these will develop on their own outside the museum sphere (e.g., GenBank for DNA sequences), and properly designed databases will be cross-referenced with museum voucher specimens. Because museums curate specimens, not publications, it strikes me as backward (not to mention wasteful) to encourage a scientist to send reprints of a molecular publication to the museum while permitting the scientist to discard the molecular extract(s) upon which the study was based.

I certainly appreciate and support Whitfield and Cameron's desire to maintain the important linkage between biological specimens and data generated from those specimens, but I would remind them that such a mechanism already exists in the form of the "specimens examined" section of a research publication, which lists specimens by museum voucher number. Unfortunately, the excitement and rapid pace of research in molecular biology have caused many scientists (as well as editors of molecular-oriented journals) to lose sight of the importance of voucher specimens as the ultimate source for data verification. In short, I believe that molecular data that lack this essential documentation should not be published.

For whatever reason, the research community seems to be largely unaware of the existence of museum repositories for their molecular samples; perhaps this letter—and the list of collections that will appear in the next edition of the Hillis and Moritz (1990) book—will help spread the word. Given the existence of ready and willing repositories for molecular samples, Whitfield, Cameron, and other concerned scientists can now take a firmer policy stance on the issue of molecular extracts taken from museum specimens. In that spirit, I recommend that the following policy be adopted by all museums that permit destructive sampling of their specimens: *DNA and other molecular samples extracted 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 molecular collection with appropriate cross-references to the original voucher specimen.* I would argue that appropriate repositories are already in place, and I offer the LSU collection as one example. This is the loan policy under which our collections operate, and I understand that more and more curators are awakening to the realization that molecular extracts are bona fide components of the original specimen and, as such, should be returned to the museum (or an alternate repository) for long-term preservation.

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Authors' Response to Hafner

To the Editor:

Dr. Hafner has pointed out the importance of long-term tissue and extract storage repositories in documenting molecular systematic research and has provided additional valuable information on locations of such repositories. We do not wish to counter his arguments for the value of long-term preservation of molecular extracts; indeed, we feel strongly that vouchering molecular research projects by deposition of extracts will become increasingly important in the future and should be encouraged, perhaps, as he suggests, required. We thank him for responding to our suggestions and for offering additional useful recommendations.

We wish to clarify, however, our position (requirement 1 under "What should museums require back?") that a museum's loan policy should include submission of the unused remains of specimens used for DNA research and that the place of deposition of the molecular extracts should also be provided (requirement 2). Dr. Hafner appears to have missed these points in suggesting that we would allow scientists to discard the molecular extracts.

We also wish to comment on several of his assertions about the roles of museums in documenting research, and on how these roles influence loan policies. Specifically:

1. Museums *are* in fact often required to document the publications that have resulted from loans of their specimens. Not only is such documentation often required for obtaining NSF or other grant funding for collection support, but it is often also required by the institutions to which the museums may be attached.

Many museums request copies of publications resulting from loans of their specimens as part of the loan agreement.

2. Even were such documentation not required, it would still be desirable to have documentation available for tracing the fate(s) of specimens originating from the same collecting lot or series, so that this information is easily available to future researchers on the group or collecting site. Such documentation might appear irrelevant for higher level phylogenetic research, but would not be so for biodiversity, ecological, or endangered species studies. Often other faunistic, ecological, or behavioral data associated with specimens are as valuable as the DNA sequences or morphological characters obtainable from them. Much recent discussion in the systematics collection community has focused on sharing specimen data through common databases (even extending to using common specimen numbering schemes such as barcodes). The goal has been to make all data obtained from, or along with, each taxonomic collection or specimen, retrievable without having to repeatedly dig through widely scattered literature, multiple museums, and notebooks kept by various researchers. To reach this goal the data must be available from some common source, be it a museum collection or a computer database. Museums are in a unique position to organize and maintain these data.

Dr. Hafner has emphasized the wastefulness of not saving DNA extracts; the same logic applies to other specimen information and data as well. We strongly disagree with Dr. Hafner's statement that research museums do (or should) not focus on data associated with their specimens. We concur, however, with his recommendations for depositing molecular extracts as vouchers in museums equipped for long-term storage of such material.

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Xantusiid Lizards, Concern for Analysis, and the Search for a Best Estimate of Phylogeny: Further Comments

To the Editor:

Hedges *et al.* (1991) employed mtDNA sequence data to address the phylogenetic relationships within the lizard family Xantusiidae and concluded that the study provided ". . . the first robust estimate of intergeneric relationships in this family. . . ." Crother and Presch (1992; CP for the remainder) disagreed, with criticisms on analytical points. In addition, CP commented on the employment of multiple data sets to obtain a best estimate of phylogeny. After reanalysis of the molecular data alone and in combination with morphological data, CP concluded that the phylogeny of xantusiid lizards remained unresolved.

Hedges and Bezy (1993; HB for the remainder) subsequently responded to the criticisms of CP and included additional data bearing on xantusiid phylogeny. Here we address some of HB's responses, especially where they bear on analytical points.

HB are to be applauded for adding more mtDNA data and for detailing some of the controversial morphological characters. Based on the additional data, we agree that some of the questions of xantusiid phylogeny are probably resolved but that other problems remain. The hypothesis of *Lepidophyma* as the sister taxon to *Cricosaura* seems likely to have been an incorrect estimate by Crother *et al.* (1986). *Lepidophyma* appears to be the sister taxon of *Xantusia*. What remains unresolved are the relationships with the genus *Xantusia*.

Morphology and Linear Transformation Series

HB questioned the informativeness of four morphological characters because they were ordered into linear transformation series. They cite Hauser and Presch (1991) to suggest that such ordered transformations may not be appropriate. Slowinski (1993) demonstrated that ordered characters increase resolution relative to unordered characters and that whenever reasonable, ordered characters should be employed. Ordered characters are not analytically problematic, but in fact are potentially beneficial to phylogenetic analysis.

Distant Outgroups

HB included sequence of the chicken *Gallus gallus* in their reanalysis to provide a second outgroup. The inclusion of distant outgroups in DNA sequence studies has been shown to be inappropriate (Wheeler, 1990; DeBry, 1992). Wheeler (1990) pointed out that if the outgroup is too distant relative to a constrained ingroup (such as xantusiids), the outgroup sequence may be equivalent to a random collection of character states and not a reflection of history.

Neighbor-Joining Phylogeny Estimates

Phylogenetic analysis attempts to recover a singular historical pattern. Given a data set comprising all possible characters, the recovery of that pattern should be possible. However, given that data sets used to reconstruct phylogeny are small, the probability of accu-