Molecules, museums and vouchers

Many ecologists and evolutionary biologists are in the habit of depositing in natural history museums voucher specimens of the organisms they study. They do this partly to provide a long-term record of their work and partly as a hedge against changes in taxonomy which could alter the interpretation of their results (for example, when a single species turns out to be several, or vice versa). The explosion of DNA-based research in systematics, ecology and population genetics is raising a number of issues about vouchers for molecular studies and the use of traditional morphological collections for DNA work. In parallel with the explosion in molecular work is an equally rapid infiltration of information technology into biology and natural history museums, which brings with it new questions about what information is to be collected and how it is to be distributed. Recent correspondence in the journal *Molecular Phylogenetics and Evolution*[1,2,3] highlights many of these concerns.

To sample, or not to sample?

The discussion centres around what questions natural history museums should be asking of molecular workers using 'loans' of archived material. I use quotes because molecular work entails partial, or, in the case of very small organisms, total destruction of a specimen. Destructive sampling of museum specimens is nothing new – morphologists often need to employ destructive techniques to see the structures they are interested in. The information obtained in this way adds value to the original collection and justifies its retention. The decision to allow destructive sampling of a specimen should rest ultimately with the curator of the collection. Responsibility for justifying the need for such sampling lies with the investigator making the request. There are many reasons why one might want to use a museum specimen for a particular project. These include the obvious (and increasingly common) case of extinct species[4–7], and situations where the time dimension available in some collections can be useful. An example of this is the search for the Lyme disease bacterium (*Borrelia burgdorferi*) in museum specimens of the deer tick, (*Ixodes dammini*) collected over several decades[8]. The bacterium was found in ticks collected well before the disease was recognized in the US.

Pääbo *et al.*[9] gave criteria they felt should be considered when making the decision to allow destructive sampling for molecular work: '(1) scientific value and feasibility of the project; (2) qualifications of the investigator/laboratory to do the research; (3) availability of samples from living collections or wild populations; (4) volume of material in the collection relative to that requested; and (5) museum staff effort required to fulfil the terms of the loan.' Whitfield and Cameron[1] reiterated these, and added to (3) above consideration of the 'need to kill or disable wild-caught individuals'. Factors such as the type-status, historical importance and rareness will also influence the decision to allow destructive sampling of a particular specimen.

What should come back to the museum?

Whitfield and Cameron[1] want to see the original specimen labels returned, along with a description of how DNA (or other molecule) was extracted and processed, where the samples are kept, references to the resulting publications, and GenBank accession numbers for any DNA sequence data. They want to make sure that molecular results are 'associated with actual morphological specimens from the same population or sample'. They stop short of asking for the return of molecular samples because at present few museums have the capability or experience to handle their long-term storage. Hafner, in his response[2], disagrees strenuously with this last point and states emphatically:

> DNA extracts from museum specimens must be returned to the museum or, if the museum is unable to store the extracts, they must be deposited in another accredited tissue collection with appropriate cross-reference to the original specimen.

He offers the frozen tissue collection at his own institution, Louisiana State University, as an example of a collection willing and able to take in DNA extracts for long-term preservation.

Many natural history museums are struggling to meet their traditional responsibilities of maintaining and making available their collections. It is not reasonable to expect them to take on new and expensive functions without additional resources. While we all hope that funding for museums will increase some day, the need is here now, and it is to be hoped that the community spirit shown by Hafner and others will spread further.

The related matter of the expense of making loans is becoming more important as the use of collections continues to increase. Everyone wants free loans of material to continue because, in spite of inevitable asymmetries in numbers of specimens moving between institutions, it is clearly best for systematics as a whole. Molecular work is expensive compared to most studies of morphology (ignoring for the moment the substantial costs involved in collecting and maintaining specimens), and often requires grant funding. It is a simple matter to include a request for a little more money to help cover the costs of loans and returns of DNA. Not so simple, perhaps, is educating grant-giving bodies of its importance.

Hafner[2] plays down the importance of returning data to the museum providing the sample, pointing out that the only essential information is the museum name and the specimen registration number. Whitfield and Cameron[3] respond by noting that many museums are 'required to document the publications that have resulted from loans of their specimens' as part of the justification for their continued funding. Apart from already existing requirements, they outline the benefits of having all the information associated with specimens in one place. These benefits are especially important for studies of biodiversity, ecology and endangered species. In addition, returning data to the source museum would facilitate the incorporation of molecular data into specimen-based databases.

The Natural History Museum (NHM) London, has developed a policy for the use of its specimens for molecular studies and specifies precisely what is expected in return (including aliquots of DNA, sequence data and publications). A database of this information is under development in conjunction with the NHM's frozen tissue and DNA collection, and it will tie into the museum's growing array of collections databases. Other museums already have, or are developing similar systems and we can look forward to the day when much of this information will be available over the Internet.

The future

Whitfield and Cameron[1] point to the need for information retrieval systems to link molecular data with actual biological material. Fortunately, efforts to improve these links are already under way. Higher-level databases, containing information about multi-species or population studies, are under development or are well ahead in the planning process. The Sequences, Sources, Taxa (SST) database, under development at the Institute for Genomic Research in Maryland[10], USA,

will contain multiple sequence alignments, along with associated collection and voucher information. SST is part of a suite of databases located at TIGR which will ultimately be available over the Internet. TreeBASE, a database for phylogenetic trees from published taxonomic studies, both molecular and morphological, is under development by M. Sanderson, T. Eriksson, W. Piel and M. Donoghue[11]. It is intended as a tool to facilitate comparative studies in systematics. A key feature of both these efforts is that they point back to the final arbiter, a curated specimen in a collection. Natural history museums will, as Whitfield and Cameron[1] say, 'play a continuing major role in organising systematic knowledge in the molecular age'.

Acknowledgements
I thank Sydney Cameron for her comments on the manuscript.

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Species as 'noise' in community ecology: do seaweeds block our view of the kelp forest?

A new text on biological oceanography[1] notes that communication between marine biologists and physical scientists is hindered because physical scientists focus first on the 90% similarities among their systems before they pursue the 10% dissimilarity, while biologists focus first on minute dissimilarities and are less aware of the 90% similarity. What constitutes a minute versus a critical dissimilarity will, of course, be a subject of considerable debate. A new study by Steneck and Dethier[2] calls for marine biologists to focus more on these similarities. They argue that species are the 'noise' of community ecology and that variance that looks unpredictable when one considers individual species becomes predictable and can be generalized if one considers functional groups of organisms – with functional groups being defined by a few general organismal features of overriding importance, such as body plan, behavior or life history.

The foundations of modern community ecology were based on studying the unique attributes of each species. Gause's[3] laboratory experiments involving competition between closely related species of protozoa produced the competition exclusion principle stating that no two species can coexist on the same limiting resource. Hutchinson[4] asked how so many species coexisted and answered that it was the uniqueness of each, which resulted in some nonoverlapping niche space, that prevented competitive exclusion. MacArthur[5] demonstrated this by concentrating on small differences, not large similarities, in habitat use among warblers. Despite the powerful conceptual impact and continued utility of these studies, recent investigators[6–8] have argued that several species within a community may be so similar as to be functionally equivalent, and that vagaries of recruitment time and priority effects may have larger impacts on community composition than modest differences in each species' niche.

If functional groups can be erected based on a few characteristics that are ecologically meaningful, then these may be a way of productively using both the species-specific and the functional-group approaches. Investigators could use the functional-group approach to see more clearly the large ecological forces that cause changes in distribution, abundance and diversity of functional groups, and they could then focus more closely on those species-specific differences that are important in determining interactions within a functional group.

In the early 1980s, seaweed ecologists noted that algal morphology and anatomy were correlated with several important ecological characteristics, such as productivity, thallus longevity and susceptibility to herbivory[9,10] (Fig. 1). This observation allowed seaweeds to be placed into polyphyletic functional groups with similar ecological characteristics, and often with similar responses to perturbations such as wave force, desiccation or herbivory[9–14]. These functional groups differed from guilds in that they were based on morphological traits that affected ecological performance rather than on similarity in resource use.

Steneck and Dethier[2] suggest that (a) two environmental parameters (productivity and disturbance potential) have a disproportionately strong effect on the structure of algal communities, (b) these structuring processes impinge on seaweeds in a form-specific manner, and (c) their model of how seaweed functional groups interact with these environmental parameters provides a simple way either to predict algal community structure based on only two environmental axes, or conversely, to learn about important environmental rigors affecting a habitat by examining the form of the common seaweeds. Productivity potential of a site is determined by factors contributing to the maximum possible rate of biomass production (light, nutrients, desiccation, water motion, etc.), while disturbance potential is determined by factors controlling the maximum possible rate of biomass loss (in this study, they address only herbivory, but note that abiotic disturbances could also be considered).

To evaluate the utility of their approach, the authors grouped algae into the forms shown in Fig. 1 and studied the distribution and abundance of these functional groups in three geographically and biologically distinct regions – the high intertidal to deep (30 m) subtidal along the coast of Maine in the western North Atlantic, the high to low intertidal on the coast of Washington state in the eastern North Pacific, and subtidal Caribbean reefs in St Croix and Jamaica (depths of 0–40 m and 1–10 m, respectively).

In each of these habitats, they determined algal percentage cover, canopy height and biomass as a function of depth or height in the intertidal. They also measured potential productivity along

