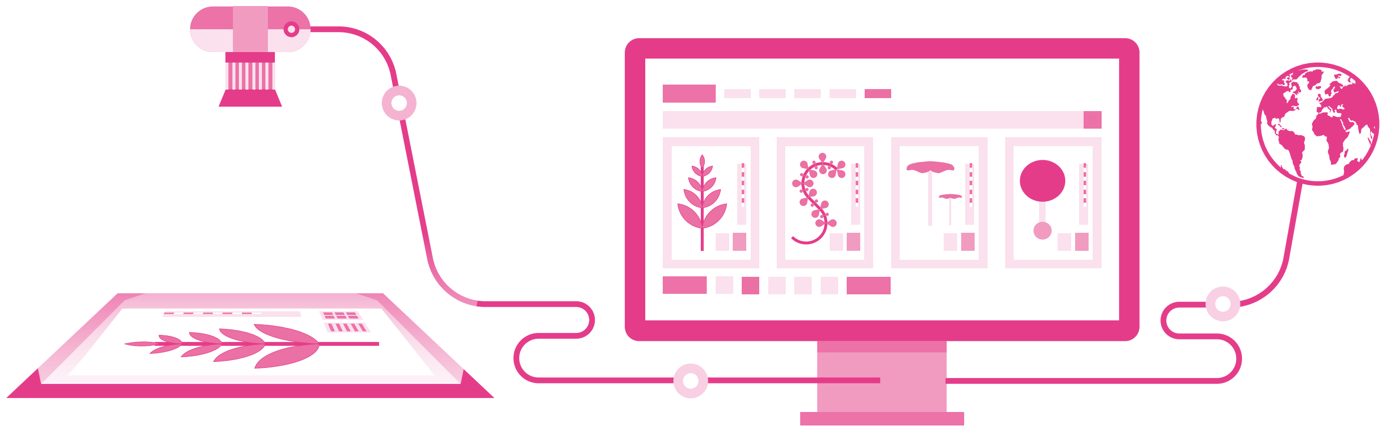

SHARING SPECIMEN DATA ACROSS THE WORLD CAN HELP TO DEMOCRATISE PLANT AND FUNGAL SCIENCE.

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State of the World's Plants and Fungi 2026 is based on, and co-released with, a special collection of academic articles entitled 'Harnessing the benefits of specimen digitisation', published by The New Phytologist Foundation in the peer-reviewed scientific journals *Plants, People, Planet* and *New Phytologist*: www.newphytologist.org/harnessing-benefits-specimen-digitisation

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Project lead: Alexandre Antonelli

Writer: Carolyn Fry

Senior science editor and project manager: Rhian Smith

Editorial team: Martyn Ainsworth, Alexandre Antonelli, Steve Bachman, Chloe Browne, Martin Cheek, Charles Davis, Felix Forest, Carolyn Fry, Paul Kersey, Isabel Larridon, Sarah Lennon, Damon Little, Mark Nesbitt, Eimear Nic Lughadha, Alan Paton, Monique Simmonds, Rhian Smith, Stephen Smith, China Williams

Design lead: Jeff Eden

Design team: Ines Stuart-Davidson, Lewis Hare, Jayne McCarthy, Emma Savage

Mapping and data team: Tim Wilkinson (mapping lead), Mounes Bakhshi, Rafaël Govaerts, Rowena Hill, Jonathan Krieger, Udayangani Liu, Robert Turner

Copyeditor: Chloe Browne

Proofreader: Andrew Lowe, Lowe Editorial Services

Picture researcher: Alex Benwell

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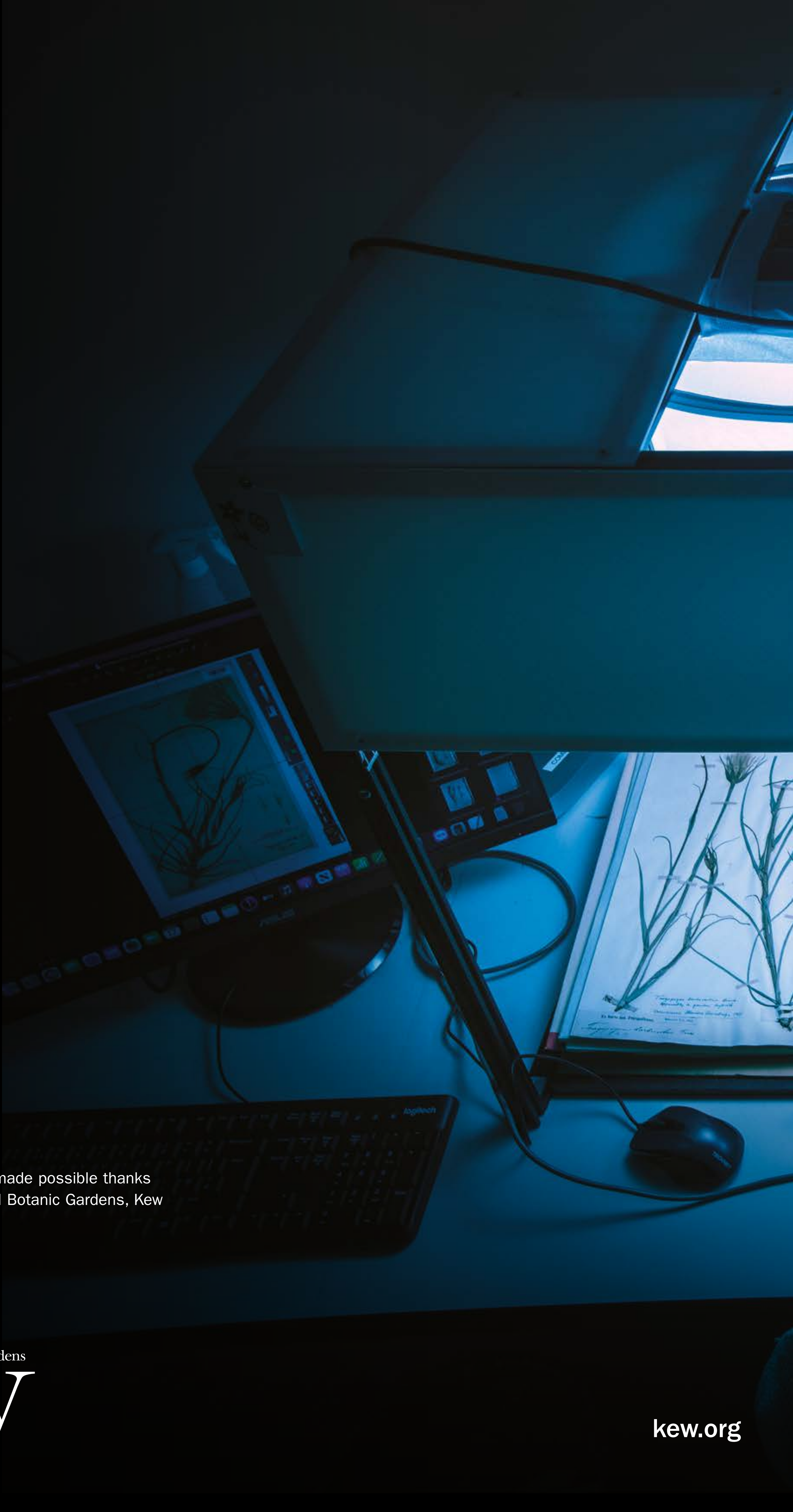

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