

- [ScienceWatch Home](#)
- [Inside This Month...](#)
- [Interviews](#)

- [Featured Interviews](#)
- [Author Commentaries](#)
- [Institutional Interviews](#)
- [Journal Interviews](#)
- [Podcasts](#)

**Analyses**

- [Featured Analyses](#)
- [What's Hot In...](#)
- [Special Topics](#)

**Data & Rankings**

- [Sci-Bytes](#)
- [Fast Breaking Papers](#)
- [New Hot Papers](#)
- [Emerging Research Fronts](#)
- [Fast Moving Fronts](#)
- [Research Front Maps](#)
- [Current Classics](#)
- [Top Topics](#)
- [Rising Stars](#)
- [New Entrants](#)
- [Country Profiles](#)

**About Science Watch**

- [Methodology](#)
- [Archives](#)
- [Contact Us](#)
- [RSS Feeds](#)



Interviews

Analyses

Data & Rankings

2008 : December 2008 - Fast Breaking Papers : L. Lacey Knowles

**FAST BREAKING PAPERS - 2008**

December 2008



**L. Lacey Knowles talks with *ScienceWatch.com* and answers a few questions about this month's Fast Breaking Paper in the field of Environment & Ecology.**



**Article Title: Delimiting species without monophyletic gene trees**

Authors: Knowles, LL; Carstens, BC

Journal: SYST BIOL

Volume: 56

Issue: 6

Page: 887-895

Year: DEC 2007

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**SW: Why do you think your paper is highly cited? Does it describe a new discovery, methodology, or synthesis of knowledge?**

There is tremendous interest in the use of genetic data for distinguishing species. The paper describes a new framework in which genetic data can be used to delimit species. The approach differs from past methods in that it is based on an explicit model of species divergence, as opposed to relying on arbitrary criteria for making inferences about species boundaries. As a consequence, it provides an approach for species delimitation which doesn't require that species exhibit monophyletic gene trees.

**SW: Would you summarize the significance of your paper in layman's terms?**

Genetic data can offer a valuable tool for identifying species. However, the way in which genetic data is interpreted can lead to misleading conclusions, and specifically a failure to recognize species.

Unlike previous methods, the approach described in our paper explicitly considers how patterns of genetic variation change over time following the formation of new species. Such an approach is not only effective at inferring species boundaries, but it also avoids the problems associated with previous methods that rely on arbitrary levels of genetic distinctiveness for delimiting species.

**SW: How did you become involved in this research, and were there any problems along the way?**

My research focuses on groups of taxa that have recently speciated. Because of their recent origin, such taxa would not be recognized based on previous genetic methods that rely on arbitrary levels of genetic distinctiveness for delimiting species. Given that population genetic models are routinely employed to make inferences about the

*"As species are being lost at an alarming rate and the fate of many taxa rests on conservation initiatives, the need for accurate species delimitation has never*

demographic and biogeographic past, it seemed that such models could naturally be extended to the species delimitation problem.

*been  
greater."*

**SW: Where do you see your research leading in the future?**

In the future, the framework developed for genetic data could be used to incorporate the temporal dynamics of morphological and behavioral data. In such a context, the lack of concordance of genetic, morphological, and behavioral data arising from differences in rates of change among data types can be distinguished from true conflict among data sets. Such a framework would represent a significant step towards a unified approach for species delimitation.

**SW: Do you foresee any social or political implications for your research?**

As species are being lost at an alarming rate and the fate of many taxa rests on conservation initiatives, the need for accurate species delimitation has never been greater. Genetic data has the potential to significantly aid in this endeavor. However, methodological approaches need to take into account how patterns of genetic variation change over time to avoid misleading inferences about species boundaries.

**L. Lacey Knowles**

**Associate Professor and Curator of Insects  
Department of Ecology and Evolutionary Biology  
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**Related information:** [Read](#) a New Hot Paper comment from Lacey Knowles from March 2004.

Keywords: genetic data can be used to delimit species, species divergence, species delimitation, monophyletic gene trees.



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[back to top](#)

2008 : [December 2008 - Fast Breaking Papers](#) : L. Lacey Knowles

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