



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.

IN THIS ISSUE:

Research Highlights	1, 4
Director's Letter	2
In the Media	3
Call for Proposals	5
Evolution 2012	6
New Awards	7

Don't miss these exciting events at Evolution 2012

There's something for everyone at the 1st Joint Congress on Evolutionary Biology in Ottawa, Ontario. Turn to page 6 for more information:

Fri. July 6: Attend a workshop for K-16 teachers on using data in the classroom

Sat. July 7: Learn to teach with data in this year's SSE Education Symposium

Sat. July 7: Vote on your favorite 3-min films at the NESCent Evolution Film Festival

Tues-Wed. July 10-11: The 3rd annual iEvoBio conference on evolutionary informatics

NEXT PROPOSAL DEADLINES:

July 1: graduate fellowships, short-term visitors

July 10: postdocs, sabbaticals, catalysis meetings, working groups, journalists-in-residence, course proposals

For more information, turn to page 5 or visit bit.ly/4trJAW

RESEARCH HIGHLIGHTS

What happens when a fast-evolving parasite switches hosts?



The house finch (*Carpodacus mexicanus*) is a common North American songbird.

PHOTO BY GEOFFREY E. HILL

A new study of a devastating bird disease that spread from poultry to house finches in the mid-1990s reveals that the bacterium responsible for the disease evolves at an excep-

"It's evolving anywhere from ten to 100 times faster than previous estimates for any other bacterium."

—Nigel Delaney, Harvard University

tionally fast rate. What's more, the fast-evolving microbe has lost a key chunk of its genome since jumping to its new host, scientists were surprised to find. The missing portion contained the genes that made up the microbe's immune

system, researchers report in a recent issue of PLoS Genetics.

When thousands of wild house finches started dropping dead from a mysterious eye infection in the Washington, D.C. area in the winter of 1994, scientists were puzzled. The birds had red, swollen, crusty eyes that left them unable to see or forage for food, until they eventually died from starvation or predation. Researchers soon identified the cause — a bacterium called *Mycoplasma gallisepticum*, a common cause of respiratory infections in turkeys and chickens that was previously known to infect only poultry.

By the time biologist Geoffrey Hill spotted his first sick bird in Auburn, Alabama, in 1995, the disease had spread through the eastern

see [PARASITE](#), p8

ABOUT NESCENT:

The National Evolutionary Synthesis Center (NESCent) is a scientific research center that supports cutting-edge, cross-disciplinary research in evolution. The center offers a range of fellowships for visiting scientists and educators and sponsors numerous scientific meetings each year. NESCent is funded by the National Science Foundation and is jointly operated by 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 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

STAY INFORMED

Subscribe to the NESCent quarterly newsletter to receive news about the Center, research and training opportunities, and upcoming events. Comments, story ideas and photo contributions are welcome. Please send corrections and suggestions for future newsletters to Robin Smith at rsmith@nescent.org

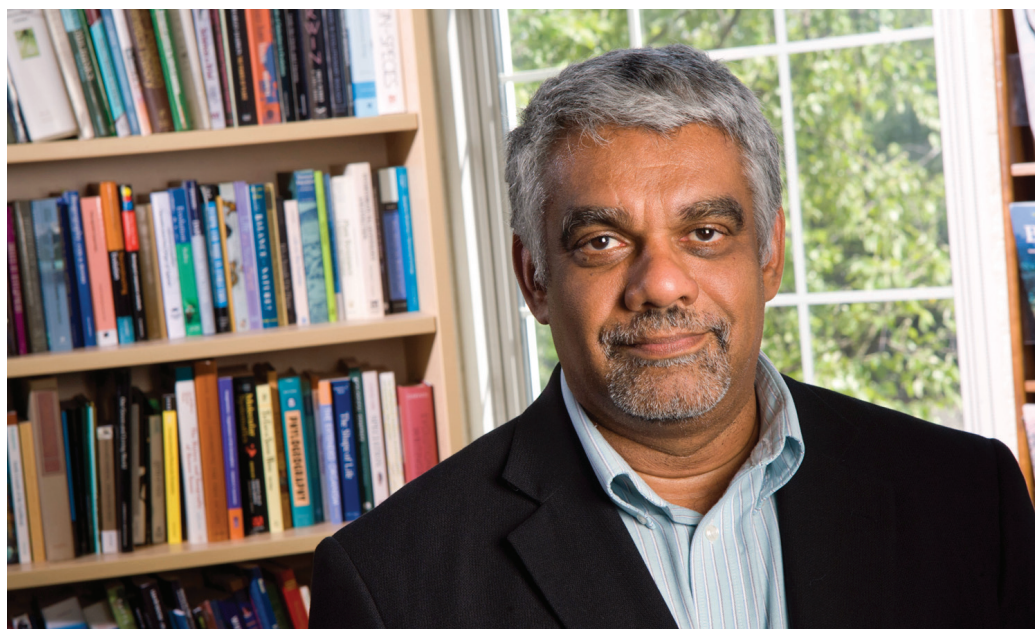
To unsubscribe fill out our online form at bit.ly/qluEWu. You can also visit NESCent on Twitter, Facebook, and YouTube.

Writer/Editor: Robin Smith
(919) 668-4544
rsmith@nescent.org

Graphic Design and Layout:
Vanessa DeJongh

LETTER FROM THE DIRECTOR

What makes NESCent special



It's not unusual for a director to be asked, "What makes your center special?"

Visitors, staff, potential donors — they all want to know. This question has become all the more critical as we get closer to the end of our second five-year grant from the U.S. National Science Foundation. NESCent is what NSF calls a "synthesis center," which means it focuses on the re-use of existing data to address 'big picture' questions.

Under current policy, NSF funds synthesis centers for a maximum of 10 years. NESCent got its start in 2004, so NSF funding for NESCent formally ends in December 2014. We have much to accomplish between now and then. Among others, we will be exploring ways to sustain the center post-2014. We plan to continue serving the scientific community as we map NESCent's future. Inside, you'll read about the next proposal deadlines for postdoctoral fellows, graduate students, sabbatical schol-

ars, short-term visitors, working groups and catalysis meetings.

We invite you to peruse research results by previous award recipients, learn what NESCent is doing to expand its international outreach efforts, and mark your calendars for exciting events at **Evolution 2012 in Ottawa**. You'll also meet the latest award recipients, including the talented and diverse undergraduates selected for travel awards to attend the meeting under the Undergraduate Diversity at SSE/SSB program. **As always, NESCent is a community resource — we want to hear from you, and we look forward to receiving your proposals.**

Allen Rodrigo

"An evolutionary theory of dentistry" (Science) Why are our teeth so rotten? NESCent scientists examine the mismatch between our diets and lifestyles and those of our ancestors: bit.ly/KPYPOg

"Why not marry your cousin? Millions do" The health risks of marrying a cousin have been grossly overstated, says a new book by NESCent visitor Alan Bittles. Read more in *West Australia Today* and *The West Australian*.

"As scholarship goes digital, academics seek new ways to measure their impact" (The Chronicle of Higher Education) Researchers, librarians, and programmers work in a loose partnership to develop alternative methods of tracking research's paths through social media. NESCent's Heather Piwowar and Jason Priem are the recipients of a \$125,000 award from the Alfred P. Sloan Foundation aimed at doing just that. Find out what they hope to accomplish at bit.ly/zTPXBu.

"Missing biologist surfaces, reunites with family" (Nature) Last fall, NESCent journalist Mike Martin worked on a story about then-missing evolutionary biologist Margie Profet which he subsequently published in *Psychology Today*. The story helped to reunite Profet with her family. Learn more at bit.ly/KJXwOp.

"The burdens of being a biped" (Science) Got back or foot pain? A NESCent working group examines the burdens of being a biped at bit.ly/NfdumJ

"For most of human history, being an omnivore was no dilemma" (National Public Radio) The feeding habits of mammals haven't always been what they are today, particularly for omnivores, finds a new study. NESCent researchers explain at n.pr/IWSkCk.

"Fitness tests reveal frisky frogs have faster-changing genomes" (Wired) Physically fit frogs have faster-changing genomes, says a new study of poison frogs from Central and South America. NESCent postdoc Juan Santos tells the full story at bit.ly/HQY6KA.

"Not all altruism is alike, says new study" (Eurekalert) From bees and wasps that die defending their nests, to elephants that cooperate to care for young, a new mathematical model by



NESCent sabbatical scholar Michael Wade pinpoints the environmental conditions that favor one form of altruism over another. Read more at bit.ly/JJc6UO

"The art of eavesdropping: nature's silent sniffers, watchers, and listeners" (Scientific American) Typically we think of eavesdropping as a human endeavor. But watching or listening in on others is ubiquitous across the animal kingdom. What are the payoffs for other species besides our own? NESCent postdoc Jennifer Verdolin explains at bit.ly/LwkJmV.

"Eight Triangle teachers named Kenan Fellows" (Durham Herald-Sun) NESCent is proud to host teaching fellow Robin Bulleri through the Kenan Fellows Program for Curriculum and Leadership Development, a program established to promote teacher leadership, address teacher retention and advance K-12 science, technology and math education. Read more at bit.ly/HQ3gpS.

"Not just for the birds: man-made noise has ripple effects on plants, too" A growing body of research shows that birds and other animals change their behavior in response to man-made noise. But human noise can have ripple effects on plants too, finds a new study. Read more in *Scientific American*, the *Christian Science Monitor*, *MSNBC*, *National Public Radio*, *Audubon Magazine*, the *Miami Herald*, *BBC News*, *Science News*, *Discovery News*, and the *New York Times*.

"James Cameron's Deep Dive" (NPR's "On Point") This March, director/explorer James Cameron dove down 6.8 miles into the deepest ocean trench on the planet. Deep sea ocean-

ographer Sylvia Earle and NESCent's Craig McClain take us on a virtual tour at bit.ly/GEzle6.

"Why do some island animals become dwarfs and others become giants?" (Futurity) A new study of huge hamsters and pint-sized porcupines puts an old idea to the test. NESCent graduate fellow Paul Durst tells the full story at bit.ly/GRx5Uf.

"Ice Age coyotes were supersized compared to coyotes today, fossil study reveals" Coyotes today are pint-sized compared to their Ice Age counterparts, finds a new fossil study. Read more in *The Huffington Post*, *Wired*, *MSNBC*, and *Science Magazine*.

"Bringing evolutionary science to the community: Center promotes Darwin Day to inspire next generation of scientists" (US News & World Report) To honor Darwin's 203rd birthday, NESCent scientists hit the road to Oregon, Washington, Missouri, Arkansas, West Virginia and Louisiana: bit.ly/xJdofU.

"Bouquet bargains" (Eurekalert) Most creatures face compromises when they reproduce – the more energy they devote to having lots of babies, the less they can invest in each one. But do the same tradeoffs hold true for plants? Find out at bit.ly/xjReKa.

"Big Pic: A Penny for Your Bivalves?" (Discovery) In a recent study, NESCent's Craig McClain explains how the distribution of marine bivalves varies across the seafloor. Learn more at bit.ly/zZ9tPf. Also featured in *Wired Magazine*.

"Prehistoric predators with supersized teeth had beefier arm bones" The toothiest prehistoric predators also had beefier arm bones, finds a new fossil study. Learn more on *The History Channel*, *Discover Magazine*, *MSNBC*, *Science Magazine*, the *Huffington Post*, *Nature* and the *UK's Daily Mail*.

"Text mining: what do publishers have against this hi-tech research tool?" (The UK Guardian) Researchers push for end to publishers' default ban on computer scanning of tens of thousands of papers to find links between genes and diseases. NESCent's Dr. Heather Piwowar and colleagues tell the full story at gu.com/p/37j9h/tw.

RESEARCH HIGHLIGHTS

A tree of life for all two million named species

A new initiative aims to build a grand tree of life that brings together everything scientists know about how all living things are related, from the tiniest bacteria to the tallest tree. The resulting tree will be digital, downloadable, and continuously updated.

“[Over the years] scientists have published tens of thousands of evolutionary trees, but there’s been very little work to connect the dots and put them all together into a single resource.”

—Karen Cranston, NESCent

Scientists have been building evolutionary trees for more than 150 years, even before Charles Darwin’s iconic sketches. But despite significant progress in fleshing out the major branches of the tree of life, today there is still no central place where researchers can go to browse and download the entire tree.

“Where can you go to see their collective results in one resource? The surprising thing is you can’t — at least not yet,” said Dr. Karen Cranston of the National Evolutionary Synthesis Center.

But now, thanks to a three-year, \$5.76 million grant from the U.S. National Science Foundation, a team of scientists and developers from ten universities aims to make that a reality.

Figuring out how the millions of species on Earth are related to one another isn’t just important for pinpointing an armadillo’s closest cousins, or determining if hagfish are more closely related to sand dollars or sea squirts. Information about evolutionary relationships has



The researchers behind the project (in alphabetical order) are: Gordon Burleigh (U. of Florida), Keith Crandall (Brigham Young), Karen Cranston (NESCent), Karl Gude (Michigan State), David Hibbett (Clark), Mark Holder (U. of Kansas), Laura Katz (Smith), Richard Ree (Field Museum of Natural History), Stephen Smith (U. of Michigan), Doug Soltis (U. of Florida) and Tiffani Williams (Texas A&M). PHOTO BY KARL GUDE

helped scientists identify promising new medicines, develop hardier, higher-yielding crops, and fight infectious diseases such as HIV, anthrax and influenza.

If evolutionary trees are so widely used, why has assembling them across all of life been so hard to achieve? It’s not for lack of research, or data. Thanks in large part to advances in DNA sequencing, thousands of new phylogenetic trees are published in scientific journals each year — most of them focused on isolated branches of the tree of life, for everything from birds to botflies.

“There’s a firehose of data,” said Cranston, principal investigator of the project. “[Over the years] scientists have published tens of thousands of evolutionary trees, but there’s been very little work to connect the dots and put them all together into a single resource.”

Part of the difficulty lies in the sheer enormity of the task. The largest evolutionary trees built to date contain roughly 100,000 taxa. Assembling the branches for all two million named species of animals, plants, fungi and microbes — not to mention the countless more still being named or discovered — will require new tools for analyzing large data sets and stitching together vast numbers of published trees.

Another difficulty lies in how scientists typically disseminate their results. A tiny fraction of all evolutionary trees that have been published — researchers estimate a mere 4% — end up in a database in a digital form. Instead, most of that knowledge is locked up in figures in journal articles, as PDFs or other file formats that are impossible for other researchers to download, reanalyze, or merge with new information.

This new initiative — dubbed Open Tree of Life (opentreeoflife.org) — aims to change all that.

What makes this project different from previous efforts, the researchers say, is its scope.

The team hopes to have a first draft of the complete evolutionary tree — compiled from the evolutionary trees that are already available in existing databases — by August 2013. The first draft that emerges will be far from finished. “There will always be new studies that come out,” Cranston said. “There will also be places in the tree where we don’t

Expanding NESCent's international outreach efforts

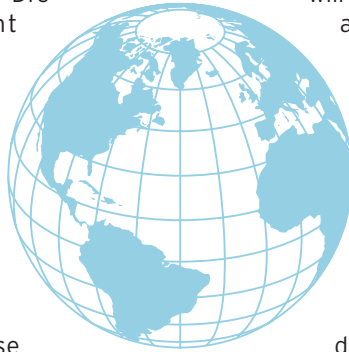
NESCent's Ambassador Program continues to send scientists and educators to developing regions around the globe to deliver short courses and workshops in evolutionary science, informatics and education.

In May, a team consisting of Drs Karen Cranston (NESCent Manager of Informatics and Training), Kate Hertweck (NESCent Postdoc), Bill Piel (Yale) and Rutger Vos (NCB Naturalis) spent two weeks at the Kenya Medical Research Institute in Kilifi, Kenya. While there, they delivered a workshop on phylogenetic analysis to 20 biomedical/infectious disease researchers from all across Africa.

In early June, Drs Jory Weintraub (NESCent Asst. Director, Education & Outreach), Rafa Rubio de Casas (NESCent Postdoc) and undergraduate Sarah Cohn (UNC Chapel Hill) visited the Galápagos Islands to lead workshops for elementary school teachers and students, as well as naturalist guides of the

islands. The student/teacher workshops were an extension of NESCent's successful "Seeing and Learning Science After-school" program (SALSA – see sidebar/adjacent story).

Finally, in the summer of 2012, NESCent will return to Bali, Indonesia, where a team visited the Indonesian Biodiversity Research Center in August 2011. This year we'll be offering courses in molecular ecology and phylogenetic inference, taught by Brian Wiegmann (NESCent's Assoc. Director of Education & Outreach), Elizabeth Sbrocco (NESCent Postdoc) and Jeet Sukumaran (a post-doctoral fellow working with NESCent Director Allen Rodrigo).



NESCent's Ambassador Program has been funded by a two-year NSF EAGER grant. As this grant wraps up, we are exploring ways to sustain and expand the program, which has now sent nearly 20 scientists/educators to eight countries in the Caribbean, South America, Asia and Africa.

"Seeing and Learning Science After-school" grows beyond NC

In our last newsletter, we profiled a new outreach program called "Seeing and Learning Science After-school," or SALSA!

Conceived in part as a vehicle for reaching out to underrepresented minority groups, SALSA! uses engaging, hands-on activities to teach elementary school children about a range of topics in evolution. This program has been growing fast.

After the first successful pilot in Chapel Hill, NC, in fall 2011, the program expanded to E.K. Powe Elementary School in Durham, NC, this spring. Based on these successes, SALSA! is now venturing beyond central North Carolina. A NESCent team traveled to the Galapagos Islands in May and June to lead SALSA! workshops in Spanish as part of NESCent's Ambassador program.

Led by postdoc Rafael Rubio de Casas, UNC Chapel Hill undergraduate Sarah Cohn, and NESCent Asst. Director of Education & Outreach Jory Weintraub, the team also trained Spanish-speaking high school students from the North Carolina Friends School, and those students subsequently delivered SALSA! workshops to children of immigrant farm workers in rural NC. Some of the students from the Carolina Friends School are also traveling to Nicaragua this summer on an exchange trip and will be delivering the activities to Nicaraguan children.

To learn more visit bit.ly/K7B450 or contact Dr. Jory Weintraub (jory@nescent.org).

CALL FOR PROPOSALS



Call for proposals

Looking for support for a graduate student, faculty sabbatical, short-term visit 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.

Proposals for short-term visits are 2 weeks to 3 months. Proposals for sabbaticals may be for up to a full year. The next deadline for short-term visitors and graduate fellowships is July 1. For sabbaticals, working groups, and catalysis meetings, the next deadline is July 10. For a limited time we also welcome proposals for two-year postdoctoral fellowships that will begin no later than January 2013. Deadline July 10.

For more information, please visit <http://nescent.org/science/proposals.php>.

THE PREMIER INTERNATIONAL CONFERENCE OF EVOLUTIONARY BIOLOGISTS

K-16 teachers invited to attend workshop on using evolutionary data in the classroom

WHERE: Ottawa Convention Centre

WHEN: Friday, July 6
8:00 AM - 4:30 PM

K-12 teachers, 2- and 4-year faculty and future faculty are invited to attend "Evo101," a one-day workshop on using evolutionary data in the classroom, to be held Friday July 6 at the Ottawa Convention Centre. Come learn about exciting research in evolution and participate in hands-on activities designed to facilitate the integration of ecological and evolutionary data into your curriculum. \$35 registration fee includes breakfast and lunch, as well as a collection of materials for teaching evolution. To register, please visit bit.ly/KBflez. Registration closes June 30. For more information visit bit.ly/N18Icq.

EVOLUTION 2012

Teaching with data

WHERE: Ottawa Convention Centre

WHEN: Saturday July 7
8:30 AM - 12 noon

Are you a faculty member who wants to learn to swim – and teach – in the data deluge? Data lies at the heart of both doing science and understanding scientific knowledge. Yet we often teach biology in data-poor classrooms. This year's SSE education symposium will directly address this challenge. Learn what we know about teaching with data. Join Sam Donovan (University of Pittsburgh), Kristin Jenkins (NESCent), Cathy Manduca (Carleton College), and Thomas Meagher (University of St Andrews) for 10+ interactive demonstrations of data resources, analytical tools and curricula from various research organizations. No registration required. For more information visit bit.ly/KhF2r8.

Ready for some REEL science?

WHERE: Ottawa Convention Centre, Room 208

WHEN: Saturday July 7
9:30 PM - 10:30 PM

Join us for the 2nd annual NESCent Evolution Film Festival. Contestants were challenged to submit an entertaining and informative video that explains a fun fact, key concept, compelling question, or exciting area of evolution research in three minutes or less. Come to the festival to view and vote on your favorite films. Winners will be announced at the farewell dinner on Tuesday, July 10. To find out more, stop by the NESCent booth or visit bit.ly/lxKns1.

Join us for 3rd annual iEvoBio conference on evolutionary informatics

WHERE: Ottawa Convention Centre

WHEN: Tues-Wed. July 10-11

What can biologists studying evolution, systematics and biodiversity learn from software developers and mathematicians? A lot, say the organizers of the third annual iEvoBio conference on evolutionary informatics. This year, iEvoBio is again held jointly with the Evolution meetings as a satellite conference. iEvoBio overlaps with the last day of the main conference and extends one day longer. The program includes a series of keynote speakers and contributed talks, as well as more dynamic and interactive elements, such as lightning talk-style sessions, a software bazaar, and Birds-of-a-Feather gatherings. You may register for iEvoBio alone or together with the main meeting. For more information, visit ievobio.org.

TREE, continued

have enough data, or where the data lead to conflicting hypotheses, or where groups of researchers simply disagree."

But with a first draft in hand, scientists will be able to go online and compare their trees to others that have already been published, or download it for further study. They'll also be able to expand the tree, filling in the missing

branches and placing newly named or discovered species among their relatives. Eventually, the team's goal is to be able to detect when new trees are published and incorporate them automatically, so that the complete tree can be continuously updated.

If the project is to succeed, one of the biggest challenges will be encouraging more scientists to publish their results in digital form. Growing numbers of

scientific journals now require authors to deposit phylogenetic data in a digital database, but many published trees never make it. "We hope to provide infrastructure and tools that will make it easier to do that, such as a more user-friendly interface for submitting data," Cranston said.

"In the long run, we hope this will become the central resource for synthesized phylogenetic data," she added. ●

Congratulations to 2012 award recipients

POSTDOCTORAL FELLOWS

Courtney Fitzpatrick (Duke University) Expanded Bateman gradients: a synthetic refinement of sexual selection theory

Joshua Martin (University of North Carolina-Chapel Hill) Quantitative predictions of RNA evolution

Jeremy Van Cleve (Sante Fe Institute) Mechanistic trade-offs and the evolution of microbial sociality, plasticity, and virulence

CATALYSIS MEETINGS

Paul Baker (Duke University) The role of mountains, climate and landscape in generating Amazon/Andean biodiversity

Nina Jablonski (Pennsylvania State University) Using genetics and genealogy to teach evolution and human diversity

Louise Mead (BEACON) K-12 Evolution Education and the Underserved

James Moody (Duke University) Ecological models and social networks: how evolutionary forces shape networks and communities

Michael Travisano (University of Minnesota) Evolutionary origins of multicellularity

WORKING GROUPS

Joshua Herbeck (University of Washington) The evolution of virulence in a human infectious disease: the case study of HIV

Andrew MacColl (University of Nottingham) Environmental and demographic determinants of natural selection

John Parker (UC-Santa Barbara) Advancing theory and research on scientific synthesis

Margaret Yacobucci (Bowling Green State University) Learning evolution for the fossil record: K-12 explorations in deep time

LONG-TERM SABBATICAL SCHOLARS

Martin Burd (Monash University) Sexual dimorphism and sexual allocation in flowering plants: a synthesis of data

SHORT-TERM VISITORS

Beaux Berkeley (James Madison University) Life history and environmental factors driving variation in mammalian sex allocation

Jonathan Marcot (University of Illinois at Urbana-Champaign) Paleontological and phylogenetic approaches to the study of diversification and extinction

Aaron Hunter (Petronas University of Technology) The evolutionary development of species gradients and hybridization in Indo-Pacific deep water crinoid populations.

Roy Plotnick (University of Illinois at Chicago) Paleontology and phylogeny of insect ears

GRADUATE FELLOWS

Matthew Pennell (University of Idaho) Angiosperm evolution and diversification with adaptive zones

Rachel Warnock (University of Bristol) 2012 sees the 50th birthday of the molecular clock, but has it reached maturity?

Pinar Yoldas (Duke University) The very loud orchestra of endangered species

COURSE PROPOSALS

Melissa Haendel (Oregon Health & Science University) Anatomy ontologies in evolutionary biology and genetics

JOURNALIST-IN-RESIDENCE

Aaron Dubrow (University of Texas-Austin) Following the sequence

KENAN TEACHING FELLOW

Robin Bulleri (Carrboro High School) Exploring evolutionary science

MSI FACULTY TRAVEL AWARDS

Michele Nishiguchi (New Mexico State University)

"UNDERGRADUATE DIVERSITY AT EVOLUTION" TRAVEL AWARDS

Chidiebere (Chidi) Akusobi (Yale University)

Marcell Cadney (California State University Long Beach)

Mario Cortes Garcia (University of California, Merced)

Talisa Erazo (CUNY- Lehman College)

Erika Espinoza (California State Polytechnic University, Pomona)

Anensshiya Govinthasamy (University of California, Berkeley)

Michelle Herrera (Salisbury University)

Emily Hsieh (University of Washington, Seattle)

Bryan Juarez (University of California, Santa Barbara)

De'Ashia Lee (Howard University)

Cullen McGovern (Colorado State University)

Douglas McKenney (Seattle Central Community College)

Devin Norman (McNeese State University)

Danielle Rivera (The City College of New York)

Barbara Rizzo (The City College of New York (CUNY))

Nichole Rota (Stonehill College)

Zoe Spanos (City College of New York)

Cong (Charles) Xu (University of Notre Dame)

For more information about these scholars and their research projects, please visit <http://bit.ly/N1fKOL>.

PARASITE, continued

part of the continent, as far north as Quebec and as far south as Florida. “This was a devastating pandemic,” Hill said.

Since its discovery, the epidemic has spread as far west as California, and is estimated to have wiped out hundreds of millions of birds. But scientists are still far from understanding how *M. gallisepticum* gained the ability to spread to house finches — which diverged from chickens and turkeys some 80-90 million years ago — or what turned it into such a sweeping killer.

In a recent study in the journal PLoS Genetics, researchers compared the genomes of a dozen strains of *M. gallisepticum* sampled from infected house finches between 1994-2007, in the years following the initial outbreak. Using a technique called pyrosequencing, “we can measure evolution on very short time scales,” said co-author Scott Edwards of Harvard University. Instead of studying the host switch years after it happened, the researchers are able to track it in real time. “We’re catching the switch in the act,” he added.

In both poultry and house finches, the researchers report, the microbe has been evolving at frightening speed. “It’s evolving anywhere from ten to 100 times faster than previous estimates for any other bacterium,” said Harvard graduate student and first author Nigel Delaney.

But when the researchers compared the DNA sequences of the poultry strains with those sampled from house finches, they found something surprising — since making the switch, some parts of the parasite’s genome have begun to break down.

M. gallisepticum has a tiny genome to begin with, with less than 1000 genes, Delaney said. But rather than acquire new genes to help it outwit its new host, the parasite has gradually lost more than



The red, swollen, crusty eyes in this house finch are the result of a highly-contagious infection caused by the bacterium *Mycoplasma gallisepticum*. PHOTO BY GEOFFREY E. HILL

50 genes — particularly those that make up the microbe’s immune system.

Mycoplasmas are parasites, but they also have parasites of their own, including naturally occurring viruses called bacteriophages. “One of the main functions [of the genes that were lost] is to help guard Mycoplasma against the attacks of bacteriophages,” Edwards explained. “It was surprising to see a part of the genome that was assumed to be so important suddenly become unimportant,” Delaney added.

It seems crazy, but “scientists have seen the same phenomenon before in HIV,” said co-author Allen Rodrigo of the National Evolutionary Synthesis Center. When HIV infects a new host, it doesn’t encounter the same threats, so it loses the specific immune defenses that protected it in its former host, Rodrigo explained. These original defenses may be expensive to maintain, Rodrigo said. Studies show that the HIV strains that lose them are able to reproduce

more quickly and spread. “It’s similar to the ‘use it or lose it’ principle,” Edwards added.

M. gallisepticum can’t be transmitted to humans. It can infect other backyard birds — including American goldfinches, purple finches, evening grosbeaks and pine grosbeaks — but none with the devastating consequences like those seen in house finches.

Researchers still don’t know which genetic changes enabled the pathogen to reach epidemic proportions in house finches. But if the house finch strains have lost the genetic machinery that protected them in poultry, then reintroducing the parasites to the bacteriophages of their former hosts could be one way to control the disease, the scientists say. Determining which specific bacteriophages those are, and whether the remnants of the *M. gallisepticum* immune system still provide some protection against them, will take much more work.

“But this study shows that there’s a third player that’s important to understand this pandemic, which are the bacteriophages. Nobody’s looked at that so far. This is the first observation that they seem to matter,” Delaney said. ●

Other authors on the paper (in alphabetical order) include Susan Balenger of the University of Turku in Finland, Camille Bonneaud of the French National Center for Scientific Research, Christopher Marx of Harvard University, Naola Ferguson-Noel of the University of Georgia, and Peter Tsai of the Bioinformatics Institute of New Zealand.

CITATION: Delaney, N., S. Balenger, et al. (2012). “Ultrafast evolution and loss of CRISPRs following host shift in a novel wildlife pathogen, *Mycoplasma gallisepticum*.” PLoS Genetics.

Data available in the Dryad Digital Repository at bit.ly/KmftoT.