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TRACKING TRENDS & PERFORMANCE IN BASIC RESEARCH

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2009 : January 2009 - Hew Hot Papers : Daniel Falush

NEW HOT PAPERS - 2009

November 2009



Daniel Falush talks with *ScienceWatch.com* and answers a few questions about this month's New Hot Paper in the field of Environment/Ecology.



Article Title: Inference of population structure using multilocus genotype data: dominant markers and null alleles

Authors: Falush, D;Stephens, M;Pritchard, JK

Journal: MOL ECOL NOTES

Volume: 7

Issue: 4

Page: 574-578

Year: JUL 2007

* Univ Oxford, Peter Medawar Bldg Pathogen Res, Oxford OX1 3SY, England.

* Univ Oxford, Oxford OX1 3SY, England.

* Univ Chicago, Dept Human Genet, Chicago, IL 60637 USA.

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

Because it allows people with a particular data type (AFLPs) to use the popular STRUCTURE software package, a free software package for using multi-locus genotype data to investigate population structure. This paper describes a new **methodology**.

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

People who work on variation in non-model, non-medically important organisms, typically in the molecular ecology field, often use technologies for assaying genetic variation that are cheap and informative but contain some inherent ambiguity. For example, AFLPs. Our paper gives access to more powerful analysis methods for people using these marker types.

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

I really regarded this as being service for the community. I personally work on bacteria and humans, where AFLPs are not used. The paper was rejected from the journal *Molecular Ecology* on the unusual grounds of it being "too short." It then sat in my cupboard for more than two years. Eventually, they changed the format of *Molecular Ecology Notes* (and later changed the name to *Molecular Ecology Resources*) to allow methodology papers of all descriptions—including shorter ones—and this impasse was resolved. This is my chance to apologize to all those who had to wait for the new methodology or had to make do with something else before this was finally published.

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

We have been developing methods that use the very rich signals of ancestry in dense

marker data to make inferences about relationships between individuals and populations that are considerably more detailed and refined than are possible with STRUCTURE. We can clearly identify and date specific events (e.g., the Mongol expansion in humans) and identify biologically informative variation in patterns of gene flow. STRUCTURE represents a great success in making methods available to a broad community, but unfortunately it will be a challenge to make these more sophisticated methods available to those without substantial computing and bioinformatic resources.

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

It is very important that people continue to work on non-model, non-medical organisms, and that we have a fuller picture of the patterns of diversity across all of life. In the modern world, if people are not made aware of what is out there and that it should be valued, then it is probably in danger.

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"In the modern world, if people are not made aware of what is out there and that it should be valued, then it is probably in danger."

Keywords: STRUCTURE software package, multi-locus genotype data, population structure, molecular ecology, biologically informative variation in patterns of gene flow.



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