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Reply from M. Edwards and D.R. Morse

To state that the burden of biodiversity research is description not identification is too simplistic. The starting point for recognizing a new species is identification, or rather failure to achieve an identification. Therefore, the identification process could be taken to encompass both identification and description.

There are three possible approaches to using computers to support identification and description. First, the approach that we outlined¹ aims to reduce the number of specimens examined by expert taxonomists. For example, under the INBio structure² part of the load on expert taxonomists is taken by parataxonomists and generalist taxonomists who filter out well-known species from reaching the expert. This filtering process could be improved by the intelligent use of computer-aided identification tools, although this does increase the cost of using parataxonomists³.

The second approach involves the development of software specifically to support the identification and description of new species. Software capable of manipulating species descriptions has two requirements. First, the descriptions must be available electronically (either on CD-ROM or over the Internet); usually this is not the case. Second, if the description is to be manipulated and compared with other descriptions, it implies that the data within the descriptions is structured and organized (using, for example, the DELTA format⁴). This implies the conversion of existing descriptions to the required format. The development of AI tools to assist with the description of new species is an extension of the 'expert systems' approach to species identification. As we noted¹, expert systems are, unfortunately, the most time-consuming tool to produce, requiring considerable input – and therefore time commitment – from expert taxonomists. We agree that 'This may be the future, but it is not the present' because it is a hard and potentially expensive problem.

The third approach to computer-aided identification would be to note the close relationship between identification of known and unknown species, and therefore to extend computer-aided identification tools to support the identification and description of new species. For example, the species × character matrix of

a multi-access key could be used to establish combinations of characters that would indicate a new species. On identifying a new species, a taxonomist would be able to update the matrix, enabling a description of the new species to be produced. For example, software associated with the DELTA format may be used to generate descriptions, conventional dichotomous keys or multi-access keys⁴. Similarly, with a suitable user interface, an expert may be able to update both hypertext keys and expert systems during the identification process. Clearly the updating facilities of such tools should only be available to expert taxonomists.

We suggest that the third approach is most appropriate for integrating routine identification with the identification of new species because it recognizes the link between the two tasks. It is also cheaper (but less effective in the long term) than developing AI tools to support the description of new species. Finally, it has the advantage that the expert is not required to use different tools depending on whether the current task is identification or description.

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The sensory exploitation hypothesis

Recently in *TREE*, Shaw¹ reviewed Ryan's² phylogenetic method for testing the sensory exploitation hypothesis. Here, we explain why the method is not a general test of the hypothesis.

The sensory exploitation hypothesis proposes a historical sequence: preferences evolve first, followed by the traits that elicit them because of sexual selection by female choice. The only selection necessary for sensory exploitation acts on male traits. The hypothesis contains no particular conceptions about the causes of preference evolution. Preferences may evolve for many reasons, before and after they mediate mate choice². Those most often discussed are selection in non-mating contexts, Fisher's or good-genes processes, and pleiotropy.

Ryan's method detects preference pre-existence only if preferences do not evolve during cladogenesis, and the preferred male trait evolves in some but not other descendant species. These are necessary conditions for the

method to show that sensory exploitation has occurred. They are not, however, necessary conditions for sensory exploitation. The sensory exploitation hypothesis predicts neither preference stasis (or change) nor the distribution of the preferred male trait among species in a clade. Hence, the method is not a general test for sensory exploitation because it cannot detect preference pre-existence if preferences evolve once they mediate mate choice, or if the male trait evolves in all species in a clade². The conditions necessary for Ryan's method to detect sensory exploitation clearly are not predictions of the sensory exploitation hypothesis.

Unfortunately, in their recent *TREE* letter³, Sherman and Wolfenbarger confounded the two. They incorrectly stated that 'sensory exploitation posits that fixed female preferences drive sexual selection' and that evidence of preference plasticity is inconsistent with the sensory exploitation hypothesis. Preference plasticity is as consistent with sensory exploitation as is preference stasis. The reasons why some preferences may^{2,4–8}, and others may not^{9,10}, evolve once they mediate mate choice are outside the explanatory domain of the sensory exploitation hypothesis.

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Parasitic infection of migratory bird species

Loye and Carroll¹ recently correctly pointed out that parasitism deserves a more prominent role in avian conservation biology. They presented a number of hypotheses as to why bird species and individuals in habitat fragments should be more susceptible to parasitic infections (they considered mainly ectoparasites but their arguments seem to apply to endoparasites and disease vectors as well) than those individuals in similar but continuous habitats. Many North American bird species that are adversely affected by forest fragmentation are migratory^{2,3}. These bird species are apparently experiencing long-term population declines⁴ and are incorporated increasingly into conservation projects⁵.