

OPINION¹

Anti-intellectualism in the DNA Barcoding Enterprise

“There are two clear-cut ways in which taxonomy should be strengthened. The first is to give more academic appointments to taxonomists who have mastered the substance, and not just the biometric methodology, of systematics, biologists who are experts on reasonably large groups of organisms on a continental or global basis. They must be allowed to take their place among the theoretical and experimental ecologists now so much in favor in biology departments”
(WILSON 1971:741).

Forty years of sentiment for an ailing scientific field is slowly turning into resentment. The short article written by WILSON (1971), from which the epigraph above is taken, highlighting the plight of taxonomy, is in strong contrast to recent calls for taxonomic innovation:

“...morphology alone is known to be inadequate to the task of species level identification in many instances” (PACKER *et al.* 2009: 42).

“We shall then ask how modern means of sharing data, especially the Internet, might be used to make taxonomy more efficient and to improve its links with its end-users.” (GODFRAY *et al.* 2008: 943).

“Taxonomists should embrace new tools that are potentially useful (such as DNA barcodes for species discovery and identification and DNA taxonomy to help test species boundaries) and catch the attention and interest of other scientists.” (AGNARSSON & KUNTNER 2007: 534).

“...taxonomists will display a regrettable lack of foresight for the future of taxonomy if we do not integrate all of the methods that are now available to delimit species boundaries into a synthetic approach.” (DAYRAT 2005: 412).

“The new excitement about taxonomy is driven partly by advances in technology, and partly by newly perceived needs given the biodiversity crisis.” (MALLETT & WILLMOTT 2003 57).

“One can make a case with some justification as to whether the science of taxonomy is evolving fast enough in the face of the demands being placed upon it by the public and by government policy makers in connection with the so-called biodiversity crisis.” (SCHRAM 2007: 23).

Thought to be no more than a service industry for end-users, such as ecologists, bioinformaticists and conservationists, taxonomy has been dumbed-down to that of a technology of a bygone era. This has created the image of dusty elitists cocooned in crumbling museums or as Luddites dismissing so-called

‘progress’ wholesale. With this increasing popular image in mind, taxonomy, as a scholarly pursuit, is undermined by what we refer to as an unwitting anti-intellectual movement within biological systematics. The movement uses “scientific” arguments to justify its use when in fact it is defying best practice.

DEFINING ‘BEST PRACTICE’ IN BIOLOGICAL SYSTEMATICS

Presently, many debates in biological systematics are argued from the perspective of ‘scientific evidence’ or ‘scientific inquiry’ when in fact the problems are of a practical rather than scientific nature. The recent ‘paraphyly debate’ for example, centers itself around finding evolutionary models to justify paraphyletic taxa, namely ancestral groups (see BRUMMITT 2002, CAVALIER-SMITH 2010). The debate cannot be resolved because genealogical arguments are being used to justify what is essentially a problem of biological classification. Seen from the point of view of ‘best practice’, paraphyly is nothing more than an indication of poor taxonomy. ‘Best practice’ in biological systematics is about quality, not quantity. We define ‘best practice’ as the highest standard of systematic practice based on the foundations of systematics. The pursuit of monophyletic taxa in biological classifications is seen as best practice within biological systematics as they define natural groups – a standard that was laid out by early taxonomists such as DE CANDOLLE (1813). Paraphyletic taxa, for instance, cannot be justified using any scientific argument because they only indicate that a particular classification is in error and needs to be revised. This means that taxonomic revisions, not ad hoc justifications, are essential to best practice procedures. Defying best practice with ad hoc argumentation leads to anti-intellectualism.

ANTI-INTELLECTUALISM DEFINED

In his 1964 Pulitzer Prize winning text, *Anti-intellectualism in American Life*, HOFSTEADER (1963) clearly separates the terms *intelligent* and *intellect*. The term *intelligent* is something

¹ The articles in the section OPINION are of sole responsibility of the authors and do not necessarily reflect the views of the editorial board.

that is ascribed to someone or something. It means cleverness, or, in the case of computers for example, it simply means ability to perform functions. Dogs and photo-copying machines can be described as being intelligent. The term intellect, however, refers to the power of knowing. An intellectual is a human who is able to question and rationalize. Within science, intellectuals are usually referred to as scholars, namely those who, for example, question the methodologies, theories and syntheses used in biological systematics. Such questions require certain knowledge of their historical interpretation while at the same time avoiding Whiggish explanations. Moreover, scholars realize that the questions we ask are limited by what we know. Science has certain limitations. For instance, methods in biological systematics are non-experimental and rely on pattern-based approaches to make hypotheses of relationships.

Anti-intellectualism, however, is defined as “opposing or hostile to intellectuals or to an intellectual view or approach” (Merriam Webster’s Online Dictionary 2009, <http://www.merriam-webster.com>). If ‘intellectuals’ are ‘scholars’ and the ‘intellectual approach’ is ‘scholarship’, then we see an anti-intellectual sentiment within science, especially biological systematics, to which this study is devoted. Given the definition above, anti-intellectualism is defined herein as any pursuit hostile to or opposing best practice in biological systematics.

FORMS OF ANTI-INTELLECTUALISM IN BIOLOGICAL SYSTEMATICS

Below we briefly outline six forms of anti-intellectualism which we believe are manifest in biological systematics. Many of these forms can be seen elsewhere (e.g. in the intelligent design debate; PIGLIUCCI 2002), whereas others are seemingly endemic to science (i.e. anti-elitism; PACKER *et al.* 2009).

1. *Anti-Elitism* is often referred to as the “democratization of science” (PACKER *et al.* 2009). For instance, there is a prevailing attitude (e.g. HEBERT & BARRETT 2005) that anyone within systematics and taxonomy has the ‘democratic’ right to comment on theories or methods outside their own areas of expertise without the necessary or required knowledge. Recent issues of the botanical journal *Taxon* for example, contain several articles by evolutionary taxonomists and horticulturalists pontificating on paraphyletic groups and their necessity (BRICKELL *et al.* 2008). The authors, who are not trained in phylogenetics, expressed a certain amount of outrage over the dismissal of well-known taxonomic groups based on phylogenetic evidence. Rather than understand why the groups they wish to preserve are not monophyletic, a new version of phylogenetics is created in order to justify, rather than change, the original taxonomic designations (see STUESSY & KONIG 2008). What is actually a taxonomic problem has now been unnecessarily further complicated (see Pseudoscience below). The disdain and distrust shown toward “experts” has led to an ‘Ivory Tower syndrome’ within science. Anti-elitists believe experts dictate or “monopolize” arguments, rather than accept that ‘experts’, by definition, are the most informed. Non-experts who have adopted a new scientific field without understanding its theory and methodology have created a dumbing-down of biological systematics. The “don’t blind me with science” attitude is prevalent in the recent ‘unitary taxonomy’ debate (GODFRAY 2002). Population geneticists and ecologists, for instance, have placed themselves in the position of ‘spokesperson’ for a field they have little knowledge or practice in. Unitary taxonomy is a response by non-taxonomists frustrated by multiple and at times conflicting biological classifications (SCOBLE 2004). Rather than understand why these problems occur and finding proper solutions, they insist on a single taxonomy for “end-users”, in effect dumbing-down what is a highly complex science.
2. *Sensationalism* in science is best illustrated by the burgeoning biodiversity crisis. Any proposed project within biological systematics not addressing the biodiversity crisis in some way is grounds for rejection (MAYO *et al.* 2008). No project within taxonomy or systematics is able to solve the biodiversity crisis. If all organisms were to be discovered and classified, it will only provide us with a single number without any context. Cataloging all life because of a biodiversity crisis is sensationalist and defeats the purpose of taxonomy and systematics. Taxonomy, like any other scientific endeavor, is about discovering and understanding the world around us. Doing so results in knowledge rather than vast amounts of information with little meaning.
3. *Populism* creates a benchmark in science against which all fields are judged. This benchmark is based on quantity of publications, citation ratings and funding opportunities. Researchers that produce a higher number in each are more likely to be offered tenure and receive further funding. This creates both a ‘publish or perish’ culture and a ‘fad science’ phenomenon. A higher number of publications with higher citation index scores do not guarantee that the author produces exceptional research. In taxonomy, for example, most breakthroughs are made within revisionary works published as monographs, which may take months to write, include one or two authors, and are often not ranked within a citation index (e.g. BRUNDIN 1966, ROSEN 1979). A successful taxonomist may therefore have few publications and a low citation rating. Populism, however, dismisses such scholarly endeavors in favor of short, speculative articles on currently popular topics (e.g. transitional fossils, exobiology, etc.) that are authored by 10 or more researchers and written for scientific magazines, such as *Nature* or *Science* (see VALDECASAS *et al.* 2000). The bane of populism rebuffs scholarship and generates an impetus for smaller research projects, which make greater assumptions and employ a greater number of researchers.
4. *Pseudoscience* in biological systematics is a procedure or system that attempts to resolve a problem but does not correspond to an appropriate scientific method. For example,

using a technology to resolve trivial scientific issues or, using a non-scientific method to resolve a scientific problem, is also pseudoscientific. The Phylocode (CANTINO & DE QUEIROZ 2007), for example, uses nomenclature, a non-scientific pursuit, in order to resolve the taxonomy within a given phylogeny. Nomenclature is a valuable resource and an essential standard for maintaining biological classifications. It is not based on any scientific method, but rather on a series of logical, standardized rules and procedures; very much like those used in legal systems. Using a non-scientific method (i.e. nomenclature) to resolve a scientific issue (i.e. classification) does not merit a scholarly endeavor within biological systematics.

5. *Fundamentalism* is prevalent in biological systematics, most notably in 2009, 200 years after the birth of Charles Darwin and 150 years after the publication of the *Origin of Species*. The various shapes and forms fundamentalism may take depend on how large the community is and what belief happens to be most popular at the time. Fundamentalism creates a vehicle for fervent dogmatic theory and links a slogan to an existing concept. The belief that anti-Darwinism equals anti-evolution is an example of fundamentalism. In this case the community of evolutionary biologists consider Darwin (1859) an originator; therefore evolution takes on the form of Darwinism. If a fundamentalist community were to consist solely of panbiogeographers, then evolution may be linked to Danielle Rosa and hologenesis (ROSA 1918). Scholarship within the history of science, however, plays a small part in validating a fundamental belief. Whiggish histories, dismissed by scholars, are essential in fundamentalism. Moreover, a strawman or opponent is required in order to justify the held belief. After all, fundamentalism cannot exist in a universe where everyone agrees. Ernst Mayr's essentialism is an example of fundamentalism in biological systematics (see WINSOR 2006). An opponent, whether real or not, is created (i.e. so-called 'typologists') and targeted (see WILLIAMS & EBACH 2008). Any other ideas diverging from the held belief are immediately labeled as 'typology' (e.g. cladistics, systematic morphology, etc.).
6. *Unreflective Instrumentalism* assumes that a valid scientific endeavor is of immediate practical value (PIGLIUCCI 2002). This dismisses scholarship as costly and timely – after all there is a biodiversity crisis and science as a practical tool is seen as a way to fix what is a recurrent problem (see discussion below). Populism results from such unreflective instrumentalism in which cost-cutting technologies, like DNA barcoding, are considered to be practical and therefore valid scientific enterprises.

DEFINING THE DNA BARCODING ENTERPRISE

An excellent example of anti-intellectualism that consists of all six forms is the DNA Barcoding Enterprise – an academic cottage industry on which this study focuses. Before we

venture into exposing the barcoding enterprise, we wish to make the distinctions clear between DNA barcoding and the DNA Barcoding Enterprise.

DNA Barcoding is a simple technique that is based in molecular sequencing technology. A marker gene (i.e. CO1 gene) is extracted for all known organisms. The barcodes can be compared to calculate genetic divergence.

The DNA Barcoding Enterprise comprises groups of individuals and consortia who wish to extract and database barcodes utilizing funds and resources allocated to academic or research institutions. The goal is to produce a product and identification service for governmental and commercial ventures (e.g. the food industry, biosecurity, and biodiversity resource management).

On the surface, barcoding and the barcoding industry seem harmless – even of limited value to systematic biology. The way in which each are portrayed within biological systematics, however, is cause for concern:

"We argue that barcodes are potentially extremely useful tools for taxonomy for several reasons. Barcodes may, for example, help to identify cryptic and polymorphic species and give means to associate life history stages of unknown identity. Barcode systems would thus be particularly helpful in cases when morphology is ambiguous or uninformative and would provide tools for higher taxonomic resolution of disparate life forms." (SCHANDER & WILLASSEN 2005: 79).

"Rather than draining support from taxonomy, the DNA barcoding initiative has the potential to inject significant new funding into museums, herbaria and individual taxonomy labs." (GREGORY 2005: 1067).

"To others, DNA barcoding will save taxonomy, servicing the rising demands of the molecular and phylogenetics community, whilst instilling new life into an aging institution. For them DNA barcoding would leave a legacy that outlives any single taxonomist and remove the uncertainty that besets traditional taxonomy." (SMITH 2005: 842).

"DNA barcodes are likely to play a major role in the future of taxonomy... This is of great utility to the end users of taxonomy, and will help make more rapid progress in traditional taxonomic work... However, we must keep open the possibility that the barcode sequences per se and their ever-increasing taxonomic coverage could become an unprecedented resource for taxonomy and systematics studies in addition to being a diagnostic tool." (SAVOLAINEN *et al.* 2005: 1807-1809).

DNA barcoding, portrayed as the 'future of taxonomy', is indeed a contentious claim. The catch phrases 'major role in the future', 'rapid progress', 'servicing the rising demand', 'inject significant new funding', and 'useful tools' all describe the limitations, rather than the advantages, of DNA barcoding. A simple technology like DNA barcoding is not an academic and scholarly endeavor and doing so verges on pseudoscience. Insisting that it can 'progress' taxonomy is sensationalist. All barcoding will do is provide the taxonomists with more data

that is formally not required within species descriptions or taxonomic revisions. Those who want barcoding are the end-users, usually an industry, government, or biodiversity management organization, rather than taxonomists. The role of taxonomy within the DNA barcoding enterprise is to provide a service, namely to check and verify data. Morphology, the basis for all taxonomic identifications and revisions, is dismissed entirely (PACKER *et al.* 2009).

The DNA barcoding enterprise is based on a business model, which follows so many others currently used in academia (Fig. 1). In exposing the DNA Barcoding Enterprise Model we hope to show that many other such models are detrimental to scientific scholarship.

THE DNA BARCODING ENTERPRISE MODEL (DBEM)

Business or enterprise models work on a solution solving basis (see Fig. 1). For instance, a stakeholder (1) consults an innovator (4) with a problem based on a demand. The innovator uses existing technologies (2) to assess the economic viability of a solution based on some form of model (e.g. a work schema). The model is developed into a beta product that is tested and the resulting data is collated (3). This information is used to develop the product (5) and dependent resources (e.g. databases, software, help desk, training, etc.). The final product is delivered to the stakeholder who makes it available to the end-user (6).

Academia, namely museums and universities have adopted this enterprise model within their own research programs. We show, using DNA Barcoding, that such enterprise models, beneficial to industries and profit margins, may be detrimental to scholarship. We use the same terminology in the figure to describe the DNA Barcoding Enterprise Model (DBEM) using recent examples and events.

1. Stakeholders

The original stakeholders in DNA Barcoding are industry and government agencies. In 2003, for example, United Kingdoms' Department for Environment, Food and Rural Affairs (DEFRA) issued a statement:

"We have been talking about techniques for encoding unique identifiers in the context of GMOs [Genetically Modified Organisms] for some time," says Howard Dalton, DEFRA's chief scientific adviser. "Any development which would help in the process of detecting and identifying GMOs would be welcomed" (GRAHAM-ROWE 2003, <http://www.foodnavigator.com/Science-Nutrition/DNA-bar-codes-for-food>).

A government that demands 'a technique for encoding unique identifiers' to detect genetically modified food would significantly outweigh any request from academia. The idea of a molecular taxonomy and DNA identification as a taxonomic tool, however, goes back earlier (e.g. KURTZMAN 1994, WILSON 1995). It is, however, most likely the demands from non-academic agencies, such as DEFRA and the resulting media attention, which has sparked renewed interest in DNA identifica-

tion (i.e. DNA Barcoding; HEBERT *et al.* 2003), rather than the potential to discover cryptic species (KNOWLTON 1993) or some concern expressed on the limitations of morphological keys. Moreover, governmental agencies and industry (e.g. primary producers and food processing companies) have the influence and resources to be viable stakeholders:

"Pyxis Genomics promises to deliver this long sought-after feature for meat processors: traceability from farm to fork. The company is developing a panel of genes for Canadian food processor Maple Leaf Foods that will form the basis for the system, the first phase of which should be implemented this fall... The company [Pyxis Genomics] is currently partnering with VIDO, Simon Fraser University and the University of British Columbia to study immunity in food animals. The three-year project, backed with \$27 million in Genome Canada funding, promises knowledge that will help keep food animals – and the food they produce – healthy and safe." (from ANON. 2003: 2).

"...Maple Leaf Foods, based in Ontario, Canada, announced that it had successfully completed research and development into producing a DNA traceability system for pork." (Meat International 2004, vol. 14: 12).

"Microchip Biotechnologies, Inc. (MBI) is pleased to announce that the Canadian Centre for DNA Barcoding (CCDB), at the Biodiversity Institute of Ontario, University of Guelph, will be the first participant to join MBI's early access program for the Apollo 100 STAR System. The Apollo 100 STAR is the first fully automated and integrated system for DNA sample preparation for sequencing. The System incorporates MBI's MOVE™ (Microscale-On-Chip-Valve) technology exclusively licensed from the University of California. 'We are delighted that the Canadian Centre for DNA Barcoding has agreed to collaborate in our Apollo 100 STAR early access program. Their commitment to this program validates MBI's overall strategic goal to develop and market front-end sample preparation systems for life science and diagnostic solutions', said Stevan Jovanovich, Ph.D., President and CEO of MBI" (Microchip Biotechnologies Press Release, April 7th, 2008: <http://www.microchipbiotech.com/news.php>).

The demand for barcodes to identify organisms has resulted in the company Genome Canada, "...a hybrid venture capital and granting council" (GODBOUT 2001: 3) through the Ontario Genomics Institute and the Natural Sciences and Engineering Research Council of Canada (NSERC), set to be major stakeholders in the Canadian Barcode Of Life Network (BOLNET) (DOOH & HEBERT 2005). On a smaller scale, DEFRA (Darwin Initiative) has also joined as stakeholder for plant DNA barcoding (CBOL Plant Working Group 2009).

2. Industry

The majority of resources used in new innovations, for instance, are borrowed from existing technologies. In numerical phylogenetics, for example, parsimony, Bayesian analysis, maxi-

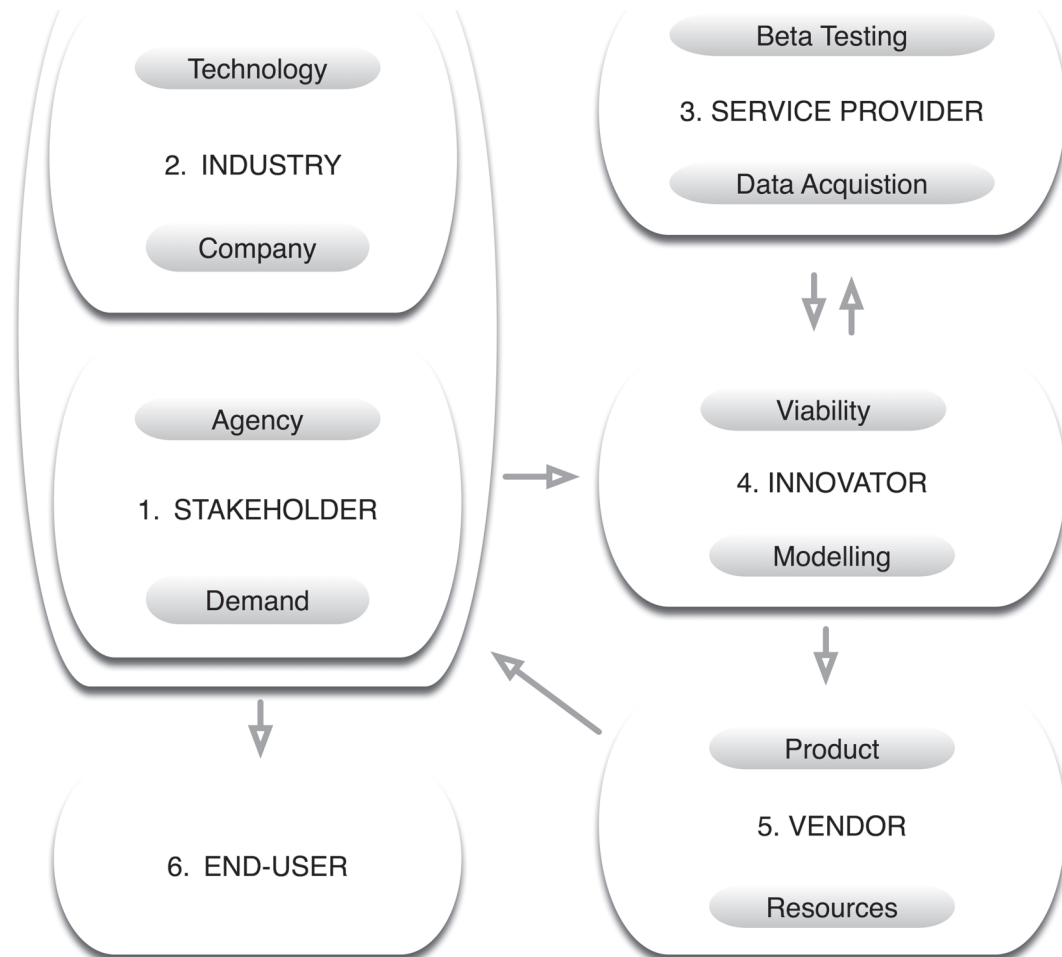


Figure 1. A business or enterprise model commonly used in academia.

mum likelihood, the binary matrix, and bifurcating trees, all originated in the statistical or mathematical sciences. Biologists have simply adopted them in order to expedite phylogenetic methods. These technologies were originally developed to deal with a vastly different abstract problem, which leads one to wonder whether they accurately represent problems within phylogenetics (see WILLIAMS & EBACH 2008). The same is true for DNA Barcoding. The ability to sequence genes and extract molecular data is a simple technology at best. It seems dubious that employing genetic divergence rates would accurately represent divergence between species. Industry provides technologies that can be integrated by innovators to develop new or modified tools.

3. Innovators

The technology produced and provided by the manufacturing industry, such as PCR machines or primers, for instance, offer innovators a quick way to assess the viability of meeting the demands of stakeholders without reinventing existing tech-

nologies. Innovators employ standards that abide to existing standards in the field the technology will be employed. Standards, for instance, have been developed for taxonomic databases in order to comply with the international codes of nomenclature. This has created the Taxonomic Database Working Group (TDWG), which issues standards for worldwide use. In some cases, innovators also create standards for data that benefit the end user rather than the source of the data, namely the taxonomists. 'Unitary taxonomies' are a standard imposed on conflicting taxonomies. While this may be beneficial for end users, it is disastrous for taxonomists (CARVALHO *et al.* 2007). Moreover, innovators are usually not representative of the field they 'represent'. DNA Barcoders for instance, who wish to 'represent' taxonomy, are usually neither taxonomists nor systematists (e.g. HEBERT & GREGORY 2005). In fact DNA barcoders are usually from a genetics background, once again highlighting the emphasis on genes and identification, rather than tax-

onomy and classification. DNA Barcoders claim to have concern for taxonomy, but in reality their interests lie elsewhere as stated in a press release for the 2nd International Barcode of Life Conference in Taiwan:

“About 350 DNA barcoding experts from 46 nations will converge in Taipei amid spiralling interest from health officials, government agencies and others beginning to realize potential applications in a range of areas – from consumer protection and food safety to disease prevention and better environmental monitoring” (COLLINS 2007).

The above represents the viability of a product. In the case of DNA Barcoding, the product of a DNA barcode reader, will be “similar to the scanners at retail checkouts” (O’CONNELL 2008), and will be of immense value to industries that require such technology to identify sources of contamination or GMOs (Genetically Modified Organisms), for example. Moreover, any new innovation requires modeling. For instance, models predict ways in which DNA barcoding will be used, the varying demands of its users, and the cost of beta testing and production. The DBEM will reveal that the demands from taxonomy and systematics alone are not enough to fulfill the required revenue to make barcoding a viable venture. Taxonomy, however, offers DNA barcoding with a resource that is viable – an identification service.

4. Service Providers

Research and development (R&D), that is, beta testing (i.e. testing software) and data acquisition (i.e. populating public databases such as the Barcode of Life Data Systems) is the most important, costly and time consuming part of any enterprise model. In the DBEM, a large proportion of R&D can be covered by using a service provider to do all the testing and data acquisition. The service provider can apply for funds from their own coffers and devote expertise and resources to R&D. Within the DBEM it is taxonomists and systematists, and the universities and museums that employ them, who are the primary service providers. The DNA Barcoding idea is marketed to taxonomists and systematists as a potential solution to taxonomic problems (HOLLINGSWORTH 2007: table I), although its benefits are far greater for non-taxonomic end-users (see below). Once sold on the idea, the taxonomic community applies for grants from traditional funding sources, or it uses its own time and resources. For example, DNA Barcoding cannot work until taxonomists and systematists have tested the viability of the CO1 gene as a reliable marker for use in DNA barcoding:

“Without traditional taxonomy, a CO1 sequence can be like an unfinished sentence” (HOLLOWAY 2006).

When most economically important groups have been barcoded, the function of taxonomists will be to apply barcoding to lesser known groups or “cryptic” taxa:

“...widely divergent taxonomic groups have reported success using CO1 for both species identification and discovery.” (SMITH 2008: 67).

“DNA barcodes can be used to identify cryptic species of skipper butterflies previously detected by classic taxonomic methods and to provide first clues to the existence of yet other cryptic species.” (BURNS *et al.* 2008: 6350).

Ironically, it is those interested in “consumer protection, food safety, disease prevention, and better environmental monitoring” that benefit from the DBEM rather than taxonomists. Take for example this statement from the CBOL-ABS brochure:

“DNA barcoding can help to achieve many of the Millennium Development Goals (MDGs) and reach the objectives of the Convention on Biological Diversity ... Controlling Agricultural Pests: Lessening Poverty and Hunger ... Identifying Disease Vectors: Combating Diseases ... Environmental Sustainability ... Protecting Endangered Species ... Monitoring Water Quality” (CBOL-ABS Brochure, <http://www.barcoding.si.edu/PDF/CBOL-ABS%20Brochure%20-%20FINAL.pdf>).

5. Vendors

Once the product has been tested it is given to a vendor to manufacture the prototype. Stakeholders satisfied with the product may request a revision of the product or order full production. DBEM has so far not produced the hand-held DNA barcoder prototype:

“Looking ahead, we expect that soon a handheld barcode reader, similar to a GPS device, will ‘read’ such a segment from any tiny piece of tissue.” (STOECKLE & HEBERT 2008: 83).

“Imagine the promise of a schoolchild with a barcoder in hand learning to read wild biodiversity, the power granted to a field ecologist surveying with a barcoder and global positioning system, or the security imparted by a port inspector with a barcoder linked to a central computer!” (Ten Reasons for Barcoding 2004, <http://www.barcoding.si.edu/PDF/TenReasonsBarcoding.pdf>).

There are, however, rumors of potential development:

“My very first ever angel investor, Sheldon Breiner, contacted me on short notice to ask if I wanted to have dinner and a brainstorm with Winnie Hallwachs and Dan Janzen, a pair of U Penn professors with a dream: a handheld barcode reader for life. The concept is that Joe Average can walk into his backyard (or his field), and find out what species there are there. What’s that ant? What bird left a feather in our garden? What’s this plant doing here?” (FRUCHTERMAN 2007).

6. End-users

The primary end-user targets within the DBEM are government agencies, and businesses like aquaculture and agriculture, rather than the taxonomists in museum and universities who catalog and curate the specimens which are vital for sequencing:

“If we could have bar-coded the species, we would have known what they were within a day and, possibly, where they came

from,' he says [David Schindel]. 'It would have been a big help for public health officials' [...] 'Agricultural groups have approached them to bar-code insects that affect Ontario crops, he says [Robert Hanner]'" (OGILVIE 2007).

"The FDA isn't the only US regulatory agency taking notice of barcoding. The Federal Aviation Administration is barcoding tissue from hapless birds involved with airplane strikes. Its intent is to prevent bird strikes by targeting specific bird species for control around airstrips. The US EPA is using barcoding to characterize the health of waterways through identifying complex assemblages of aquatic species that would otherwise require intense and time-consuming taxonomic study to characterize. The US Department of Agriculture is using barcoding data from CBOL's fruit fly working group to better control the agricultural pest" (GRANT 2007).

The benefits for taxonomists, the prime end-users of taxonomic data, are minimal (see EBACH & HOLDREGE 2005a).

'BEST PRACTICE' IN TAXONOMY, YET AGAIN

Before explaining the forms of anti-intellectualism in the DBEM it is important to understand 'best practice' in taxonomy. Taxonomy is a field that is either poorly misunderstood as merely 'stamp-collecting' or seen as a service industry for 'end-users' (GODFRAY *et al.* 2007). Regardless of what non-taxonomist end-users feel about taxonomy, the field itself adheres to a standard. The naming of taxa must adhere to one of several codes of nomenclature. Moreover, taxonomists working within each taxonomic group also follow strict guidelines. For example, trilobites are always described from head (cephalon) to tail (pygidium). For most, if not all, taxonomists geographical locality does not define a taxon. These are all 'best practices' that are based on rational argument and practicality. Morphology and not geography, for instance, gives us the vital information we use in classification. Naming a trilobite from cephalon to pygidium standardizes the way we describe taxa and makes finding characters in a text much easier. 'Best practice' in taxonomy also extends beyond how we name and describe taxa. Taxonomy is a field that has all its knowledge based in the expertise of taxonomists (CARVALHO & EBACH 2010). A database, no matter how well atomized or sorted, cannot replace the knowledge of a taxonomist. As a tool the database is invaluable, but as a source of knowledge of a particular group, it is inadequate. When databases, for instance, start to out-number taxonomists the knowledge is not replaced – only nomenclature, descriptions and hypothetical phylogenetic relationships are recorded. If we wish to increase the productivity in taxonomy then quite obviously we increase the number of taxonomists and demand from them products of high quality. This adheres to best practice.

DNA Barcoding, however, does not adhere to best practice in taxonomy simply because it is not taxonomic in nature. Taxonomy, for instance, is purely morphological and not molecular. Unless there is a morphological character to distinguish

a new taxon, then DNA Barcoding is extremely limited as a taxonomic tool. In the case for identification purposes, such as keys, DNA Barcoding is again limited. Unless a barcode is explicitly linked to a specimen that signifies a whole species, then DNA Barcoding is of little use. Firstly, this means that the specimen in question, a type, is properly assigned. It is unusual for a single specimen to show all the morphological variation with a proposed species. Until the taxonomic workers of a particular group can be satisfied that a single specimen, or sample of specimens, are properly designated as types, and that the morphological variation corresponds to the molecular variation, then the barcode is most likely a molecular representation of a species. In any case, whether this is true for all barcodes is highly questionable (see SONG *et al.* 2008); does uncontextualized molecular variation really signify new taxa anyway? Furthermore, barcodes adhere to 'best practices' elsewhere, outside of taxonomy, complicating the matter further.

The DBEM however, goes against all best practices in biological systematics. This is because it uses scientific arguments to justify what is essentially poor practice in managing systematic biologists. Justification for this poor practice has led to anti-intellectualism. Unfortunately, the DBEM is often confused as DNA Barcoding itself. We refer the reader to the large body of literature dedicated to the scientific justifications of DNA Barcoding (see WILL 2005). Herein, however, we look at the DBEM and investigate the forms of anti-intellectualism found in poor practice within biological systematics.

THE DNA BARCODING ENTERPRISE MODEL AS AN EXAMPLE OF ANTI-INTELLECTUALISM

Anti-Elitism: democratizing science and the end-user lobbyist

Comparative biology and most other sciences do not lend themselves to democracy:

"We propose DNA barcoding as a reliable, consistent, and democratic tool for species discrimination in routine identification of parasitic nematodes" (FERRI *et al.* 2009).

Systematics, for instance, is a science and an academic pursuit that consists of experts who are knowledgeable of the groups they study. In order to democratize systematics, or any other comparative science, we immediately reject the need to reduce the importance of such knowledge. This irrefutably damages the field. Take for instance:

"Janzen and Hallwachs want biological knowledge to extend beyond experts, to move out of the hands of the one person in the world who can identify a certain spider, to reach everyone. They see a handheld barcode device – which doesn't exist yet – democratizing information, bolstering bioliteracy, making gardeners of us all" (HOLLOWAY 2006).

Gardeners or parataxonomists (see below) do not have the experience to practice taxonomy. Technology cannot replace knowledge gained over many years of experience. A world

filled with parataxonomists will result in partially correct identifications and generally low-quality descriptions:

“Parataxonomy does not fulfil the criteria of a scientific method” (KRELL 2004: 795).

The call for faster species identifications and descriptions is not made so we can better understand the natural world:

“We examine the crafting of publics in the global Barcoding of Life Initiative (BOLI) – seen as crucial for re-invigorating, and democratizing, early-twenty-first-century taxonomic sciences and hence for actually achieving biodiversity protection” (ELLIS *et al.* 2009).

‘Biodiversity protection’ is not a goal of systematics or taxonomy but rather of conservation biology, and protecting biodiversity is a task that lies outside science altogether. For instance, what are we protecting biodiversity from? Poor systematic classifications or clumsy taxonomic diagnoses, which endanger systematics, are seemingly of little relevance to biodiversity protection. Linking systematics to biodiversity, as we show below, is sensationalist and of little relevance to biological classifications.

Sensationalism: the biodiversity crisis

Implying the inadequacies of describing new species and revising current taxa in light of the burgeoning biodiversity crisis is a sensationalist claim promoted by the DNA Barcoding Enterprise. For instance, we will have no control over the biodiversity crisis if all known species are described, catalogued and their taxonomic groups fully revised. All systematics can contribute is in providing a single number of species. Given this number, we may be able to monitor the rate of loss, but identifying and preventing the causes of extinction are well beyond the goals and abilities of systematics. The DNA barcoding enterprise is well aware that a single number and related statistics can sell an idea. Too much emphasis however is placed on a quantitative measurement of biodiversity:

“Current estimates of the number of species range from 5 to 30 million, with a best working estimate of 8 to 14 million; of these, only around 1.8 million have been described” (IUCN 2008).

DNA Barcoding alone cannot describe each and every new DNA species. In fact, it requires the knowledge that lies within taxonomy and systematics. The tactic used to promote the DNA Barcoding Enterprise works as follows. First establish an academic link to taxonomy. For example, show how DNA Barcoding can work with taxonomy to facilitate faster identifications:

“The taxonomic enterprise is entering a renaissance for many reasons, including new tools like DNA barcoding. Traditional taxonomists realize the need for a more streamlined system of data gathering, analysis, and publication. Researchers in related fields (e.g., ecology, evolutionary biology, and agriculture) recognize that taxonomic names provide the basic vocabulary and information framework for biodiversity. Taxonomy as a field has always been tightly

knit at the level of individual scientists but loosely organized at an institutional level. In recent years, a series of cooperating intergovernmental activities and nonprofit organizations have been created to build a more integrated taxonomic enterprise.” (MILLER 2007: 4775).

Once testimony has been given to the usefulness of DNA barcoding, the deficiencies and inadequacies of taxonomy needs to be provided. This justifies the decrease of taxonomists due to the lack of technology and validates new technologies like DNA barcoding as economically praiseworthy and ‘scientific’:

“DNA barcoding has emerged at a critical time for taxonomy. Economic development and increased international commerce are leading to higher extinction rates and the introduction of invasive and pest species. As a result, local, national, and international user communities are demanding more and faster species identification services and better information about their biodiversity than ever before. At the same time, taxonomy as a field faces huge funding challenges and a dwindling professional workforce. Barcoding is emerging as a cost-effective standard for rapid species identification. It has the potential to accelerate our discovery of new species, improve the quality of taxonomic information, and make this information readily available to nontaxonomists and researchers outside of major collection centers” (MILLER 2007: 4775-4776).

DNA Barcoding has been elevated to the level of a classificatory ‘science’ by justifying new technologies in taxonomy. This sensationalist approach has no scientific merit. Taxonomy is not an identification service and does not answer to ‘economic development’ or ‘local, national, and international user communities’. In order to expedite taxonomy, greater investment into training taxonomists is needed as well as a greater number of available positions. A long-term vision, such as identifying all the species on Earth, requires long-term investments. Unfortunately, DNA Barcoding is sensationalism that promotes new technologies, which are not able to perform the same functions as taxonomists, is damaging systematics and taxonomy.

Populism: taxonomy as a service industry

The DNA Barcoding enterprise is making use of the populist image of taxonomy, a term that is becoming synonymous with ‘service’. For instance, taxonomy is measured by the number of described species, rather than the quality of the descriptions and revisions. The impression given is that of a good service rather than of a good science:

“We live in an exciting time. A new generation of tools are coming online that will vastly accelerate the rate at which we are able to discover and describe species,” says Wheeler. “Most people do not realize just how incomplete our knowledge of Earth’s species is or the steady rate at which taxonomists are exploring that diversity. In 2006, for example, an average of nearly 50 species per day were discovered and named” (WHEELER in <http://www.biologynews.net/ar->

chives/2008/05/23/scientists_announce_top_10_new_species_issue_sos.html).

DNA Barcoders, however, use this impression of a slow 'service' to state their case:

"Barcoding gathered momentum quickly because its early proponents bemoaned the slow pace of taxonomy to quantify global biodiversity (HEBERT *et al.* 2003) and sought a faster, better way" (RUBINOFF 2006: 1549).

Taxonomy, seen as a service provider, has resulted in identification tools that carry the taxonomic prefix without any reference to meaningful 'taxonomic classifications'. A 'taxonomic key' for example, helps us identify a named taxon, whereas 'taxonomic checklists' provide a list of known named species within an area:

"Taxonomic species lists should be based on the best taxonomic data at hand, and instability will reflect the continuous flux of taxonomic knowledge" (PADIAL & DE LA RIVA 2007 865)

Identification keys do not necessarily use data of vital taxonomic relevance (i.e. diagnostic characteristics) or reflect natural classifications, as they rely upon any morphological, behavioural, ecological or physiological data that distinguish among taxa that are similar. More often than not taxonomic keys reflect artificial rather than natural classifications, the latter of course being a legitimate goal of taxonomic endeavor.

'Taxonomic' keys are not representative of taxonomy per se, as they represent a consequence or a secondary end-product of a taxonomic study, and are not directly involved in species discovery (i.e. new diagnoses and descriptions) or systematic revisions (i.e. new hypotheses of natural classifications). Taxonomic data, however, are often misinterpreted as distributional or nomenclatural information, both of which are not taxonomic in nature. Moreover, taxonomic data is often interpreted as 'specimen data', that is, data pertaining to an individual rather than to a species or a classification:

"An essential part of improving taxonomic data is the preservation of voucher specimens" (MILLER 2007: 4776).

The populist interpretation of the term 'taxonomy' as a service industry directly affects the field. Taxonomy, measured as a service to describe new species, loses its perceived importance as an academic field:

"If the original estimates hold and between 873 and 1,750 new species of catfishes are described, the cost will have been between \$2,700 and \$5,400 per species. Completing the taxonomy, with revisions, identification keys, field guides, and websites with distributional and other information on all 4,500 species of catfish, will have been done for a cost of approximately \$1,000 per species. At this rate, and if estimates of 5 million to 10 million species of organisms on Earth are correct, the cost of completing an inventory of the biodiversity of the planet will be only \$5 billion to \$10 billion. This is a trivial amount considering modern expenditures for the military and health care, and it would

produce an unparalleled source of information about the planet Earth and its resources" (PAGE 2006).

Taxonomy, reduced to a service that is equivalent to 'health care', may easily be equated by populist means to a technology like DNA Barcoding. In so doing, DNA barcoders can justify their aims. If taxonomy is more than a manual way to produce species identifications and descriptions, then it obviously can benefit from a faster and more cost-effective technology. The populist image of a new fangled technology coming to the aid of ancient machinery helps sell the DNA Barcoding Enterprise and undermine taxonomy.

Pseudoscience: DNA Barcoding and cryptic species

DNA barcoding is a limited technology. For instance, the differing rates of genetic divergence that DNA barcoding may uncover is not directly correlated to taxonomic divergence. Taxonomic justification for erecting a new species is based on various morphological characteristics found in, usually, a larger number of specimens. The divergence in a single sequence from the CO1 region of a single gene derived from several specimens is not evidence for taxonomic designation. Why, then, do HEBERT *et al.* (2005) happily accept that such minor genetic variation between morphologically indistinct species justifies separate identification (i.e. cryptic species)?

"In 'DNA barcoding' a short section of DNA sequence is used to identify species. Neither the idea nor the technology behind DNA barcoding is novel. What is new and controversial is the idea of using just a small portion of a single gene to identify species from a wide taxonomic range, including animals such as birds, fish and insects... As well as correctly identifying known species, a number of probably cryptic species have been discovered within what had previously been thought to be single morphologically based species. This apparent success has fuelled speculation that accurate species identification is now possible by anyone with access to DNA sequencing even if they lack taxonomic expertise. The methodology used in DNA barcoding has been straightforward. Sequences of the barcoding region are obtained from various individuals. The resulting sequence data are then used to construct a phylogenetic tree using a distance-based 'neighbour-joining' method. In such a tree, similar, putatively related individuals are clustered together. The term 'DNA barcode' seems to imply that each species is characterised by a unique sequence, but there is of course considerable genetic variation within each species as well as between species. However, genetic distances between species are usually greater than those within species, so the phylogenetic tree is characterised by clusters of closely related individuals, and each cluster is assumed to represent a separate species" (DASMAHAPATRA & MALLET 2006: 254).

A similar plea was made several years before under the guise of DNA Taxonomy:

"The basic procedures of DNA taxonomy would be straightforward. A tissue sample is taken from a collected individual

and DNA is extracted from this. This DNA serves as the reference sample from which one or several gene regions are amplified by PCR and sequenced. The resulting sequences are, as a first approximation, an identification tag for the species from which the respective individual was derived. This sequence is made available via appropriate data bases, together with the species description and other associated information, ideally including its taxonomic status with appropriate references. The sequence now serves as a standard for future reference, together with the type specimen and the respective DNA preparation, which will be deposited in museum collections. Once a significant sequence data base has been built up, new samples can be checked against these existing sequences to assist species re-identification or to assess whether a new species description might be warranted. The data base could also serve to resolve questions about the taxonomic identity of specimens that are derived from larval life stages, or for identification of artefacts from trade with endangered species and so on. In the early phases of this initiative, concerted efforts must be made to achieve good coverage of all known species (or some specifically targeted subgroups), but once the data base is sufficiently complete, these comparisons, aided by the phylogenetic analysis of query sequences, will readily place any sequences from new specimens" (TAUTZ *et al.* 2003: 70-71).

However, others beg to differ:

"The concept of DNA taxonomy as proposed by TAUTZ *et al.* (2003) is essentially based on the barcoding approach as its practical component. It goes much further, however, in demanding that DNA sequences – not morphological data – be used as the main criterion for taxonomic decisions. The advocates of DNA taxonomy claim that the current practice in taxonomy is not adequate to achieve the aim of a more or less complete inventory of animal life in a reasonable period of time... The main criticism of DNA taxonomy, however, deals not with these minor aspects of practicability. It is rather concerned with the lack of intellectual content... In summary, DNA taxonomy promises something that it cannot deliver. This meagre concept provides neither a serious alternative to the well established system of taxonomy nor a useful scaffold in which the existing system can be embedded. While this concept should be buried, the use of DNA sequences remains most valuable in biological systematics and certainly will attain growing influence in the future" (KOEHLER 2007: 45-46).

This statement exposes the contradictory nature of the DNA Barcoding Enterprise. KOEHLER (2007) rejects DNA Taxonomy because it rejects morphology while DNA Barcoding itself rejects morphology as inadequate for the purposes of discovering "cryptic" species (see PACKER *et al.* 2009). It is as if cryptic species are solely demonstrated by molecular approaches – morphological systematists, entrenched in their endeavor to

tease apart variation and unravel patterns of relationships, commonly deal with cryptic species themselves (i.e. cryptic patterns of relationships), a very obvious fact overlooked by barcoders.

We are told DNA barcoding aims to identify named taxa, but at the same time it is offered as a way to discover cryptic species (see HEBERT *et al.* 2004). Which is it? DNA Barcoding, by its own admission, is unable to completely do or replace taxonomy; how then can it discover new species?

"We have suggested that when DNA barcoding is compared to traditional taxonomy in the areas where barcoding is likely to be most useful – cryptic species recognition, it nearly always outperforms morphology which often simply does not work at all. In this respect, it is perhaps ironic that new species are readily described on the basis of subtle morphological variation, yet there is a general reluctance to describe species on the basis of genetic evidence alone, which suggests that data chauvinism (R. Mayden, personal communication) is alive and well within the taxonomic community." (PACKER *et al.* 2009: 47).

'Data chauvinism' or not, DNA barcoding, like DNA Taxonomy, promises something that it cannot deliver. Individuals that display only trivial variations or a significant lack of differences at the morphological level cannot be justified as representing different species due to variations within single DNA sequences. DNA barcoding alone cannot justify species representative of a single gene. After all, the aim of barcoding is species identification, not species discovery or a replacement for taxonomy:

"CBOL's mission is to promote the exploration and development of DNA barcoding as a global standard for species identification" (<http://www.barcoding.si.edu/>).

"...DNA barcoding would benefit, not compromise, taxonomic science" (GREGORY 2005: 1067).

"Species discovery is really the job of taxonomy and hence cannot solely use DNA barcodes as the arbiter of the discovery of new species" (RACH *et al.* 2008: 237).

Apparently, practitioners of the DNA Barcoding Enterprise are starting to think otherwise:

"Certainly an organism's DNA barcode might be considered as simple compared to its entire morphology... But, it brings an entirely independent set of data to bear on the study of organismal diversity and thereby helps to calibrate the level of taxonomic uncertainty in the existing system. This should be seen as being advantageous to the process surely?" (PACKER *et al.* 2009: 44).

Technology in and of itself is not science, but a tool which expedites the work process. Real innovation is born in ideas and not techniques (see also CRISCI 2006, CARVALHO *et al.* 2008). DNA barcoding is at best pseudoscientific and held together by a fundamental belief that molecules speak the 'truth' and technology 'saves' (see SMITH 2005).

ANTI-INTELLECTUALISM AND THE DNA BARCODING ENTERPRISE LEGACY

The End-user Phenomenon

There is a growing concern about the end-users of taxonomic data. As discussed above, these data primarily consist of diagnostic descriptions, synonymies and images of type material. The end-users of taxonomic data, however, are:

“... the ecologists, environmentalists, other biologists, and amateurs, [who] would have an unambiguous recommendation that they could use in their work...” (GODFRAY *et al.* 2007: 950).

GODFRAY *et al.* (2007; see also GODFRAY 2002) want a single user-friendly classification that will suit end-user needs. The fact that many classifications conflict and that taxonomists cannot agree on any one taxonomy seems to be irrelevant. Moreover, the conflict that exists between different classifications usually lies at the ordinal or familial level, rather than at the level of species, the unit of taxonomy that concerns ‘ecologists, environmentalists, other biologists, and amateurs’. However, it is the differences in taxonomic conclusions that has lead end-users to despair, so much so that:

“[Current taxonomic practice] also undermines arguments for investing more resources in taxonomy: if further taxonomic work leads to an increase in the size of the accumulated fragmented taxonomy with no synthesis for the end-user, it will fare badly in the intense competition for science funding” (GODFRAY *et al.* 2007: 943).

This argument that a field in crisis does not require more investment is one also favored by DNA Barcoders. One cannot help but interpret GODFRAY *et al.* (2007) as underselling taxonomy. As a woefully underfunded field, taxonomy cannot sort out complicated problems. It needs more funding, training and support – not a ‘synthesis’ for the end-user. GODFRAY *et al.*’s (2007) populist, that is, anti-intellectual, viewpoint hinders taxonomy. The suggestion that this would ‘fare badly in the intense competition for science funding’ most likely reflects the view of funding bodies, which prefer a technological solution. This sentiment is stated in a recent invitation to tender under NERC’s ‘UK Taxonomy & Systematics Review’ in response to “to the recent House of Lords Science and Technology Committee inquiry into systematic biology research and taxonomy” (NERC, 2009: <http://www.nerc.ac.uk/research/themes/biodiversity/events/documents/taxonomy-itt.pdf>):

“...an identification of topics, technologies or mechanisms that need research and development to most effectively ramp up taxonomic and systematic biology work to meet societal needs, including rapid taxonomic techniques, metagenomics and novel methods based on new sequencing technologies” (NERC 2009:2).

The perceived ‘inability’ that taxonomy is unable to function without access to ‘technologies or mechanisms’ is incorrect (see EBACH & HOLDREGE 2005b, CARVALHO *et al.* 2008). These

new technologies that funding bodies consider innovative and worth funding are the same technologies that end-users demand for faster species identification. Taxonomy, which cannot meet these demands, has been usurped by the DNA Barcoding Enterprise:

“Leading genomic researchers, industry technology developers and end-user regulatory agency scientists gathered in Toronto’s MaRS Centre on 18 February 2009 to explore the market-readiness of DNA barcoding... It is clear that DNA barcoding – which was invented and has been largely validated in Ontario by Dr. Paul Hebert and his colleagues at the University of Guelph’s Biodiversity Institute of Ontario – has the potential to speed up and decrease the cost and uncertainty of traditional approaches to identifying individual species in exploratory, regulatory, forensic and educational settings’ said Dr. Christian Burks, President and CEO of OGI. ‘As with other genomics research, translating this innovation into much broader applications will be driven by the involvement of industry partners and end-user uptake’” (Ontario Genomics Institute News, <http://www.ontariogenomics.ca/media-centre/news/2009-3-05/320>).

The end-user in DNA barcoding is a different beast altogether. The original stakeholders, who demanded DNA barcoding, are now benefiting from the DNA Barcoding Enterprise. Taxonomy, reduced to a service industry in the minds of the public and several of its practitioners, has as a service provider beta tested the technology to resolve the ‘uncertainty of traditional approaches to identifying individual species in exploratory, regulatory, forensic and educational settings’.

So far the benefit for taxonomists and end-users of taxonomic data is limited. As a service provider it receives funding to do DNA Barcoding rather than taxonomic revisions. End-users have a rudimentary identification service and database, which may be of value once hand-held devices become available, which are used and maintained by a new generation of technicians or parataxonomists.

CONCLUSIONS

“Whence springs this taxonomic worldview that ignores the needs of humankind?” (PACKER *et al.* 2009: 48).

Under the auspices of ‘taxonomy’ and the ‘biodiversity crisis’, the DNA Barcoding Enterprise Model has succeeded in creating a product for a non-taxonomic stakeholder, namely industry, governmental departments, fisheries, agriculture, applied ecology and conservation. The DBEM is not designed to help taxonomy, nor does it further taxonomic research or promote scholarship. Rather the DBEM is an exercise in poor practice, demoting the importance of taxonomy via faint praise, by adding to the taxonomic ‘toolbox’ as if taxonomy were a mere technology in aid of mechanical advancement. A new generation of parataxonomists and barcoders is unsustainable within biological classification. Rather than helping taxonomy it will create a service industry to help measure the biodiversity crisis.

Many reading this work may shrug at the march of technology and embrace the DBEM as providing a potentially useful tool. They do so at their own peril. The DBEM is a cash-cow that may or may not inadvertently fund taxonomic or systematic projects. The whole enterprise, however, is anti-intellectual and is characterized by non-scientific aims and methods. As taxonomists and scientists we question the need of the DBEM and its scientific relevance.

ACKNOWLEDGEMENTS

We wish to thank David M. Williams for his invaluable input and advice. We also thank Gary Nelson and two anonymous reviewers for their comments. MCE is grateful to the ARC for awarding a Future Fellowship (FT0992002). MRdeC is grateful to the CNPq for a research fellowship (303061/2008-1).

LITERATURE CITED

- AGNARSSON, I. & M. KUNTNER. 2007. Taxonomy in a changing world: seeking solutions for a science in crisis. *Systematic Biology* **56**: 531-539.
- ANON. 2003. **Bringing home the bacon**. Newtrition, Summer, p. 2.
- BRICKELL, C.D.; M. CRAWLEY; J. CULLEN; D.G. FRODIN; M. GARDNER; C. GREY-WILSON; J. HILLIER; S. KNEES; R. LANCASTER; B.F. MATHEW; V.A. MATTHEWS; T. MILLER; H.F. NOLTIE; S. NORTON; H.J. OAKELEY; J. RICHARDS & J. WOODHEAD. 2008. Do the views of users of taxonomic output count for anything? *Taxon* **57**: 1047-1048.
- BRUMMITT, R.K. 2002. How to chop up a tree. *Taxon* **51**: 1-41.
- BRUNDIN, L. 1966. Transantarctic relationship and their significance. As evidenced by chironomid midges with a monograph of the subfamilies Podonominae and Aphroteniinae and the austral Heptagytiae. *Kungliga Svenska Vetenskapsakademiens Handlingar* **11** (1966): 1-472.
- BURNS, J.M.; D.H. JANZEN; M. HAJIBABAEI; W. HALLWACHS & P.D.N. HEBERT. 2008. DNA barcodes and cryptic species of skipper butterflies in the genus *Perichares* in Area de Conservacion Guanacaste, Costa Rica. *Proceedings of the National Academy of Sciences* **105**: 6350-6355.
- CANTINO, P.D. & K. DE QUEIROZ. 2007. **International Code of Phylogenetic Nomenclature**. Version 4. Available online at: <http://www.ohiou.edu/phylocode> [Accessed: 06/IV/2010]
- CARVALHO, M.R. DE; F.A. BOCKMANN; D.S. AMORIM; C.R.F. BRANDÃO; M. DE VIVO; J.L. DE FIGUEIREDO; H.A. BRITSKI; M.C.C. DE PINNA; N.A. MENEZES; F.P.L. MARQUES; N. PAPAVERO; E.M. CANCELLO; J.V. CRISCI; J.D. MCEACHRAN; R.C. SCHELLY; J.G. LUNDBERG; A.C. GILL; R. BRITZ; Q.D. WHEELER; M.L.J. STIASSNY; L.R. PARENTI; L.M. PAGE; W.C. WHEELER; J. FAIVOVICH; R.P. VARI; L. GRANDE; C.J. HUMPHRIES; M. EBACH & G.J. NELSON. 2007. Taxonomic impediment or impediment to taxonomy? A commentary on systematics and the cybertaxonomic-automation paradigm. *Evolutionary Biology* **34**: 140-143.
- CARVALHO, M.R. DE; F.A. BOCKMANN; D.S. AMORIM & C.R.F. BRANDÃO. 2008. Systematics must embrace comparative biology and evolution, not speed and automation. *Evolutionary Biology* **35**: 150-157.
- CARVALHO, M.R. DE & M.C. EBACH. 2010. Death of the specialist, rise of the machinist. *History and Philosophy of the Life Sciences* **31** (2009): 467-470.
- CAVALIER-SMITH, T. 2010. Deep phylogeny, ancestral groups and the four ages of life. *Philosophical Transactions of the Royal Society of London B* **365**: 111-132.
- CBOL Plant Working Group. 2009. A DNA barcode for land plants. *Proceedings of the National Academy of Sciences* **106**: 12794-12797.
- COLLINS, T. 2007. Amid spiralling government interest, world's top 350 DNA barcode scientists meet in Taipei. Consortium for the Barcode of Life (CBOL) Public release 14-Sep-2007. Available online at: http://www.eurekalert.org/pub_releases/2007-09/cftb-asg090707.php [Accessed: 06/IV/2010]
- CRISCI, J.V. 2006. One-dimensional systematists: perils in a time of steady progress. *Systematic Botany* **31** (1): 215-219.
- DARWIN, C.R. 1859. **On the origin of species by means of natural selection, or the preservation of favoured races in the struggle for life**. London, John Murray.
- DASMAHAPATRA, K.K. & J. MALLETT. 2006. DNA barcodes: recent successes and future prospects. *Heredity* **97**: 254-255.
- DAYRAT, B. 2005. Towards integrative taxonomy. *Biological Journal of the Linnean Society* **85**: 407-415.
- DE CANDOLLE, A.P. 1813. **Théorie Élémentaire de la botanique**. Paris, Déterville.
- DOOH, R. & P.D.N. HEBERT. 2005. **The Canadian Barcode of Life Network**. Available online at: <http://www.bolnet.ca> [Accessed: 06/IV/2010]
- EBACH, M.C. & C. HOLDREGE. 2005a. DNA barcoding is no substitute for taxonomy. *Nature* **434**: 697.
- EBACH, M.C. & C. HOLDREGE. 2005b. More taxonomy, not DNA barcoding. *BioScience* **55**: 822-823.
- ELLIS, R.; C. WATERTON & B. WYNNE. 2009. Taxonomy, biodiversity and their publics in twenty-first-century DNA barcoding. **Public Understanding of Science**. doi: 10.1177/0963662509335413
- FERRI, E.; M. BARBUTO; O. BAIN; A. GALIMBERTI; S. UNI; R. GUERRERO; H. FERTÉ; C. BANDI; C. MARTIN & M. CASIRAGHI. 2009. Integrated taxonomy: traditional approach and DNA barcoding for the identification of filarioid worms and related parasites (Nematoda). *Frontiers in Zoology* **6**: 1-12.
- FRUCHTERMAN, J. 2007. **Beneblog (December 16, 2007)**. Available online at: <http://benetech.blogspot.com/2007/12/barcoding-life.html> [Accessed: 06/IV/2010]
- GODBOUT, M. 2001. Mapping Canada's genome: in conversation with Genome Canada's president, Dr. Martin Godbout. **Biotechnology Focus** **4** (5). Available online at: http://www.genomecanada.ca/media/biofocus_july-august2001.pdf [Accessed 19/XI/2009]

- GODFRAY, H.C.J. 2002. Challenges for taxonomy. *Nature* **417**: 17-19.
- GODFRAY, H.C.; B.R. CLARK; I.J. KITCHING; S.J. MAYO & M.J. SCOBLE. 2007. The Web and the structure of taxonomy. *Systematic Biology* **56** (6): 943-955.
- GODFRAY, H.C.; S.J. MAYO & M.J. SCOBLE. 2008. Pragmatism and rigour can coexist in taxonomy. *Evolutionary Biology* **35**: 309-311.
- GRAHAM-ROWE, D. 2003. Britain wants genetically modified food to have DNA bar codes. *New Scientist* **177**: 5.
- GRANT, B. 2007. Cataloging Life. *The Scientist* **21**: 12. Available online at: <http://www.the-scientist.com/article/display/53881> [Accessed: 06/IV/2010]
- GREGORY, T.R. 2005. DNA barcoding does not compete with taxonomy. *Nature* **434**: 1067.
- HEBERT, P.D.N.; E.H. PENTON; J.M. BURNS; D.H. JANZEN & W. HALLWACHS. 2004. Ten species in one: DNA barcoding reveals cryptic species in the neotropical skipper butterfly *Astraptes fulgerator*. *Proceedings of the National Academy of Sciences* **101**: 14812-14817.
- HEBERT, P.D.N. & R.D.H. BARRETT. 2005. Reply to the comment by L. Prendini on identifying spiders through DNA barcodes. *Canadian Journal of Zoology* **83**: 505-506.
- HEBERT, P.D.N. & T.R. GREGORY. 2005. The promise of DNA barcoding for taxonomy. *Systematic Biology* **54** (5): 852-859.
- HEBERT, P.D.N.; A. CYWINSKA; S.L. BALL & J.R. DE WAARD. 2003. Biological identifications through DNA barcodes. *Proceedings of the Royal Society of London B* **270**: 313-322.
- HOFSTADTER, R. 1963. *Anti-intellectualism in American life*. New York, Knopf.
- HOLLINGSWORTH, P.M. 2007. DNA barcoding: potential users. *Genomics Society and Policy* **3**: 44-47.
- HOLLOWAY, M. 2006. Democratizing taxonomy. *Conservation in Practice* **7**: 14-21. Available online at: <http://www.conservationmagazine.org/articles/v7n2/democratizing-taxonomy> [Accessed: 06/IV/2010]
- IUCN. 2008. *Red List Report*. Available online at: http://cmsdata.iucn.org/downloads/state_of_the_world_s_species_factsheet_en.pdf [Accessed: 06/IV/2010]
- KNOWLTON, N. 1993. Sibling species in the sea. *Annual Review of Ecology and Systematics* **24**: 189-216.
- KOEHLER, F. 2007. From DNA taxonomy to barcoding – how a vague idea evolved into a biosystematic tool. *Zoosystematics and Evolution* **83**: 44-51.
- KRELL, F.-T. 2004. Parataxonomy vs. taxonomy in biodiversity studies – pitfalls and applicability of ‘morphospecies’ sorting. *Biodiversity and Conservation* **13**: 795-812.
- KURTZMAN, C.P. 1994. Molecular taxonomy of the yeasts. *Yeast* **10**: 1727-1740.
- MALLET, J. & K. WILLMOTT. 2003. Taxonomy: renaissance or Tower of Babel? *Trends in Ecology and Evolution* **18**: 57-59.
- MAYO, S.J.; R. ALLKIN; W. BAKER; V. BLAGODEROV; I. BRAKE; B. CLARK; R. GOVAERTS; C. GODFRAY; A. HAIGH & R. HAND. 2008. Alpha e-taxonomy: responses from the systematics community to the biodiversity crisis. *KEW Bulletin* **63**: 1-16.
- MILLER, S.E. 2007. DNA barcoding and the renaissance of taxonomy. *Proceedings of the National Academy of Sciences* **104**: 4967-4972.
- O’CONNELL, S. 2008. DNA barcoding all our flora and fauna. *Daily Telegraph Online* **21 Oct 2008**. Available online at: <http://www.telegraph.co.uk/science/science-news/3353660/DNA-barcoding-all-our-flora-and-fauna.html> [Accessed: 06/IV/2010]
- OGILVIE, M. 2007. New frontier for DNA team: A bar code for every animal. *Toronto Star* **15 September 2007**. Available online at: <http://www.thestar.com/article/256975> [Accessed: 06/IV/2010]
- PACKER, L.; J. GIBBS; C. SHEFFIELD & R. HANNER. 2009. DNA barcoding and the mediocrity of morphology. *Molecular Ecology Resources* **9**: 42-50.
- PADIAL, J.M. & I. DE LA RIVA. 2007. Integrative taxonomists will use and produce DNA barcodes. *Zootaxa* **1586**: 67-68.
- PAGE, L.M. 2006. Planetary Biodiversity Inventories: A Response to the Taxonomic Crisis. Available online at: <http://www.actionbioscience.org/biodiversity/page.html> [Accessed: 06/IV/2010]
- PIGLIUCCI, M. 2002. *Denying Evolution: Creationism, Scientism and the Nature of Science*. Sunderland, Sinauer.
- RACH, J.; R. DESALLE; I.N. SARKAR; B. SCHIERWATER & H. HADRYLS. 2008. Character-based DNA barcoding allows discrimination of genera, species and populations in Odonata. *Proceedings of the Royal Society B* **275** (1632): 237-247.
- ROSA, D. 1918. *Ologenesi*. Firenze, Bemporad, p. XI, 305.
- ROSEN, D.E. 1979. Fishes from the uplands and intermontane basins of Guatemala: revisionary studies and comparative geography. *Bulletin of the American Museum of Natural History* **162**: 267-376.
- RUBINOFF, D. 2006. Utility of mitochondrial DNA barcodes in species conservation. *Conservation Biology* **20**: 1548-1549.
- SAVOLAINEN, V.; R.S. COWAN; A.P. VOGLER; C.K. RODERICK & R. LANE. 2005. Towards writing the encyclopedia of life: an introduction to DNA barcoding. *Philosophical Transactions of the Royal Society* **360**: 1805-1811.
- SCHANDER, C. & E. WILLASSEN. 2005. What can biological barcoding do for marine biology? *Marine Biological Research* **1**: 79-83.
- SCHRAM, F.R. 2007. Taxonomy/Systematics in the 21st Century, p. 21-32. *In*: T.R. HODKINSON & J.A.N. PARNELL (Eds). *Reconstructing the tree of life: taxonomy and systematics of species rich taxa*. Baton Roca, CRC Press.
- SCOBLE, M.J. 2004. Unitary or unified taxonomy? *Philosophical Transactions of the Royal Society B* **359**: 699-710.
- SMITH, V.S. 2005. DNA Barcoding: Perspectives from a “Partnerships for Enhancing Expertise in Taxonomy” (PEET) Debate. *Systematic Biology* **54** (5): 841-844.
- SMITH, V.S. 2008. The new taxonomy. *Systematic Biology* **57** (4): 660-663.

- SONG, H.; J.E. BUHAY; M.F. WHITING & K.A. CRANDALL. 2008. Many species in one: DNA barcoding overestimates the number of species when nuclear mitochondrial pseudogenes are coamplified. **Proceedings of the National Academy of Sciences** **105** (36): 13486-13491.
- STOECKLE, M.Y. & P.D. HEBERT. 2008 Barcode of life. **Scientific American** **299**: 82-86.
- STUESSY, T.F. & C. KÖNIG. 2008. Patrocladistic classification. **Taxon** **57**: 594-601.
- TAUTZ, D.; P. ARCTANDER; A. MINELLI; R.H. THOMAS & A.P. VOGLER. 2003. A plea for DNA taxonomy. **Trends in Ecology and Evolution** **18**: 70-74.
- VALDECASAS, A.G.; S. CASTROVIEJO & L.F. MARCUS. 2000. Reliance on the citation index undermines the study of biodiversity. **Nature** **403**: 698.
- WILL, K. 2005. The Perils of DNA Barcoding and the need for integrative taxonomy. **Systematic Biology** **54** (5): 844-851.
- WILLIAMS, D.M. & M.C. EBACH. 2008. **Foundations of Systematics and Biogeography**. New York, Springer.
- WILSON, E.O. 1971. The plight of taxonomy. **Ecology** **52**: 741-741.
- WILSON, K.H. 1995. Molecular biology as a tool for taxonomy. **Clinical Infectious Diseases** **20** (Suppl.): 192-208.
- WINSOR, M.P. 2006. The creation of the essentialism story: an exercise in metahistory. **History and Philosophy of the Life Sciences** **28**: 149-174.

Malte C. Ebach^{1, 3} & Marcelo R. de Carvalho²

¹ School of Biological, Earth and Environmental Sciences, University of New South Wales. Sydney, NSW 2052, Australia. E-mail: mcebach@gmail.com

² Departamento de Zoologia, Instituto de Biociências, Universidade de São Paulo. Rua do Matão, Travessa 14, no. 101, 05508-900 São Paulo, São Paulo, Brazil. E-mail: mrcarvalho@ib.usp.br

³ Corresponding author.

Submitted: 02.XII.2009; Accepted: 30.III.2010.

Editorial responsibility: Walter P. Boeger