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work on almost every insect-related topic imaginable. With this in mind, the RES trustees have agreed to fund and oversee an ambitious project in collaboration with the whole RES membership that will culminate in a “state of entomology” paper to outline the major challenges ahead in entomology. These will then be unpacked to reveal specific research questions related to each wider challenge. Dr Lynn Dicks FRES (University of Cambridge) will be the lead researcher on a survey of the RES membership. The aim is to use the wealth of experience and knowledge of the Society to inform policymakers, funding bodies and the public about the challenges ahead and how entomology might offer solutions. To achieve this, Dr Dicks’ project will run from January to September 2020 and every Member, Fellow and Honorary Fellow will receive a survey in order to take part in this exciting initiative. The information gathered will then be synthesised and summarised using workshops and global experts to compile a report.

I sincerely hope that you will choose to participate and help to create a valuable “state of entomology” paper that will act as a manifesto for the future of global insect science. You should expect to hear from Dr Dicks in the near future. Please add your experience to the project.



Journals and Library

New ways for old specimens – museomics is transforming the field of systematic entomology

Christiane Weirauch, Peter S. Cranston, Thomas J. Simonsen and Shaun L. Winterton

Editors of *Systematic Entomology*

Natural history collections have preserved and housed natural objects since the “cabinets of curiosities” of the Renaissance period. Still, only a minute proportion of their vast holdings is on display in the public galleries of these natural history museums. The remaining billions of biological specimens worldwide are archived behind the scenes, in what might be envisioned as dusty and dark vaults reluctant to reveal their treasures. Until the second half of the 20th century, these collections have almost exclusively served as resource for the cataloguing and classifying of past and present biodiversity including the discovery and documentation of taxa so far unknown to science. This started to change before the turn of the millennium, when scientists launched the first large initiatives to “unlock the vault” and bring the vast biodiversity data harboured in biological collections out into the open by creating digital records of the metadata associated with a specimen (locality, date, collector, host plant, etc.), imaging of specimens, and by making these data freely available online. This biodiversity informatics revolution was spearheaded initially by museum scientists and curators focussed on vertebrates and plants, because of the larger size, greater public interest, more manageable number of specimens, and the 2D quality of herbarium specimens that facilitate workflows. Although more challenging because of the enormous number of specimens, comparatively small size, diversity of preservation techniques, and position of metadata on a label underneath the specimen, a growing number of specimens in entomological collections worldwide have been, or are currently being, digitized^{1,2}. By documenting past and present and predicting future species distribution ranges, these

museum-derived datasets have enabled research on areas including biodiversity change in relation to climate change, biological invasions, and arthropod vectors of public and veterinary health concerns, impacting fields far beyond systematic entomology^{3,4}.



Fig. 1. Samantha Smith (Weirauch lab, UC Riverside) collecting emesine assassin bugs for phylogenomic projects on Barro Colorado Island, Panama.

We are now at a point where an on-going revolution in DNA-sequencing techniques and bioinformatics methodology allows us to unlock this vault of treasures even further⁵. Starting in the mid-2000s, advances in sequencing technology have launched research that is now referred to as “museomics”, a legacy approach to genetic sequencing of specimens from museum collections. In contrast to more



Fig. 2. Madison Hernandez (Weirauch lab, UC Riverside) preparing assassin bug museum specimens for next-generation sequencing.

traditional molecular systematics projects that required targeted field-work (Fig. 1) and careful preservation of tissues to ensure that DNA remains largely intact, these new approaches take advantage of the billions of specimens that are already deposited in natural history collections (Fig. 2). Using genetic material and data from specimens in natural history collections, scientists can now trace evolutionary origins, model past and future spread of pests and diseases, offer insights into the evolution of insecticide resistance, and revolutionize our understanding of human evolution using ancient DNA.

Similar to the biodiversity informatics revolution, museomics was spearheaded initially by the vertebrate and botanical communities, but despite the unique set of challenges when applied to small, dry biological specimens, insect scientists have made great strides towards embracing and advancing this field⁶⁻⁸. Studies range from targeting relatively few genes to entire mitochondrial and/or nuclear genomes. Entomologists have explored the feasibility of extracting and amplifying DNA from pinned insect specimens with fragmented and degraded DNA and subsequent Sanger sequencing for more than two decades⁹. However, only the use of next-generation sequencing (NGS) protocols that has increased substantially during recent years has started to make museomics in the entomological field a cost-effective and more widely used alternative to traditional approaches. This is largely due to the fact that NGS protocols involve steps that “shear” or fragment intact DNA, so using already fragmented DNA from pinned insect specimens should not pose a problem - at least theoretically. In the real world, entomological museomics offers great opportunities, but also significant challenges, in particular for pinned, dry museum specimens that represent the bulk of entomological collections.

Due to centuries of field expeditions to all corners of the world, natural history collections are the most comprehensive and accessible representation of biodiversity, offering a tremendous opportunity for scientific discovery. They also house rare species that even targeted expeditions frequently fail to find again; these are often represented only by the original type specimens. Another great benefit of using museum specimens for genetic research is that generations of taxonomists may have worked on a given collection and the proportion of specimens authoritatively identified to species level is consequently high. Given that NGS approaches have recovered sequence data for insect

specimens that were collected more than a century ago, museomics also has the potential to uncover historical signatures in genetic sequences, allowing, e.g., an improved understanding of the evolution of insecticide resistance¹⁰ and similar phenomena such as cryptic (genomic) changes within, and between, populations due to well-documented environmental and anthropogenic changes. Generating and making publicly available genetic resources is also a key element of the Nagoya Protocol on Access to Genetic Resources, a supplementary agreement to the Convention on Biological Diversity. Furthermore, in the face of the current biodiversity extinction crisis, museum specimens including bulk samples from large survey and passive trapping projects may be the only specimens remaining after the site surveyed is no longer intact. Museomics may thus be the only way to acquire unique genomic insights into the biological, evolutionary and biogeographical importance of now extinct populations.

Despite these overwhelming benefits, there are still challenges to applying museomic approaches to insect specimens. The number of insect species, both known to science and remaining undescribed, is staggering and the number of insect specimens in collections is overwhelming (300 million in North American collections alone²); the availability of genome-scale datasets for all, or even just the majority of, insect species is therefore a distant dream. In addition, many insects are small and the amount of DNA that can be retrieved from a single specimen may be too little for reliable sequencing without destruction of the entire specimen. Depending on collecting methods and preservation conditions, pinned insect specimens can be heavily degraded and even overgrown by fungi, posing additional challenges to both the wet lab protocols and bioinformatics procedures required to sort useful sequence data from potential contaminants. Additionally, primary types are the only known specimens for many species, making the advancement of protocols for largely non-destructive sampling imperative in like manner as currently employed for procedures such as genitalic dissections.

Although NGS approaches are now cost-effective compared to Sanger-sequencing projects, sampling of a large number of individuals for relatively low-profile projects such as genus-level taxonomic revisions will benefit from further refining protocols for maximal effectiveness. On-going research is further adapting and optimizing NGS methods for pinned museum specimens in an attempt to make them affordable and widely used^{11,12}. The challenge for museomics will be how to integrate with the rapidly growing field of environmental DNA that reveals almost inconceivable diversity in terrestrial and especially freshwater aquatic systems, with much deriving from insects¹³. While NGS barcoding allows rapid and low-cost association of insect life stages¹⁴ allowing identifications against well-populated ‘libraries’ of organisms, the data produced in such studies already seem likely to overwhelm even the most dedicated museomic practitioners. Yet, without such connections with historic named specimens, we can ask what value such metagenomic revelation of diversity can have in a world of biodiversity losses.

A conclusion might seem to be that field expeditions and the collection of large-scale specimens are things of the past. This is, however, far from the truth. Not only is field-work necessary to study and document the biology, ecology and behaviour that museomics may allow us to put into an

evolutionary context, but also continuous collecting activities aimed at building collections for the future are essential to document and explore both spatial and temporal cryptic changes in molecular diversity – changes that are often preceding more obvious phenological, phenotypic or ecological changes. In fact, this makes collecting activities even more important in the current age of accelerating biodiversity changes. Indeed, museomics simply provides an opportunity to exploit the vast wealth of legacy genetic

information already available in present collections, to then use this data source to strategize future research efforts, including field-work. We argue that any decrease in collecting activities (among both professional and amateurs), or funding for collecting and collection maintenance, threatens to deprive future researchers of the opportunity to study and publish research on our biodiversity in the Society's journals in the same way that we have benefited from the collecting activities of past generations.

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