



Newsletter of the National Evolutionary Synthesis Center, an NSF-funded collaborative research center operated by Duke University, the University of North Carolina at Chapel Hill, and North Carolina State University.

UPCOMING DEADLINES:

JULY 1: graduate fellowships; short-term visitor proposals

JULY 10: meetings, sabbaticals, and course proposals

DECEMBER 1: meetings, sabbaticals, and postdoctoral fellowships

For more information, turn to page 2-3 or visit nescent.org/science/proposals.php

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ABOUT NESCENT:

NESCent is a scientific research center dedicated to cross-disciplinary research in evolution. Funded by the National Science Foundation (award #EF-0905606), NESCent is a collaborative partnership between Duke University, the University of North Carolina at Chapel Hill, and North Carolina State University. For more information about research and training opportunities at NESCent, visit www.nescent.org

SENIOR LEADERSHIP:

Allen Rodrigo Director

Susan Alberts Associate Director of Science and Synthesis

Todd Vision Associate Director of Informatics

Brian Wiegmann Associate Director of Education and Outreach

RESEARCH HIGHLIGHTS

Flowering plants may be much older than we think

Debates over different approaches to dating tree of life



A new analysis of the land plant family tree suggests that flowering plants may be considerably older than the fossil record suggests. PHOTO BY ERIC GREENE

Flowering plants may be millions of years older than previously thought, says a new study by NESCent postdoc Stephen Smith and colleagues.

Previous studies suggest that flowering plants, or angiosperms, first arose 140 to 190 million years ago. Now, a paper published in *Proceedings of the National Academy of Sciences* pushes back the origin of angiosperms to 215 million years ago, some 25 to 75 million years earlier than either the fossil record or previous molecular studies suggest.

“If you just looked at the fossil record,

you would say that angiosperms originated in the early Cretaceous or late Jurassic,” said Michael Donoghue of Yale University. “Most molecular divergence times have shown that they might be older than that,” added Yale biologist Jeremy Beaulieu. “But we actually find that they might be Triassic in origin,” said Beaulieu. “No one has found a result like that before.”

If confirmed, the study could bolster the idea that early angiosperms promoted the rise of certain insects. Modern insects like

see **FLOWERS**, p7

Letter from the Director

At the end of last year, NESCent was re-funded by the National Science Foundation for another five years. This means that we can continue to work with scientists and educators to ensure that evolutionary research expands beyond traditional boundaries and disciplines, that we are able to reach young and energetic



ALLEN RODRIGO
DIRECTOR

students and emerging researchers, and that we can continue to foster links between colleagues across the nation and the globe. In February this year, I took over as Director from Kathleen Smith.

We also have a new Associate Director of Science and Synthesis: Susan Alberts takes the reins from Joel Kingsolver. For Susan and me, it has been a painless transition, thanks to Kathleen's and Joel's professionalism and commitment to NESCent and its future.

So where does NESCent go from here?

What are our plans for the next five years? Let's take a step back. NESCent recognises that its most valuable resource is the community that stands behind it. And so, whether we are designing courses, or deciding what new areas of evolutionary science deserve our attention, we want to hear from you. In this issue, you will see details on how you can let us know what you think we should deliver.

NESCent will continue to support interdisciplinary research through its program of Catalysis Meetings and Working Groups. We have a vibrant group of postdoctoral scholars, sabbatical fellows and short-term visitors who make NESCent an exciting venue for creative thinking. We have allocated additional resources to support Working Groups with tasks and activities that need to be undertaken between meetings. Additionally, we will support graduate students for a semester, if they work on Working Group projects or with members of NESCent's in-house community.

Science does not respect national bound-

aries – it is a social enterprise, and like other social networks, knowledge increases exponentially with the number of collaborations we can enlist. NESCent will strengthen its links with organisations of equivalent scope in other countries. We expect to develop opportunities for US scientists to work with their international colleagues.

Evolutionary science is entering a new and exciting phase. The parallel developments of genomic and computational technologies, and the realisation that evolutionary principles underlie everything from medicine to macroeconomics, present evolutionary scientists with more challenges and opportunities than in any other period in the discipline's history. NESCent expects to lead the charge, and I look forward to seeing you in Durham, North Carolina.

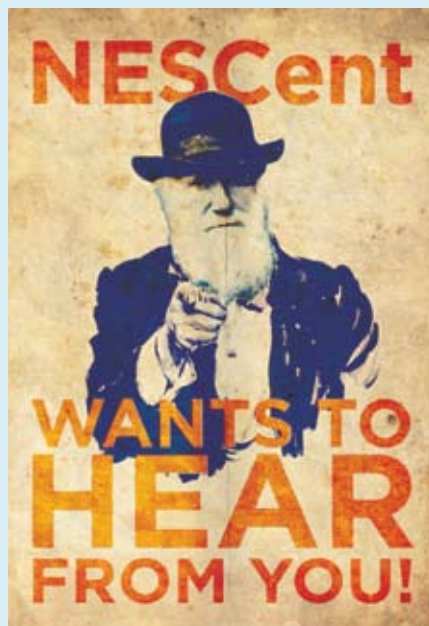
Allen Rodrigo, Director of NESCent

CALL FOR PROPOSALS

We Want You!

Looking for support for a sabbatical, postdoc, or meeting? NESCent welcomes your proposals. We are looking to support innovative approaches to outstanding problems in evolutionary biology. In particular, proposals that have a clear interdisciplinary focus, or involve evolutionary concepts in non-traditional disciplines, are strongly encouraged, as are proposals that demonstrate international participation and a mix of senior and emerging researchers, including graduate students.

NESCent is now accepting applications for postdoctoral and sabbatical fellowships, short-term visitors, and meetings. The next deadline for short-term visitors is July 1. For sabbatical fellowships, working groups, and catalysis meetings, the next deadline is July 10. For postdoctoral fellows, the deadline is December 1 annually.



New: Graduate Fellowships

Next deadline July 1

NESCent is now adding graduate training to our portfolio by offering one-semester fellowships for graduate students to pursue research, either with a NESCent sabbatical scholar or with a NESCent Working Group. The research should be in line with the goals of the sabbatical scholar and/or working group and may include integrating datasets, developing databases, performing analyses, programming and software development, etc.

Interested graduate students should consult with the Principal Investigator of a Working Group or Sabbatical scholar before submitting an application through our online proposal system.

Learn more at nescent.org/science/GraduateFellowships.php

For more information, visit nescent.org/science/proposals.php

CALL FOR PROPOSALS

Share your ideas
for evolution courses

Deadline July 10

What courses would you like to see offered to the evolution community? NESCent is expanding its course offerings and would like your suggestions. NESCent welcomes ideas and proposals for postgraduate-level short courses (1-2 weeks) on topics of relevance to synthetic evolutionary science.

Do you have a bright idea? Please let us know. Course proposals from those interested in being instructors are due July 10, 2010.

For a list of current and previous courses offered at NESCent, visit nescent.org/courses. For more information about preparing and submitting a course proposal, please visit nescent.org/courses/proposals/

Targeted sabbaticals
for faculty at minority-
serving institutions

Next deadline July 10

As part of NESCent's commitment to increasing diversity in evolutionary biology, we offer targeted sabbatical opportunities to evolutionary biologists from Minority-Serving Institutions (MSIs) to undertake projects that will increase minority participation in evolutionary science and/or develop evolution education activities.

NESCent provides stipends up to the equivalent of a full salary (monthly stipend equal to 1/12th of a 9-month salary at home institution). A housing allowance up to \$1,000/month can also be provided.

Deadlines for NESCent Targeted Sabbaticals are July 10th and December 1st each year. For more information, visit nescent.org/science/targetedsabbatical.php or contact **Dr. Jory Weintraub** (jory@nescent.org).

Job Openings

Interested in employment opportunities at NESCent? Our Center runs with the help of a dynamic team of programmers, financial experts, event planners, and other specialists. To find out about job openings as they become available, visit nescent.org/about/employment.php

UPCOMING EVENTS

Join us in June for a new conference
on evolutionary informatics**Where: Portland, Oregon****When: June 29-30, 2010**

What can biologists studying evolution and biodiversity learn from software developers and mathematicians? A lot, say the organizers of an exciting new conference on evolutionary informatics.

"Biologists have tons of fascinating questions. Mathematicians and software developers have tons of tricks and tools.

Together, they can do so much more than they could ever do on their own," said co-organizer Cecile Ane.

The National Evolutionary Synthesis Center (NESCent) and the Society for Systematic Biology (SSB) are pleased to announce a new 2-day conference, dubbed *iEvoBio*, to be held June 29-30 in conjunction with the Evolution 2010 meetings in Portland, Oregon. Those who are already attending the Evolution meetings are encouraged to extend their stay by a day and take part in what promises to be an exciting new annual event.

The organizers hope the meeting will facilitate an exchange of ideas and spur the development of new tools for answering biological questions. "We are in the age of 'big data'," said organizing committee chair Rod Page. "Whether it is the ever-growing flood of DNA sequences, the vast numbers of natural history museum specimens being digitized, or the tens of millions of pages of biodiversity literature being scanned and released onto the web. Making sense of these data requires skills in analysis, computing, and visualization, as well as the ability to ask interesting questions," said Page.

Nearly 200 people – both seasoned practitioners and newcomers to informatics – are expected to attend the inaugural meeting, which will include a series of keynote speakers, contributed talks, and

live demonstrations of informatics tools.

Attendees are also invited to compete in a 'grand challenge' to develop new methods for visualizing evolutionary data. "Evolutionary biologists now handle data sets that are so large and so complex, that just looking at the data is difficult," said co-organizer Cynthia Parr of Encyclopedia of Life.

Entries could range from geophylogenies, to visualizing extremely large phylogenetic trees, to mashups showing relationships between lineages and other types of data, the organizers say. The conference participants will vote on the winner, who will receive a \$1000 cash prize. "The entries will likely be interesting both to those who develop visual tools, but also to those who need them.

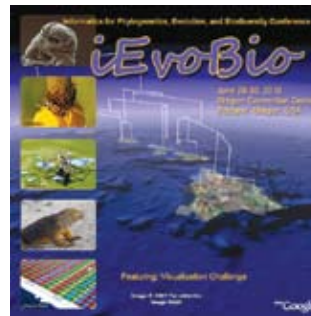
And they should be pretty to look at and fun to use," Parr added.

The organizers ask that all challenge entries be produced by software that is available as open-source. "That way, anybody can look at the source code to learn how it works," said Page. "By making the code open we ensure that people can learn from the entries. They can say 'ah, so that's how they do it,' instead of 'wow, that's really cool, but how does it work?'"

In addition to the visualization challenge, attendees can expect a range of other activities. "Birds of a feather" sessions will allow people with common interests to get together and discuss a specific topic. "We will also have 'software bazaar' so people can show off their work informally, and 'lightening talks' that are very short, 5-minute contributions, so that everyone has a chance to present," said keynote speaker Rob Guralnick.

"There has never been anything quite like *iEvoBio* in my opinion," Guralnick added. "We are sure it will continue for many years."

For more information, visit ievobio.org.



TreeBASE is back

Phylogenetic database completely rebuilt

If scientists have identified some two million species, where can you find the latest information about the tree of life that unites them all? A vastly improved database gives scientists and educators access to state-of-the-art knowledge about the evolutionary relationships among living things.

TreeBASE – a database designed to help scientists store, share, and study evolutionary trees – was first developed in the mid-1990s as way to archive the vast amounts of phylogenetic information accumulating in the literature.

“Phylogenies were being published at an explosive rate,” said Bill Piel of Yale University. “What we needed was a database where we could compile them so people could use them later.”

The database allows researchers to archive and retrieve published phylogenetic trees and data from different studies. “People can store sequence alignments, morphological character sets, and the resulting phylogenetic trees – all in digital form. They can also be recovered and reanalyzed or combined with other data,” Piel said.

Since the first prototype was developed, researchers have contributed more than 6,500 trees from over 2400 articles, describing the relationships among well over 60,000 terminal taxa. A variety of journals now require their authors to deposit phylogenetic data in TreeBASE, and peer reviewers are given anonymous access to the data prior to publication.

Now, a team of biologists and computer scientists is releasing a new version that is completely rebuilt. Years of work have gone into improving and upgrading the original version. “At some point we knew we had to make it bigger and better,” said Michael Donoghue of Yale University. With this upgrade, the database is poised to become an increasingly valuable resource for a number of fields, including conservation biology, biogeography, and education, developers say.

“We have introduced a wide variety of



After years of work spent improving the original prototype, TreeBASE has a host of new features and a new home at NESCent.

features that didn't exist before,” said Val Tannen at the University of Pennsylvania. “In terms of data deposition and how users interact with it, it has taken a huge leap forward,” Donoghue added.

For one, TreeBASE can now store much richer information. “Trees can contain information such as the length of each branch, which is important for studying the timing of evolutionary events,” Piel explained. The database also has an improved system for making sure that information such as taxonomic names and DNA sequence IDs match those found in other sources.

Researchers will also be able to take advantage of a more user-friendly interface and more advanced search techniques. “There are things you can query now that you couldn't before,” said Piel. “For example, you can search for trees that share

a certain topology.”

“The visualization tools have also received a major upgrade,” Piel added. “For example, now users can manipulate large trees and zoom in and out.”

A number of advanced features have also been introduced that will allow bioinformaticians to do new and creative things with the data without being blocked by the user interface, said Piel. These include support for new machine-readable phylogenetic data exchange and web service standards. In addition, the metadata in TreeBASE are being made available for harvesting en masse.

According to Rutger Vos of the University of Reading, “all these features basically mean that TreeBASE plays nice with other Linked Data resources on the web, allowing the next generation of web applications

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TreeBASE, continued

to automatically understand the connections among different biological data resources.”

In addition to getting a major makeover, the database also has a new home. Most recently housed at the San Diego Super-computer Center with support from the CIPRES project, TreeBASE is now being hosted by NESCent in Durham, North Carolina.

NESCent has made an initial commitment to host TreeBASE for up to five years, explained Todd Vision, Associate Director of Informatics at NESCent. “This partnership enables TreeBASE to continue serving the scientific needs of the community and to keep pace with technological innovations,” said Vision.

“We have introduced a wide variety of features that didn’t exist before.”

–Val Tannen, University of Pennsylvania

Looking to the future, the team has established a non-profit foundation to ensure the database’s long-term sustainability. “The foundation will become a caretaker of TreeBASE and other phylogenetic resources, such as the Tree of Life Web (ToLWeb) project,” said Piel.

To enable wider participation in TreeBASE’s future development, the code has been made open source and is hosted by SourceForge. The developers now communicate on a public forum. “In essence, this allows anyone with the necessary skills to participate in TreeBASE development, whether small or large,” says Hilmar Lapp, Assistant Director for Informatics at NESCent.

“The really good news is that we now have a much better product – much more stable, much more industrial-strength – and we have an arrangement with NESCent that’s going to be very successful,” Donoghue added. “Now that we have a new home for it, we can service it, we can build it, and we can continue to modify it,” he added. “This is a good place to be right now.”

TreeBASE is freely available online at www.treebase.org.

NEW AWARDS

Congratulations to the newest award recipients for 2010

NESCent is pleased to announce the following new awards:

POSTDOCTORAL FELLOWS

Peter Umack

A GIS based approach to a priori prediction in aquatic biogeography

Jenny McGuire

Examining paleontological extinction patterns to predict modern extinction vulnerability

Jennifer Verdolin

Integrating behavioral syndromes into social networks: optimal distribution of phenotypes and group stability

Clinton Francis

Acoustic signal space conservatism: a framework for signal flexibility in noise

Rafael F Rubio de Casas

Dispersal evolution in the angiosperms: the origin of heterocarpy

LONG-TERM SABBATICAL SCHOLARS

James H. Hunt (North Carolina State University)

The origins of arthropod sociality

Armin Moczek (Indiana University-Bloomington)

The nature of nurture: how environmental and genetic information interact to shape development and evolution

Dorothee Huchon (Tel-Aviv University)

Current view of rodent phylogenetic relationships

Tal Pupko (Tel-Aviv University)

Evolutionary models accounting for multi-layer selection pressures

SHORT-TERM VISITORS

Claire Williams (Forest History Society)

Domesticating forest carbon: a synthesis on forest adaptation to climate change

Shane Lavery (University of Auckland)

Connectivity of New Zealand coastal marine communities: a synthesis of datasets

CATALYSIS MEETINGS

Richard Moore (Miami University-Oxford)
Tia-Lynn Ashman (University of Pittsburgh)

Emergence of gender and sex chromosomes: evolutionary insights from a diversity of taxa

James H. Hunt (North Carolina State University)

Evolution of insect sociality: an integrative modeling approach

Greger Larson (Durham University);
Dolores Piperno (National Museum of Natural History); **Dorian Fuller** (University College-London); **Michael Purugganan** (New York University); **Robin Allaby** (University of Warwick)

Domestication as an evolutionary phenomenon: expanding the synthesis

Sarah Reece (Institutes of Evolution, Immunology and Infection Research); **Andrew Read** (Pennsylvania State University); **Nick Savill** (University of Edinburgh); **Nicole Mideo** (University of Edinburgh)

Evolution of infectious diseases: Integrating empirical and modeling approaches

WORKING GROUPS

John Gowdy (Rensselaer Polytechnic Institute); **David Sloan Wilson** (Binghamton University)

Integrating evolutionary theory with behavioral economics

MSI FACULTY TRAVEL AWARDS

James Archie (California State University, Long Beach)

Jason Munshi-South (Baruch College, The City University of New York)

Aditi Pai (Spelman College)

To apply for future faculty travel awards please visit nescent.org/eog/2010facultytravelaward.php

RECENT PUBLICATIONS

Recent publications by NESCent authors

Anthes, N., P. David, et al. (2010)

"Bateman gradients in hermaphrodites: An extended approach to quantify sexual selection." *American Naturalist*. In press.

Balhoff, J. (2010)

"Phenex: Ontological annotation of phenotypic diversity." *PLoS ONE* 5(5): e10500. doi:10.1371/journal.pone.0010500.

Dahdul, W. M., J. G. Lundberg, et al. (2010)

"The Teleost Anatomy Ontology: Anatomical representation for the genomics age." *Systematic Biology* 59. DOI:10.1093/sysbio/syq013.

Edwards, E., C. Osborne, et al. (2010)

"The origins of C4 grasslands: Integrating evolutionary and ecosystem science." *Science* 328(5978): 587 - 591.

Edwards, E. and S. Smith (2010)

"Phylogenetic analyses reveal the shady history of C4 grasses." *Proceedings of the National Academy of Sciences*. DOI:10.1073/pnas.0909672107.

Elias, D., C. Botero, et al. (2010)

"High resource valuation fuels "desperado" fighting tactics in female jumping spiders." *Behavioral Ecology*. In press.

Hazkani-Covo, E., R. Zeller, et al. (2009)

"Molecular poltergeists: mitochondrial DNA copies (numts) in sequenced nuclear genomes." *PLoS Genetics* 6(2): e1000834.

Hunt, J., F. Wolschin, et al. (2010)

"Differential gene expression and protein abundance evince ontogenetic bias toward castes in a primitively social wasp." *PLoS One*. In press.

Johnson, M. A., L. J. Revell, et al. (2010)

"Behavioral convergence and adaptive radiation: Effects of habitat use on territorial behavior in *Anolis* lizards." *Evolution* 64 (1151-1159).

Korall, P., E. Schuettpelz, et al. (2010)

"Abrupt deceleration of molecular evolution linked to the origin of arborescence in ferns." *Evolution*. DOI:10.1111/j.1558-5646.2010.01000.x.

Lacey, E. P., M. B. Lovin, et al. (2010)

"Floral reflectance, color and thermoregulation: What really explains geographic variation in thermal acclimation ability in ectotherms?" *The American Naturalist* 175: 335-349.

Laikre, L., F. Allendorf, et al. (2009)

"Neglect of genetic diversity in implementation of the convention on biological diversity." *Conservation Biology* 24(1): 86-88.

Lindenfors, P., L. J. Revell, et al. (2010)

"Sexual dimorphism in primate aerobic capacity: A phylogenetic test." *Journal of Evolutionary Biology*. DOI:10.1111/j.1420-9101.2010.01983.x.

Logsdon, J. (2010)

"No sex please." *Science* 328(5976): 310.

Logsdon, J. and M. Neiman (2010)

"Evolution of sex and recombination: in theory and practice." *The Journal of Heredity* 1(Supplement 1).

Lovely, K. R., D. L. Mahler, et al. (2010)

"The rate and pattern of tail autotomy in five species of Puerto Rican anoles." *Evolutionary Ecology Research* 12: 67-88.

Mahler, D., L. Revell, et al. (2010)

"Ecological opportunity and the rate of morphological evolution in the diversification of Greater Antillean anoles." *Evolution*. In press.

McClain, C., L. Lundsten, et al. (2010)

"Bathymetric patterns in diversity, abundance, and community structure on a Northeast Pacific Seamount." *Marine Ecology*. In press.

Meachen-Samuels, J. (2010)

"Comparative scaling of humeral cross-sections of felids and canids using radiographic images." *Journal of Mammalian Evolution*. DOI:10.1007/s10914-010-9133-y.

Plotnick, R., S. Dornbos, et al. (2010)

"Information Landscapes and Sensory Ecology of the Cambrian Radiation." *Paleobiology* 36(2): 303-317.

Pryer, K., E. Schuettpelz, et al. (2010)

"DNA barcoding exposes a case of mistaken

identity in the fern horticultural trade." *Molecular Ecology Resources*. DOI:10.1111/j.1755-0998.2010.02858.x.

Revell, L., D. Mahler, et al. (2009)

"Non-linear selection and the evolution of variances and covariances for continuous characters in an anole." *Journal of Evolutionary Biology*. In press.

Richards, C., O. Bossdorf, et al. (2010)

"What role does heritable epigenetic variation play in phenotypic evolution?" *BioScience* 60(3): 232-237.

Rosenberg, M. (2010)

"A Generalized formula for converting chi-square tests to effect sizes for meta-analysis." *PLoS ONE* 5(4): e10059.

Scott, A., F. Kenig, R. Plotnick, et al. (2010)

"Evidence of multiple late Bashkirian to early Moscovian (Pennsylvanian) fire events preserved in contemporaneous cave fills." *Palaeogeography, Palaeoclimatology, Palaeoecology*. DOI:10.1016/j.palaeo.2009.06.008.

Sidlauskas, B., G. Ganapathy, et al. (2010)

"Linking big: The continuing promise of evolutionary synthesis." *Evolution* 64(4): 871-880.

Slater, S. Price, et al. (2010)

"Diversity versus disparity and the radiation of modern cetaceans." *Proceedings of the Royal Society B*. In press.

Smith, S., J. Beaulieu, et al. (2010)

"An uncorrelated relaxed-clock analysis suggests an earlier origin for flowering plants." *Proceedings of the National Academy of Sciences*. DOI:10.1073/pnas.1001225107.

Strier, K., J. Altmann, et al. (2010)

"The Primate Life History Database: A unique shared ecological data resource." *Methods in Ecology and Evolution*. DOI:10.1111/j.2041-210X.2010.00023.x.

Williams, C. G. (2010)

"Long-distance pine pollen still germinates after meso-scale dispersal." *American Journal of Botany* 97(5): 1-11.

FLOWERS, continued

bees and wasps rely on flowers for nectar and pollen. “The fossil record suggests that a lot of these insect groups originated before angiosperms appeared,” said Stephen Smith of the National Evolutionary Synthesis Center. This study shifts the oldest angiosperms back farther in time towards the origin of groups like bees and flies, the scientists say. “If you take our dates and superimpose them on the evolutionary tree for these insect groups, all of a sudden you get a match,” said Beaulieu.

To trace the origins of flowering plants, the researchers used genetic comparisons of living plants and clues from fossils to reconstruct the relationships among more than 150 terrestrial plant species. While their results support previous age estimates for other plant groups, they suggest an older age for angiosperms. “Many of the dates that we get correspond really well to the known fossil record, at least for the origin of land plants and the origin of vascular plants and seed plants,” said Donoghue. “But we got a much older date for the origin of angiosperms – one that’s really out of whack with the fossil record,” Smith added.

“As we develop better molecular methods, people would like it if the molecular dates reconciled with the fossil record. But instead the gap is getting wider. And in the end, that might actually be interesting.”

–Michael Donoghue, Yale University

This disconnect between molecular and fossil estimates is not unheard of, the authors explained. “We see the same kind of discrepancy in other groups too, like mammals and birds,” said Donoghue.

Why the mismatch between different approaches to dating the tree of life?

One possibility, the researchers explained, is that the first flowering plants



A new study of angiosperm origins fuels ongoing debates over different approaches to dating the tree of life. PHOTO BY MILA ZINKOVA, WIKIMEDIA COMMONS

weren’t diverse or abundant enough to leave their mark in the fossil record. “We would expect there to be a time lag between their origin and when they became abundant enough to get fossilized,” said Smith. “The debate would just be how long.”

“Imagine a long fuse burning and then KABOOM! There’s a big explosion. Maybe angiosperms were in that fuse state,” said Donoghue. “But it’s hard to imagine flowering plants would have had a big impact on the origin of major insect groups if that were the case,” he added.

Another possibility, the researchers allow, is that the molecular methods may be amiss. “If the angiosperms originated 215 million years ago, then why don’t we find them in the fossil record for almost 80 million years?” said Beaulieu. “It could also suggest that our dates are wrong.”

To improve on previous studies, the researchers used a method that allows for variable rates of evolution across the plant family tree. “Older methods assume

that rates of molecular evolution don’t change too radically from one branch of the evolutionary tree to another,” Beaulieu explained. “But this newer method can accommodate some fairly major rate shifts.”

Although researchers have come up with some savvy statistical tricks to account for rate shifts, said Donoghue, the problem hasn’t entirely disappeared. “We’ve done the best analysis we know how to do with the current tools and information,” he said.

“As we develop better molecular methods, people would like it if the molecular dates reconciled with the fossil record,” said Donoghue. “But instead the gap is getting wider,” he said. “And in the end, that might actually be interesting.”

The team’s findings were published online in the March 15 issue of *Proceedings of the National Academy of Sciences*.

CITATION: Smith, S., J. Beaulieu, and M. Donoghue. (2010). “An uncorrelated relaxed-clock analysis suggests an earlier origin for flowering plants.” *Proceedings of the National Academy of Sciences* doi/10.1073/pnas.1001225107.

STAY INFORMED

In the Media

"Pine pollen gets flight miles"

(*Science News*) A new study suggests that pollen from the loblolly pine—the most commonly planted tree in the southern US—can still germinate after drifting long distances. Far-flung pollen makes it difficult to contain transgenic trees, says visiting scientist Claire Williams. sciencenews.org/view/generic/id/58360/title/Pine_pollen_gets_flight_miles

"Paradox of dining in deep, wet mud"

(*Science News*) Surplus food can be a double-edged sword for animals in the ocean deep. While extra nutrients give a boost to larger animals on the deep sea floor, the feeding frenzy that results wreaks havoc on smaller sediment dwellers buried below, says a new study by Assistant Director Craig McClain. sciencenews.org/view/generic/id/58558/title/Paradox_of_dining_in_deep_wet_mud

"Stephen Smith: the botanist hacker"

(*The Scientist*) Postdoctoral fellow Stephen Smith shows off his musical roots the-scientist.com/article/display/57180/

"Monster bug? It's no joke!" (MSNBC)

Assistant Director Craig McClain debunks myths about deep-sea isopods cosmiclog.msnbc.msn.com/archive/2010/03/31/2253964.aspx

"The Evolutionary history of jogging"

(*Duke Today*) If humans evolved to run barefoot, how do running shoes change the way we move? Evolutionary anthropologist Dan Schmitt explains how people run differently in shoes and bare feet. ondemand.duke.edu/video/21753/the-evolutionary-history-of-jogging

"DNA barcode exposes 'fake' ferns for sale"

(*Futurity*) DNA testing of garden ferns sold at plant nurseries in North Carolina, Texas, and California has found that plants marketed as American natives may actually be exotic species from other parts of the globe. Postdoctoral fellow Eric Schuettelpelz and colleagues tell the full story in the journal *Molecular Ecology Resources*. futurity.org/science-technology/dna-barcode-exposes-fake-ferns-for-sale/

Calling all K-12 teachers!

Two workshops on teaching evolution

WHAT: Evo 101: Hands on Evolution for K-12 Teachers (and college faculty)

WHEN: June 25, 2010

WHERE: Portland, OR

Science educators in the Portland area, and visitors to the area for the Evolution 2010 meetings, are invited to participate in "Evolution 101"—a one day workshop to be held at the Portland Convention Center on June 25. Come learn about recent research in the field of evolution, talk with evolutionary biologists, and attend sessions that feature hands-on activities for teaching evolution to all ages.

Teachers can register for the workshop at evolutionsociety.org/SSE2010/Register.html. Evolution 2010 meeting participants interested in attending the workshop, contact Louise Mead (mead@ncse.org) or Kristin Jenkins (kjenkins@nescent.org).

For more information, visit evolutionsociety.org/SSE2010/Workshops.html



WHAT: Evolution 2010: A Workshop for Educators

WHEN: June 21st - 23rd, 2010 (Application deadline May 31)

WHERE: Durham, NC

Please join us for three fun-filled days of exploring evolution. Reinforce key evolutionary concepts and explore cutting-edge topics in evolutionary biology with biologists and educators at the National Evolutionary Synthesis Center (NESCent).

Participants will receive continuing education units (CEUs), a \$25/day stipend, and a collection of resources and materials for teaching evolution. Travel awards are available for participants from outside the Raleigh-Durham-Chapel Hill area.

This workshop will include two educational field trips: one to tour the **Duke Lemur Center**, one of the foremost prosimian research centers in the world, and the second to the **North Carolina Museum of Life and Science in Durham, NC**.

Workshop will be held at NESCent in Durham, NC. Approximate hours each day are 8:30 AM to 5:00 PM.

For more information, and to apply, please see www.nescent.org/courses/2010/eogsummer. If you have questions about the workshop, please contact Jory Weintraub (jory@nescent.org).

Application deadline: Monday, May 31st, 2010

Notification of acceptance will be sent by June 1st, 2010

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