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**SPECIAL ISSUE:
ANIMAL GENOMES, BODIES AND TISSUE IN SCIENCE AND SOCIETY**

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Contents

Guest Editorial

by MATTHEW HARVEY ii

Editorial Essay

Animal genomics in science, social science and culture
by MATTHEW HARVEY 1–28

Articles

The Barcode of Life Initiative: synopsis and prospective societal impacts of DNA
barcoding of fish
by FILIPE O. COSTA & GARY R. CARVALHO 29–40

Commissioned Responses to Costa & Carvalho

Real but modest gains from genetic barcoding
by JOHN DUPRÉ 41–43

DNA barcoding: potential users
by PETER M. HOLLINGSWORTH 44–47

The Book of Life goes online
by PETTER HOLM 48–51

The Barcode of Life Initiative: reply to Dupré, Hollingsworth and Holm
by FILIPE O. COSTA AND GARY R. CARVALHO 52–56

Socialising animal disease risk: inventing Traceback and re-inventing animals
by ANDREW DONALDSON 57–69

The reification of life
by MICHAEL HAUSKELLER 70–81

Exploring biopower in the regulation of farm animal bodies: genetic policy
interventions in UK livestock
by LEWIS HOLLOWAY & CAROL MORRIS 82–98

Animal genomics and ambivalence: a sociology of animal bodies in agricultural
biotechnology
by RICHARD TWINE 99–117

Author Biographies 118–119

Editorial: Animal Genomes, Bodies and Tissue in Science and Society

The papers in this issue address the field of animal biotechnology and, particularly, animal genomics. Together they seek to understand the context and shaping of the science of animal genomics, reflect on connections between this science and the social position and cultural construction of animals and human-animal relationships, and explore current and future regulation and policy. Each paper emerged from a multi-disciplinary workshop convened by the ESRC Genomics Policy and Research Forum, University of Edinburgh to discuss animal genomics in April 2006. Some participants at the workshop, and some authors here, have long been interested in animal genomics and biotechnology, whilst others were asked to bring knowledge developed in other fields and with other case studies.

Underpinning the workshop, and followed through in this issue, was a recognition that genomics uses and studies a lot of animals, combined with concern that the otherwise flourishing social science of genomics has passed them over. The strength of concern is variously expressed. In my own editorial essay, I ask only that the animal becomes more conspicuous. Others call for something stronger: Donaldson, for example, argues that we need to rethink our idea of society or the social in such a way that the inclusion of nonhuman animals becomes obvious.

Whichever route is adopted, a handful of themes recur, including: whether animal genomic science is reductive; the extent to which it aligns with narratives of instrumentalism; the potential for animal genomics to render animals efficient sources or accumulators of capital; whether animal genomics functions as an instrument of biopower; and whether animal genomics alters both what we can and do know about an animal, and the animal that is known. On the way we visit the farmyard (Donaldson, Holloway & Morris, Twine), the laboratory (Harvey, Hauskeller), and the sea (Costa & Carvalho), although as Twine points out, genomics means that it is increasingly difficult to separate such spaces.

Although final judgement rests with the reader, I hope this issue makes a valuable contribution both to the social scientific and philosophical analysis of genomics, and to the growing field of animal studies. It also contains a new venture for the journal. The issue includes a broadly technical paper on DNA barcoding by molecular ecologists Filipe Costa and Gary Carvalho. Inclusion of a technical paper is new in itself, but moreover, this is followed by three short commissioned responses from John Dupré, a philosopher, Pete Hollingsworth, a conservation geneticist, and Petter Holm, a social scientist. Costa and Carvalho provide a final response and together these papers make for a very interesting discussion. Many aspects of animal genomics have been discussed before within social science journals, and sometimes from multiple perspectives in this way, but probably not DNA barcoding.

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Guest Editor

The Barcode of Life Initiative: synopsis and prospective societal impacts of DNA barcoding of Fish

FILIPE O. COSTA AND GARY R. CARVALHO¹

Abstract

Almost 250 years after the publication of the taxonomy-founding work *Systema Naturae*, by Carl Linnaeus, the inventory and catalogue of the planet's biodiversity is still far from complete: only *ca* 1.5 to 1.8 million of an estimated 10+ million species are so far described. Notwithstanding the remarkable merits of the Linnean system, the task is too vast ever to be completed using current conventional approaches. Such a staggering reality, and the customary difficulty that the scientific community and society in general experience to access taxonomic knowledge, has prompted the search for novel tools or approaches for species identification. Such a tool has been recently proposed in the form of a standardised short DNA sequence from an agreed-upon region of the genome, which is expected to ultimately provide a means of fast and robust identification of any species on the planet: the DNA barcode. Received with as much enthusiasm by some as skepticism by others, this novel tool was set in motion on a worldwide scale by means of an international consortium of organisations (the Consortium for the Barcoding of Life), thus becoming a large-scale horizontal genomics project. While anchored within the knowledge and principles of taxonomy, DNA barcoding possesses unique characteristics which anticipate a diverse scope of new applications and benefits for society. Notably, it places the completion of the biodiversity catalogue within the reach of a single generation, with the promise to assist greatly in the discovery of new species. Alongside long-term, ultimate goals, such as democratisation of access to taxonomic knowledge and assistance in writing the encyclopaedia of life, there are several more prosaic applications that may also impact society, not only in certain scientific fields, but also in a range of social and economic activities. Here, we will use DNA barcoding of fish as an example to illustrate foreseen applications, and as a basis to stimulate reflection on potential societal impacts of this horizontal genomics project.

Synopsis of the Barcode of Life Initiative

DNA barcoding: why and what for?

The realisation of the paucity of our knowledge about the world's biodiversity, together with the limitations of current approaches to biodiversity diagnosis, are the main driving forces behind new approaches to species identification. Estimates of the number of existing eukaryotic species range from the most conservative 3.6 million up to 100+ million, with 10 million favoured by most analysts as the nearest order of magnitude.² Circa 1.5 to 1.8 million species have been described to date.³ Even considering the lower estimates, we still know only a minor fraction of the immensity of life's diversity. The current rates of discovery - about 10,000 new species are described per year⁴ - are inadequate if such a huge gap is to be closed in the near

future. Moreover, no more than 5% of the named organisms are known in any biological detail.⁵

Taxonomists and systematists constitute the scientific frontline for addressing issues of life's diversity. They have the central role of delineating species, naming, classifying and describing, and unravelling their phylogenies and placement in the tree of life. Ideally, these experts should make use of multiple sources of evidence and follow a hypothesis driven approach to resolve species identities and relatedness. Hence taxonomy and systematics are disciplines with high and pivotal intellectual content⁶ that depend on only a few taxon-specific experts.

However, intervention of experts is frequently required beyond species delineation and goes as far as routine species identification, the very basis of most research involving organisms. For those who work in other areas of science this will likely come as a surprise. In fact, learning the nuances that separate closely-allied species assemblages is so complex that few biologists, even those who have devoted their careers to taxonomy, can critically discriminate more than 1000 species. This serious constraint to the diagnosis of biodiversity is exacerbated by various peculiarities of current taxonomic protocols. Many such protocols rely heavily on phenotypic characters, and frequently require lengthy and detailed inspection of the specimens, and even dissection. There is no master key that could work for different groups of taxa, or even for a single species across its different life stages. Reliable identification depends on experts who have climbed a long learning curve and who are focused on a specific group of organisms. There is also a bias of focus in particular groups such as vertebrates and insects. Taxonomic literature is often difficult to locate, and the description of a new species does not assure its future recognition.⁷ The compounded outcome of these difficulties, together with the shortage of taxonomic experts and resources allocated to taxonomy, impose a taxonomic impediment to understanding, utilising and conserving biological diversity.^{8,9} Indeed, this taxonomic impediment extends to the whole scientific community and society in general, which experience a customary difficulty to access taxonomic knowledge.

In 2003, Hebert and co-authors introduced the concept of a DNA barcode, and proposed a new approach to species identification,¹⁰ which offered great promise to counter many of the limitations above. The new approach is based on the premise that the sequence analysis of a short fragment of a single gene (eg. cytochrome c oxidase subunit 1), enables unequivocal identification of all animal species. Hence, analogously to the barcodes used in commercial products, the DNA barcode would provide a standardised tool for fast, simple, robust and precise species identification. Such a 'barcode region' would also have to evolve at a rate that would distinguish species from each other while remaining more or less identical for all members of the same species. Finally it would have to be flanked by conserved DNA regions so as to make the polymerase chain reaction (PCR), a method of targeted gene replication, practical.¹¹

DNA barcoding differs in many ways from conventional taxonomic identification tools and approaches, over which it offers several advantages. It permits the identification of species from fragments, and from any life-history stage, as well as

the standardisation of a universal master key in a format that reduces ambiguity and enables direct comparison of specimens to a global reference database.

Before the introduction of DNA barcoding, various molecular methods were already applied to species identification,¹² though often these were of limited scope. None had the ambition, scale and, most importantly, the degree of standardisation of barcoding. Soon, it was proposed that the DNA barcoding concept be expanded in order to embrace all eukaryotic life forms, and promised to revolutionise taxonomy and influence other allied disciplines.¹³ The emergence of controversy among the scientific community was not, however, unexpected.¹⁴ Some critics are concerned about known limitations of the approach (see next section), and question the ability of a single gene to provide sufficient information for such an ambitious project.^{15,16} Others fear that DNA barcodes will overrule conventional methods and become the unique standard for species delineation (which is different from species identification, as explained above). Or even that this fashionable and democratic tool will make species identification a frivolous, apparently straightforward task, leading to the abandonment of conventional methods, and the gradual demise of the whole scientific discipline of taxonomy and its essential intellectual input into the biological sciences.^{17,18,19} As explained in the next section, some of this criticism may result from misconceptions about the rationale and approach of DNA barcoding.^{20,21,22}

Rationale and approach

Hebert and co-authors²³ suggested a 650 base pair (bp) sequence of mitochondrial gene cytochrome *c* oxidase subunit 1 (COI) as the reference DNA barcode for all animal life. This gene occurs in the mitochondria of all eukaryotic organisms, and the initial appraisal revealed consistent resolving capability at the species level for many animals. There are a few recognised limitations of this barcoding region, namely the possible lack of resolution for recently diverged species or for particular animal taxa (eg, cnidarians), or the inability to detect cases of introgressive hybridisation. These exceptions are thought to represent only a minor percentage of the target species on a global scale. Moreover, it is expected that these limitations can be tackled using additional or alternative barcoding regions in a comparatively small number of exceptional cases. Thus, while COI has been elected as the prime DNA barcode for identification of animals (and probably for macroalgae, too²⁴) the pursuit of regions of the genome appropriate for use as DNA barcodes in other eukaryotic life forms (eg, plants,²⁵ fungi^{26,27}) is in progress.

The rationale and approach of DNA barcoding are essentially the same whichever region of the genome is selected. The basic premise is that for each currently known species an unequivocal match can be established with the DNA barcode obtained by reading a selected region of its genome. The DNA barcode sequence is not necessarily invariable within a species. Instead, the rationale is that individuals of a species share very similar sequences and that the barcode arrays for different species are usually distinct. This “matching hypothesis” constitutes the key starting point for launching and implementing the new bioidentification system. Every known species must be checked for the validity of this hypothesis. In doing so, a database linking a given species and respective DNA barcode array will be built. Reference barcoded

specimens of each species that have been identified by experts are deposited in a museum and therefore available for double-checking and for long-term study. Once this reference database is complete, it can be used to assign an unknown sample to a known species.

In comprehensive DNA barcoding studies conducted so far with Lepidoptera,²⁸ birds,²⁹ fish³⁰ and crustaceans,³¹ a match between a DNA barcode and a known species has been found in more than 95% of the cases. Failure to obtain an unambiguous match may result from insufficient resolution of the DNA barcode (which can be the case when screening recently diverged species). However, as is the case with the studies above, ambiguities may also flag the presence of potentially unrecognised species that were overlooked by conventional methods. It is precisely in this type of setting that DNA barcoding can be of great assistance in the discovery of new species; it provides a molecular basis to test species hypotheses when data are not congruent with known species boundaries.^{32,33}

It should be emphasised that DNA barcoding does not substitute the conventional protocol for delineating new species.^{34,35,36} A hypothesis-driven approach should be followed to address potential new species supported by DNA barcoding screening. Ideally, new species hypotheses should be tested against various sources of evidence (morphological, ecological, reproductive, other molecular evidence, etc.)^{37,38} which will continue to rely on the input of the taxonomic expert. Indeed, this novel tool will assist taxonomic experts greatly in their research efforts, and not only by releasing them from routine identifications; it also provides a fast means of screening and triage for large numbers of samples, enabling quick detection of potential new species, with consistent identification of morphologically distinct or cryptic life history stages and gender. Most importantly, the efforts of experts in the delineation and description of new species will have an immediate effect, since the new species can be readily tracked down using DNA barcoding. As new species are discovered and identifications revisited by experts, voucher specimen identifications and the global reference database can be updated and immediately effective.

Organisation and framework

In May 2004, little more than a year after the publication of Hebert and colleagues' seminal paper,³⁹ an international consortium of organisations - the Consortium for the Barcoding of Life (CBOL)⁴⁰ - instigated the worldwide implementation of DNA barcoding, thus launching a unique large-scale horizontal genomics project. CBOL's mission is to explore and develop the potential of DNA barcoding for research and as a practical tool for species identification. Consortium members include museums, herbaria, zoos, biodiversity research institutes, universities, conservation organisations, government agencies and private companies.

Since its inauguration, CBOL has experienced rapid development, which was particularly intense after the First Conference for the Barcoding of Life, held in February 2005 at the Natural History Museum, London. This conference constituted the first large forum for discussing DNA barcoding, and the proceedings were compiled in a special issue of *Philosophical Transactions of the Royal Society*.^{41,42}

There was also progress in organisational aspects of CBOL with the establishment of five working groups to target specific aspects of DNA barcoding.

Currently CBOL counts more than 150 organisations from 45 countries in its membership. The first global DNA barcoding campaigns - the Fish Barcode of Life (FISH-BOL)⁴³ and the All Birds Barcoding Initiative (ABBI)⁴⁴ - have been launched, with the intention of assembling a reference database of DNA barcodes for all fish and bird species respectively. FISH-BOL expects to complete most of the inventory of all known fish species of the world by 2010. More recently, a campaign was launched for DNA barcoding all Lepidoptera, which already exceeded 8 600 species barcode records.⁴⁵ Finally, a thematic international network, Barcoding of Invasive and Pest Species,^{46,47} is also in operation.

CBOL coordinates and promotes DNA barcoding on a worldwide scale, and endorses public access to DNA barcoding data. Both the Barcode of Life Database (BOLD)⁴⁸ and existing public genomic repositories (namely the GenBank of the National Center for Biotechnology Information (NCBI), the European Molecular Biology Laboratory (EMBL) and the DNA Data Bank of Japan (DDBJ)) will provide free access to DNA barcoding data. The Barcode of Life Initiative intends also to be both integrative and integrated with other worldwide taxonomic initiatives⁴⁹ such as the global Taxonomic Initiative for the Convention for Biological Diversity and the Global Biodiversity Information Facility (GBIF).

Currently DNA barcoding is a fully established approach, as recognized for example by the setting up of a 'Barcode' keyword for the identification of standard DNA barcodes in public genomic repositories⁵⁰ and by the creation of a specific theme-section for submission of DNA barcoding studies in the journal *Molecular Ecology Notes*.⁵¹ There is also 'The Barcode Blog'⁵² at Rockefeller University, which, since June 2004, has been alerting the community to new studies on barcoding.

The promise of DNA barcoding

*'Imagine a world in which any person, anywhere, at any time can identify any species at little or no cost. That world is technologically upon us.'*⁵³

By contributing to a break up of the 'taxonomic impediment', DNA barcoding promises to open doors to a diverse array of scientific and social applications and for a variety of end-users, from the scientific expert, to the individual citizens. Our improved ability to recognize existing and cryptic species will be of benefit to environmental sciences, forensics,⁵⁴ pharmaceuticals, agriculture, conservation, biological and molecular evolution, to countermeasures to biological warfare, to name but a few.⁵⁵ We describe some of the applications to fish biology and fisheries in the next section, but first we shall deal with more general impacts.

The scientific field of taxonomy itself may well be one of the most immediate beneficiaries from DNA barcoding. With this new and powerful tool, taxonomists can be freed from maintenance and routine tasks, and focus instead on the description and

investigation of newly discovered species,⁵⁶ thus greatly accelerating the rate of new entries in the encyclopaedia of life. However, crucially for addition of any species' DNA barcode to BOLD, it will remain necessary to deposit a voucher specimen,⁵⁷ a requirement that emphasises the intended integration of DNA barcoding with the Linnean system.

Benefits will likely extend to more than purely technical aspects, and many view DNA barcoding as a key opportunity to revitalize the scientific discipline of taxonomy,⁵⁸ which has progressively become one of the most underfunded within biological sciences.⁵⁹ In fact, different views on the potential impacts of DNA barcoding in taxonomy have been a source of lively debate:⁶⁰ some critics suggest it will sound the death knell for a moribund but vital discipline,⁶¹ while for others it is a valuable opportunity to revolutionise and revitalise the subject.^{62,63,64}

Such a debate might soon become a redundant one, since the prime concept and current practice of DNA barcoding is built upon establishing a match between a known vouchered species and a DNA sequence. Thus, the success of DNA barcoding is a corollary of progress in taxonomy and biodiversity inventories. The Barcode of Life Initiative has already started to draw attention to the value of taxonomy and the key role of taxonomists, and has attracted new sources of funding for the discipline. DNA barcoding has prompted unprecedented large-scale biodiversity inventories, which will provide new raw materials for taxonomy and systematics. It is raising standards for incorporating taxonomic information into genomic data repositories.^{65,66} Moreover, it is establishing a new and valuable type of genetic bank (by means of archiving tissue samples or DNA extracts) from which the genome of each species can be accessed in the future.^{67,68} Hence, benefits start to emerge, not only for taxonomy, but also for other disciplines within biological sciences and related scientific fields.

The impacts of the Barcode of Life Initiative are expected to extend beyond the scientific arena and ultimately influence society as a whole. Through improved knowledge of the planet's biodiversity, societies will be able to manage biological resources in a more sustainable and responsible manner. Ironically, the taxonomic impediment is most acute in developing countries, where biodiversity is highest.⁶⁹ Features of DNA barcoding such as rapid, accurate and cost-effective specimen identification have the potential to democratize access to taxonomic information in all regions of the globe, and open the gates of biodiversity information to the ordinary non-expert citizen.

One of the most emblematic visions of the Barcode of Life Initiative is the ultimate creation of a handheld device that could be used to identify any life form anywhere and anytime at little or no cost.^{70,71} Such a 'Bio-pod',⁷² would not only provide a species identification, but would also enable an Internet link with the corresponding entry in the encyclopaedia of life, with images and related information about that species. Below is a commentary on an article about DNA barcoding posted in a free access website.⁷³ It synthesises in a rather spontaneous fashion the type of reaction that the ordinary citizen may have to the idea of a Bio-pod:

This could be fantastic. If there's something in it for the end user, millions of people will be turned into field taxonomists. A known plant gives ID; a weird one means you contribute to science. Upload your location at the same time, and you have new types of data: scientists could get plant coverage. With such data useful in climate research, a person could feel good everytime they ID a plant.

Reading through Jamais' previous post, I can see this opens up a whole pandora's box of problems with patents and the openness of the whole model.

Hopefully there's a wikipedia like model for this. Are these machines available now to non-researchers? What is their cost?

This comment also captures many of the hopes for the societal benefits of the Barcode of Life Initiative, in particular the high expectations for improvements in bio-literacy.⁷⁴ In this respect, DNA barcoding could become to biodiversity what the printing press was to literacy.⁷⁵ A more bio-literate society as a whole would be able to take better and more responsible decisions about the management of our planet's biological heritage. The ordinary citizen would have the opportunity to become familiar with the surrounding biological diversity, and acquire a different perception of its relevance.⁷⁶ It may trigger a curiosity for living organisms, and improve awareness of biodiversity threats, and the perception of how human actions can have a detrimental impact on rates of species extinctions and ecosystem change. Eventually, a more bio-literate society could produce 'greener' individuals, who are more environmentally-responsible in their daily actions, and willing to undertake pro-active measures to minimize their own impact on the planet's biodiversity.

The example of fish DNA barcoding

Fish provide a suitable model for testing the implementation of DNA barcoding at a worldwide scale. Although they constitute the largest vertebrate group (about 50% of all vertebrate species), they have a manageable number of species: c.20,000 marine species (15,648 in Fish Base; 91 with subspecies); c.15,000 freshwater species (13,544 in Fish Base; 152 with subspecies) (705 species occur in both marine and freshwater systems); and c.80 brackish species (82 in Fish Base; 1 with subspecies). They are very diverse systematically, comprising three major groups of organisms: the jawless fish (Superclass Agnatha), such as lampreys hagfish; the cartilaginous fish (Class Chondrichthyes), including sharks and rays; and the immense variety of the bony fish (Superclass Osteichthyes) which include lungfishes, eels, tunas, sea horses, etc.⁷⁷

Fish are also of economic value as a food source. Global figures for the value at first sale in 2000, is circa US\$81 billion for capture fisheries and about US\$52 billion for aquaculture (excluding plants).⁷⁸ In the same year the estimate for retail trade for ornamental fish in the USA alone was US\$3 billion, and in 1984 in Australia the value of recreational sports fishing was estimated in US\$2 billion.

Fish and fisheries resources comprise a key target group from which it is anticipated that DNA barcoding will bring larger and more immediate benefits.⁷⁹ Such a system

will offer a simple – and increasingly rapid and inexpensive – means of unambiguously identifying not only whole fish, but fish eggs and larvae, fish fragments, fish fillets and processed fish. This capability will yield more rigorous and extensive data on recruitment, ecology and geographic ranges of fisheries resources, and improved knowledge of nursery areas and spawning grounds, with evident impacts at the fisheries management and conservation levels. For example, the possibility of rigorous identification of fish species from eggs and larvae could be particularly fruitful, since phenotypic identification of early life stages can be especially difficult.⁸⁰ A study testing the application of molecular techniques in species identification of fish eggs revealed that over 60% of the eggs were misidentified when phenotypic characters were used.⁸¹ Eggs from haddock and whiting may have been reported as cod's eggs in previous surveys, possibly leading to an inflation of stock assessments of cod in the Irish Sea. Moreover, early stage haddock eggs were detected in the Irish Sea, indicating the presence of a spawning stock of this species previously unknown to that region.⁸² In a context of environmental change, induced, for instance, by global warming, the ability to rigorously identify fish species at all life history stages from egg to adult is particularly useful to assess changes in geographic distribution ranges, spawning grounds and nursery areas.

Another valuable application envisaged for DNA barcoding is the identification of prey-remains from predators' stomach contents. This could provide more detailed information about aquatic trophic chains, revealing which fish species are preyed upon by other fish species⁸³ or seabirds.⁸⁴ This type of information could then be incorporated into ecological models and provide new data for use in management and conservation.

Potential forensic applications of fish DNA barcoding include the monitoring of fisheries quotas and by-catch, inspection of fisheries markets and products, the control of trade in endangered species, and improvements in the traceability of fish products. In Australian waters, for example, sharks are illegally captured, largely for their fins alone. Quality sharks' fins can sell for \$6,000-\$8,000/kg in Hong Kong, and it is estimated that globally more than 100 million sharks are killed every year. Sharks are a particularly susceptible animal, since they are slow growing, long lived, undergo a long gestation and have low fecundity. Many species are morphologically very similar, and many are protected.⁸⁵ A tool enabling precise identification of shark species from fins, from the fisheries boat to the soup in the restaurant, could be of great utility for law enforcement and conservation of endangered species.⁸⁶ Such a tool could also be used for detection of fraudulent species substitutions in fish markets and fish food products, a practice that is generating concern among consumers.⁸⁷ A striking example comes from the Red Snapper (*Lutjanus campechanus*), which is one of the most economically important fisheries in the Gulf of Mexico, and which has been subject to stringent fishing restrictions due to stock depletion. Marko and colleagues⁸⁸ used sequences of the mtDNA gene cytochrome b, in an approach very similar to DNA barcoding, to show that as much as 77% of the *L. campechanus* fillets were mislabelled in USA markets. This level of mislabelling may adversely affect estimates of stock size and contribute to the false impression among consumers that the supply of fish is keeping up with demand.

In this section we have illustrated several potential and actual applications of fish DNA barcoding, which can have direct impacts on various activities from fisheries management to traceability of products in the food supply chain. These are in addition to the scientific applications mentioned in previous sections, such as detection and tracking of undescribed species, clarification of taxonomic uncertainties (eg, cryptic species) and identification of historical, archived and museum material.⁸⁹

Conclusions

Humankind's outstanding technological and scientific achievements during the late 20th century include space exploration, the unravelling of the human genome, and the cloning of mammals. In the face of such accomplishments, the paucity of our knowledge of the world's biodiversity is both puzzling and disappointing.

Tackling the inventory of the planet's biodiversity is in itself a colossal task. The Barcode of Life Initiative promises to accomplish that task in the timescale of a single generation. Only time will tell if it succeeds. Like the Human Genome Project, DNA barcoding is not free of controversy. While in the aftermath of the Human Genome Project it became evident that information *per se* does not generate knowledge, there is today broad recognition of the value and relevance of that project, to the extent that various genome projects of other organisms have followed.

Among other virtues, DNA barcoding has already focused attention on problems of biodiversity. There is little doubt of the worth of the numerous applications of the technology, as for example described in the context of fish and fisheries. The success of various wider and more ambitious historical, philosophical, and sociological goals of barcoding will depend initially on the approach of the scientific community, but also on current and future recognition, investment and support from society.

Perhaps the decisive test for DNA barcoding will be the ability to effectively convert the immense information to be collected into tangible scientific knowledge - the completion of the encyclopaedia of life. Accomplishing this task will improve citizen bio-literacy of the world's biodiversity, and possibly engender a new vision and attitude towards non-human life-forms and their conservation and sustainable utilisation. The role of the classical amateur naturalist so typical of the Victorian era, would become extended to those with limited taxonomic knowledge, although taxonomic expertise would still underpin all barcoding applications. Should DNA barcoding succeed in its mission, the concurrent progress in taxonomy may rank among the most important scientific legacies of the early 21st century.

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Commissioned response to Filipe O. Costa & Gary R. Carvalho, 'The Barcode of Life Initiative: Synopsis and Prospective Societal Impacts of DNA Barcoding of Fish'

Real but modest gains from genetic barcoding

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Costa and Carvalho² make a compelling case for the practical utility of barcoding fish. Essentially the barcode, the precise sequence of a carefully chosen few hundred base pairs of a mitochondrial gene found in all eukaryotes, is intended as a definitive taxonomic criterion that can be added to the existing description of a species, but that has the enormous advantage of being applicable to any part of the organism. No existing part of most taxonomic descriptions can be applied to a fish finger, remains of animals in a fish's stomach or, probably, a detached shark's fin. Since, as they explain, there are important practical contexts in which it is desirable to relate such objects to their species of origin, detecting fraudulent fishmongers or violations of fishery preservation law, for example, the potential benefits are clear. They might also, in imaginable future circumstances, come to be of considerable benefit in providing definitive classifications for field biologists without easy access to relevant kinds of taxonomic expertise.

It is much more difficult to understand how the introduction of this technique will revolutionize the practice of taxonomy or enable the 'completion of the biodiversity catalogue within the reach of a single generation'. I'll leave aside for a moment the fact that this project is explicitly limited to eukaryotes (and in practice has only so far been applied with much success to animals), and therefore that this hypothetical catalogue will be missing out the very large majority of organisms and probably the majority of *kinds* of organisms. My first point is merely that the limiting factor in cataloguing life will surely continue to be the number of properly trained taxonomists.

Perhaps the most important theoretical point is that the introduction of genetic barcodes does nothing to solve the traditional problem of determining what a species is. A few decades ago, partly due to the effective advocacy of Ernst Mayr, it was widely believed (if by no means universally by professional systematists) that species could be defined as reproductively isolated groups—the so-called Biological Species Concept. Unfortunately it became increasingly clear that reproductive isolation was neither a necessary nor a sufficient condition for maintenance of the morphologically stable kinds generally agreed to be species. That reproductive isolation was not necessary was classically illustrated by the case of oaks,³ in which distinct species appeared to have existed for long periods of time despite continuous and substantial interbreeding, but it now appears that many other groups of organisms might have been chosen to make the point. Lack of sufficiency was demonstrated by the existence of species dispersed among isolated populations, physically unable to interact and mate, yet showing no significant divergence.⁴

The biological species concept assumed a picture of evolution as consisting of a branching tree in which the initiation of a branch could be defined by reference to the establishment of reproductive isolation between the organisms represented by the new and the originating branches. If a group of organisms conforms to this model, and a reasonable period of time has passed since the occurrence of the speciation event marked by the branch in the tree, an appropriate mitochondrial gene sequence is likely to provide a good criterion for species membership.⁵ However, a likely explanation for the problems with the biological species concept is that local diversity within a genus or even higher taxon is maintained by ecological differentiation rather than reproductive isolation. A compelling reason for believing this is the fact that interspecific hybridization is proving to be far more common than had for a long time been thought, even in groups such as birds, which have been widely taken to be a paradigm for application of the biological species concept.⁶ Hybridization involves, by definition, exchange of genetic material, and hence makes the use of a genetic test for species membership unreliable. Using reproductive isolation as a definition of species will effectively deny the existence of a great deal of diversity that has traditionally been captured by descriptions of species.

Putting the matter another way, the Mayrian vision sees the cutting edge of evolution as isolated populations—incipient species—forging off into the future to find their unique destiny. A different view, made increasingly likely by the growing evidence of hybridization, proposes that many evolving groups will consist of a set of more or less hybridizing, though ecologically separated, kinds—but kinds sufficiently stable and robust to meet most traditional understandings of the species. Which of these pictures is correct is, at any rate, surely an empirical matter, and judging where and to what extent the latter situation obtains will again require the continuing engagement of taxonomists. And of course if it is not to be wholly question-begging, the relevant judgments will need to be based on a variety of criteria—morphological, behavioural, reproductive, etc. So the usefulness of genomic (barcode) taxonomy will be subject to the judgments of taxonomists, and the limiting factor on ‘cataloguing life’ will remain the availability of this expertise.

Costa and Carvalho also make the much more speculative suggestion that barcoding might greatly increase the interest in taxonomy among the general public, and thereby provide impetus for conservation measures. The basis for this suggestion is the vision of a hand-held barcoder—something that anyone could buy for \$10, according to one of the websites Costa and Carvalho reference for this proposal—connected by wireless link to a central databank. Though it is certainly easy to underestimate the rate of technical change in an area such as this, I am a little sceptical about this prediction. Still, let us assume for the sake of argument that such a thing is indeed forthcoming in a few years time. I remain sceptical as to whether such a product would find a mass market. As a (very) amateur taxonomist of wild plants, it is my experience that most people find the identification of flora and fauna decidedly uninteresting. And I suspect that those who do not, find the acquisition of the (currently) necessary skills a large part of the attraction of the practice. But more interestingly, and paralleling my point about professional taxonomy, it strikes me that the sort of knowledge people already interested in such matters have had to acquire would be necessary to make the use of the barcode reader rewarding. The great

majority of plants, say, are, by definition, common. It is the expertise that enables one to pick out the uncommon or difficult-to-classify specimens that would make access to such a machine attractive. Constantly identifying brambles and stinging nettles would soon become tiresome.

I certainly don't wish to deny that the barcoding project has potential value to many kinds of users from professional taxonomists to enforcers of fishery protection legislation and amateur botanists and no doubt many others. It may even be a good investment of the very substantial resources it has attracted. But as with so many novel scientific projects nowadays, it has also attracted its fair share of hype. Suggestions that it will bring about the rapid cataloguing of all biodiversity, or that it will create a wave of popular excitement about taxonomy seem to me to belong in this category.

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DNA barcoding: potential users

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The current popularity of DNA barcoding relates to its potential power coupled with its intuitively pleasing simplicity. It is based on the premise of using a standard short region of DNA as a universal tool for identifying organisms.² The aim is to establish a large-scale reference sequence database against which unknown samples can be queried for identification. Where sequences are found that are divergent from others in the database, the corresponding specimens are flagged up as potential new species warranting further investigation. Costa and Carvalho³ describe some of the potential societal benefits of DNA barcoding in the context of fish identification and also summarise some of the potential benefits to the discipline of taxonomy itself.

Who will benefit most from DNA based identification?

Table I lists some examples of people who identify organisms and some of the approaches they may use. Much of the debate around DNA barcoding has focused on its implications for taxonomists and taxonomy. However, if DNA barcoding can be made accessible and cheap, arguably the greatest beneficiaries will be the many professionals whose work involves biological identifications, but whose job is not to carry out taxonomy *per se*. For this category of people, DNA identification can potentially offer a direct route to the knowledge generated by taxonomists, and avoid them having to spend their time learning how to identify organisms. The opportunities here are immense, given the range of professions that involve biological identifications, and particularly with the growing importance of biodiversity conservation. Of course, there will be limitations. Resource constraints will limit application in some circumstances. A pre-requisite for user confidence is validation of the approach in the taxonomic group of interest, and even a perfectly functioning DNA barcoding system will be dependent on the samples that are fed into it. For example, in field-based surveys targeting the appropriate habitats to sample can require considerable expertise, and the untrained field collector may miss some key species by not knowing where to sample in the first place. Nevertheless, once a sample is available, many professions would benefit from access to automated identification systems (Table I).

The likely use of DNA identification by the broader public is more difficult to quantify. Amateur naturalists are potential beneficiaries in that a cheap and easily accessible DNA identification service could represent a useful training/feedback tool as they are 'getting their eye in' on a given group of organisms. However, given that their enthusiasm is underpinned by an interest in morphological and ecological aspects of biodiversity, there are likely to be limitations as to the extent of uptake and their perceived relevance of DNA barcoding technologies.

Table I. Some examples of users of taxonomic information and their potential interest in DNA-based identification.

	User	Identification need	Typical source of information for identification	Identification skills	Interest in taxonomy	Potential direct beneficiary of DNA identification?
	Taxonomist	Assessments of diversity and distributions	Specialised literature, museum collections, field guides, databases, colleagues	High	High	Yes (for routine identification & sub-optimal specimens)
Non-taxonomic professionals	Ecologist/life scientist	Assessments of diversity and distributions, verification of research sample identity	Specialised literature, museum collections, field guides, databases, taxonomists, colleagues	Variable (low-high)	Variable (low-high)	Yes
	Conservationist	Assessments of diversity and distributions, identification of specimens to conserve	Field guides, images, databases, taxonomists, colleagues	Variable (low-high)	Variable (low-high)	Yes
	Legal (police, customs)	Identifications based on fragmentary material, forensic samples, wildlife crime/illicit trade	Field guides, images, targeted key, databases, taxonomists	Variable (low-high)	Variable (low-mid)	Yes
	Human/animal health	Identification of species with harmful attributes or medicinal properties	Field guides, images, targeted key, databases, taxonomists	Variable (low-high)	Variable (low-mid)	Yes
	Environmental protection	Identification of indicator species, identification of invasive/pest species	Field guides, images, targeted key, databases, taxonomists	Variable (low-high)	Variable (low-mid)	Yes
	Biodiversity utilisation (e.g. agriculture, fish management, forestry, horticulture)	Identification of species with useful attributes, identification of species that impede utilisation (pests/invasives etc)	Field guides, images, targeted key, databases, specialist colleagues, taxonomists	Variable (low-high)	Variable (low-mid)	Yes
Public	Amateur naturalist	Assessments of distributions and diversity	Specialised literature, museum collections, field guides, databases, taxonomists	High	High	Yes (as a training/feedback tool)
	Passively interested public	Occasional curiosity driven interest	Field guides, images	Low	Low	Possibly (may encourage interest in biodiversity)
	Uninterested public	-	Nothing	Low	Low	No

For the more general public, by improving accessibility to information, there is the potential to generate interest and to instil a greater degree of environmental responsibility.⁴ Costa and Carvalho follow up this point and discuss the potential impacts of easy access to DNA barcoding for the ‘ordinary citizen’ and note that:

It may trigger a curiosity for living organisms, and improve awareness of biodiversity threats, and the perception of how human actions can have a detrimental impact on rates of species extinctions and ecosystem change. Eventually, a more bio-literate society could produce ‘greener’ individuals, who are more environmentally-responsible in their daily actions, and willing to undertake proactive measures to minimize their own impact on the planet’s biodiversity.

However, it remains to be seen whether a simple technological solution to identifying organisms will have a major impact on public awareness of biodiversity. Access to a hand-held DNA ‘barcoder’ might lead to an increased interest in biodiversity, but this may be transient as technological developments in other walks of life compete for attention. In considering how society responds to resources available for identification, it is worth reflecting on situations where a high density of information already exists. In well characterised regions of the world which have comparatively low numbers of species such as the British Isles, there are many easy-to-use illustrated field guides which enable the identification of organisms from a range of taxonomic groups. However, this has not led to comprehensive bioliteracy.⁵ In cases such as this, access to taxonomic information *per se* is not the limiting factor. Rather it is more likely to be attributable to the level of interest/enthusiasm/need being insufficient to acquire the knowledge, even with the necessary tools at hand. A hand-held DNA ‘barcoder’ may make identifications and access to associated information easier, but it still requires an inclination for use in the first place. The main drivers for environmental awareness for the general public seem likely to remain day-to-day contact with biodiversity⁶ and exposure to captivating environmental reportage in the mainstream media.

The future use of DNA barcoding

DNA barcoding represents the key foundation step in the process of coordinating the use of DNA for taxonomy at the species level.⁷ It has already accelerated the routine establishment of ‘DNA ready’ collections for herbaria and museums. It has triggered a formalisation of links between sequence data and voucher specimens in Genbank, and the development of informatics systems linking specimens, sequences, names and associated information. It has without doubt stimulated biologists using DNA data at the species level to pay much greater attention to coordinating activities and to think beyond producing local solutions for individual studies.

The vision put forward by Herbert et al,⁸ Janzen⁹ and colleagues for DNA barcoding has in turn prompted considerable debate. Several biologists have questioned both the scientific validity of the approach, and its broader implications for the future of taxonomy.¹⁰ However, given the general benefits that have emerged from the

coordinated use of genetics in other disciplines and the societal need for biological identifications, it seems difficult to imagine that an appropriately implemented coordinated use of genetics in species level taxonomy can be anything other than beneficial. The exact form of this approach can be expected to evolve as technologies develop, and the future will undoubtedly involve approaches that go beyond single gene sequencing. But as long as there is a demand for the conservation and utilisation of species (eg, Table I), there will be a need for their identification. A system which enables this to be automated has to be worth developing.

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The Book of Life goes online

PETTER HOLM¹

A walk in the park

It's a beautiful day for the great outdoors. You have decided to take a break from city life. Sunny fall weather; it's drying up from the rain last week. Perfect for picking mushrooms. You bring a basket, small brush, sharp knife. And the biopod, the latest generation life barcoder, 'Tricorder' edition.² After a short walk to your own secret mushroom place, you spot a patch of nice-looking specimens. Caps are 5–10 cm across, with slightly depressed centres. Slightly sticky. Colour brownish to dark brick-red. Gills close together. It could be the delicious 'Flirt' (*Russula vesca*). Or is it the poisonous 'Sickener' (*Russula emetica*)? You quickly scan it with the barcoder. There is a barely-audible hum as the device goes online. A few seconds later, the display shows *Russula vesca*. Great! Scrolling down the tiny screen, you're informed that its mild flavour goes well with lamb stew. Serve with a light red Italian. You fill the basket, and head to the supermarket for the rest of the ingredients you need to prepare a fine meal.

Linnaeus in the sky

This sort of scene becomes possible to envisage from Costa and Carvalho's synopsis on the Barcode of life initiative.³ At first glance, it has a Star Trek feel to it: a landing party is beamed from the safety of the starship onto some planet 'where no one has gone before', equipped with tricorders serving as lifelines and generalised information gadgets. Whereas a real-life version of this scenario might have been dismissed as pure fiction a few years ago, the rapid rise of GSP and mobile 'phones have made it more realistic. The Barcode of Life Initiative extends just slightly what is now a familiar scene. Instead of dispensing with a map, compass and navigation skills, as the GPS did, the life barcoder promises easy access to the identity of the wildlife along your track. When one is equipped with such a hand-held device, it is as if the mushroom comes fixed with a label. Instead of the cumbersome task of teaching yourself how to be a taxonomist, or bringing one along from the local museum, you simply consult the virtual Linnaeus in the sky.

From Costa and Carvalho's fine review, we already know how the Barcode of Life pulls off this feat. The barcoder analyses DNA from a tissue sample taken from the target specimen and links it to a barcode. With this barcode, the identity of your specimen is fixed as a specific location in a DNA-based species classification system, which also provides easy access to other relevant information, be it, in the mushroom case, the appropriate antidote or the wine that best brings out its flavour.

Barcoding and the Encyclopedia of Life

A virtual Linnaeus would be a wonderful thing. Such a system, fully operational, comes with a number of advantages. It can identify species from tissue fragments and regardless of life-history stage. Ambiguity is reduced and identification of look-alikes becomes straightforward. The identification of known species can now be safely left to amateurs, allowing the experts to focus on unknown species.

While Costa and Carvalho are excellent guides to the advantages of a fully functional barcode-of-life system, they are less explicit when it comes to the investment required before the system can go online. How much and what kind of work does it take to make a virtual Linnaeus? The key here is the classification system by which the DNA sequence from a specific genome region is linked to some (hierarchically ordered) list of named species. For a lay person to use a barcoder to identify species, the databases by which these links can be made must already be in place. There must be an 'Encyclopedia of Life', with information linked to barcodes. If a specimen's barcode is not registered, the amateur will remain uninformed.

This problem is comparable with one commonly encountered in supermarket checkout queues, when an item - usually from the fruit and vegetable section - lacks a barcode. When the cashier is confronted with a species exotic to him - is this a cantaloupe or a galia? - he must become an old-fashioned taxonomist, consulting, first, the super-market version of a field-guide. If this is unsuccessful, he must call up a real expert from the back of the shop somewhere to identify it. Only then can you pay for your merchandise and take it away with you.

A sizable supermarket contains around 50,000 items. Here, classification is reasonably easy: not only are there relatively few species, but all have been classified and priced prior to sale. The problem is not one of knowing the identity of your species, but making that information available at the checkout. Nature, by comparison, is a far grander kind of supermarket, storing many millions of items. Here, the inventory is not pre-established, but must be built from scratch. While the barcoder allows the lay person easy access to the labelled checked entries, there remains a problem with the un-labelled species. Since the barcode is encoded in the specimen itself, you will of course always get a reading. But if the species in question has not already been named and entered into the Encyclopedia of Life, your query will remain unanswered.

Setting up an Open Writing Workshop

A complete Encyclopedia of Life is not the only advantage of the Barcode of Life Initiative. Another major attraction is the ease by which entries can be added. To use Costa and Carvalho's vocabulary, barcoding will speed up species *delineation* as well as species *identification*.

Assume the Initiative produces the first draft of a DNA barcode 'Encyclopedia of Life' by adding the relevant DNA key to the list of all conventionally named and classified species. In the process, improvements such as the definition of the true identity of similar species will already have been made. Nevertheless, the basic problem is much the same as before, namely that most species remain unclassified. How could the DNA barcoding technology help fill in the blanks?

The first point emphasised by Costa and Carvalho concerns the economy of expertise. Since barcoding makes identification of labelled species easy, the professional taxonomists can concentrate their work on the uncharted territories. However, the taxonomist community should perhaps not rely on this, since the number of taxonomists in society is not a constant. Can we assume that resources freed up by an efficient species identification technology will be allocated to the task of species delineation? Given the tight budgets of the organizations employing taxonomists, and the constant struggle among worthy causes, the answer to this is unclear.

Another, perhaps more interesting point, concerns how a barcode classification system allows for the process of species delineation to be organised differently. Imagine that a cluster of unknown barcode readings has been reported by reliable sources, which leads to the formulation of a hypothesis of a new species. While the rejection or confirmation of such hypotheses will still require expert opinion, the barcoding technology invites broad participation in the collection of the information required to test it. Working from the fixed point of DNA-based identification, a protocol on data collection can be set up and distributed. In this way, authorship of the Encyclopedia of Life changes. Instead of the expert taxonomist working alone in the dusty dungeons of the museum, the Encyclopedia becomes a collaborative effort involving many different people.

A related point here concerns the status of the conventional taxonomist as expert. Initially, as underlined by Costa and Carvalho, the barcode classification of a given species is a hypothesis to be checked against the conventional classification. The conventional taxonomist's expertise with the tools of the trade mean that he remains first author and gate keeper for DNA-based classification. If and when the technology proves itself, however, this is turned on its head. The conventional classification changes status, and becomes the hypothesis that must be checked against the barcode classification. The real experts, set to judge between true and false Linnean classification, are those who master DNA-based technologies. While this may look problematic from the point of view of today's taxonomy profession, such is the normal destructiveness of progress. Indeed, the re-organisation of the taxonomy profession is an important feature of barcode technology. With the DNA barcode as classification key, folk taxonomy becomes, just as the Linnean classification did before, a new and interesting source of hypotheses for species identity.

A few dark possibilities

Will the world become a happier and more just place with the success of the Barcode of Life initiative? As always, new technologies produce both winners and losers when

they are let loose on the real world. A major question here is how barcoding might affect the balance of power in an already unfair world. Who stands to gain: the resource-rich of the North or the impoverished of the South?

Wouldn't it have been nice if the DNA barcoding, on top of everything else, also helped the poor and powerless? But this is not the case. The Encyclopedia of Life – in both its conventional and DNA-barcode versions – is more complete for the North than the South. The broad, democratic access to species identification by way of barcoding technology will therefore be of most relevance in the North. In the South, where most unlabelled species are to be found and the lack of resources to fill the blanks are most obvious, its usefulness is less clear. It could be argued, of course, that the efficiency of DNA-based delineation will give developing countries a chance to make inventories of their natural riches. Another, darker possibility is that such inventories will be of most interest to capitalist firms on bioprospecting excursions. While DNA barcoding may allow indigenous people to be co-authors of the Encyclopedia of Life, it may be the modern pharmaceutical giants that stand to reap the financial rewards.

Do you want to live in a supermarket?

The rich stand to gain while the poor lose out. In the face of this, the have-nots should organise and fight as best they can. Not to ban the technology, of course, but to reformat it in a way that can serve their interests. While we wait for this upcoming struggle, we can take time to consider whether a barcoded world is desirable. A romantic might put it thus: 'Do you really want to live in a supermarket - a world where every species comes pre-labelled for reading with a handheld device?' To the romantic, the answer is 'no', of course. To him, barcoding is but an extension of the iron cage of rationality, a place where the disenchantment of the world has reached an extreme, and all wilderness has been emptied of mystery and turned into yet another supermarket.

While I acknowledge this fear, however, I do not share it. The wilderness of the world simply cannot be contained in a classification scheme. Just like a map, classification does not really reduce the complexity of the world, but allows you to travel more effectively within it. The barcoder offers a fine meal of 'Flirt' mushrooms instead of violent vomiting induced by the 'Sickener'. Just like Star Trek's tricorder, the barcoder will not prevent the adventure, but serve as a valuable companion for your travel to places where 'no one has gone before.'

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² A tricorder is a handheld device used for scanning an area, interpreting and displaying data from scans to the user, and recording information. A tricorder is a prop in the Star Trek Universe. See www.startrek.com

³ F.O. Costa and G.R. Carvalho. The Barcode of Life Initiative: synopsis and prospective societal impacts of DNA barcoding of fish. *Genomics, Society and Policy* 2007; 3 (2): 29-40.

The Barcode of Life Initiative: Reply to Dupré, Hollingsworth and Holm

FILIPE O. COSTA AND GARY R. CARVALHO¹

We are grateful to John Dupré, Peter Hollingsworth and Petter Holm for their insightful and constructive responses to our article.² As with any new and increasingly applied approach, DNA barcoding has provoked considerable discussion, even though the basic technology employed is essentially a refinement of existing molecular approaches to systematics.³ What characterises DNA barcoding is the attempt to standardise the molecular approach by focusing on one or a few genes with appropriate levels of among-species divergence, and to secure global accessibility to a common database. Additionally, although one gene, cytochrome oxidase I (COI), has proven to be informative across diverse taxa, the aim of DNA barcoding has not been to identify a single common gene, but rather to maximise standardisation across related taxa to ensure high comparability. DNA barcoding is essentially a practical tool that can be applied to compare a target DNA sequence with a reference DNA sequence that may confirm species identity or generate alternative hypotheses of species delineation. It is crucial therefore to appreciate that rather than replacing conventional approaches to taxonomy, which rely heavily on ecological, morphological and behavioural characteristics, DNA barcoding can in many cases render the Linnaean system more accessible. A recent cover of *Nature*⁴ illustrating a modern-age Linnaeus wearing a contemporary naturalist's outfit and holding a barcode in his hand could not be more paradigmatic.

Rather than rehearse many previous discussions and articles on the merits and limitations of DNA barcoding, here we focus on just a few of the key points raised by Dupré, Hollingsworth and Holm. One of the initial points raised by John Dupré is the relative bias of existing DNA barcoding databases towards eukaryotes, especially animals. While the balance of current information is indeed skewed toward animals, the utilisation of alternative standardised gene sequences is being increasingly used in other groups, including land plants,⁵ fungi^{6,7} and other protists.⁸ The driving characteristic of such inventories of biodiversity is to ensure high comparability and quality of reference databases. While it is clear, as with any technology, that certain taxa may remain recalcitrant to standard barcoding approaches, occasional combination of additional sequences, might be anticipated to disclose species identity for many organisms.

A major point made by Dupré is the link between DNA barcoding and the biological species concept. Although DNA barcoding may provide novel insights into the species concept,⁹ it is certainly not the primary aim. While there may be direct concordance between presumed species status and reproductive isolation,¹⁰ barcoding is potentially a practical tool that may facilitate the classification of ecological or morphological diversity within a taxonomic framework. It is not disputed that closely related species experiencing intermittent or frequent hybridisation will not be detected using conventional DNA barcoding approaches. However, where there appears to be

an uncoupling between observed ecological, behavioural or morphological heterogeneity and reproductive or molecular divergence, DNA barcoding can serve to facilitate the testing of alternative hypotheses or the application of alternative species concepts. Thus, rather than being constrained by or restricted to only those taxa conforming to Mayr's vision of biological species, DNA barcoding can extend taxonomic approaches to test evidence obtained at other biological levels.¹¹

A further point raised by Dupré is the necessary limitation of any molecular taxonomy by the availability of high level taxonomic expertise. Coincident with the inclusive biological nature of DNA barcoding, is the recognition that highly trained taxonomists remain a crucial component of the species identification procedure. However, James Hanken,¹² in an historical overview of the rates of species discovery, suggests that, indeed, taxonomy should rely on technological innovation rather than expecting an improbable substantial enlargement of the community of taxonomic experts. Thus, a more realistic solution would be the implementation of innovative technologies into an integrative taxonomy framework, including digital imaging, high resolution X-rays, information technologies, DNA barcoding and other genomic approaches.

It is expected, however, that barcoding may extend the taxonomic process to those individuals lacking such skills, depending of course on the availability of a matching DNA sequence in the reference database. This point is linked to the more general issue of how DNA barcoding may facilitate interest in taxonomy among the general public, thereby serving to promote a case of conservation measures. It is accepted that many people, including the interested amateur naturalist, are motivated by an innate interest in the nature and patterns of biological diversity that will not necessarily be enhanced by molecular taxonomy. However, non-specialists within conservation bodies, museums and various government laboratories where molecular expertise might not exist can still submit samples to commercial companies for DNA sequencing, enhancing access. Such accessibility will enhance public awareness through the disclosure of new species, as well as increasing the profile of threatened species or risks posed by invasive species. The availability of the so-called 'Tricorder', although a seductive and distinctive vision for the future of DNA barcoding, is only one aspect. The recent discoveries of new species in what are considered well-documented taxa, such as birds,^{13,14} lepidopterans,¹⁵ and fish,¹⁶ enhance the awareness of biodiversity among the general public that may relate more readily to the discovery of new species in easily recognisable and familiar taxa. Such disclosures can then serve as a framework for emphasising the much higher levels of hidden biodiversity and cryptic speciation in less familiar organisms, especially among microbes.

Peter Hollingsworth points out that one of the main drivers for environmental awareness for the general public is likely to remain the day-to-day contacts with biodiversity. While this is undoubtedly true, it is not necessarily exclusively so. As indicated above, increased awareness of environmental issues, which has been driven by such things as climate change and habitat destruction, has focused increasingly on the role of species in ecosystems. Thus, a more precise cataloguing of the levels and distribution of species diversity across the globe can only help to generate a case for public engagement in environmental and conservation policies.

While Petter Holm promotes many of the virtues of DNA barcoding, he questions the level of investment necessary to generate 'a virtual Linnaeus'. Considerable global effort is already underway with various DNA barcoding campaigns and other biodiversity surveys (eg, Census of Marine Life¹⁷). However, there were two recent and important developments that will have a major impact in accelerating the availability of the 'virtual Linnaeus'. One of them is the International Barcode of Life (iBOL),¹⁸ an international consortium that aims to generate DNA barcodes for 500,000 species over a period of five years, starting in 2009. While such efforts will of course take time and considerable manpower and funding, they will be rewarded by gains in efficiency - in terms of both time and expenditure - by the scale of activity, the high throughput analysis and automation. It is difficult to envisage how such efficiencies could be generated by the hitherto taxonomic and geographically fragmented efforts to log biodiversity, especially where quality assurance and access to curated voucher specimens is more variable. Another recent salient development, The Encyclopedia of Life (EoL),¹⁹ brings together the currently scattered global biodiversity initiatives, thereby 'materializing' the virtual Linnaeus. The EoL is conceived as an 'ecosystem of websites that makes all key information about life on Earth accessible to anyone, anywhere in the world'. Ten years is the estimated time for the completion of the species pages for the 1.8 million known species, the first pages are expected to be available sometime in 2008. Inspired by Wikipedia, EoL intends also to consider the contribution of individual citizens, though all published information will be subject to authentication by scientists. DNA barcoding will dovetail well with this project, playing a key role, for instance, in providing unequivocal links between different source databases, such as between museum specimens and genomic databases (eg, GenBank). It is precisely the combined influence of such expansive biodiversity projects that we expect to have a significant impact in the bioliteracy and appeal for biodiversity of future generations.

Holm also raises the ethically important and timely issue of balancing such access and value to DNA barcoding efforts with geographic variability in biodiversity and infrastructure. The Consortium for the Barcode of Life aims to catalogue global biodiversity through the existence of various regional working groups associated with particular taxa. Obtaining and describing such diversity where it is at its greatest in the tropics, for example, but where infrastructure and expertise may be more variable, is a particular challenge. While such issues will serve to constrain overall activity, it is only through the generation of a global effort that sufficient resources and manpower might be mobilised to address such imbalance. The existence of what Holm refers to as 'dark possibilities', whereby DNA barcoding inventories may be exploited by capitalist firms or bio-prospecting excursions, is a possibility where information is available to all. Such activities are of course not new, and although the ethos of DNA barcoding would be counter to such exploitation, scenarios can be envisaged where useful products or species may be disclosed for use not just by the developed world. A case in point is the current DNA barcoding efforts in mosquitoes,²⁰ which of course are associated with considerable distribution of disease and mortality.

Concluding remarks

It is a useful exercise to critically evaluate the application and implications of new approaches to tackling well established problems such as taxonomy and species identity. DNA barcoding has often been regarded as an alternative or exclusive approach to generate a “new taxonomy”. As seen from many published studies on DNA barcoding, it is an approach that is by its nature dependent upon comprehensive reference to other biological levels of organisation. Genes evolve in individuals that often aggregate into populations that live in specific habitats, and it is crucial therefore to examine the extent to which biological heterogeneity may coincide with recognisable species groupings. Where a convenient genetic tag (stable, heritable and discrete) can be developed to recognise such entities, such as a DNA barcode, then this can be a useful practical tool that may, or may not, be used in conjunction with other independent corroboratory information. The integration of molecular approaches with conventional Linnaean taxonomy has in many cases stimulated new levels of investment in taxonomy.²¹ While the prognosis for DNA barcoding appears sound, there will continue to be a need for conventional taxonomic expertise, though one might hope for increased integration and communication across the molecular and non-molecular divide. The key is not to claim exclusivity for DNA barcoding, but rather to promote awareness of the complexity and in some cases the fragility of diversity in the natural biological world.

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² F.O. Costa and G.R. Carvalho. The Barcode of Life Initiative: synopsis and prospective societal impacts of DNA barcoding of fish. *Genomics, Society and Policy* 2007; 3 (2): 29-40; and commissioned responses in same issue.

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⁷ All Fungi DNA Barcoding Planning Workshop <http://barcoding.si.edu/fungi.html>.

⁸ Report of the Workshop on 'Protistan Barcoding, Reference Material and Cultures', November 6-7, 2006, Portland, ME USA. Protist here are defined as 'mostly microscopic eukaryotic organisms commonly referred to as algae, aquatic fungi, and protozoa'. Available at <http://www.barcoding.si.edu/PDF/Protist%20Workshop%20Report%20-%20FINAL.pdf>

⁹ S.E. Miller. DNA barcoding and the renaissance of taxonomy. *Proceedings of the National Academy of Sciences* 2007; 104 (12): 4775-4776.

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- ¹⁷ Census of Marine Life (CoML): <http://www.comlsecretariat.org/>
- ¹⁸ The International Barcode of Life (iBOL) <http://www.dnabarcoding.org/>
- ¹⁹ The Encyclopedia of Life (EoL) www.eol.org
- ²⁰ N. Kumar Pradeep et al. DNA Barcodes can distinguish species of Indian mosquitoes (Diptera: Culicidae). Journal of Medical Entomology 2007; 44 (1): 1-7.
- ²¹ Miller, op. cit. note 9.

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John Dupré is a philosopher of biology who has held posts at Oxford, Stanford, and Birkbeck College, London. In 2006 he held the Spinoza Visiting Professorship at the University of Amsterdam. He is currently Professor of Philosophy at the University of Exeter and Director of the ESRC Centre for Genomics in Society (Egenis). His publications include *The Disorder of Things* (Harvard, 1993), *Human Nature and the Limits of Science* (Oxford, 2001), *Humans and Other Animals* (Oxford, 2002) and *Darwin's Legacy: What Evolution Means Today* (Oxford, 2003).

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