

Rethinking the value of biological specimens: laboratories, museums and the Barcoding of Life Initiative

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Abstract

This paper explores the shifting values and fragilities of museum biological specimens as they have recently become enrolled in the Barcoding of Life Initiative (BOLI); a global techno-scientific project which seeks to provide the 'barcode' to 'anyone anywhere' as a ubiquitous species naming device for all species on the planet. The reliance of BOLI upon museum collections for the industrialized high throughput sequencing necessary to rapidly accumulate DNA barcodes, I argue, positions museum specimens in a newly configured relationship with a 'global populace' assumed to require instantaneous species information. I discuss how museum specimens, as scientific, epistemic objects are sites of evolving and contested meaning as alternative approaches to the potential (classificatory and possibly commercial value) of DNA barcodes continue to be negotiated within the taxonomic community. As such they are sites of lively and ever-emerging forms of material culture in natural history museums as they speak for multiple natural orders.

Key words: taxonomy, specimens, DNA, global techno-science, value

Introduction

Specimen collections, housed and meticulously curated in the world's natural history museums and herbaria, stand for – be it in an incomplete sense – the ordering of the variation of life on our planet. More accurately speaking, they embody an entanglement of life burgeoning beyond the walls of collection enclosures and a human endeavour to collect, describe and classify nature in all its variety. Since the very first natural history collections appeared in the sixteenth century, arrangements of specimens, in the form of whole organisms and their fragmented parts stored in cabinets, boxes, vials and more recently, as frozen tissues in cryogenic storage facilities, have continued to provide taxonomists the world over with an ever-growing indispensable resource against which to examine and classify new species and to posit spatial and evolutionary re-arrangements for those groups of organisms already known.

Yet the meaning elicited from collections is more unstable than first meets the eye. Systematics, the science of describing, identifying and classifying biological organisms, is renowned for its internal creative turbulence in that, over the last decades in particular, the selection and stabilization of methods for classification, combined with a questioning around the wider societal benefits of taxonomic knowledge are continually (re)negotiated.¹ As a result, an understanding of evolutionary processes and geographical distribution of life on the planet is presented as contested terrain. Specimen collections on the one hand thus present a solid and tangible arrangement of artefacts speaking for possible natural orders. On the other hand, collections - and the nature(s) they both embody and represent - are valued in multiple and constantly (re)emerging ways, even if this variety of meanings is not always explicitly in view. More recently, certain policy-driven assumptions concerning society's needs for particular forms of taxonomic information can be seen to be shaping the ways in which nature is deemed knowable and what utility this knowledge might have. Laying a claim to the value(s) of biological specimens thus raises a whole range of questions concerning what a specimen can ultimately

stand for and forces us to imagine what it might mean to 'scale-up' from the specimen in a mahogany drawer or in a deep freeze to an appreciation of (potentially multiply constituted) 'life itself'.

Positing an underlying order to nature – however tentatively – is no mean task and is a rather precarious business. Moreover, the ontological status of specimens as they speak for order, is not something that can be assumed but is something that is worked hard to achieve. The patterns taxonomists divulge through close and lengthy examination and comparison of different organisms, if to be presented to the taxonomic community (and society) as a credible theoretical classification, require material guarantors against which research can be assessed and calibrated. This evidence takes the form of 'voucher' specimens deposited and preserved in permanent collections.² For taxonomy then, the value of biological specimens and the natural order(s) they are taken to represent, are upheld by meticulously observed chains of connections vitally linking the specimen to information, to nature and back again.

Despite the fact that the classification of nature has been widely acknowledged as a quintessentially human activity (Foucault 1966), and one closely associated with and shaped by hopes for its protection and exploitation (Grove 1995, Müller-Wille 2003, Spary 1996, Thomas 1984), the taxonomic sciences were, arguably until 1992, perceived as a rather esoteric set of knowledge generating practices somewhat disassociated from the more urgent needs of society. One consequence of the signing by over 150 nations of the Convention of Biological Diversity (CBD) in 1992 was an unprecedented focus of global attention upon the significance of taxonomic knowledge as an underpinning prerequisite for the protection of an ever dwindling global biodiversity.

One result of placing systematics on the biodiversity policy agenda were calls for the modernisation of the taxonomic sciences to meet public policy expectations and to propel themselves into the twenty-first century (Godfray 2002, House of Lords Select Committee Report 1992, 2002). Hopes for modernization included visions of a democratized taxonomy: the creation of digitized collections (Hine 2008) and interoperable databases (Bowker 2005a), for example, arose from the premise that accessibility of information for a range of users (both taxonomic and non-taxonomic) was of paramount importance. As collections and taxonomic practice become increasingly enrolled in and aligned to global techno-scientific - and public - initiatives, the meaning and value of specimens and of biodiversity takes on an emergent and changing quality.³

The Barcoding of Life Initiative

A project which exemplifies the drive to democratise taxonomy and to render its products persuasively accessible to a wide range of users is the *Barcoding of Life Initiative* (BOLI).⁴ BOLI is an ambitious global techno-scientific project designed to standardize specimen identification methods and to provide instantly accessible species-level information to 'anyone anywhere' on the globe and has been hailed as nothing less than a revolution for the taxonomic sciences. Whilst visible characters have been taken for centuries by taxonomists to distinguish levels of similarity and differences between organisms and a range of molecular characters have complemented the use of these since the 1950s (Avice 1994, Hull 1988, Nelson and Platnick 1981, Schuh 2000), what was potentially revolutionary about the first barcoding proposals, was that one short gene sequence from a standardized position of the genome could be used to tell species apart.⁵ The use of sequencing and databasing technologies by DNA barcoding, could convert the chosen gene segment into an easily represented, simple, digital barcode available to everyone. The broad aim of BOLI has been therefore to establish DNA barcoding as a 'global standard for assigning biological specimens to correct species'.⁶

The finding that one selected gene segment worked so well to tell species apart, inspired the creation of the Barcoding of Life Database (BOLD) designed both to centrally bank all validated DNA barcodes and also to operate as a 'work bench' (Ratnasingham and Hebert 2007) for any individual or institution wanting to identify a biological organism.⁷ The sequenced DNA of this organism is 'blasted' or checked against all DNA barcodes in the database and its identity revealed.⁸ DNA barcoding will only work effectively for its user communities, once the Barcoding of Life Database is filled with quality, validated DNA barcodes.⁹ In attempts to reach

its aim, BOLI has had to work hard to encourage the world's main taxonomic institutions to participate in the initiative. This has meant that natural history museums and botanic gardens have opened up their whole specimen and frozen tissue collections as raw material for the industrialized high throughput sequencing necessary to barcode life on the planet (see fig. 1).¹⁰



Fig. 1. Cryogenic nitrogen storage facilities, Laboratory for Analytic Biology, Smithsonian Institution, Washington DC. Picture taken by Claire Waterton, July 2007.

The value of biological specimens

In this paper I will discuss BOLI's dependency upon the world's main natural history specimen collections as the main donors of samples for sequencing. In some ways DNA barcoding's use of specimens is continuous with more conventional taxonomic uses of raw materials, in that molecular characters are interpreted as revealing a certain understanding of species. In many ways it nevertheless introduces a certain discontinuity in specimen use and their corresponding valorization. The scale of their circulation and the enrolment of sequencing laboratories, has effectively opened them out to a breadth of enquiry unprecedented. The exchange of specimens, their frozen parts, and eventually DNA sequences, has lengthened the 'analytical chain' between raw material and information and has introduced a further degree of fragility to the practices of taxonomic scientific enquiry. A DNA sequence without a direct and transparent (clearly audited) route to the voucher specimen, for example, becomes a meaningless artefact, or as one collection curator stated;

The only thing a voucherless DNA sample can tell you is that vials or data labels got switched or that the specimen was misidentified before it flew away.¹¹

If high-quality taxonomic information is to be made available to a 'global populace' and so circulate beyond an exclusive taxonomic community, such a material guarantor for otherwise 'virtual' accounts of species becomes even more important. This, as I will describe below, has worked to raise the profile of the importance of voucher specimens stored in museum collections. It also highlights the fact that their epistemic and ontological status is a micro-

managed achievement. Furthermore, the alignment, through DNA barcoding, of systematics with bioinformatics and genomics inspired technologies and approaches to knowledge production, has introduced debate concerning what kind of specimen – whole or part – counts as a voucher able to provide legitimate back up for barcoding research. It is essential, I argue therefore, to consider the fragility of the DNA barcode and the work undertaken to render it a meaningful object, as integral to the creation and circulation of its different forms of value derived from specimens themselves.

There is a further, more marked difference in taxonomic practice introduced by BOLI which has particular implications for the natural order(s) imagined and in turn promoted by DNA barcoding. At present the taxonomic community is not entirely in agreement as to exactly what kind of order the DNA barcode is capable of representing. The meaning which has come to be most obviously stabilized and promoted, is one of an ability to reveal *species identification*. This kind of taxonomic knowledge provides a horizontal (synchronic) mapping of species level biodiversity, or in the words of one British botanist, 'It allows us to look at the tips'.¹² Arguably, the stabilization of this use and value of DNA barcodes is shaped by the urge, described above, to democratize taxonomy, together with ideas of what kind of knowledge is envisaged to be useful for society.

A small contingent of the taxonomic community mines the minute genetic fragment for far more complex information about the organism's evolutionary history (Vogler and Monaghan 2006), although this approach is not (yet) officially endorsed or supported by BOLI. The corresponding natural order revealed by this alternative approach may be characterized as an account of the (historical) coming into being of life as we know it and is thus more complex in spatial and especially temporal terms. Some taxonomists were however concerned by Hebert *et al.*'s initial claims that genetic barcodes could be used to delimit species relationships – something that requires consensus on the 'species concept' itself (Lipscomb, Platnick and Wheeler, 2003, Tautz *et al.* 2003, Will *et al.* 2005). In more general terms, concerns were also voiced about the fact that the amount of information held within the DNA barcode was insufficient to determine the relationships between organisms on the basis of tracing their descent from a common ancestor.

The discrepancy is significant; it tantalizingly demonstrates the ability of the DNA barcode (and of the specimen from which it is derived) to accommodate quite different claims as to what kind of natural order may be revealed and connected to by one genetic fragment. Furthermore, it raises questions concerning BOLI's efforts to align a global taxonomic and bioinformatic community in accordance with a standardized set of protocols established to validate DNA barcode knowledge production, in which the voucher specimen plays a salient role. This is still a matter for fiery discussion but BOLI decided, somewhat strategically, to promote the role of DNA barcoding strictly as a practical and cheap tool for ascertaining species identity and diversity only (and not relationships between species). At present, as I will describe below, the BOLI promoted standards for DNA barcode production, only consider what is required to maintain the DNA barcode as a meaningful object in function of its ability to reveal species identity and name. If a deeper, phylogenetic reading of DNA barcodes was to gradually become accepted by BOLI as a legitimate use of the genetic fragment, it follows that quite different, and possibly more complex validation procedures would have to be set in place, again carrying relevant implications for the valorization of museum specimens.

Two further things interest me about the divergence in barcode meaning described above. On the one hand it is important – at a time when DNA barcoding is still relatively new and its future uncertain – to document the co-emergence of the value(s) of DNA barcodes and biological specimens with hopes and expectations of how nature can and should be known. On the other hand, as Rheinberger (1992, 1997, 2000) and Knorr-Cetina (1999) remind us, scientific-epistemic objects are best characterized by their state of continual (re)emergence. One classificatory value (species identification or naming value) and its associated validation procedures, might at present prevail, encouraging the museum specimen to speak for a rather a-temporal natural order. It is important to remain attentive however, to simultaneous, historically rich natural orders revealed by an alternative reading of DNA barcodes, which may or may not contribute to the emergent value(s) of DNA barcodes and specimens as scientific objects.

In invoking the conceptual category of 'value' in a context of taxonomic classification, my analysis is also informed and further complicated by a consideration of research into biological value which has proliferated during the last decade, mainly by anthropologists and sociologists with an interest in biotechnology and biomedicine. This research has tended to define biological value as the potential for the commercialization of biological material (and knowledge). DNA barcoding is characterised by its advocates as a branch of 'pure' science with no (explicit) commercial future. Yet, as earlier and ongoing research has demonstrated, the commercial potential of nature is itself shaped and unleashed by its prior classification and the corresponding identification and description of species, *genera* and the relationships between these natural groupings.¹³ Theorization of the relationship between the classification of nature and the instrumental uses to which it is put (commercial or otherwise), has emphasized the co-production of classificatory systems with broader political, economic, social and ethical frameworks.

My approach, therefore, to understanding the classificatory value(s) residing in biological specimens, stabilized and circulated in a particular way by the DNA barcode, reflects upon how certain (normative) hopes and expectations concerning the way nature should be known - whether for purely intellectual pursuits, instrumental ends or for the likely intersection between these - have already shaped and will continue to shape the future of this technoscientific approach to taxonomy. In this paper, I thereby ask certain questions about what the entanglement of instrumental (and possibly commercial) characterizations of the value of nature might imply for the new emerging valorization of museum specimens.

The research project from which this article derives employs multi-sited ethnographic research methods (Marcus 1995), including participant observation, semi-structured interviews and focus group discussions with a variety of individuals and institutions key to the barcoding venture in the UK and the USA¹⁴. In order to explore the creation, stabilization and circulation of value of museum specimens, I describe what I believe are salient moments in the creation of DNA barcodes and examine what work is required to sustain their value as useful objects with which to document and know the natural world. To do so, I define the object under analysis as the whole specimen, its tissue parts and its digital representation (the DNA barcode). By incorporating insights from scholars, who over the past two decades, have explored what it means to unravel the multiple biographical trajectories of objects, some of which play a vital role in the production of knowledge, I demonstrate that biological specimens and their digital representations are scientific-epistemic objects constitutive of lively and ever-emerging forms of material culture in contemporary natural history museums in an encounter with the visions and practices of global techno-science (Daston 2000, Knorr-Cetina 1997, 1999, Rheinberger 1992, 1997).

Attention to the multiplicity not only between but also within objects, as brought about in part by the changing (human, material, epistemic) relationships in which they participate, raises important questions concerning what might play a role in bringing about the emergence and shifting epistemic and ontological nature of biological specimens. As Suchman notes, 'Objects are not innocent, but fraught with significance for the relations they materialise' (2005: 279) and indeed, DNA barcodes embody and tell rich biographies which are both generative of - and witness to - far-from-innocent and vitally different possibilities for the orderings of nature. It is these possibilities, I argue, which need to be perceived as being folded into the object as some of its vital biographical constituents. This requires identifying and following scientific-epistemic objects as they travel and are transformed in their journeys between different specific sites, communities of practice and epistemic expectations - and in so doing are invested with different kinds of classificatory value as they are held to stand for or 'tag' varying accounts of a natural order.¹⁵

Appadurai (1986) is widely acknowledged as pioneering the notion that objects as well as persons are relationally composed and live and move through social lives.¹⁶ By demonstrating that objects move between and are witness to different cultural worlds and multiple 'regimes of value', Appadurai argues for a recognition of these circuits of value as biographical constituents of objects. Appadurai does not however consider that an object's biography can also contribute to its value.¹⁷ That is, there is a mutuality between an object, the relations which constitute it as such, and its 'value' as perhaps multiply defined. By highlighting the embodiment, by biological

specimens, of multiple regimes of value I will acknowledge an enfolding within the object of past, present and future social lives or biographies as contributing to and shaping the forms of value that are perceived to reside within them. I seek in this way to further contribute to what has already emerged as a fruitful convergence between science and museum studies exemplified by the work of scholars including Alberti (2005), Bennett (2005) and Gosden and Marshall (1999) whose work explores museum objects in biographical terms, as mobile, polysemic and transformative of institutional and human relationships. I will firstly clarify what a DNA barcode is.

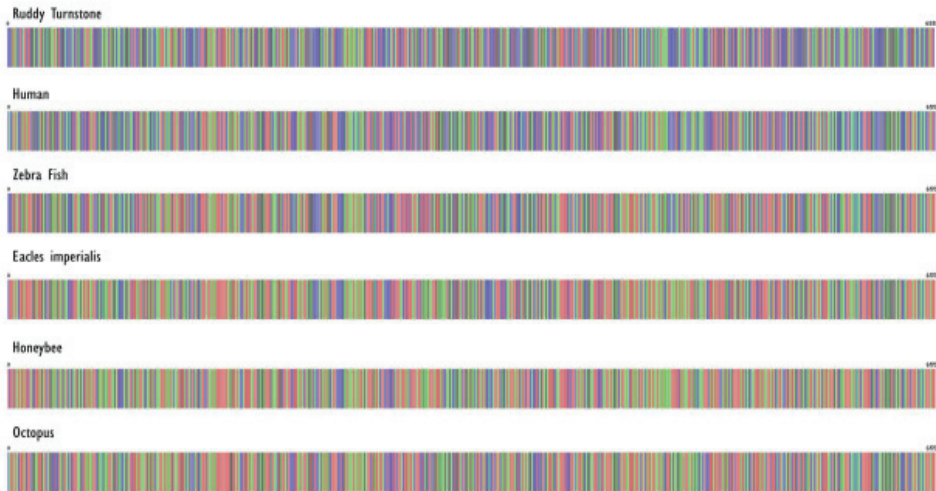


Fig. 2. DNA barcodes. Image provided by Sujeevan Ratsingham, Canadian Centre for DNA barcoding.

The DNA barcode

The DNA barcode (see fig. 2) perhaps most captivates the human imagination when observed as a shimmering sequence of blue, red, green and black bars on the computer screen – and even more so, if you are privileged enough to observe the process of its gradual fabrication and emergence. It is a four-coloured digital representation of a selected gene fragment portraying the sequential order of the nucleotide bases – A, C, G, T. Consistent differences in the sequential order of bases between species are used by taxonomists to identify them.

I describe here certain crucial moments in the DNA barcode's fabrication, observed at the Canadian Centre for DNA Barcoding and presently the main hub of DNA barcoding activity and where the DNA barcode was originally 'invented'.¹⁸ Being accompanied around the barcoding laboratory by the Lead DNA Scientist, allowed me to observe the equipment, materials and human work in interaction as digital sequences are created. It also allowed me to ask her what she perceived to be robust or vulnerable about the sequence of events necessary for the emergence and stabilization of the DNA barcode as a meaningful scientific object.

Any process of DNA sequencing consists of sequential stages: tissue extraction, DNA extraction, isolation and amplification of the segment of DNA required – the DNA marker – which, in the case of animal barcoding, is *Cytochrome Oxidase I*, and finally the alignment of the DNA sequence itself.¹⁹ Each of these stages requires the administration of carefully prepared cocktails of the chemical and biological reagents necessary for the corresponding treatment of the DNA.²⁰ As the Lead DNA Scientist led me around the different components of the laboratory space and explained the workings of the robotic machinery and reagents, she highlighted the need to erase the possibility of human misjudgement and error which would compromise the validity of the final DNA sequence. At the Canadian Centre for DNA barcoding, for example, the entire building has been designed around the need to separate 'wet lab'

conditions – tissue and DNA extraction - and ‘dry lab’ conditions – digital DNA sequencing - so to avoid any risk of enzyme and chemical contamination and to ensure that the DNA extracted and processed is pure and of a quality good enough to sequence (see fig. 3).



Fig. 3. Specimen sequencing preparation facilities, Laboratory for Analytic Biology, Smithsonian Institution, Washington DC. Picture taken by Claire Waterton, July 2007.

Once the DNA has been extracted and separated from the remaining tissue, the piece required (the ‘marker’) is selected and amplified and the nucleotide bases – A, C, G and T are sequentially aligned in order to be able to assess variation between the DNA of different specimens. This requires a complex chemical reaction whereby dyes that bind specifically to the different nucleotide bases allow a laser to read the sequence of the bases and create what is known as a ‘trace file’. A ‘trace file’ depicts the different concentrations of A, C, G, T in a certain order. Sometimes a ‘trace file’ presents a very clear portrayal of the DNA sequence. On other occasions, the ‘trace file’ is not immediately legible and the lines of colour reveal no clear prominence of any one dye which could be read as the correct nucleotide location (correct nucleotide location is paramount as it is the subtle differences between these locations between different species which are diagnostic of specimen similarity or difference). It is at these times that a decision has to be made concerning the identification of the nucleotide base – a decision which can leave the greatest room for ambiguity.²¹

When I asked the Lead Scientist about what I perceived to be a ‘leap of faith’ necessary for her to ‘believe’ in the representational status of the barcode, she stressed the importance of being able to link the sequence back to the original voucher specimen from which the DNA was extracted. This realization conveys the sense that both the DNA barcode and the voucher specimen itself - as objects which stand for a natural order - are rendered meaningless artefacts if not clearly labelled and linked by data (for example in the form of ‘trace files’) to sustain their meaning. The establishment of the ‘analytical chain’ which links a voucher specimen to a barcode and finally to the user(s) of a barcode (and back again), is a part of a rather complex alignment of rather risky techno-scientific practices, demonstrating how the DNA barcode’s classificatory value is fully contingent upon a careful accommodation and negotiation of fragility.

Meeting global barcoding standards

What I have described are the endeavours of one small part in a chain of connections that can contribute towards creating and maintaining the Barcoding of Life Initiative. BOLI's proposals for DNA barcoding require however that it enrolls the participation of museum collections and laboratories worldwide – a participation which needs also to be aligned ontologically and epistemically with BOLI. Crucially, they need to accept and adopt the standards and protocols it is currently establishing.

In July 2007, the first Leading Labs meeting, bringing together key players in collection management (museum curators) and DNA sequencing (laboratory managers) for barcoding, was convened at the Smithsonian Institution in Washington, with a view to smoothing out some of the complications arising from specimen and data travel on an unprecedented global scale. An indication of how high the stakes are for BOLI to achieve their standardizing aim and to ensure the legitimacy of the DNA barcode as a scientific-epistemic object, was perhaps best voiced by one of the meetings participants;

What we don't want is for people to search for a species in BOLD and come out with something worse than if they had looked under a microscope.²²

The emphasis of the discussions at the Leading Labs meeting, lay upon defining the means by which a genetic sequence could meet the so-called 'barcode grade'. This label would differentiate the barcode's status as a reliable identification tool, from other DNA sequences created under less stringent data control conditions and submitted to the same public sequence database Genbank. The donning of barcode status requires adherence to a number of criteria. The DNA barcode must, for example be accompanied with information about the use of different chemical reagents necessary for DNA extraction, amplification and sequencing, together with information about the corresponding voucher specimen as material evidence to back up its virtual representation. Other criteria include the requirement that the barcode sequence should be at least 500 base pairs long and that ambiguity in reading of 'trace files' to assemble the sequence should be less than 1%. Finally, each moment in the analytical chain should be coded using software to enable interoperability between institutions and between the uses for which information is gathered and processed.²³

The point here is not that these kinds of procedures are new but what BOLI is doing is different, both in terms of the scale of the initiative, but also in its emphasis upon the need to achieve global acceptance of the Barcode standards as integral to the definition of the artefact and of its ability to stand for species identification as a key to the diversity of the natural world. By introducing and encouraging the adherence to 'barcode flag' criteria, BOLI is developing a form of insurance to back up and legitimate this ability.

To return briefly to the importance of voucher specimens as evidence, it is interesting to note recent moves to extend 'voucher' status to parts of the organism (as opposed to the whole organism). The decision, for example, taken at 'The All Bird Barcoding Initiative' meeting in September 2005, that a hierarchy of voucher specimen standards be used, reflects one of the consequences of an alignment between the knowledge practices of systematics, bioinformatics and genomics, which characterizes DNA barcoding.²⁴

Whilst this disciplinary encounter has been indispensable in order to propel BOLI forward as a global techno-scientific endeavour, it has also required nuanced negotiations concerning the material cultural underpinnings of taxonomic research. Most importantly, for this paper, these negotiations concerning voucher status, play a crucial role in (re)configuring the value(s) of museum specimens - and their parts - for taxonomy. Furthermore, and in light of this paper's focus upon what might be included as salient in the biography of the object as a move towards understanding its value(s), I suggest that the meticulous auditing of a transparent analytical chain, as part of a general effort to sanitize and control DNA barcoding, is becoming central to the making of knowledge about biodiversity and in the stabilization of the DNA barcode as a scientific epistemic object. Interestingly, the chair of the Barcoding Database Working Group has often publicly stated that the real revolutionary potential of DNA barcoding lies less in its taxonomic potential and more in its ability to 'clean up' the process of producing, archiving and distributing taxonomic information. As such DNA barcoding, drawing upon centuries of

taxonomic tradition and its rigour, dedication, and an eye for the value of audit, has important implications for both genomics and for the valorization of specimens in museum collections. In the following section, I complicate this account by returning to the thorny issue of what the barcode is actually deemed capable of representing and what different possible 'readings' of DNA might imply for the instrumental use of DNA barcodes and the corresponding valorization of nature.

Shallow and deep natural orders and rethinking the biological value of museum specimens

A brief consideration of the shifting emphases and approaches to natural history since the eighteenth century (Farber 2000, Foucault 1966, Stermerding 1991) reveals that the portrayal of natural order(s) by taxonomists depends very much upon what properties of organisms are considered indicative of order. As Foucault's (1966) oft cited work on the history of natural historical pursuits demonstrates, the classification system developed in the seventeenth and eighteenth century that became known as the Linnaean hierarchy, essentially operated – and continues to do so today – as a linguistic device equipped to lay out a grid of the observable qualities of organisms, organized according to the measurements of similarities and differences between them. It is this linking of organisms to order as being exemplary of and brought about through the 'classical episteme' of the time. An organism's place in the world became defined in that it 'exists in itself only in so far as it is bounded by what is distinguishable from it' (1966: 158). From the beginning of the nineteenth century, a growing sense of dissatisfaction with the limits of the Linnaean linguistic naming and classificatory tool encouraged natural historians to explore the temporal complexities of the relationships between organisms and they began to present natural orders as evolutionary achievements with a propensity for further change.²⁵

These shifts, only briefly outlined, occurred centuries ago, and as Foucault argues, together with Cuvier's focus upon the vital processes or functions of parts of organisms as necessarily integral to their classification, marked an emergence of the life sciences out of but separate from the humble naming and grid like mapping pursuits of classification. Today, the central tenets of the Linnaean system remain relevant to taxonomic practice, but usually only in so far as they are made sense of by advances in taxonomic practice which seek to understand the relationships between organisms in terms of being able to trace them back to a (hypothetical) common ancestor.²⁶ The difference between a static – and named – natural order and a more temporally complex evolutionary informed natural order is important for understanding the shifting classificatory value of biological specimens since the advent of DNA barcoding.

I have described so far in this paper the work undertaken by BOLI to establish the DNA barcode as a legitimate tool with which to identify and map species – a role for the DNA barcode which I have suggested has emerged by virtue of the assumption that a public need for taxonomic knowledge is one satisfied by species level identification only. I have also mentioned how contemporary systematics involves an array of far more complex intellectual pursuits than species naming but that the use of DNA barcodes to further phylogenetic or evolutionary research has been relegated to the domain of 'bad science'. It is nevertheless important to remember that this role for DNA barcodes remains lurking in the wings of the DNA barcoding community and it is quite possible that with time, its role will be legitimated.²⁷ The effort undertaken to standardize the practice of DNA barcoding and to painstakingly secure the status of the DNA barcode as a legitimate naming device, does not (yet) however include a consideration of alternative standards and protocols to enable the DNA barcode to safely work towards more complex taxonomic ends.

It is fair to say that for the moment, DNA barcoding, as it has been established and enabled through a series of globalized, standardization mechanisms discussed above, has put to one side the advances in natural history initiated since the nineteenth century and as such, DNA barcoding resonates strongly with the eighteenth-century focus upon species naming and mapping propounded by Linnaeus. This I argue, has serious implications both for the natural orders which become selected as important and revealed through DNA barcoding and for the corresponding value of museum specimens as they are whipped up into the energetic global efforts to know, document, protect and use biodiversity by means of rendering species information accessible to 'anyone anywhere' on the planet.

At the beginning of this paper, drawing upon insights of Suchman and Appadurai, I argued that scientific objects – in this case DNA barcodes and museum specimens – are far from neutrally composed, and take on and perform multiple layers of meaning and value as they travel in and between different sites, communities of practice and epistemic expectations. I further suggested that the complexities of the biographies of scientific objects could contribute to the value they accumulate (Graeber 2001). In order to return to this point, I underline the argument, rehearsed by many, that classificatory systems, rather than providing passive representations of natural order(s), are shaped by preferred imagined human relationships to the natural world and in turn play a performative role in shaping human relationships to nature. Classificatory value, in this way, is created and in turn plays a role by virtue of its intersection with other, ostensibly quite different ‘regimes of value’.

One well rehearsed approach to the performative role of classification has been to demonstrate that classificatory pursuits are inseparable from dominant political and economic trajectories (Anderson 1991, Bowker 2000, 2005a, 2005b, Bowker and Star 1999, Foucault 1966, Grove 1995, Müller-Wille 2003, Richards 1993, Scott 1998, Spary 1996, Thomas 1984, Waterton 2002, 2008). The aforementioned authors and others have all, in different ways, demonstrated the tendency for classificatory systems to harbour political and economic visions which in turn have been consequential for the politics and economies of a nation. Scott, for example, demonstrates how the commercialization of timber in eighteenth-century Germany, was enabled by the grid-type classificatory practices of the time. Spary discusses how the merging of a natural and national economy in eighteenth-century France could be observed through Buffon’s re-ordering of natural classifications as dependent upon indicators of a so-called ‘vegetable economy’. Bowker (2005a, 2005b) brings such a focus upon the co-emergence of natural order(s) with prevailing political and economic forces to bear upon an understanding of the contemporary valorization of biodiversity. His work is particularly relevant for my understanding of how one classificatory value of the DNA barcode – as ‘simply’ species identification – takes precedence over an alternative classificatory value which reveals nature in its evolutionary and spatio-geographical complexity.

Bowker’s approach to biodiversity value takes as its premise a very general point about value as a concept which amalgamates matters of price and the meaning of desire. In so doing, he immediately demonstrates how classificatory value intersects with alternative ‘regimes of value’, including ways in which nature is deemed both knowable and useful. Biodiversity, according to Bowker, has enjoyed success as a conceptualization of nature, capable of mobilising economics and politics, precisely because it converges price (something Bowker analyses as both the unit value of money and the selection of a meaningful unit of biodiversity as species) and meaning (nature of the universe), and thus plays at the intersection of moral and monetary value. Bowker shows how the workable valorization of biodiversity – both for policy and the market – becomes recognisable as a list of species units. He continues to argue that the reduction of nature to list, creates a biodiversity ‘currency’ as a ‘singular’ and flattened nature ignoring both a multiplicity of social values attached to nature and the temporal complexity of evolution; it ignores what he poetically names the ‘mnemonic deep’;

In the case of biodiversity, the currency move is collapsing emergence into units (the commodity form) that circulates in a very flat, linear time and space. (Bowker 2005a: 213)²⁸

For Bowker, the value of biodiversity is shaped by a certain political and economic vision of the way in which nature should be known; classification becomes normative. It would seem that the vision of DNA barcoding advocates for the speeding up of accurate species identification and a corresponding inventorying or mapping of global nature, reflects – in extreme form – the kind of valorization of biodiversity foregrounded by Bowker. To sum up, DNA barcoding at present epitomizes and further promotes this list-like representation and performance of the natural world and it does so at the risk of relegating more historically and social complex natures to the shadows of the scientific and policy imaginary.

Bowker’s analysis provides a useful bridge with which to potentially link the (purely academic) classificatory value of DNA barcodes and specimens with a distinct but related form of biological value, characterized by a number of scholars as an organism’s commercial

potential. Recent literature focusing upon the domains of biotechnology and biomedicine explores the co-emergence of forms of capitalism with humanity's knowledge and use of biology, in the wake of proliferating (post) genomic developments (Franklin and Lock 2003, Hayden 2003a, 2003b, Helmreich 2007, Rose 2007, Sunder Rajan 2005, 2006, Waldby 2000, 2002). This literature defines biovalue as the actual or hoped-for capital created and circulated by unleashing the potential of genetic function as it is transformed into information. The commodifiable characteristic of biology, as the following assertion of Hayden suggests, is active biological function (rather than the revelation of order which is described in more passive ontological terms):²⁹

For these enterprising practitioners of plant screening, describing new plant compounds has little worth if its is not accompanied by a description of their efficacy: *what a plant has and what a plant does* are two different questions... patent claims on substances derived from nature revolve around a newly vital emphasis *not on what life is, but on what life does* (2003a: 198, emphasis added).

One of the most interesting contributions of the aforementioned authors to an understanding of the entanglement of the market and biology, is the analysis of the ability of market forces to play a role in defining the workings of biological life. Helmreich is one of the few scholars to explore the implications of such insights for biodiversity. In his study of the prospecting of marine microbial biodiversity by biotechnology practitioners, he asserts that certain characteristics of the biological functioning of marine biodiversity in Hawaii, are elicited - or using his vocabulary, they are 'naturalized' - through the hopes and visions of energy and labour encapsulated by commodity regimes of value employed by biotechnology practitioners. This is a compelling idea illustrated well by the following:

A belief in the irrepressible generativity of biological life forms themselves is often called upon to warrant the promissory character of biotechnology, as though biotechnology has inherited the potentiality associated with genes. Biotic substance is considered to be the source of mutations and recombinations that create 'newness' (Helmreich 2007: 288)

I draw upon Helmreich's insights to understand the selection of one form of classificatory value over another by the DNA barcoding community. I suggest that the pressure and desire to know nature in flattened, cartographic form feeds into the interpretation of the role of the barcode gene (Cytochrome Oxidase I) as being one which reads natural order as one of species name and position in a grid-type order. In Helmreich's terms, the assumption that nature is best knowable and most useful in this form has worked to 'naturalize' the ordering potential of the genetic segment as indexing species identity. If, instead the use-value of a more complex, phylogenetic reading of natural order prevailed, a quite alternative classificatory genetic potential could have been - and might be in the future - naturalized.

This process of classificatory rather than functional 'naturalization' I suggest plays a vital role in determining the biographical trajectory of the museum specimen and DNA barcode. What I have suggested so far is that the prevailing value of the DNA barcode as species identifier only, arguably cuts its biography short. Whilst it contemplates the biographical travels of the specimen between collections, laboratories and as digital information is eventually deposited on a database - and hence accumulates all the work done to legitimate its classificatory value - it does not incorporate the relevance of its evolutionary history as relevant biographic (and value producing) information. Of course, this multiplicity of meaning has always resided in museum specimens, but I reiterate that the globalizing force of DNA barcoding potentially places it in a position to connect museum specimens and a 'global populace' with very particular - and potentially reduced - natural order.

The authors discussed above are predominantly interested in the infusion of capital regimes of value into the generation of knowledge concerning life processes. At first glance, the hopes and visions for how nature can and should be known, expressed by DNA barcoding advocates, are not explicitly informed by expectations of the commercial potential of this knowledge. BOLI currently promotes DNA barcoding as being associated purely with 'academic'

rather than 'commercial' ends. This would suggest that the classificatory value I suggest is 'naturalized', is not one which would necessarily circulate or achieve an exchange value as part of a commercial 'regime of value'. The insistence upon such a division of 'regimes of value' appears rather naïve however; as Appadurai points out, most objects can circulate within and between a multiplicity of these. Parry (2004) in her informative account of the bioprospecting of museum botanical collections – a phenomenon she characterizes as 'micro-sourcing' – perhaps makes the most literal links between two 'regimes of value' and in so doing complicates Hayden's distinction between a nature that *is* and a nature that *does*.

The collections of biochemical compounds, living or cryogenically stored materials, and even herbarium specimens that have been created by systematists ... are more likely to have been accurately identified and classified. They are also less likely to have been patented, as they have been investigated for purely academic purposes in publicly funded institutions (2004: 176).

Parry again reminds us that the distance created by taxonomists between their humble interest in natural order and the possible uses to which this knowledge might be put, could be subject to a more complex entanglement of different schemes of valorization of biological material than first meets the eye. To reiterate; I am arguing that it is the DNA barcode's ability to rapidly identify species and so propound a certain natural order that the biological value of specimens entangles what biology does with what biology is; classificatory value thus becomes highly active rather than passive. Arguably, this indicates the impossibility of separating the ontological status of species from the uses to which they are (or will be) put in a contemporary cultural climate which places such a high emphasis upon instrumentality.

Conclusion

There are some aspects of BOLI which, as I have described above, have become established within the global DNA barcoding community and there are other dimensions of BOLI which remain considerably uncertain. One implication of this is a certain (creative) uncertainty of future attributions of value to museum specimens. I have discussed, for example, the work undertaken to sanitise and standardize the practices associated with DNA barcoding, from annotating voucher specimen information through to adhering to strict protocols designed to stabilized DNA barcoding as 'good science'. At present most BOLI participants across the globe are gradually aligning themselves to these closely audited procedures. What is certain is that these endeavours work to establish the DNA barcode as a legitimate species identifier and in so doing they attribute a particular classificatory value to biological specimens which is further linked to a particular kind of natural order. What is rather less certain is whether this portrayal of what is important and knowable about nature will in fact achieve global purchase; whilst all BOLI eyes are presently upon the rate at which the Barcoding of Life Database (BOLD) gradually fills with authenticated species barcodes, an air of uncertainty remains around the question of user uptake of barcode information. A further unknown is the likelihood of BOLI accommodating increasing global pressure to officially legitimate the use of DNA barcodes for phylogenetic research.

In the final section of this paper, by suggesting an intersection between classificatory and more instrumental regimes of value, I raise the question of the potential commercialization of DNA barcoding and its products. Whilst, as I mentioned, this is not something explicitly entertained by BOLI, all DNA barcoders await with anticipation the appearance on the market of a hand-held sequencer which will provide instant validated species information to anyone, anywhere on the globe. But there are more subtle interconnections between DNA barcoding and market forces; traditional scientific funding bodies in the US, UK and Canada, such as the US National Science Foundation, have not so far funded any DNA barcoding projects. Instead these have been funded by institutions such as Genome Canada with an explicit interest in the results of DNA barcoding for crop protection and pest control. Such funding sources have hitherto been untapped by more conventional taxonomic projects and have injected the community with unprecedented financial support.

What is far from certain is the likelihood of a commercial future for the more temporally

complex information released by the marginal use of DNA barcodes for phylogenetic research. Of course evolutionary biological research has long been put to instrumental and commercial uses. Plant breeding, for example, depends upon knowledge of the history of a plant to determine how its exploitable 'traits' have developed (Kloppenborg 2004). At present, BOLI not only is reluctant to establish parallel standards and protocols which would uphold a phylogenetic classificatory value of the DNA barcode, they are concerned that in so doing, the standards they have stabilized for the 'shallow' reading of the DNA barcoding risk a certain de-stabilization as the credibility of the whole project of DNA barcoding - as one which is presently one of species naming - is jeopardised by the risk of 'bad science'.

Nevertheless, given the interest across the globe in using DNA barcodes for phylogenetic research, it is necessary to reflect upon the following questions: what might a historically rich natural order revealed through the big-science endeavour of DNA barcoding look like? What kinds of instrumental/commercial 'regimes of value' might this use of the DNA barcode intersect with and be informed by? What forms of guarantee to uphold the evolutionary classificatory value of the DNA barcode might in the future be deemed credible?

In this paper I have explored a particular way in which museum specimen collections are being re-valued as they are opened out beyond the walls of museums thanks to their enrolment by global techno-scientific projects such as BOLI. Whilst demonstrating the stabilization by BOLI of one form of classificatory value over another as specimens are converted into DNA and through their voucher status, remain attached to DNA barcodes, it is important to remember that specimens remain sites of contested classificatory meanings. I have suggested that these meanings are inseparable from forces, lying beyond museums, which shape the preferred uses to which taxonomic information are put. Moreover their status as objects with an ability to reveal a variety of possible natural orders is one which is subject to an uncertain future. The inevitability of this is perhaps supported by Rheinberger's and Knorr-Cetina's assertions that scientific-epistemic objects are best characterised by their state of continual (re)emergence. Information, knowledge, practice, materials, multiple human investments of meaning and finally the application of objects, are relationally produced in a way which engages past, present and future hopes and expectations, in this case for the valorization of biodiversity.

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Notes

- ¹ In this paper, I will use the terms systematics and taxonomy interchangeably. Literally speaking, 'Taxonomy is defined in the Dictionary of Ecology, Evolution and Systematics, as 'The theory and practice of describing and classifying organisms' and 'Systematics' is defined as 'The classification of living organisms into hierarchical series of groups emphasizing their phylogenetic interrelationships; often used as equivalent to taxonomy' (Lincoln *et al.* 1987). See Hine 2008 for a description of the concerns voiced within the taxonomic community since the flurry of debates during the 1960s and 1970s and their changing emphases in more recent years. Hull 1998 provides an exhaustive analytical account of the cladistics versus phenetics debates of the 1960s and 1970s.
- ² The dependency upon these vouchers is but one sign of the rigour and discipline which have characterised the taxonomic sciences since the mid nineteenth century. See Daston 2004 for a history of the characterisation of 'type' specimens – those specimens which serve as a permanent reference point for classified organism's name.
- ³ My interest in the alignment of specimen value with an (imagined) public need for species information complements Rader and Cain's (2008 in this issue). Whilst they explore the implications of changing relationships between science and its publics for the North American museum display of specimens in the mid twentieth century, I concentrate on the implications of democratised science for the valorization of specimens for behind-the-scenes taxonomic research.

- 4 See Ellis, Waterton and Wynne 2008 for an analysis of DNA barcoding's 'publics' and what has been characterised by some as the rhetoric of 'democratisation' associated with DNA barcoding.
- 5 The selected gene for animals is 648 base pairs of the mitochondrial gene Cytochrome Oxidase I or CO1. What Hebert *et al.* (2003a, 2003b) found was that the rate of substitution of nucleotide bases was high enough between the genetic fragments of different species, to index species difference. CO1 does not work to identify plant species so efficiently and the botanical community are still in the process of negotiating the selection of a combination of two to three gene regions which will eventually be used as the plant DNA barcode.
- 6 See BOLI website for further information on the Barcoding of Life Initiative: <<http://www.dnabarcodes.org>>.
- 7 For a discussion of BOLI's potential user communities, see Ellis, Waterton and Wynne 2008.
- 8 This is of course in cases when the organism under investigation has already been identified, and its DNA barcode submitted to BOLD. In cases where the identification is unknown, the investigator will be advised that the species is a 'new' one requiring classification. DNA barcoders are clear that, in these cases, taxonomists and other users will need to use more 'conventional' classification methods than those of rapid species identification provided by DNA barcoding itself.
- 9 Furthermore, DNA barcoding as a taxonomic technique which relies upon blasting a sequence from an unknown organism against a bank of sequences from known specimens, produces better calibrated matches between sequences if a large number of sequences for each organism are banked. This means that the larger the number of samples supplied for high through-put sequencing the better.
- 10 Barcode data on the Barcoding of Life Database is organized according to ongoing and completed barcoding projects. Each project indicates the provenance of its tissue samples and the project 'Birds of North America', for example demonstrates that virtually all of its 437 specimens were derived from the Royal Ontario Museum. As an example of a slightly more esoteric project – ACG Belvosia – a group of parasitoids – the research collection appears as one privately owned by the project researchers.
- 11 Email from a North American Collection Manager, 24 January 2008.
- 12 UK botanist from the Natural History Museum: transcript, October 2006
- 13 See Parry 2004 for the most thorough account of the changing valorization of collections with a particular emphasis upon the way in which bioprospecting, over the last two decades, has introduced imperatives to collect specimens of commercially valuable genetic and biochemical potential.
- 14 Funded by the ESRC and undertaken at Lancaster University in collaboration with the Botany Department at the Natural History Museum, London, Taxonomy at a Crossroads: science, publics and policy in biodiversity is a sociological study of the Barcoding of Life Initiative. It began in 2006 and will end in 2009. The author is the main researcher on the project and Claire Waterton (Lancaster), Brian Wynne (Lancaster) and Johannes Vogel (Natural History Museum) are the project's Principal Investigators.
- 15 'Tag' is Charis Thomspson's characterization of the ability of Kenyan elephants to stand for quite 'competing philosophies of nature' (2002: 167). See also Bowker and Star 1999, Latour 1999, Law and Mol 2002, Roth and Bowen 1999, who all in different ways, argue that artefacts both harbour political, social and ethical visions and in turn stretch out to connect with and take part in a playing out of the world.

- ¹⁶ See also Kopytoff 1986.
- ¹⁷ See Graeber 2001 for a thorough critique of Appadurai in his effort to synthesise and appraise changing anthropological approaches to exchange and value since Mauss 1954.
- ¹⁸ See website for the Canadian Centre for DNA Barcoding: <<http://www.dnabarcoding.ca/>>.
- ¹⁹ See Rabinow 1996 for a full description of the Polymerase Chain Reaction which is the process by which minute quantities of DNA are amplified into a form with which sequencing and relevant experiments can be carried out.
- ²⁰ For full details on the reagents required for DNA Barcoding, see Ivanova *et al.* 2006, 2007.
- ²¹ See MacKenzie 1990 and Shackley and Wynne 1996 for analyses of the way in which uncertainty is negotiated by producers of scientific knowledge. They highlight in particular the tendency for scientific knowledge to be presented in more certain terms, the further the knowledge product ventures from the site of its production for policy or public application. See Lahsen 2005 for a critique of Shackley and Wynne's use of MacKenzie's 'certainty trough' in their analysis of climate change modelling.
- ²² Leading Lab participant, 11 July 2007.
- ²³ A software tool called LIMS – Laboratory Information Management System has been developed as an integral part of the Barcoding of Life Database (BOLD) to facilitate the data flow between institutions.
- ²⁴ 'The preliminary hierarchy of acceptable voucher specimens is: Gold Standard: male study skins with breeding plumage, females, alcohol preserved specimens; Silver Standard: skeleton, skin sample; Bronze standard: feather, digital image' (Baker *et al.* 2005:13). This agreement should be appreciated as arising in a context of encounter between the domains of genomics and systematics. As Hine (2008) has described, these scientific domains foster a very different relationship with the biological material with which they work. Very few sequences on Genbank - the public database which eventually houses DNA barcodes, but is best renowned for its human genome sequences – are linked to voucher specimens.
- ²⁵ See Foucault 1966: 162–6 for a full appreciation of the changing approaches to temporality in eighteenth- and nineteenth-century classificatory methods and practices.
- ²⁶ This evolutionary approach to taxonomic practice is known as 'phylogenetics', defined by the *Dictionary of Ecology, Evolution and Systematics* (Lincoln, Boxshall and Clark 1987) as 'pertaining to evolutionary relationships within and between groups'.
- ²⁷ Interestingly, at the second of BOLI's global meetings held in Taipei in September 2007, many of the presentations from South East Asia demonstrated the region's use of DNA barcoding for phylogenetic purposes. The sense at this meeting was that BOLI will gradually have to find ways to accommodate uses for DNA barcoding beyond its officially established role as a species naming device. See also Vogler and Monaghan 2006.
- ²⁸ See Tsing 2005: 155 for alternative reflections concerning the liveliness of biodiversity lists; 'The lists acknowledge an acclaimed global biodiversity by conserving a local space within it'.
- ²⁹ This selection of function over having or being echoes with Cuvier's determination, at the beginning of the nineteenth Century, to demonstrate the importance of understanding life's processes as revealed through an examination of the parts of organisms, as superseding the importance of the linguistic importance of their observable characteristics. See Farber 2000, Foucault 1966. Cuvier's work, as I have already suggested above, marked a separation of the developing life sciences from natural history and is a separation felt today

which positions taxonomy as a science which provides indispensable knowledge necessary to underpin the pursuits of the bio-sciences as well as human efforts to preserve biodiversity. – Laboratory Information Management System has been developed as an integral part of the Barcoding of Life Database (BOLD) to facilitate the data flow between institutions.

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