

EDITORIAL

Leveraging Natural History Collections to Understand the Impacts of Global Change

Leveraging natural history collections to understand the impacts of global change

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If you have been lucky enough to visit a natural history museum and you are reading this, it is highly likely that you found that visit inspirational. It is also highly likely that natural history museums still inspire you. Of course, behind the scenes at most natural history museums are the collections, where, there are often dozens, if not hundreds of curators, researchers, students, collections managers, and others curating, contributing to, and using the collections to ask any number of questions about the ecology and evolution of extinct and extant taxa. To us, their work is as inspiring as the displays in the museum. Their work is also critical, and largely underappreciated, in an era of rapid global change that is leading to shifts in species distributions, genotypes, phenotypes, and interactions. The collections harboured by natural history museums span time, taxa, and geographic regions, and, as a result, provide unparalleled opportunities to explore questions in global change biology. This Special Feature provides more than 30 examples of how our colleagues around the world are addressing fundamental questions on the impacts of global change using natural history collections.

Over 200 authors contributed to more than 30 papers in *Journal of Animal Ecology*, *Functional Ecology*, *Journal of Ecology*, and *Methods in Ecology and Evolution*. The sheer diversity of life that is covered in this Special Feature is impressive, as is the diversity of questions addressed, approaches taken, and methods used and proposed. Broadly speaking, the papers fall into four general categories: the impacts of global change on phenotypes; the impacts of global change on phenology; the impacts of global change on diversity, ranges,

or population sizes; and the impacts global change on interactions among species. There are also a number of toolkits, R packages and guidelines to facilitate collections based research in the future. Perhaps the most generally applicable one is *plantR*, an open-source R package to edit, format and standardize data from herbarium data repositories or collections (de Lima et al., 2021).

1 | THE IMPACT OF GLOBAL CHANGE ON PHENOTYPES

Intraspecific variation among phenotypes is driven by variation in climatic conditions, biotic interactions, and a whole host of other factors. Ongoing climate change has also been implicated as a cause of phenotypic change through time, such as reductions in body size, for some (e.g. Weeks et al., 2020) but not all taxa (Siepielski et al., 2019). Clearly, specimens from museums provide a wealth of opportunities to explore how phenotypes might change through time. For example, in *Journal of Animal Ecology*, Arce et al. (2023) document the degree of fluctuating asymmetry—a potential proxy for developmental stress—in the forewings of four bumblebee species from five natural history collections over 100 years. They found that fluctuating asymmetry generally increased over the course of the 20th century, which could have implications for the health of bumblebee populations.

Crittenden et al. (2023), in *Journal of Ecology*, used contemporary surveys along a nitrogen deposition gradient in Wales, and

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herbarium collections dating back to 1820, to show how nitrogen deposition has led to the loss of the ability to fix nitrogen in montane lichens.

Two papers highlight how spatial variation in climate and ongoing climate change affect the extended phenotype. In *Journal of Animal Ecology*, Vanadzina et al. (2023) examined how nest size of passerine birds varied along a climatic gradient. Of the 1117 species they examined, 412 came from museum specimens. They found that nests tended to be larger in colder climates and suggest that the ability to alter nest structure in response to climate change could influence species persistence. In *Methods in Ecology and Evolution*, Teixeira-Costa et al. (2023) review what is known about parasitic plant specimens in herbaria around the world. Impressively, there are upwards of 1,000,000 records (476,000 of which are georeferenced) of more than 4300 species. They point out the huge potential to explore how global change affects the 'extended specimen', including the host species, herbivores and the phenology of interactions between the host and the parasite.

Several other papers in *Methods in Ecology and Evolution* in the Special Feature provide new and/or improved approaches for examining phenotypic change through time. For instance, Theriot et al. (2023) examine whether published studies on changes in mammalian body sizes through time are repeatable (they mostly are not) and suggest a number of ways these kinds of studies could be improved, not just for mammals, but for other taxa as well. Wilson et al. (2023) introduce Mothra, a computer vision pipeline to phenotype specimens. Manual measurements of the 184,533 specimens would take >3000 days to measure manually, but Mothra accomplished that in less than a week. Using Mothra, they found that, for most of the species they examined, butterfly size is increasing with temperature. Weeks et al. (2023) introduce Skelevision, a method for rapidly handling, photographing, and measuring skeletal specimens. They use Skelevision to estimate 11 traits from 11 different bones from 12,450 specimens of 1882 passerine birds, with a handling time of ~1 min per specimen. It is clear that Skelevision could lead to rapid accumulation of measurements of how traits have changed in response to global change. Kothari et al. (2023) show how reflectance spectroscopy can be used to nondestructively measure a suite of functional traits on pressed plants from herbaria, opening the door to reconstructing trait responses to global change using the many hundreds of millions of specimens in herbaria around the world.

2 | THE IMPACTS OF GLOBAL CHANGE ON PHENOLOGY

The evidence from museum specimens for shifts in phenology (i.e. the timing of biological events) in recent decades and centuries (Vitasse et al., 2022; Willis et al., 2017) in response to global change continues to accrue, and features in more than half a dozen papers in this Special Feature. Belitz et al. (2023), in *Functional Ecology*, provide a framework and methodological checklist to address key questions in broad-scale phenological patterns, using museum specimens on

North American lepidopterans as a test case. Similarly, Dorian et al. (2023) analysed 168 years of museum specimens and sighting data to assess phenological shifts for 70 species of solitary bees and found that, like many taxa, solitary bees have advanced their phenologies and lengthened their flight period. Woods and McGarvey (2023) do something comparable with the odonates (dragonflies and damselflies) producing slightly more complicated results; they found that degree days had a bigger effect on emergence timing than did photoperiod or precipitation, which other studies had indicated were important. Woods and McGarvey also argue for combining specimen data and community science data to get a more system-level understanding of phenology.

In birds, Bates et al. (2023) examined nesting dates for 72 bird species using 1550 historical museum nest and egg collection records along with 3038 contemporary records of bird nesting dates from Northeastern Illinois over a 143-year period (1872–2015) to examine nesting phenology over time. Overall, egg laying dates are advancing, though there is of course variation among species, in both the intensity of the response, and even the direction of the response. Some bird species have significantly advanced their laying dates, while exhibit no response, and one species has a lay date that is actually later in the year.

It is probably true that most phenological studies to date are on plants, and temperate plants in the northern hemisphere in particular. In *Journal of Ecology*, Miller et al. (2023) use 3083 herbarium specimens collected between 1870 and 2019 in eastern North America to quantify leaf-out and flowering times of 21 species. They found interesting differences between native and nonnative species. In particular, nonnative plants tended to have much more variability in their phenological sensitivity. Everingham et al. (2023), also in *Journal of Ecology*, raise the important point that phenological shifts might vary between the northern and southern hemispheres; they showed that fewer than 60% of species in the southern hemisphere were advancing flowering times, compared to more than 80% of species in the northern hemisphere.

And, just as most phenological studies have been done in the northern hemisphere, more have undoubtedly been conducted in temperate rather than tropical ecosystems. Park et al. (2023) show that herbarium specimens from Brazil, because they typically represent a much broader sampling across geographic and climatic space than do field observational data, can be a better source of data to test phenological hypotheses. The data already reside in herbaria, and phenological estimates from herbarium specimens align well with those collected in the field.

3 | THE IMPACTS OF GLOBAL CHANGE ON GENETIC DIVERSITY, RANGES OR POPULATION SIZES

Investigators are increasingly developing novel ways to use museum specimens to examine historical changes in population genetics, genome sizes and species distributions. In *Journal of Ecology*, Závada

et al. (2023) extract chloroplast DNA sequences and 12 microsatellite nuclear markers from herbarium specimens from as early as 1884 (from one of the famed botanist Asa Grey's mounting sheet, no less) to document temporal genetic changes in populations of the nonnative chicory (*Chichorium intybus*) in New England. In *Methods in Ecology and Evolution*, Mullin et al. (2023) employ next-generation sequencing approaches developed for retrieving and analysing ancient DNA to investigate genome-level changes over time, from bumblebee specimens up to 113 years old. They also assessed phenological shifts for 37 Australian species using herbarium records, historical data and contemporary data collection and again found the striking result that only four species had advanced their flowering time, eight had delayed flowering time, and the remaining 25 species showed no phenological shift.

Occurrence records can be easy to obtain from museum specimens if collectors provide a precise record of where and when they collected the specimen. Such data have been compiled in places like the Global Biodiversity Information Facility (GBIF) and Integrated Digitized Biocollections (iDigBio). To date, these databases contain more than two billion records of species occurrences. While these databases are impressive and widely used to examine changes in occupancy and ranges, they have their shortcomings; for instance, they are 'presence-only' data. In this Special Feature, Shirey et al. (2023), in *Methods in Ecology and Evolution*, develop a set of best practices and a workflow to look at how changes in the occupancy and detection of species, along with collector frequency, influence model performance for datasets with presence-only records. Trethowan et al. (2023) in *Journal of Ecology*, use over 7000 herbarium specimens to assess how current and future climate change interact with biogeographic origin to shape species occurrence and richness of plants on Mount Jaya, in New Guinea, the tallest mountain on any island in the world. They found that species of Sunda origin (i.e. Borneo, Sumatra, Java, Mainland Asia) are more likely to occur in warmer lowlands and species of Sahul origin (New Guinea and Australia) species are more likely to occur in cooler higher elevation sites. Trethowan et al.'s (2023) models suggest that Sahul species are also less likely to persist in the face of ongoing increases in temperature.

Similarly, in *Journal of Animal Ecology*, Davis et al. (2023) propose a framework that integrates specimen data from museums with contemporary field-collected data, with the possibility of examining long-term trends in insect populations, and Boyd et al. (2022) in *Methods in Ecology and Evolution*, provide a tool called ROBITT (Risk Of Bias In Temporal Trends in ecology) to help investigators identify sampling bias through time and space when using museum records to explore trends in abundances or diversity. Also in *Methods in Ecology and Evolution*, Gotelli et al. (2021) assembled 1,405,316 field observations and 73,039 museum records from 17 coupled field and museum datasets to show that relative abundances in museum collections are correlated with relative abundances from field observations, highlighting that it might be possible to examine long-term changes in relative abundance of particular species from carefully curated museum occurrence records.

In *Journal of Ecology*, Harris et al. (2023) compiled traits of African angiosperm species to estimate trait hypervolumes. They then used hierarchical clustering to identify 12 potential biogeographic regions and map them. They point out that because herbaria have specimens with both trait and locality information that this could be done for other regions around the world, and perhaps be used to develop models that link traits, distributions and ecological strategies to forecast shifts in both species ranges and biogeographic regions.

4 | THE IMPACTS OF GLOBAL CHANGE ON INTERACTIONS AMONG SPECIES

A standard way that ecologists try to understand interactions among species is by doing an experiment: we build a fence around some plots to exclude large herbivores or we remove a keystone species from some bits of rocky intertidal shoreline but not others. Studying how global change factors might influence interactions among species usually involves manipulating some climatic factor (e.g. studying plant-insect interactions under rain-out shelters or in open-top chambers) or working along some environmental gradient. But how could we study how climatic change over the previous 50 years has shaped interactions among species? Leveraging natural collections is the answer, and there are a number of excellent examples in this Special Feature.

Rakosy et al. (2023) in *Functional Ecology* provide an excellent road map for trying to reconstruct and understand how global change over decades influences the structure and dynamics of plant-pollinator interactions. Ivison et al. (2023) in *Journal of Ecology* examined 2200 herbarium specimens from 26 species over 195 years and found little support for the enemy release hypothesis. In *Methods in Ecology and Evolution*, Donald et al. (2023) describe how to use precision glycerine jelly swabs to remove pollen from pinned insect specimens, which might allow for reconstructing historic pollination networks.

Though for a completely different set of interactions (parasite-host interactions), Wood and Vanhove (2023) similarly argue in *Journal of Animal Ecology* that parasite ecologists can reassemble time series of host-parasite interactions from specimens in natural history collections; they go on to offer an explicit, step-by-step framework for how to do that, what the constraints are, and what the possibilities might be.

Moura et al. (2023) examined 8847 preserved specimens of 58 snake and 22 amphisbaenian (worm lizards) species, deposited in 61 collections from 11 countries to examine the influence of life history and environment on autotomy—a defensive behaviour that entails the loss of a body appendage to escape predation. They propose that examining more specimens through time and space could shed light on how predation pressure might change with ongoing climate change. Using a completely different toolkit—stable isotopes—on 68 museum specimens of kea (*Nestor notabilis*), a threatened alpine parrot native to New Zealand, Wehi et al (2023) showed how their diet perhaps became less diverse from 1880 to the 2000's.

Finally, Ivison et al. (2023) show that it is possible to test ecological hypotheses about the success and failure of invasive species using herbarium records. In *Journal of Ecology*, they analysed over 2200 specimens of 26 native and nonnative species collected over 195 years in Norway to test the “enemy release hypothesis”—the idea that some invasive plants thrive in their introduced range because they have escaped their enemies in their native range. Though their results suggest that the enemy release hypothesis is likely not at play in Norway, they point to the power of using herbarium specimens to examine plant-herbivore interactions through time.

5 | SUMMARY

Natural history collections have been key repositories of knowledge about the world for centuries. Their usefulness and importance have only increased as we are increasingly faced with the doubly vexing biodiversity and global change crises. This Special Feature clearly demonstrates how contemporary investigators can leverage natural history collections to understand changes in biodiversity and the impacts of global change on genotypes, phenotypes, and interactions among species. It is our hope that readers of this Special Feature will be inspired to visit their nearest or favourite Natural History Museum collection, and, in collaboration with a curator or collections manager, come up with new ideas and questions to ask about how ecology, evolution and global change have shaped, and will shape, the diversity of life on Earth.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

DATA AVAILABILITY STATEMENT

Data have not been archived because this article does not use data.

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