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JILL WEGRZYN AND COLLEAGUES SEQUENCE SUGAR PINE GENOME AND TRANSCRIPTOME

NEW YORK (GenomeWeb) – A University of Connecticut and University of California, Davis-led team of researchers has sequenced both the genome and transcriptome of the sugar pine.

In a pair of studies appearing in *Genetics* and *G3: Genes, Genomes, Genetics*, the researchers report on the 31-billion-basepair genome of *Pinus lambertiana* Douglas and the transcriptomes of about a dozen of its tissues. With this data, the researchers explored the region harboring a pathogen resistance gene as well as lineage-specific Dicer-like proteins within the sugar pine that may give insight into its oversized genome.

"The recent availability of a draft *P. lambertiana* genome sequence, coupled with transcriptomics, offers opportunities to study basic questions about the biology of conifers as it relates to genome evolution and gene expression," UConn's Jill Wegrzyn and her colleagues wrote in the *G3: Genes, Genomes, Genetics* paper.

The UC Davis researchers <u>first announced</u> last year that they'd sequenced the California sugar pine. It's one of the world's tallest trees, reaching 76 meters in height, and may have a lifespan of more than 500 years. In recent decades, though, it has suffered damage from white pine rust, caused by the fungus *Cronartium ribicola*.

In their *Genetics* paper, UC Davis' Charles Langley and his colleagues wrote that to sequence *P*. *lambertiana*, they <u>adapted the approach</u> they'd used to sequence the loblolly pine genome. In particular, they used haploid DNA from a single sugar pine megagametophyte to serve as the basis for their assembly, which they then filled in using mate-pair library reads from diploid needle tissue. From this, they generated some 1.9 trillion basepairs, reflecting 62X coverage of the *P. lambertiana*, which they estimated to be 31 gigabasepairs in size.

Much of the sugar pine genome, though, is repeats. Transposable elements make up 79 percent of the *P*. *lambertiana* genome, slightly higher than the 74 percent found in loblolly pine, the researchers reported. Of those transposable elements, two thirds are long terminal repeat retrotransposons. The researchers estimated the median LTR insertion time for *P. lambertiana* to be 16 million years ago, more recent than that of loblolly.

This high number of repeats and their age gives credence, the researchers said, to the hypothesis that the sugar pine genome, like that of other conifers, got to its massive state by undergoing transposable element expansions.

The researchers noted that being able to use SNP genotyping to uncover resistant trees would speed up reforestation efforts.

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Sugar Pine Genome and Transcriptome sequenced con't....

While sugar pines in general have suffered from *C. ribicola* damage, some trees have resistance to the fungus. Previous work has mapped a biallelic locus, $Cr1^{R}/Cr1^{r}$, that confers resistance, and Langley and his colleagues used their newly generated genome sequence to uncover SNPs in association with $Cr1^{R}$. They uncovered 14 genes annotated on the scaffolds genetically linked to $Cr1^{R}$, one of which — PILA_lg017786 — stood out to the researchers as a candidate gene as it contains domains typically found in disease-resistance genes.

Meanwhile, <u>in *G3: Genes, Genomes, Genetics*</u>, UConn's Wegrzyn and her colleagues reported that they conducted deep sequencing of RNA from tissues representing the tree's embryo state, female cones nearing pollination, stems, and roots, among others, to generate the sugar pine transcriptome.

The researchers used a combination of Illumina MiSeq, HiSeq, and Pacific Biosciences sequencing to pull together the transcriptome. Overall, they uncovered 278,812 transcripts, 30,839 of which could be functionally annotated.

Because of their role in transposable element proliferation and how that might have influenced the hefty size of conifer genomes, Wegrzyn and her colleagues focused part of their analysis on Dicer-like (DCL) proteins.

Within the *P. lambertiana* transcriptome, the researchers uncovered 12 transcripts that exhibited similarity to DCLs, six of which were supported by gene models. Through a phylogenetic analysis drawing on conifers, monocots, dicots, and an outgroup, the researchers identified DCLs that the sugar pine shared with other trees as well as DCLs it shared only with other conifers.

In sugar pine, conventional DCL1 transcripts and one DCL4 transcript were found across all samples the researchers analyzed, while the other DCL4 transcripts were found in cones and DCL3 expression was restricted to reproductive tissues. The profiles of conifer-specific DCL1 transcripts, they added, varied: one was barely expressed, one was ubiquitously expressed, and one had a differential profile in reproductive tissues.

"Expression analysis derived from sequencing data further supports a biological role of these variants," the researchers said in their paper. "The results presented here highlight the peculiarities of this pathway in conifers and identifies similarities with ancient land plants."

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EEB IN THE NEWS

EEB has been making headlines. Below are a few of the articles, on a wide variety of subjects, that may interest you:

Grand challenges for the study of cultural evolution (Turchin) - <u>http://www.nature.com/articles/</u><u>s41559-017-0070</u>

'Goldilocks Fires' can enhance biodiversity in Western Forests (Tingley)- <u>http://</u> today.uconn.edu/2016/10/goldilocks-fires-can-enhance-biodiversity-western-forests/

Study says the ocean's largest life is under threat of extinction (Bush) - <u>http://</u>today.uconn.edu/2016/09/study-says-largest-ocean-life-threat-extinction/

Critical information needed in fight to save wildlife (Urban) - <u>http://today.uconn.edu/2016/09/</u> critical-information-needed-fight-save-wildlife/

Social Instability lies ahead, researcher says (Turchin) - <u>http://today.uconn.edu/2016/12/using-social</u> -science-to-predict-the-future/

Researchers say natural regeneration an overlooked but low-cost option for forest restoration -Mongabay (Chazdon) - <u>https://news.mongabay.com/2016/12/researchers-say-natural-regeneration-</u> an-overlooked-but-low-cost-option-for-forest-restoration/

How 'elite overproduction' and 'lawyer glut' could ruin the U.S. - (Turchin) <u>http://</u><u>news.nationalpost.com/full-comment/peter-turchin-how-elite-overproduction-and-lawyer-glut-could-ruin-the-u-s</u>

New science writing course aims to make science accessible for all - (Rubega) <u>http://</u> <u>dailycampus.com/stories/2016/11/30/new-science-writing-course-aims-to-make-science-accessible-for-all?rg=rubega</u>

This American sparrow could be gone in 50 years, say conservationists—(Elphick) <u>http://</u>www.csmonitor.com/Environment/2016/1128/This-American-sparrow-could-be-gone-in-50-years-say-conservationists

At UConn-Avery Point, a new approach to teaching - (Finiguerra) <u>http://www.theday.com/</u> <u>local/20161016/at-uconn-avery-point-new-approach-to-teaching</u>



AWARDS

FACULTY

Sixteen EEB faculty, lecturers and staff on three campuses were awarded <u>2016 Teaching Excellence</u> <u>Awards</u>. Storrs Campus: Janine Caira, John Cooley, Adam Fry, Elizabeth Jockusch, Cindi Jones, Louise Lewis, Jane O'Donnell, Margaret Rubega, Eric Schultz, Morgan Tingley and David Wagner. Waterbury Campus: Melissa Durstin, Paula Philbrick and Susan Preston-Berlin. Claudia Kramer from the Stamford Campus and Michael Finiguerra from the Avery Point Campus also received awards. Excellence in Teaching Award recipients have displayed commitment to innovative and exceptional pedagogy.

Michael Willig, UConn Board of Trustees Distinguished Professor of Ecology and Evolutionary Biology, was named a Fellow of the American Association for the Advancement of Science. The AAAS grants Fellow status based on scientifically or socially distinguished efforts to advance science or its application; it publishes the journal *Science* and several other publications.

Chris Simon was elected as an Honorary Fellow of the Royal Society of New Zealand. This honor recognizes her distinguished research career. It is one of the highest honors accorded a foreign scientist.

Elizabeth Jockusch received the Edward C. Marth Mentorship Award. This award is the highest honor presented in recognition of leadership and dedication to excellence in mentoring graduate students. The award was established by UConn AAUP to honor Ed Marth, former Executive Director of the CT AAUP Chapter.

Gene Likens received a Frontiers of Knowledge in Ecology and Conservation Biology Award from the BBVA Foundation recognizing his pioneering work on the discovery causes of acid rain and his long-term experimental studies of the impacts on ecosystems.

GRADUATE STUDENTS

Dustin Ray, working in Cindi Jones' lab, was awarded the 2016 Katherine Esau Award for best student paper delivered to the Development and Structural Section at the Botanical Society of America annual meeting.

Samantha Apgar, working in Chris Elphick's lab, was awarded a USFWS Pathways Internship. This program pays students to do work for the USFWS while conducting their studies, and comes with a range of professional development benefits as well as potential employment opportunities within the FWS after graduation.

ALUMNI

Lily Lewis, Ph.D. 2015, Dr. Bernard Goffinet, advisor, was awarded the 2016 Greg and Mona Anderson Best Dissertation Award. The cash award and certificate are presented for the best thesis in the general areas of systematics and/or ecology and evolution.

GRANTS

FACULTY

Robert Bagchi, in collaboration with Chris Phillipson at ETH Zurich, has been awarded a grant to study ecosystem multifunctionality at a landscape scale in degraded tropical forests in Borneo. "FORESTER: Functioning & Resilience of Ecosystem Services in Tropical Rainforests"

Michael Finiguerra, Avery Point campus, was awarded a NSF REU site grant (Mystic Aquarium) for "Collaborative Research: Investigating the consequences of global change on marine organisms and their ecosystems."

John Silander received an award from NASA/National Aeronautics and Space Administration/ Research Foundation for the State University of New York for his project, "Detecting Dimensions of Biodiversity in a Mega-Diverse Region of Southern Africa: From Traits to CommUnities to Ecosystems."

Jill Wegrzyn received a grant from the NSF/BIO/Directorate for Biological Sciences/Washington State University for her project, "Standards and Cyberinfrastructure that Enable "Big-Data" Driven Discovery for Tree Crop Research." In addition, **Dr. Wegryzn** received a USDA/National Institute of Food and Agriculture/North Carolina State University award for her project, "Development and Use of Genomic Tools to Improve Firs for Use as Christmas Trees."

Charlie Yarish received an award from the DOC/National Oceanic and Atmospheric Administration/ Woods Hole Oceanographic Institution for his project, "Integrating Mussel and Kelp Longline Culture Structures and Management." **Dr. Yarish** also received an award from the Suffolk County Government, NY/ Cornell University for his project, "Proposed Cornell Cooperative Extension of Suffolk County and University of Connecticut Collaboration of Kelp Growth Trials in the Peconic Estuary, Long Island, New York."

GRADUATE STUDENTS

Val Milici, working in Robi Bagchi's lab, received a grant from the Tinker Field Graduate Research Fund for her field research in Panama.

Annette Evans, working in Elizabeth Jockusch and Mark Urban's labs, received a research grant from the Society of Integrative and Comparative Biologists to support her research in the red-backed salamander, *Plethodon cinereus*.

Andrew Frank, working in Elizabeth Jockush's lab, was awarded a research grant from the Chicago Herpetological Society for his California field work on juvenile skinks.

Manette Sandor, working in Chris Elphick's lab, received a 2017 Doctoral Dissertation Improvement Grant.

ALUMNI NEWS

Dr. **Chris Martine**, Ph.D. 2006, Bucknell University, received a 2016 Passion in Science Award from the New England BioLabs. Chris' award was a Science Mentorship and Advocacy award. Passion in Science awards acknowledge scientists for inspirations and innovative work that transcends the boundaries of pure science, and has profound impact on other fields include the arts, humanitarian service, environmental stewardship and science mentorship.

Dr. **Anne Bruneau**, MS 1986, University of Montreal, was awarded the 2016 Le prix Michel-Jurdant in Quebec for her work regarding the preservation of biodiversity in this time of plant fragility. Dr. Bruneau, who, earned her Ph.D. at Cornell, was instrumental in creating de l'Institut de Recherche en Biologie Végétale and serves as it's Director.

Dr. Saul Cunningham, Ph.D., 1995, has been appointed Director of the Fenner School of Environment and Society at the Australian National University in Canberra.

Dr. **Gregory Miller,** Ph.D., 1987, has been names President and CEO of NatureServe in Arlington, VA. NatureServe is a top international conservation biology science program.

Dr. **Susan Letcher,** Ph.D. 2008, has accepted a tenure-track position at the College of the Atlantic in Bar Harbor, ME.

Dr. **Suegene Noh,** Ph.D., 2010, has accepted a tenure-track position at Colby College in Waterville, ME as Assistant Professor of Biology (Computational Biologicist/Genomicist)

Dr. **Frank Smith**, Ph.D., 2013, has accepted a tenure-track position as an Assistant Professor of functional genomics at the University of North Florida in Jacksonville, FL,

Dr. **Brian Klingbeil**, Ph.D. 2015, recently completed a UConn Postdoctoral Fellow position in Chris Elphick's lab and has accepted a Post Doc position with Dr. Chris Lepczyk at Auburn University in Auburn AL.

EEB COLLECTIONS BENEFITS FROM 2016 SUMMER FELLOWSHIPS

EEB'S Collections Endowment provided fellowship funds for undergraduates Timothy Pullen (EEB BS/MS '18) and Jake Perfetto (Bio '17) to assist with projects associated with the Mammal and Herpetology collections respectively. Jessica Cebelius (ECSU '17) volunteered in the bird collection, rounding out a summer of labwork at ECSU with curatorial experience. Their primary objective was to bring our specimen data to full conformation with Darwin Core standards. Once the projects are finished, the data will be submitted to VertNet to be published online.

In natural history collections, it's usually better to have more rather than fewer specimens, but this summer Tim Pullen's task was to reduce the number of specimen entries in the mammal database - by eliminating duplicate records. Many of these nearly 5000 records turned out to be skulls stored separately from their skins, which he tracked down and reunited - with one specimen record. Discrepancies in earlier data-entry efforts were not uncommon, especially regarding collecting locations. Correcting these led Tim down the Trans-Chaco Highway of Paraguay, along the routes of several collecting expeditions, where in addition to geo-referencing many collecting events, he ultimately learned quite a bit about the geography of that country.

After Tim's summer efforts, 2445 new specimen records will be sent to VertNet, to be added to UConn's mammal dataset of 9889 records, published in April 2016. The next major database overhaul, in preparation for its online debut, will be that of the reptiles and amphibians. Jake Perfetto, BIO '17 and EEB PhD candidate Annette Evans both worked with the Herpetology collection this summer, on tasks ranging from the inventory of gallon jars of wood frogs to making sense of specimens on the "problems" shelf. For both, the goal was to ascertain that our specimen data was as accurate as possible.

Jake's main focus was to comb through an excel file containing a veritable mountain of frog and salamander collecting data, to format names, dates and locations. Usually the specimen accession ledger would help clarify details of collecting events, but sometimes it further confused - for example, it listed at least three variations on the same collecting location. Using a combination of written description and Google Earth maps, Jake was able to clarify spelling errors and geo-reference that specific salamander collecting event, placing it along the Long Trail in Vermont's Green Mountains.

Jessica Cebelius, an undergrad in Biology at ECSU, volunteered in the bird collection this summer, taking a one-day per week diversion from her studies in marine sciences. Aside from the novel experience of being in a natural history collections environment, one highlight of Jessica's hours spent with the bird database was correcting old location errors. This process usually began with coming across a somewhat vague collecting locality. If the tag on the actual bird skin shed no new light, she back-tracked to the accession ledger, then to the original data card where she would usually discover the source of the error.

Using GoogleEarth, Jessica was able to pinpoint collecting localities for two tanager species to a mountain slope not far from Bogota, in central Colombia. Four specimens of these tropical birds, *Tangara vitriolina* and *T. heinei*, are now quite precisely geo-referenced, and hence far more valuable as study skins than we previously thought.

As a finale to a summer of data-entry, all three students spent time in the vertebrate preparation lab, learning how to make bird study skins. The results will be added to the Biodiversity Research Collection ... as soon as the collecting localities are geo-referenced!

Article by Susan Hochgraf, EEB Collections Vertebrate Manager

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