@NESCent

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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:

Don't miss these exciting events at Evolution 2014 in Raleigh, NC

- Attend workshops on women in science, software tools for phylogenomics, and teaching evolution
- View and vote on your favorite videos at the Evolution Film Festival
- Participate in the 5th annual iEvoBio conference on evolutionary informatics
- Don't miss "DNA Portraits," a traveling exhibit on molecular anthropology by artist Lynn Fellman
- Immerse yourself in interactive science and technology exhibits at the Tuesday night Super Social
- Participate in a citizen science project to study face mites

For more information turn to page 2, or visit evolution 2014.org/

RESEARCH HIGHLIGHTS

A new study using ancient DNA suggests that today's domestic chickens may look far different from the chickens of just a few hundred years ago.

Ancient DNA offers clues to how barnyard chickens came to be

Ancient DNA adds a twist to the story of how barnyard chickens came to be, finds a study published in *Proceedings of the National Academy of Sciences*.

Analyzing DNA from the bones of chickens that lived 200-2300 years ago in Europe, researchers report that the domestic chickens of just a few hundred years ago may have looked far different from the chickens we know today.

The results suggest that some of the traits we associate with modern domestic chickens—such as their yellowish skin—only became widespread in the last 500 years, much more recently than previously thought.

"It's a blink of an eye from an evolutionary perspective," said co-author Greger Larson at Durham University in the United Kingdom.

The study is part of a larger field of research that aims to understand when, where and how humans turned wild plants and animals into the crops, pets and livestock we know today.

Generally, any mutations that are widespread in domestic plants and animals but absent from their wild relatives are assumed to have played a key role in the process, spreading as people and their livestock moved across the globe. But a growing number of ancient DNA studies tell a different tale.

Chickens are descended from a wild bird called the Red Junglefowl, which humans started raising roughly 4,000-5,000 years

see CHICKENS, p 8

ABOUT NESCENT:

NESCent is a scientific research center dedicated to cross-disciplinary research in evolution. The center's mission is to promote the synthesis of information, concepts and knowledge to address significant, emerging, or novel questions in evolutionary science and its applications. NESCent achieves this by supporting research and education across disciplinary, institutional, geographic, and demographic boundaries.

NESCent is a collaborative partnership between Duke University, the University of North Carolina at Chapel Hill, and North Carolina State University, and is funded by the National Science Foundation (award #EF-0905606). 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

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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

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evolution 2014

"DNA Portraits," a traveling exhibit by artist Lynn Fellman

WHEN: on display through July 2014
WHERE: North Carolina Museum of Natural Sciences

Find out where art and genomic science meet. A special exhibit for the Evolution 2014 conference will be on display at the North Carolina Museum of Natural Sciences, just six blocks from the Convention Center. Multimedia artist Lynn Fellman's traveling exhibit, "DNA Portraits," features five portraits and companion storyboards that translate complicated stories of human migration and evolution into art and narrative.

The portraits are based on data from the Genographic Project, a longitudinal molecular anthropology project launched in 2005. Each participant met individually with Fellman in her art studio to begin the portrait process. She gave them DNA lab kits, explained how to take their DNA sample, and where to mail it for sequencing. When the data from the lab was available, Fellman reviewed with them their DNA results and preliminary sketches of their portrait. With an individual's data in hand, she proceeded to complete the portraits combing landscape and haplogroup paths with drawings of their face.

The exhibit has travelled to museums, science conferences, and universities across the United States. Originally commissioned by the University of Minnesota, the portraits and storyboards were revised and reprinted for display during the Evolution 2014 conference.

About the artist: Lynn Fellman is a multimedia artist and designer who works with scientists to communicate the value of their research to the public. Fellman lived in North Carolina for six months in 2013 during her tenure as artist-in-residence at NESCent. See more of Fellman's work at www.FellmanStudio.com

"Crossing Beringia" is a DNA Portrait by Lynn Fellman of a Native American man from Minnesota. DNA data are from the Genographic Project.

Tracking the trail of big data

WHEN: 8:30 a.m.-5 p.m., Tues.-Wed. June 24-25
WHERE: Raleigh Convention Center

Are you interested in the intersection of biology, software, and mathematics? Come to the iEvoBio Meeting on June 24-25, in conjunction with Evolution 2014 in Raleigh, North Carolina.

The iEvoBio Meeting brings together biologists working in evolution, systematics and biodiversity with software developers and mathematicians. Enjoy two full days of 5-minute lightning talks on bioinformatics, software demos, and "birds of a feather" sessions—informal groups of meeting participants with a common interest.

You'll also see talks by two fabulous keynote speakers, Drs. Scott Edwards and Cyndy Parr.

Get the latest program details, find answers to frequently asked questions and more at ievobio.org/

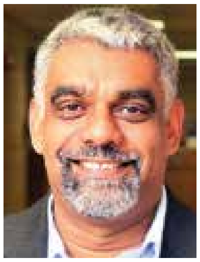
Join us for the 4th annual evolution film festival

WHEN: 8-10 p.m. on Saturday June 21
WHERE: Raleigh Convention Center Rm 402

Ready for some REEL science? Join us from 8-10 p.m. on Saturday, June 21, in the Raleigh Convention Center for free popcorn and drinks and a two-part screening of evolution-themed films. We'll kick off with a preview of the latest short film on evolution produced by HHMI's BioInteractive team. In the second half of our show, we'll show a series of 3-minute evolution-themed videos produced by students and scientists like you. View and vote on your favorite videos at the 4th annual NESCent/HHMI Evolution Film Festival. Your vote will determine the winners, who will be announced at the 'Super Social' at the North Carolina Museum of Natural Sciences on Tuesday June 24. To find out more, visit http://filmfestival.nescent.org/.

Letter from the director

As of this writing, Evolution 2014 is just days away. We look forward to welcoming you to Raleigh for the joint annual meeting of the Society for the Study of Evolution (SSE), the Society of Systematic Biologists (SSB), and the American Society of Naturalists (ASN), to be held June 20-24. Join more than 2000 people from 38 countries for four full days of science and socializing. A few highlights include:



ALLEN RODRIGO

- A full program that includes 1200 talks and 450 posters. If you browse the session titles you'll see some familiar themes you may recognize from previous years, such as molecular evolution, speciation, life history evolution, genomics, phylogenetics and phylogeography. You'll also find some newer themes among the session titles too— such as avian evolution, toxins and toxicity, honey bee evolution, migratory behavior, venom evolution, plant organelles and sociality. Back by popular demand, this year's conference will also feature nearly 70 five-minute lightning talks, split into two separate sessions on Monday and Tuesday mornings. Think of it as the haiku version of the traditional presentation format.
- Social activities will include an opening reception, mixers with each evening poster session, and a Super Social at the North Carolina Museum of Natural Sciences on the last night of the conference, just six blocks away from the Convention Center. When you are at the Museum, check out the artwork by former NESCent artist-in-residence Lynn Fellman, whose traveling exhibit, "DNA Portraits," will be on display on the skyway bridge that connects the main Museum building to the adjacent Nature Research Center. At the conference, also look out for the evolution film festival sponsored by NESCent/HHMI on Saturday night—all of these mixers and receptions are included with registration.
- For the 5th year in a row, we will meet jointly with the iEvoBio conference, which brings together biologists interested in evolution, systematics, biodiversity, software and mathematics.
- We've gone digital. Only a limited number of print copies of the program will be available onsite for those who did not pre-order, so please plan accordingly. Browse the program for specific sessions, titles, authors or keywords using the searchable online program at http://www.xcdsystem.com/evolution2014/program/, or build your own personalized itinerary to print as a pdf using the itinerary builder at http://www.xcdsystem.com/evolution2014/itinerary/index.cfm.
- Attendees can also stay up to date with a free smartphone app. Search speakers and sessions, find maps, receive announcements about schedule changes and other news, or join the Twitter conversation about the meeting – all at your fingertips. The free app is available for iOS devices, including iPhones and iPads, and Android devices, including smartphones and tablets. Download the app by searching for "Evolution 2014" in your device's app store. Once the app is downloaded, it will prompt you to install the information for the 2014 annual meeting. Users can also view the same content on their laptops using Chrome or Safari and the following URL: m.xcdsystem.com/evolution2014.

We'd like to extend a special welcome to those who are attending the Evolution meeting for the first time. Those include many of our 800+ graduate and undergraduate students, as well as our K-12 attendees, who will be presenting posters on Saturday night—be sure to stop by.

Whatever your career stage, we hope you have a great conference, meet lots of people, and learn a great deal of interesting science. On behalf of the Evolution 2014 Organizing Committee, again WELCOME!

Allen Rodrigo, Director of NESCent and chair of the organizing committee for Evolution 2014

Dr. Allen Rodrigo
Director of NESCent and chair of the organizing committee for Evolution 2014

RESEARCH HIGHLIGHTS

Apply for open access publishing support fund

Past and present NESCent-sponsored scientists are eligible for open access publishing support funds from NESCent. NESCent will reimburse Article Processing Charges for articles published in qualifying open-access journals. Funds can be used to support article-processing fees for publication in any peer-reviewed journal that is listed in the Directory of Open Access Journals, is a member of the Open Access Scholarly Publishers Association, and is published in a fully open access format based on a published schedule of article processing fees. The fund cannot be used to support "hybrid" open access publishing, where individual articles from journals that are generally subscription access only are made openly available when author fees are paid. Only journals that do not charge readers or institutions for access to peer-reviewed content are eligible. All reimbursement is on a first come, first served basis up until the funding for a given year is exhausted. To apply for reimbursement please contact NESCent's operations manager Barbara Mitchell (mitchelb@duke.edu) and cc our Associate Director of Informatics, Todd Vision (tjv@bio.unc.edu)

RESEARCH HIGHLIGHTS

In the age of open science, repurposing and reproducing research pose their own challenges

Reproducibility is a laudable goal, but making it a reality can be tricky. NESCent researchers discovered this firsthand when they tried to answer a seemingly simple question: what percentage of plants in the world are woody?

Growing numbers of researchers are making the data and software underlying their publications freely available online, largely in response to data sharing policies at journals and funding agencies. But in the age of open science, improving access is one thing, repurposing and reproducing research is another. In a study in the *Journal of Ecology*, a team of researchers experienced this firsthand when they tried to answer a seemingly simple question: what percentage of plants in the world are woody?

They thought the answer would be easy to find. After all, scientists have been distinguishing between woody and herbaceous plants for over 2000 years, ever since Plato's student Theophrastus—often considered the "father of botany"—made the distinction in 300 BC. Researchers already know when the first woody plants came to be, how wood develops and decomposes, and that woody plants like trees and shrubs evolve slower than herbs.

"We thought that if we just dug through the literature enough we would find the answer," said co-author Will Cornwell of the University of New South Wales.

But online searches weren't much help. Google didn't have the answer. Bibliographic tools like Web of Science didn't offer any clues, either.

Expert opinion didn't get them any closer. An informal survey of nearly 300 researchers from 29 countries revealed little consensus even among trained scientists, with guesstimates ranging from 1% to 90%. "[Surprisingly] it didn't matter how much research experience they had, or how familiar they were with plants," said co-author Matt Pennell of the University of Idaho, who was a graduate fellow at NESCent at the time of the study.

Thankfully public data were available. Before they could turn to existing databases, however, they had to deal with an additional problem: Even the largest plant trait database to date—a global woodiness database containing nearly 50,000 species—contains less than 20% of the more than 300,000 plant species known to science. Simply calculating the fraction of species in the database that are woody gave misleading results, due to missing data and sampling bias towards economically important or temperate species.

By applying statistical tricks to account for sampling bias, the researchers were able to determine that between 45 - 48%, or just under half, of the world's plants are woody. "[The take home lesson is that] all big databases are biased, but by acknowledging that bias is universal and accounting for it we can make better use of them," said co-author Rich FitzJohn of Macquarie University

The researchers learned another lesson when they published their work. Their goal was to make enough information about their methods available such that other researchers could retrace their steps. Could someone—using the same data and code, but a different computer—get the same or similar results?

In an ideal word, reproducing the analyses should be as simple as installing the necessary software, downloading the data and hitting 'run.' But software changes from one version to the next. Analysis standards evolve. Analyses that run on one machine don't always work on another.

Making a study easily reproducible, they found, requires a significant amount of time and technical skill. They made sure that everything needed to download and manipulate the data and even create the figures, was written into the code, and explained the thinking behind each snippet of code. They also provided links to tools that would enable researchers to compare changes between different versions of software and restore and run previous versions if need be.

"Nobody denies that researchers should try to make their work reproducible so that others can check their results, but actually making that feasible is easier said than done," FitzJohn said. ●

CITATION: FitzJohn, R., et al. (2014). "How much of the world is woody?" *Journal of Ecology.*

PUBLICATIONS

Recent publications by NESCent authors

Barber, P., et al. (2014). "Advancing biodiversity research in developing countries: the need for changing paradigms." *Bulletin of Marine Science* 90.

Abraham, J., et al. (2014). "The Dominance Concept Inventory: a tool for assessing undergraduate student alternative conceptions about dominance in Mendelian and population genetics." *CBE-Life Science Education.*

MacLean et al. (2014). "The evolution of self-control." PNAS (product of working group led by Charlie Nunn and Brian Hare).

Arnold, S. (2014). "Phenotypic evolution: the ongoing synthesis." *American Naturalist* 83(6): doi: 10.1086/675304.

Bachtrog, D., et al. (2014). "Sex determination: why so many ways of doing it?" *PLoS Biology* in press.

Basey, J., et al. (2014). "Impact of pre-lab learning activities, a post-lab written report, and content reduction on evolution-based learning in an undergraduate plant biodiversity lab." *Evolution: Education and Outreach* 7(1): 10.

Blackmon, H. and J. Demuth (2014). "Estimating tempo and mode of Y chromosome turnover: explaining Y chromosome loss with the fragile Y hypothesis." *Genetics* 197(2).

Comas, L., et al. (2014). "Patterns in root traits of temperate AM and EM woody species: implications for the evolution of belowground strategies." *Ecology and Evolution* in press.

Consortium, T. T. o. S. (2014). "Tree of Sex: A database of sexual systems." *Nature Scientific Data* in press.

Doust, A., et al. (2014). "Beyond the single gene: How epistasis and gene-by-environment effects influence crop domestication." *PNAS* 111: 6178-6183.

FitzJohn, R., et al. (2014). "How much of the world is woody?" *Journal of Ecology*.

Fitzpatrick, C., et al. (2014). "Sources of variance in a female fertility signal; exaggerated estrous swellings in a natural population of baboons." *Behavioral Ecology and Sociobiology* doi: 10.1007/s00265-014-1722-y.

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Gerbault, P., et al. (2014). "Storytelling and story testing in domestication." *PNAS* 111: 6159-6164; doi:6110.1073/pnas.1400425111.

Govindaraju, D. (2014). "Opportunity for selection in human health." *Advances in Genetics* 87(in press).

Gremillion, K., et al. (2014). "Particularism and the retreat from theory in the archaeology of agricultural origins." *PNAS* 111: 6171-6177; doi:6110.1073/pnas.1308938110.

Gross, B. and Z. Zhao (2014). "Archaeological and genetic insights into the origins of domesticated rice." *PNAS* 111(6190-6197; doi:10.1073/pnas.1308942110).

Jones, A., et al. (2014). "Epistasis and natural selection shape the mutational architecture of complex traits." *Nature Communications* 5(3709): doi:10.1038/ncomms4709.

Kraft, K., et al. (2014). "Multiple lines of evidence for the origin of domesticated chili pepper, Capsicum annuum, in Mexico." *PNAS* 111: 6165-6170; doi:6110.1073/pnas.1308933111.

Ksepka, D. (2014). "Flight performance of the largest volant bird." *PNAS.*

Larson, G., et al. (2014). "Current perspectives and the future of domestication studies." *PNAS* 111: 6139-6146.

MacLean, E., et al. (2014). "The evolution of self-control." *PNAS* doi: 10.1073/pnas.1323533111

Marshall, F., et al. (2014). "Evaluating the roles of directed breeding and gene flow in animal domestication." *PNAS* 111: 6153-6158; doi:6110.1073/pnas.1312984110.

McClain, C. and J. Barry (2014). "Beta-diversity on deep-sea wood falls reflects gradients in energy availability." *Biology Letters* 10(4).

Meachen, J. and T. Roberts (2014). "A novel multi-scale assessment of community assembly across time, space, and functional niche." *American Naturalist* 183(5): doi: 10.1086/675758.

Metcalf, J., et al. (2014). "Integrating multiple lines of evidence into historical biogeography hypothesis testing: a Bison bison case study." *Proceedings of the Royal Society* B 281(1777).

Moczek, a. (2014). Towards a theory of development through a theory of developmental evolution. Towards a theory of development. A. Minelli and T. Pradeu, *Oxford University Press.*

Murren, C., et al. (2014). "Evolutionary change in continuous reaction norms." *The American Naturalist* 183(4): doi: 10.1086/675302.

Normark, B. and L. Ross (2014). "Genetic conflict, kin and the origins of novel genetic systems." *Phil. Trans. R. Soc.* B. 369(1642).

Otto, S. (2014). "Selective maintenance of recombination between the sex chromosomes." *J Evol Biol* doi: 10.1111/jeb.12324.

Patten, M., et al. (2014). "The evolution of genomic imprinting: theories, predictions and empirical tests." *Heredity.*

Price, R., et al. (2014). "The Genetic Drift Inventory: a tool for measuring what undergraduates have mastered about genetic drift." *CBE-Life Science Education* 13(1): 65-75.

Ramírez, M. and P. Michalik (2014). "Calculating structural complexity in phylogenies using ancestral ontologies." *Cladistics* DOI: 10.1111/cla.12075.

Redelings, B. (2014). "Erasing errors due to alignment ambiguity when estimating positive selection." *Molecular Biology and Evolution* doi: 10.1093/molbev/msu174.

Spencer, H. and A. Clark (2014). "Non-conflict theories for the evolution of genomic imprinting." *Heredity* doi: 10.1038/hdy.2013.129.

Spencer, H. and A. Clark (2014). "Non-conflict theories for the evolution of genomic imprinting." *Heredity.*

Stringer, J., et al. (2014). "Post-natal imprinting: evidence from marsupials." *Heredity.*

Verdolin, J., et al. (2014). "Key players and hierarchical organization of prairie dog social networks." *Ecological Complexity.*

Wang, X. and A. Clark (2014). "Using next-generation RNA sequencing to identify imprinted genes." *Heredity* doi: 10.1038/hdy.2014.18.

Willis, C., et al. (2014). "The evolution of seed dormancy: Environmental cues, evolutionary hubs, and diversification of the seed plants." *New Phytologist.*

Wolf, J. and Y. Brandvain (2014). "Gene interactions in the evolution of genomic imprinting." *Heredity.*

Wolf, J., et al. (2014). "Imprinted gene expression in hybrids: perturbed mechanisms and evolutionary implications." *Heredity.*

***NESCent publications have been cited more than 10,000 times**

In the Media

"Overriding their animal impulses" (The New York Times) When it comes to animal intelligence, don't ask which species is smarter. "Smarter at what?" is the right question. A NESCent working group on comparative cognition is leveraging a worldwide network of scientist collaborators to test ideas about how cognitive differences in the animal kingdom came to be. Read more in the New York Times at nyti.ms/1nIBNNf, or in National Geographic at bit.ly/1kyjilf. Also picked up by the daily newsfeed of the National Science Foundation.

"Plants with dormant seeds give rise to more species" (Eurekalert) Seeds that sprout as soon as they're planted may be good news for a garden. But wild plants need to be more careful. In the wild, a plant whose seeds sprouted at the first warm spell or rainy day would risk disaster. More than just an insurance policy against late frosts or unexpected dry spells, it turns out that seed dormancy has long-term advantages too: Plants whose seeds put off sprouting until conditions are more certain give rise to more species, finds a new study. NESCent researchers Rafael Rubio de Casas and colleagues tell the full story at bit.ly/1mKyboP.

"Scientists pinpoint the origins of human influence on everything from chickens to chili peppers" (Public Radio International) About 12,000 years ago, the first human "genetic engineers" started introducing small changes to plants and animals to produce benefit for humans. Now scientists are working together to illuminate the story of how animal breeding and food cultivation got started. They are examining everything from genetics to archaeological records to linguistics to fill in the missing pieces.

Learn about the latest research from the NESCent working group on domestication at bit.ly/1kyjilf. Also picked up by Nature, Science Friday and Ars Technica.

"Hundreds of high school students learn about science at Darwin Day Roadshow" (Montgomery Advertiser) NESCent travels to schools across the country every February to celebrate the Feb. 12 birthday of Charles Darwin, and to get more students interested in science. More than 250 students participated during their visit to Montgomery, Alabama. Read more at on.mgmadv.com/1oOXV8r.

"Montana scientists refine knowledge, gather useful data at North Carolina center" (Missoulian) The phrase "room full of bird-brains" doesn't automatically imply intellectual firepower. But there they were – about 30 Ph.D.'s, post-doctoral researchers and graduate students gathered for "A Deeper Look into the Avian Brain: Using Modern Imaging to Unlock Ancient Endocasts" conference. Learn about NESCent's recent avian brain conference, the latest meeting on the microbes that inhabit our homes and offices, and other scientific events at bit.ly/1tCrCXP.

"A marine biologist explains Godzilla's exponential growth" (io9) In 1954, Godzilla was 164 feet tall. With each successive appearance over the past 60 years, his height has increased, so that he now stands at 492 feet. Not bad, given that it took cetaceans 55 million years to go from 8.2 feet to 98 feet in length. Can evolutionary theory help explain Godzilla's rapid growth spurts? NESCent's Craig McClain has the answer, and it's not pretty: bit.ly/1lUkHsw.

"The marine creatures that only live on land plants" (National Geographic) In November 2006, NESCent's Craig McClain sailed into the Pacific Ocean, threw 36 logs overboard, and created several new worlds. Learn about a group of marine creatures that live only on land plants, thanks to special adaptations that allow them to digest wood: bit.ly/1qqOliF

COMING SOON

Add your dataset to a special collection from the publishers of *Nature*

Interested in making research data easier to find and reuse? This May, Nature Publishing Group launched a new open-access online-only publication aimed at recognizing scientists who invest in making valuable datasets widely available and reusable. Scientific Data is currently planning a special collection to highlight data resources from NESCent-sponsored scholars. The first round of NESCent papers are in review, but we hope to add publications to the collection over time. If you're interested in contributing to the collection, please contact Dr. Karen Cranston, NESCent's Training Coordinator & Bioinformatics Project Manager, at karen.cranston@nescent.org, or NESCent's Associate Director of Informatics Dr. Todd Vision at tjv@bio.unc.edu.

COMING SOON

Workshop offers skills and tools for dealing with data

If you're looking for better tools and practices for dealing with data, you're not alone. On May 8-9, 2014, more than 30 researchers converged at NESCent to learn better ways of managing and analyzing their data, such as how to get data out of Excel and into more powerful tools, manage data in R, query databases using SQL, and other skills. This is just the beginning. Sponsored by the Data Observation Network for Earth (DataONE), other Data Carpentry workshops will soon be coming to an NSF-funded BIO Center near you. The next Data Carpentry workshop is slated for July 24-25, 2014, at BEACON at Michigan State University. There will likely also be future workshops at iDigBio at the University of Florida, iPlant at the University of Arizona, and SESYNC at the University of Maryland. Look out for announcements from these and other centers and get more done in less time, and with less pain.

AWARDS

Congratulations to the newest award recipients for 2014

SABBATICAL SCHOLARS

Boris Igic (University of Illinois at Chicago) *The history and consequences of self-incompatibility in flowering plants*

Carola Borries (Stony Brook University) *Principles of primate life histories*

CATALYSIS MEETINGS

Amy Balanoff (Stony Brook University School of Medicine) *A deeper look into the avian brain: using modern imaging to unlock ancient endocasts*

Seth Bybee (Brigham Young University) *New resources for ancient organisms—enabling dragonfly genomics*

Robert Lanfear (Australian National University) *Realizing the full potential of long-term evolution experiments*

Cristine Legare (University of Texas at Austin)*Developing best practices for teaching evolution in the social sciences*

Elena Litchman (Michigan State University) *Evolution and community ecology of host-associated microbiota*

Jonathan Shaw (Duke University) *Scaling evolution from genomes to ecosystems in peatmosses (Sphagnum)*

SHORT-TERM VISITORS

Rachel Adams (University of California, Berkeley) *Meta-analysis of microbial datasets from built environments*

Ashley Bateman (University of Oregon) *Meta-analysis of microbial datasets from built environments*

Beaux Berkeley (James Madison University) *Summarizing a multi-model analysis of biased birth sex ratios in captive prosimians at the Duke Lemur Center*

Holly Bik (University of California, Davis) *Meta-analysis of microbial datasets from built environments*

Christina Caruso (University of Guelph) *The strength of phenotypic selection on floral traits*

Breana Hall (University of Washington)*An improved web tool to assess recombination*

Hafiz Maherali (University of Guelph) *Physiological and climate niche consequences of genome duplication in angiosperms*

James Meadow (University of Oregon) *Meta-analysis of microbial datasets from built environments*

Tamra Mendelson (University of Maryland Baltimore County) *New directions in sexual selection: a synthesis in preparation for a book*

Rebecca Safran (University of Colorado, Boulder) *New directions in sexual selection: a synthesis in preparation for a book*

Rob Gysel (University of California-Davis) *Why are read-overlap graphs computationally tractable?*

Jessica Kissinger (University of Georgia) *Tools to study the evolution of host-pathagen interations*

Frans Plooji (International Research-Institute on Infant Studies)*Translation of field notes for developmental study of chimpanzee vocal communication, Part 2: Adults*

Emanuele Serrelli (University of Milano Bicocca) *What is evolutionary synthesis? The NESCent experience*

Yonas Takle (Spelman College) *In search of the molecular signs of sex in Amoebozoa*

COURSES

Samantha Price (University of California-Davis) *Paleobiological and Phylogenetic Approaches to Macroevolution*

Tracey Heath (University of California-Berkeley) *Phylogenetic analysis using RevBayes*

GRADUATE FELLOWS

Lomax Boyd (Duke University) *Enhancing the synthesis of new evolutionary models of fertility using new media*

Barbara Dobrin (University of Arizona) *Tracing the origins of an endemic flora, and extending a study of divergence dating disparity*

Libby Liggins (University of Queensland) *Nestedness and turnover in the genetic diversity of marine species in the Indo-Pacific Ocean*

Kate Thomas (Duke University) *Physical and ecological parameters driving the evolution of bioluminescence*

Kara Walker (Duke University) *Personality and transfer outcomes in female chimpanzees at Gombe National Park*

David Zonana (University of Colorado, Boulder)*How do sexual signals mediate social interactions? Social network theory and the evolution of dynamic signal traits by sexual selection*

Alannie-Grace Grant (University of Pittsburgh) *Do selfers have greater habitat diversity in their range than outcrossers?*

JOURNALISTS IN RESIDENCE

Robert Chaney (Missoulian) *Wilderness at 50*

Mark Moffett (Smithsonian Institution) *Human identity and the evolution of societies*

Suhail Yusuf *Paleostan—or—Fossilstan—the untold story of fossils from Pakistan*

EVOLUTION 2014 TRAVEL AWARDS FOR FACULTY FROM MINORITY-SERVING INSTITUTIONS

Thomas Backman (Nothwest Indian College)

Mary McKenna (Howard University)

Florentine Riquet (Brooklyn College)

"UNDERGRADUATE DIVERSITY AT EVOLUTION" TRAVEL AWARDS

Usmaan Basharat (Arizona State University)

Emily Behling (University of Connecticut)

Anna Blick (Texas A&M University)

Jennifer Brannon (Rockford University)

Andrew Brown (University of Mississippi)

Susanna Campbell (UMBC)

Austin Cole (University of Minnesota Twin Cities)

Samantha Cooke (California Polytechnic University)

Kiera Coy (George Mason University)

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Megan Frayer (Michigan State University)

Margarita Hernandez (University of Florida)

Alexandria Igwe (Howard University/ Texas A&M)

Sarah Khalil (Cornell University)

Tess Linden (Harvard College)

Jose Maldonado (University of Texas at Arlington)

Natrieifia Miller (University of North Carolina at Asheville)

Michael Rivera (The University of Arizona)

Amie Settlecowski (Tulane)

Andrea Thompson (Harold Washington College)

Gabriel Trujillo (Lake Forest College)

Anna Vinton (University of Colorado at Boulder)

Sophie Wang (Pomona College)

Daniela Zarate (Williams College)

For more information about these scholars and their research projects, please visit bit.ly/N1fKOl.

CHICKENS, continued

ago in South Asia. To pinpoint the genetic changes that transformed this shy, wild bird into the chickens we know today, researchers analyzed DNA from the skeletal remains of 81 chickens retrieved from a dozen archeological sites across Europe dating from 200 to 2,300 years old.

The researchers focused on two genes known to differ between domestic chickens and their wild counterparts: a gene associated with yellow skin color, called BCDO2, and a gene involved in thyroid hormone production, called TSHR.

"[Many of] the pets and livestock we know today–dogs, chickens, horses, cows–are probably radically different from the ones our great-great-grandparents knew."

—Greger Larson, Durham University

Though the exact function of TSHR is unknown, it may be linked to the domestic chicken's ability to lay eggs year-round—a trait that Red Junglefowl and other wild birds don't have.

When the team compared the ancient sequences to the DNA of modern chickens, only one of the ancient chickens had the yellow skin so common in chickens today. Similarly, less than half of the ancient chickens had the version of the TSHR gene found worldwide in modern chickens.

The results suggest that these traits only became widespread within the last 500 years—thousands of years after the first barnyard chickens came to be. "Just because a plant or animal trait is common today doesn't mean that it was bred into them from the beginning," Larson said.

"It demonstrates that the pets and livestock we know today—dogs, chickens, horses, cows—are probably radically different from the ones our great-great-grandparents knew," he added.

Less than 5000 years separate this domestic chicken from its wild ancestor, a bird called the Red Junglefowl. Researchers are trying to pinpoint the genetic changes that transformed the Red Junglefowl into the chickens we know today.

"…They are subjected to the whim of human fancy and control, [so] radical change in the way they look can be achieved in very few generations."

The study is part of a collection of articles in a special edition of PNAS devoted to domestication. This study and others featured in the special issue stemmed from a meeting that took place at NESCent in 2011. Learn more about the meeting—titled "Domestication as an Evolutionary Phenomenon: Expanding the Synthesis"—at domestication.groupsite.com/main/summary. ●

Other authors of the study include Linus Flink, Richard Allen and Ross Barnett of Durham University; Helena Malmström, Jonas Eriksson and Leif Andersson of Uppsala University in Sweden; Joris Peters of Ludwig Maximilian University in Munich, and Keith Dobney of the University of Aberdeen in Scotland.

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