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Adrian Van Allen

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Pinning beetles, biobanking futures: practices of archiving life in a time of extinction

Adrian Van Allen *

National Museum of Natural History, Smithsonian Institution, Washington, DC, USA

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Museums have been apparatuses for articulating knowledges, power and natures into an ordered whole for centuries, practices that have extended through to contemporary museums and their genetic collecting programs. Focusing on negotiations at the Smithsonian National Museum of Natural History between 2014 and 2016 I examine the integration of biotechnology into museums, exploring how life is being “archived” and for what imagined futures. Engaging the practices of making and organizing genomic collections, I examine a specimen’s ontological instability as it is created and circulated. Learning to pin beetles, take genetic samples and extract DNA, I contrast these processes with a debate over whether a genetic sample could serve as a voucher specimen – a permanently preserved physical reference. I argue that the capacities and limitations of materials are a vital part of understanding how cryo-collections are enacted into being through different practices and are framed by an orienting ethic of preservation in biodiversity biobanking.

Keywords: practices; museums; biobanking; ontologies; genomics; material culture

Introduction

With an estimated 50% of all species potentially heading towards extinction by mid-century (IUCN 2017), projects to preserve dwindling biodiversity have taken on multiple forms. One such form is the emergence of genomic biobanking projects in natural history museums, where the living world, from plants and animals, to microbes and environmental samples, are being sampled and frozen in liquid nitrogen, “archived” for uncertain futures. This paper is an ethnography of one such project, the Global Genome Initiative (GGI) at the Smithsonian National Museum of Natural History (NMNH) in Washington D.C., a project that strives to “preserve and understand the genomic biodiversity of life on earth” (GGI 2013), working towards cryopreserving half of the taxonomic

*Email: adrian@adrianv.com

family-level species known to exist within the next five years. Based on fourteen months of fieldwork in the museum between 2014 and 2016, I followed scientists and their specimens behind the scenes as they worked towards this goal, processing new collected organisms into specimens, tissue samples and genomic data, and debating the proper relationships between the “unbound biologies” (Helmreich 2009, 280) of their increasingly molecular specimens. The Smithsonian is a site where collecting practices and policies are rapidly changing with the integration of genomic technologies in response to increasing extinction rates – a return to encyclopedic collecting with biotechnological tools.

The collected life amassed worldwide in museums and herbaria is estimated to be as high as 3 billion specimens (Bi *et al.* 2013), yet according to taxonomic scientists only 5–12% of species have been collected, documented and preserved (Winker 2004). To “fill the gaps” in biodiversity knowledge requires collecting specimens, for “to know what is being lost, it is necessary to know what is here in the first place” (Rainbow and Lincoln 2003, 11). Within museum communities this has provided an ethical imperative to collect “all life” (as defined by taxonomists) before it vanishes in the face of mass biodiversity loss. Coupled with the ever cheaper and faster tools of biotechnology, this has created the condition of possibility for genomic collecting projects in museums to emerge. However it is the larger cultural shift towards reducing life to the molecular, as many have argued (cf. Franklin and Lock 2003; Rose 2009) that makes projects such as the GGI conceptually possible.

As living things unravel into increasingly molecular forms the links between pieces of an organism are a source of on-going negotiations between competing disciplinary views within the museum. As these new kinds of museum objects are produced, such as tissue samples and extracted DNA, museum communities struggle to sort out the relationships between these new molecular objects and the organism from which they originated. Through examining these relational ontologies within museum genomics – that is, how each specimen or sample is constructed as a new kind of object, by what audiences, and bound up with what imagined futures of potential value and utility – provides a deeper understanding of the co-constitutive social, technical and material aspects of creating a biobank of “the genomic biodiversity of life on earth” (GGI 2013). In doing so I open up the internal workings of a natural history museum’s biodiversity biobank in order to highlight the multiple kinds of material and discursive work that goes into transforming living things into museum specimens, from the morphological (a pinned beetle) to the molecular (DNA extracted from a beetle leg). I argue that genetic collections are made to matter as ontological embodiments, and further that each of these ontological embodiments (pinned beetle, genetic sample, DNA extract, genomic data) are enacted into being (Mol 2003) through the practices of their construction. It is through a close attention to these practices – that is, how they are created, the negotiations for their use, and their continuing re-evaluation – that the ways they become increasingly vulnerable and increasingly valuable objects becomes visible.

The goal of this paper is to ground an inquiry into the ontological instability of genomic specimens in material practices, to engage with the materials of making them first hand. To do so I bring together three ethnographic episodes from working with Global Genome Initiative (GGI) scientists at the Smithsonian NMNH. I begin by pinning beetles and pulling off their legs as genetic voucher specimens, tracing a history of the connections between specimens and their parts as they are distributed across the museum. I then turn to extracting DNA from a beetle leg using a butterfly “primer,” or segment of genomic data used to assess different characteristics. Through this I discuss the implications of “reading” life through another species, exploring the impact of human biomedical techniques that have migrated into the natural sciences. In conclusion I compare these material practices of “molecularizing” life with the discursive practices in a debate at the Smithsonian NMNH’s monthly genetics meeting. Discussion between administrators, curators, biorepository and collection managers focused on the potential relationships between original specimen, its genetic samples and genomic data.

Through these three episodes – comparing my experiences in the work rooms of the museum with a different perspective gained from a policy meeting – I ask, what are the relationships between specimen, sample and data and how are each of these constructed as objects through the different museum practices? That is, what are they articulated as being by different stakeholders, but further what are the potential relationships between these new kinds of objects? As Mol (2003) among many others¹ has suggested, the ontological instability of an object does not necessarily reflect different perspectives of a discrete, stable object, but instead creates a multiplicity of objects. Following this concept, I argue that the different views of genomic collections at the Smithsonian, rather than reflecting simply competing visions of what they are and what they should do, are in fact constructions of different objects made through different sets of practices.

Contrasting these views, from material and semiotic perspectives, provides insight into the specific kinds of practices, imagined future uses, and shifting ontological statuses of these specimens as they unravel into multiple objects. The value of these unfolding objects shifts as new relationships emerge, not just in their immediate capacity to answer questions about taxonomic mapping or biodiversity conservation, but most pointedly in their imagined future uses, in their envisioned potential (cf. Jasanoff 2015; Svendsen and Koch 2013). The Smithsonian beetles, whole and in pieces, can from one perspective be thought of as simply parts of one organism, a view shared by many if not all of the Smithsonian scientists I interviewed. Yet from another perspective the beetle pieces are being fundamentally remade into entirely new kinds of objects, each capable of carrying different value and meaning, with different visions for the future folded into the practices of their making.

Practices of making an archive of life

Scholarship on the political nature of archives has emphasized the implications of what is preserved versus what absent, the narratives these choices create, and in doing so how they standardize the objects and information they contain and maintain (cf. Bowker 2005; Derrida 1996; Stoler 2010). Archives both reveal and hide, and in doing so “harbor their own tacit politics, histories, and powers” (Waterton 2010, 4). I use the term “archive” here as a larger conceptual category that includes different structures used to collect, inventory and preserve both objects and knowledge for future uses. Archives, from this perspective could include, as Waterton suggests, “forms as diverse as the simple spreadsheet, the species inventory, the computerized database, and the museum” (2010, 4). Natural history museums, including the Smithsonian, are working to transform biodiversity into stable, standardized objects to enable its collection, preservation, analysis and use, in effect, to “archive” life in the cabinets, liquid nitrogen tanks and databases of the museum. In these practices the rarity of the species, the high molecular weight of the sample, and the analytical chain between vouchers and samples are preserved for uncertain futures.

As biotechnology has entered museums it has reshaped the taxonomic research going on in the hive of offices and laboratories behind the scenes, where scientists continue to collect, classify, name and order “nature.” The Smithsonian has recently articulated its role in the face of what has been called the current sixth mass extinction (Ceballos *et al.* 2015) as being uniquely situated to “archive” species before they disappear (Smithsonian Institution, Living in the Anthropocene Consortia 2015). Within this framework of impending loss and the crisis of on-going extinctions, Smithsonian scientists have framed their collecting programs within an ethical imperative to preserve vanishing biodiversity before it disappears.² To do so, they combine the tools of taxonomy with those of genomics to collect and preserve life for uncertain ecological futures. Although the “archive” of biodiversity has been called into question as a problematic metaphor (Sayre 2017), it can still be understood as the underlying logic driving biodiversity biobanking projects such as the GGI, with a goal to “capture and understand the Earth’s genomic biodiversity, preserve it on ice in biorepositories worldwide, and make it accessible to researchers everywhere – in perpetuity” (GGI 2013).

This on-going process of creating new kinds of museum specimens, transformed into the molecular, has caused debate over the status of these objects – what they are, how they should or could relate to the organism they were derived from and what their future potential uses may be. In other words, museums genomics is a site full of ontologically unstable objects. While various social science scholarship has explored how realities are enacted into being (cf. Ingold 1993; Kohn 2013; Latour 1999; Law and Mol 2002) the goal of this paper is to ground an inquiry into the ontological instability of genetic museum objects in material practices,

to engage with the materials of making genomic specimens first-hand and in doing so understand how these different beetle-objects are enacted into being.

Mol's work (2003) on diagnosing and treating atherosclerosis, described by doctors as a gradual hardening of the arteries, does not produce a stable, fixed disease but instead multiple iterations of both the disease and the bodies it affects. This does not imply a fragmentation, but instead these multiples are made to cohere through a variety practices such as consultations, medical imaging, and paperwork. This focus on thinking through the creation of multiple objects through practices is relevant to my thinking here about the practices of making beetles in the context of biodiversity biobanking. I argue that as beetle bodies are transformed into different kinds of specimens – pinned whole, a leg pulled as a genetic sample, or dissolved into protein sequences as a DNA extract – new kinds of objects are brought into being and made to cohere through the on-going labor of museum work. My point here is that the museum object of a “beetle” is a distinct type of object that is created through the processes of transformation as it is pinned, named, stored, sampled, extracted into DNA and sequenced into a genome. Each of these aspects of a museum-beetle-object is assembled into one “beetle,” but one that is called into question as new technologies and accompanying ontological frameworks emerge, that is, as museum communities question what objects exist within their ontologies and the relations between them.

The importance of materials and an attention to techniques has long been a part of STS (cf. Latour 1999) as well as anthropology (cf. Ingold 2012), particularly in the following of the “operational chain” (*chaîne opératoire*) of how materials and ideas are wound together into processes (Coupaye 2009; Dobres 1999; Lemonnier 2004). Examining the practices of making living things into data, scholars have studied of the evaluation of microbial life (Helmreich 2009), the “obliteration of life” as it is transformed into genomics (Zwart 2016), and an analysis of the shifting value of specimens as they are translated into DNA barcodes (Ellis 2008). Scholars have also examined the debates on the relationship of information to site from which it derived, including the “latent life” of futures made in and through frozen samples of blood (Radin 2013), and an analysis of the “circulating references” made by soil scientists as they move their samples from field to museum (Latour 1999), or by botanists as they circulate plants and genomes (Parry 2004). This paper is located at the intersection of these lines of inquiry, however while I stress the importance of examining techniques and the practices that re-inscribe different ontologies, I also emphasize what the materials themselves can communicate when experienced first-hand, what Tsing has called the “sticky materiality of practical encounter” (2005, 12).

My approach is one of engaging with the material culture of museum genomics in the “back of the house,” a place usually invisible and inaccessible to the public. Instead of focusing on the negotiations for power and authority in the public exhibit spaces of the museum (cf. Bennett *et al.* 2017; Karp and Lavine 1991), I moved into

the behind-the-scenes workspaces where matter and meaning were woven together in the daily routines, techniques and narratives. For this mode of engagement I draw on concepts of learning-through-making, analyzing materials as a method for thinking through things (Henare, Holbraad, and Wastell 2007) as they are enacted into being. Becoming part of the daily work at the Smithsonian NMNH I integrated myself into various communities of practice (Lave 2011) which provided me with “a view from below” (Harding 2008), that is, access to the wealth of mundane details and occasional moments of epiphany that constitute museum work.

The Global Genome Initiative

Within the biological sciences “life” is increasingly understood as a network of living things, systems, and processes (Bowker 2000; UNEP 2010). Natural history collections have also transformed into networks, with vouchers specimens, tissues, and data dispersed across the museum as well as dispersed globally in museums, research centers, zoos, botanical gardens, and biorepositories (Prendini, Hanner, and DeSalle 2002). The Smithsonian Natural Museum of Natural History is one of the world’s largest museums with a collection of over 145 million objects, and through its extension via these global networks of collaborating institutions it has expanded its collections and the power it can leverage for genetic collecting projects.

One such project is the Smithsonian’s Global Genome Initiative (GGI). Begun in 2010 as part of a five-year Strategic Plan at the National Museum of Natural History, the GGI is a project tasked with “preserving and understanding the genomic biodiversity of all life on earth” (GGI 2013) within the next five years. The GGI has positioned itself both within the museum and within a growing global network of collaborating institutions (including museums, zoos, herbaria, research centers), as the central authority that will collect and synthesize existing collecting protocols and preservation workflows into one standardized document. With the stated goal of creating an open-source genome databank to be utilized for nature conservation and biodiversity research, the GGI has situated itself as a natural progression in collections-based research – a move from studying anatomical to genomic similarities in order to expand taxonomic knowledge. While the GGI seeks to archive a synoptic sample of the “Tree of Life,” importantly it will also train the next generation of genomics researchers in biodiversity science, contouring the shape of future conservation genetics. The expanding technological and computational capacity to sequence genomes has facilitated the increasingly central role of DNA sequences in both evolutionary theory and ecological investigations, and has in turn created the capacity for making a genomic archive of life.

The Global Genome Initiative (GGI) began with a six million dollar gift from a private donor, with the total estimated budget of fifteen million dollars to complete its goal of preserving genome-quality tissue samples of each family of eukaryotic³

life on earth. The GGI staff have identified “family-level” as a plausible number of samples to gather within their timeframe and budget.⁴ Classified between Order and Genus, “Family” is one of the eight major taxonomic ranks in biology, with an estimated 10,000–20,000 on earth, and approximately 7500 currently biobanked by the GGI and its partner institutions (GGBN 2018) [Figure 1]. Funding for the GGI has provided the means for genomic collecting on a large scale at the Smithsonian NMNH, through creating infrastructure in the form of freezers, liquid nitrogen tanks and salaries for technicians and administrators, as well as providing resources for genomic collecting expeditions in accordance with the GGI’s collecting protocol. In setting out to standardize collecting methods the GGI is also standardizing biodiversity into comparable and computable units that will fit precisely in their liquid nitrogen vats and databases. This can be understood in a long history of specimens-as-data within museums dating back to early modern cabinets of curiosity (Findlen 2002; Strasser 2012), as well as in the molecularization of life in a modern era of genetics and biotechnology (Rose 2009). These two threads – museums and biotechnology – converge in the project of the GGI, a project to “archive” all life using the tools of genomics.

In the following sections I unbind the biology (Helmreich 2009, 280) of beetles in three ways, from pinning a voucher specimen, to pulling off a leg as a genetic sample, to extracting beetle DNA. In following my beetle and its genetic samples I examine the ontological instabilities of these objects and the kinds of labor required for their creation and maintenance.

Pinning beetles, pulling legs: making specimens into multiple objects

Biological specimens and the natural orders they are held to represent are key to taxonomy’s project of mapping life in order to preserve it, through “meticulously observed chains of connections vitally linking the specimen to information, to



Figure 1. The Smithsonian Biorepository (December 2014). Photo by author.

nature, and back again” (Ellis 2008, 173). These “chains of connections” are built from data derived from the materials of the specimens, from what is preserved versus what is discarded. Each discipline values and discards different pieces of an organism as they craft specimens and take genetic samples. For instance, a Smithsonian’s parasitologist defines her “field site” as the intestines of birds, part of the specimen that would have been thrown away by the ornithologists, categorized as biowaste (Van Allen 2017).

When I met with a pair of Smithsonian entomologists who were testing genomic collecting workflows in 2015 they detailed the practical matters they faced while field collecting. This included tasks that ranged from obtaining liquid nitrogen in remote parts of the world, to the extra labor required to fit non-standardized insects into a standard 2 ml cryovial that had been approved for use in the Smithsonian Biorepository. “Getting a butterfly in there is like shoving a damn wet bird into the tube,” as one wasp-expert described it.⁵ Wasps fit easily in the tubes, but butterflies wings did not, and had to either have their wings removed and glued onto a strip of cardboard (a time consuming process), or rolled up to fit in the tube.

Although the Hymenopterists (scientists who study wasps, bees sawflies and ants) and Lepodopterists (scientists who study butterflies and moths) were in the same Department of Entomology, the parts of their respective creatures that they valued and preserved were radically different: “We trap our wasps, they fall into the jar of ethanol below, great. Pin them or freeze them whatever ... Pull the butterflies out and they’re like wet birds, wings all over the place.”⁶ When collecting unfamiliar categories of life they encountered the material capacities and limitations of those species, some fitting neatly into workflows (tube-compatible wasp bodies) while others overflowed (a butterfly like a “wet bird” that was not).

To understand how these different practices shaped the objects they created I learned to preserve beetles myself, pinning and pulling legs as genetic samples in the workrooms of the Smithsonian’s Department of Entomology in January 2015. Walking through the corridor I passed rows of white metal cabinets that held millions of insects – from bees to beetles, flies to spiders, butterflies to wasps – collected at every stage of development from pupae to adult. Though their subjects are tiny, the Entomology collections comprise the majority of specimens in the natural history collection, and along with the insects also include their nests, cocoons, their food sources of leaves, flowers, tree sections riddled with holes. To be able to do their research, entomologists collect not a few individuals but hundreds or thousands of the same species and pin them, preserve them in ethanol, or freeze them, depending on their intended or imagined future uses.

Sitting in a workroom in the Entomology Department I pass the pin all the way through the beetle and into a foam block to hold it in place. Using the tip of a pin I carefully arrange the legs and the antennae as evenly as possible, anchoring them with more pins as the beetle dries. Key diagnostic features for the beetle are the shape of the claws and the antennae. Tiny and brittle, I’m told legs, antennae and even heads fall off all the time, but there’s a special insect adhesive and

“you can just glue them back together like a model airplane.”⁷ As I learn, the important thing is to arrange specimens so that the key features – diagnostic attributes – are arranged symmetrically so you can, in the words of a collections manager “see variation by looking down a drawer.”⁸ Pushing the beetle a thumb-width down on its anchor pin, I leave space so it can be picked up without damaging the specimen in the future [Figure 2].

Different preparators, different fingers, different spaces left at the top of pins. I think about the millions of insects pinned in the collections, and the different fingers that have grasped the top of each pin over a hundred years – an alternative view of this archive, one of the measurements of the people who have made and used the collections, measured out in finger-widths. The traces of human practices left in the collections by generations of preparators mark time in different ways. These histories are layered into the materiality of the specimens, and highlight the value placed on the meticulous, the ordered, and the reproducible in the museum workrooms. Through standardizing techniques to make perfect, systematic specimens museum preparators have worked to make certain kinds of variation visible by “looking down a drawer.” In doing so, the mark of human hands is integrally bound up in every part of the collections—from thumb-widths on pins, to handwritten labels on DNA extracts, to the intricately crafted structure of databases and the biodiversity data they contain. Each of these objects not only shows the mark of human hands, but it is precisely through the integration of practices and materials that these objects are enacted into being as new kinds of objects, with each embodying specific kinds of imagined futures.

Thinking through these various kinds of imagined futures, rendered differently through making specimens, samples or data I returned several months later in April 2015 to the Department of Coleoptera (Beetles) to learn how to take a



Figure 2. A beetle pinning workstation (Department of Entomology, Smithsonian NMNH, March 2015). Photo by author.

genetic sample from a preserved beetle. The workflows we were testing would inform the first version of the GGI Genomic Collecting Module. “You can smell the wax and honey on the floor with the bees,”⁹ one bioinformatics staff member told me, though on this particular day the lingering smell was of mothballs, residue from the pesticide in the collection cabinets. Some insects were deemed worth preserving in perpetuity, while other living insects were intent on consuming them. My own task was, in a sense, to destroy a precious insect but in doing so to produce two new objects.

In a room lined with microscopes and trays of pinned beetles we sit down to work. By selecting a variety of specimens preserved at different times (from last year to 50 years ago), and using by different methods (pinned or preserved in alcohol) we were learning how to remove the left hind leg while leaving the rest of the beetle intact. This proved a meticulous task, as the carabid beetles that were our subjects were about the size of a grain of rice [Figure 3]. The pinned beetle with its stack of labels spun under the microscope as I tried to find the correct angle to carefully extract a leg.

As the creature loomed into focus, I learned how to see in a completely new way. I was trying to see the beetle body as its parts, to see where it could be broken apart into a set of discrete objects. A small crack and the leg of my beetle split off cleanly. Behind me voices mixed with the click of tweezers and glass as staff placed their beetle legs into a 96-well plate, a container for genetic samples. Held at the ends of our forceps were tiny valuable objects that we pulled apart to create new valuable parts. These new, tiny objects would be labeled and tracked first in Entomology database and then, as they were consumed and transformed into genetic data, in the Laboratory of Analytical Biology database. Our current goal was to keep the beetle body as pristine as possible, so that it could serve a voucher specimen for

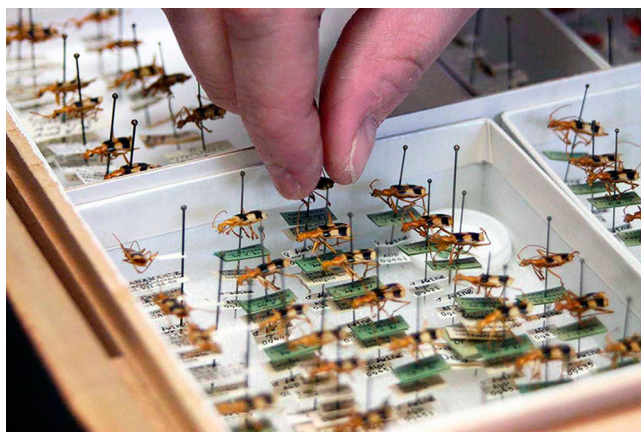


Figure 3. Selecting a beetle for genetic sampling. (Department of Entomology, Smithsonian NMNH, March 2015). Photo by author.

the genetic samples that would be produced from the legs. Two objects from one, and each created to carry specific kinds of data, value and meaning.

This process of building futures into specimens was visible in other parts of the museum practices. For example, during collecting expeditions the Entomology Department amasses large quantities of specimens, filling jars of ethanol with thousands of insects ready to be pulled out, identified and pinned. However, if individuals of the species are very small, for example tiny wasps only a millimeter long (e.g. microhymenoptera), multiple insects may be needed to obtain a viable genetic sample. In this case another individual of the same species is collected and serves as a so-called paravoucher. This means the preparator has to imagine various future uses for the specimen and its associated genetic samples throughout the process. The implication here is that the one-to-one relationship of individual specimen to tissue sample to data is disrupted – an issue at the core of the debates over genetic voucher specimens. Importantly for standardizing practices across the museum, the key difference is the relationship between a genetic sample and its origin, or voucher. Within the museum community a voucher is literally what vouches, or “speaks for,” the authenticity of that genetic sample, verifying the chain that binds it to its source. For some museum genomicists vouchers tie all research results to specific, permanently preserved specimens deposited in museums and as such, they are “the basis of reproducibility, an essential part of the scientific method” (Funk *et al.* 2005, 127). Yet other museum scientists have different views of what constitutes a valid relationship between specimen and genetic sample. For now I follow my disassembled beetle across the Smithsonian, from the Department of Entomology to the Laboratories of Analytical Biology, where I learn to extract DNA from my carefully disarticulated beetle leg.

The unbound biologies of extracting beetle DNA

From pinning beetles and pulling a leg off as a genetic sample I now move to the Laboratory of Analytical Biology (LAB) at the Smithsonian NMNH, where in March 2015 I helped conduct tests to assess the “genomic potential” for museum specimens, transforming a beetle leg into genetic data. Working with the GGI’s lab technician we assessed the amount of DNA we could extract from beetle specimens [Figure 4]. Some were pinned months earlier, while others were more than fifty years old. Using one leg we would leave the rest as a voucher specimen, a reference for the genetic samples and data we would produce. First dipped in liquid nitrogen to make them brittle, we crushed the beetle legs with a mortar and pestle. The resulting powder was mixed with a “buffer,” one of several types of acid that break down the protein bonds, separating the hard outer casing of the beetles from the DNA-rich muscle tissue inside.



Figure 4. Cryo-tubes ready to be filled (Smithsonian Biorepository, March 2015). Photo by author.

“We’re using a lep [short for *Lepidoptera*, or butterfly] primer for these,” the lab technician tells me.

They were developed awhile ago and they’re pretty solid, they are used for lots of things that aren’t actually leps. Must be some conserved genes in there that cut across [taxonomic] families. ... I’m used to working with vertebrates—much better DNA.¹⁰

Bundled into this conversation is a long and complex history of the flow of biotechnology. From human-centered medical research, where a great deal of social and financial capital concentrated, emerged a number of technologies and techniques for extracting, sampling, sequencing and banking biological materials.

As categories of “life,” including biodiversity, are increasingly defined by molecular biology¹¹, DNA has been described as a text to be written or rewritten. This has rearranged “nature” biotechnologically, with standardized human biomedical data “overflowing” (Hoeyer, Tupasela, and Rasmussen 2017) into techniques for collecting genomic samples of exotic biodiversity. Species, in this conceptual framework, become their genomes in a sense – the protein sequences extracted from frozen samples, “read” and sorted into a “book of life,” are ready to be read or rewritten as needed with emerging technologies such as CRISPR genome engineering (CRISPR/Cas9 Guide 2016; Wright *et al.* 2016). The Human Genome Project – a “single-species mammal project,”¹² as one Smithsonian geneticist wryly described it – slowly spread to other contexts such as museums and zoos, and then to other species, such as mammals, out to other warm-blooded vertebrates such as birds, then to vertebrates in general including snakes, reptiles, and fish, and then to invertebrate zoology with hard-bodied insects and soft-bodied worms and snails, and finally to plants that proved useful as raw material for human medical biotechnology.

The materials at work on the lab bench in front of me were bound up in these specific histories of making the world – techniques from human biomedical domains migrating into natural history laboratories, fundamentally shaping how I transformed the beetle’s DNA into a new type of data object through the filter of another species. Carefully following the protocol scribbled in the lab notebook, I used a pipette to distribute microliter droplets of DNA, buffer and stain into a tiny grid on a plastic container. After going through the centrifuge, washed in ice-cold ethanol, centrifuged again and then suspended in more buffer I had extracted, amplified and stained beetle DNA floating at the bottom of each well. Putting these precious droplets through an electrophoresis gel, I photographed them under UV light and we used the resulting image to assess the amount of DNA in each beetle sample. Beetle transformed from a leg, to powder, to tiny protein bundles that were extracted, stained, expanded, photographed and evaluated. In reassembling these forms of knowledge I was amplifying the DNA of a beetle through that of a butterfly to assess the “quality” of that beetle (*vis-à-vis* butterfly) DNA, to in turn deem it valuable enough as a genomic sample to be part of the GGI’s collection.

As the beetle unbound into these increasingly disembodied objects – from a leg to powder, from a droplet of liquid to lines in a lab book – the material qualities of the insect receded. In parallel, the labor needed to transform it became increasingly apparent; as did the continuing work to keep those pieces bound together and render each of them meaningful. As I learned through this process and many others, the material capacities and limitations of specimens are at the core of different disciplinary ontologies within the museum. For example, Entomology organizes the natural world and the relationships between beetles in a fundamentally different way than Botany organizes relationships and differences between plants. Each discipline preserves and discards different parts to form a unique and coherent disciplinary ontology – that is, a world made up of a distinct set of objects and the possible relations between them. As specimens are taken apart into increasingly disembodied pieces, each new piece becomes a distinct entity capable of carrying different values. As a new type of object, genetic samples begin to trouble traditional relationships. For example, a beetle can be transformed into an assemblage of parts including a pinned specimen, a beetle leg as a genetic sample, extracted beetle DNA frozen in a tube and genomic data on a server. The “proper” relationship between these parts, as well as their ontological statuses as discrete objects, are under continuing debate as cross-disciplinary genomic standards are developed and implemented, as I discuss in the next section.

How to build a biorepository: a debate on genetic voucher specimens

Classification can be seen as a system of cultural forms used to carry meaning – one that requires its collective construction as well as multiple kinds of labor to maintain the relationships between classes of things (Bowker 2005; Daston 2004).

Making collective meaning continues across cultures (Bell 2017; Bleichmar and Mancall 2011), but changes in the materials, forms and details of how a classification system is “anchored” over time, for example in what counts as a “proper” voucher for the genetic samples and data derived from a specimen. A voucher specimen ties all tissue samples, DNA extracts, data sets and the resulting research results created from that data to a particular preserved specimen permanently deposited in a museum. As such, voucher specimens are mutually agreed upon conventions that enable the taxonomic natural sciences to function. Collections of voucher specimens deposited and preserved in museums around the world serve as the material guarantee of the evolutionary structures proposed by taxonomists as they collect, describe, categorize, and order life using specimens, in whole or in part.

However, the ontological status of voucher specimens is neither “natural” nor stable, as many have argued (cf. Daston 2004; Waterton, Ellis, and Wynne 2013), but requires meticulous work to render it meaningful. What a beetle pinned in a drawer is, versus what it does (Hayden 2003) has been continually changing apace with the discipline of taxonomy as it is transformed by museum genomics. The shift towards disarticulating specimens into genetic samples – such as beetle legs and DNA – continues to demand the re-articulation of a specimen’s state of being (what it is) and its instrumentalization (what it does), two distinct objects that are bound together by the threads of data between a specimen and its parts.

To contextualize these molecular specimens I now turn to debate at the Smithsonian NMNH in 2014 centered around what constituted a “proper” voucher – the traditional reference for all things derived from that specimen – from physical characteristics to tissue samples, from extracted DNA to genomic sequence data. The lack of providing voucher specimens for molecular samples has been a source of increasing concern in the “museomics” community¹³, and multiple definitions of “voucher” were in circulation at the Smithsonian [Figure 5]. “We don’t really speak the same language as IZ [Invertebrate Zoology],” a Botanist told me, “Their ontologies aren’t our ontologies ... Why should they be?”¹⁴

It is important to note that several versions of “ontology” were at work at this moment. The “ontologies” the Botanist referenced are informatics ontologies, a branch of information science that builds a stable set of terms and the relationships between them to facilitate knowledge transfer. These intentionally reductive views of the world are designed to represent certain aspects for a specific purpose, and are used by, for example, by computer scientists designing data types for a database, bioinformaticians defining types for lab repositories, or taxonomists describing categories of life in the natural sciences.

Another kind of “ontology” at work in this context is a philosophical ontology that is concerned with the “nature of being,” or what the world consists of and the ties that bind it together. With branches in science and technology studies (cf. Barad 2007; Pickering 2010) and anthropology (cf. Descola 2013), among

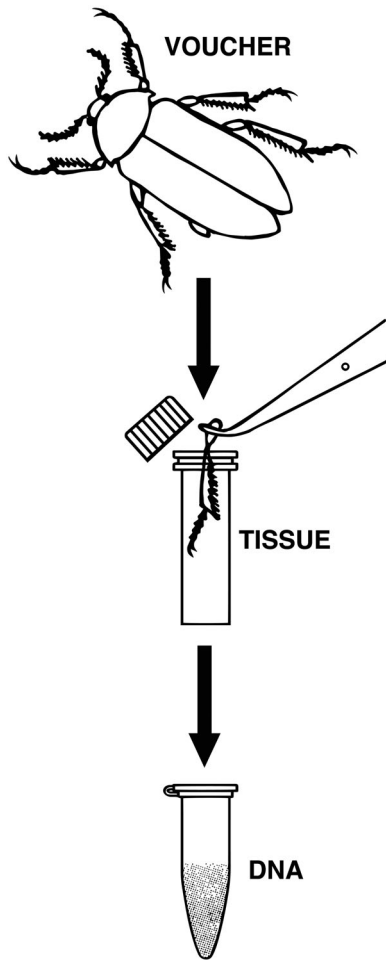


Figure 5. Optimal relationship between a voucher specimen and the samples derived from it, based on interviews with Department of Entomology staff at the Smithsonian NMNH, 2014–2016. Illustration by author.

others, it is a systematic account of existence that describes criteria for types of objects (such as concrete or abstract, real or ideal) and the potential relationships between them (such as relational or dependent). The ontological instability of the genomic specimens and samples hangs somewhere between these first two definitions, where different disciplines in the Smithsonian define their samples and the relationships they have to voucher specimens in distinct and often incompatible ways – some firmly grounded in a representative taxonomic ontology while others described sets of objects that were fundamentally different from other disciplines. As a new a type of object genetic samples complicated these disciplinary understandings of the objects that existed within the natural world in profound ways.

The friction between these different, layered and intersecting visions of genomic collections unfolded in one particular episode.

In February 2015 during the monthly Genomics Meeting a discussion began about how to define a standardized “genetic voucher” specimen across the different disciplines at the Smithsonian. Questions were raised about whether a genetic sample – or indeed an even more abstracted piece of amplified DNA – could serve as a voucher specimen. The following is a transcript of the conversation that ensued in the meeting between ten individuals who represented key stakeholders in the museum’s genomics projects. These included curators in Birds, Botany, Mammals and Invertebrate Zoology, a collections manager from Entomology, project directors for several large-scale genomic projects at the museum, and staff from the Bioinformatics department who were trying to synthesize these different practices into a coherent, ontologically-stable and mutually-agreed-upon whole:

Invertebrate Zoology Curator 1: “Can DNA or tissues be vouchers? I certainly think so. I’ve done it.”

Mammal Curator and Bird Curator in unison: “A voucher is a voucher.”

Bioinformatics Staff Member: “We’re figuring out what you actually do—a paravoucher in IZ [Invertebrate Zoology], versus a phenotype voucher in Entomology ... We want to choose one.”

Invertebrate Zoology Curator 2: “On a coral you take one polyp and sequence it, then use the polyp next to it as the voucher.”

Botany Curator: “We do population sampling too, but we don’t voucher like you do.”

Genetics Project Director 2: “If Botany isn’t going to quite agree with IZ’s [Invertebrate Zoology’s] definition then we’re just sitting here gilding the taxonomic lily. If it’s propagated and then split up as individuals, then they’re different vouchers.”

Genetics Project Director 1: “We’re talking about concepts specific to different collection methods. The member/set relation is different than the part/whole relationship ... Member/set is a clone organism such as a tree or a coral; part/whole is a bird, fish, insect, etc. Clone, exemplar, voucher: we’re here attempting to define the usage within each Division.”

Invertebrate Zoology Curator 1: “So, the parent of the DNA is a tissue sample, but that often gets consumed.”

Bioinformatics Staff Member 2: “You have a parent at every single level, but the highest level might not be a whole organism, it might just be a tissue or even just a DNA.”

Genetics Project Director 2: “We’re reinventing something taxonomists spent a hundred years trying to erase and decided was obsolete ... I also don’t personally see the use of ‘living voucher.’ Some vouchers are living, some are dead. Sooner or later that organism will be dead and it will be a dead voucher. Then your records will be wrong.”

Entomology Collections Manager, making air quotes around the word “Living”:
“‘Living’ is just another preparation type—it’s just walking around instead of pickled in a jar, pinned in a drawer, or glued to a page.”

Genetics Project Director 1, with a smile: “So herbarium pages [botany specimens pressed on sheets of paper] are ‘catch and release’? Plants just don’t get away very fast?”

Genetics Project Director 2: “Let’s not go back to the idea that you need a pristine whole organism just as God made it to be a voucher. We’ve moved beyond that—a DNA can be a voucher itself.”

Entomology Collections Manager: “If it’s going to be completely consumed then it can’t be a voucher because the point is to be reproducible.”

Genetics Project Director 1: “What we’re talking about is the record of a thing in the collection. If there’s nothing in the collection left, then there’s no voucher.”

Genetics Project Director 2: “There’s the record of its use in the records.”¹⁵

From this exchange between the different stakeholders in the Smithsonian’s project to standardize its objects, a view of the very different objects each discipline both creates and privileges comes to the fore. Some voices were adamant that “they” (meaning the institution of the Smithsonian, and further the discipline of biology as a whole) had moved beyond “whole pristine organisms” as vouchers. Others were adamant that “a voucher was voucher” – that is, an organism, in part or preferably whole, was pinned, “pickled” in alcohol, stuffed or frozen somewhere, preserved as an enduring, tangible reference in perpetuity. From this I suggest that for these assembled scientists genomic sequences on servers existed in a different ontological category than the extracted DNA, with digital files of genetic code as an inherently different type of object than that same (unprocessed) genetic material bound up in a frozen tube of DNA. What constitutes a “proper” voucher continues to be negotiated not just at the Smithsonian but at other institutions the world over that serve as repositories—museums, herbariums, botanical gardens, zoos, and, increasingly, laboratories and biobanks (Rocha *et al.* 2014). Within a long history of museums making living things into scientific tools, the practices what was left out what just as important as what was left in for making specimens as much as for making data. While this perspective is not new – exploring how humans make and remake their worlds has been of enduring interest to anthropologists, sociologists and historians¹⁶ – I would argue that their form in

the genomic “archive” of life is new in the materials and tools they employ as well as the specific visions for the future that are bundled into the process. In the discourse of the museum what is preserved now will provide the materials for future research and continuing preservation efforts, and forms a vital part of the museum’s self-described role in preserving an increasingly endangered natural world.

Conclusion: crafting specimens, biobanking futures

Collections articulate “nature” in specific ways based on the materiality of the life they utilize in the context of their distinct disciplinary histories. Through pulling beetle legs, extracting their DNA and following the debate on the relationship within genomic collections between these objects, I have examined how museums are transforming living things into multiple kinds of new museum objects that assembled together constitute an “archive” of life crafted in response to the threat of on-going extinctions. Focusing on the material practices for making these collections has highlighted the ways that the daily practices at the workbench directly shapes not only policy debates about their use, but further constructs multiples of that object that together constitute the specimen. Choices made in what to preserve, how to preserve it and for what kinds of uncertain futures shape the collection and the specimens they contain. Tracing the ontological instability of these genomic collections as they shift between contexts and domains I have underscored the skill, thought and negotiations required to make and maintain these objects. Yet these practices also render possible specific kinds of futures.

Each specimen—be it a pinned beetle, a tissue sample or extracted DNA – reflects for the scientists who create them a complex and evolving genomic Tree of Life and an imperfect and dwindling biosphere. Practices of “archiving” life in natural history museums has always broken down individual creatures into pieces and parts, such as a skin and a skeleton. However the move towards molecular specimens shifts these practices into new types of abstraction and disembodiment, transforming individuals into tangled webs of data and matter where discrete subjects become increasingly difficult to locate. As one collections manger said, “Tissue tubes don’t have much, well, personality ... its just a little bit of meat or an insect part or a leaf, or sometimes just powdery dust of some kind ... you just never know what you’re looking at.”¹⁷ Examining how materials and practices shape genomic collections requires thinking through the capacities and limitations of what the collections are made from – a beetle leg that dissolves into a viable droplet of DNA, or the dozen tiny wasps needed for similar genetic sample – and what visions for the future they are built for. Making specimens, I argue, also makes new kinds of museum objects that are enacted into being by this complex web of relations and practices.

Each specimen’s life history can be seen as a collection of moments, important events as it is collected, prepared, accessioned, and sampled—events in the

“afterlife” of the specimen that begin after death but reach into imagined futures uses for each new object. Following Mol’s (2003) analysis of how objects are multiply constituted by the practices through which they come into being, I suggest that these moments of un-making and re-making in a specimen’s trajectory combine with the materials it acquires or loses in these processes, an on-going assemblage that consists of multiple objects bound into one. For as much as the different disciplines within the Smithsonian were struggling to integrate standardized genomic collecting protocols into their ways of doing things – as seen in genetic sampling techniques or standardizing terminology around vouchers – each discipline also continued to modify practices. Changes accumulate over time and eventually naturalize different methods into a set of codified practices, transforming shared knowledge into standardized workflows and sets of objects.

In making and naming genomic specimens I have sought to clarify their ontological instability, underscoring their contingent and constructed nature – such as a pinned beetle contextualized by its stack of labels [Figure 6]. Small details locate the specimen in a particular moment, as a product of a web of unfolding relations, from the metal of the pin (stainless or spring steel), to the quality of the paper for the labels (cotton rag or cardstock) to the information on the labels (handwritten or printed). These relations include the techniques of different

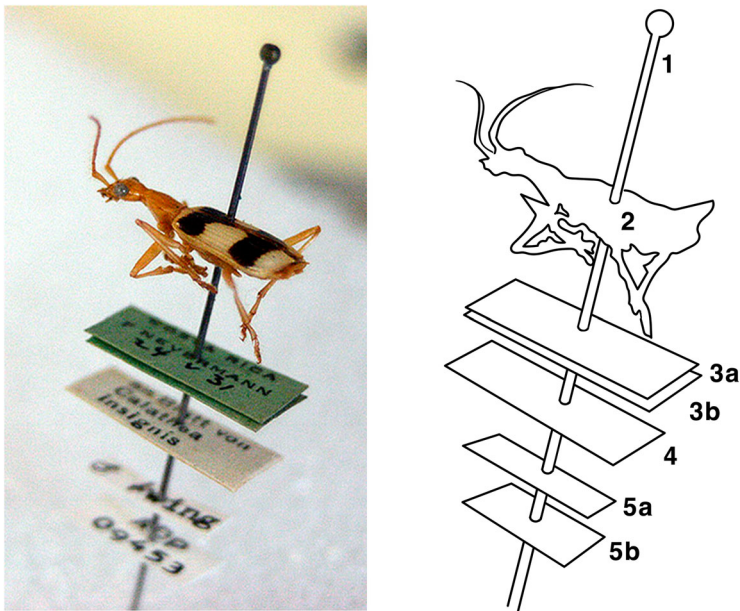


Figure 6. A pinned insect assemblage includes: [1] Entomology pin; [2] Insect; [3a] Label with collection data (locality, date) collector and species identification; [3b] Second half of information from 3a if it won’t fit on one label; [4,5a, 5b] Other “life histories” of the specimen, which may include re-identification of species, genetic sampling or movement between museum collections. (Department of Entomology, Smithsonian NMNH, March 2015). Photo and illustration by author.

collectors, changes in industrial production such as the cost and availability of stainless steel and paper, and the pressures of global economies in granting collecting permits before and after policies such as the Convention on Biological Diversity (CBD 1992).

In the practices of the museum formerly living things are transformed into multiple kinds of objects, made into unique assemblages that combine biological materials (such as beetle legs, extracted DNA), concepts of nature (such as species and trees of life), the skilled labor and tools used to make them (such as tissue tubes and entomology pins), and the regimes of value they embody (such as “banking” precious biodiversity and global collecting networks). These assembled specimens circulate within the museum and beyond to other museums, institutions, and research sites. In doing so they carrying with them visions for the future being constructed in museums, one beetle leg, DNA extract and genome at a time.

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Notes

1. Work on the ontological instability of objects has been widely developed in the social sciences, see: Latour and Woolgar (1979), Haraway (1997), Rheinberger (1997) and Law and Mol (2002).
2. Genetic collecting programs at the Smithsonian include the Global Genome Initiative (GGI 2013), part of an international coalition, the Global Genome Biodiversity Network (GGBN 2018), as well as DNA barcoding projects such as the Barcode of Life Initiative (BOL 2017) and the Genome 10k Project that is gathering genomic data for 10,000 vertebrate species (Genome 10K Project 2016).
3. Eukaryotic “life” is defined by the natural sciences as multi-cellular organisms, characteristic of all life forms except bacteria and other primitive microorganisms.
4. From interview notes with GGI staff, 3 March and 10 April 2015. All interviews took place at the Smithsonian National Museum of Natural History, Washington D.C., with an approved human subjects protocol from the Smithsonian Institution and UC Berkeley.
5. From interview notes with two Lepidoptera curators, 2 February 2016.

6. From interview notes with two Lepidoptera curators, 2 February 2016.
7. From interview notes with a Coleoptera collections manager, 27 January 2015.
8. From interview notes with a Coleoptera collections manager, 28 January 2015.
9. From interview notes with a Bioinformatics staff member, January 2015.
10. From interview notes with a GGI genomics lab technician, 19 April 2015.
11. For human genomics projects see Rabinow (1997), Fortun (2008) and Radin and Kowal (2017), for non-human genomics see Parry (2004) and Waterton, Ellis, and Wynne (2013).
12. From interview notes with a genomics project director, 12 April 2015.
13. On museum vouchering and genomics see: Astrin, Zhou, and Misof (2013) Coddington *et al.* (2007) and Nachman (2013).
14. From interview notes with a Botany curator, 12 February 2015.
15. From notes during Genomic Meeting, 12 February 2015.
16. On classification practices see: Durkheim and Mauss (1963), Bowker and Star (1999), and Lampland and Star (2009).
17. From interview notes with a Mammal collections manger, 20 February 2015.

ORCID

Adrian Van Allen  <http://orcid.org/0000-0002-5990-3381>

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