

The Plant Press



Smithsonian
National Museum of Natural History

Special Symposium Issue - see page 9

New Series - Vol. 12 - No. 2

April-June 2009

Botany Profile

Genome Scientists Express Themselves

By David Erickson

This year's Smithsonian Botanical Symposium, held on 27-28 March at the National Museum of Natural History in Washington, DC, brought together scientists from the academic genomics community with scientists from the natural history and applied research fields to highlight and promote collaboration. The eighth annual symposium, "Genes, Genomics and Genome Evolution in Plants," hosted by the Department of Botany, was held in collaboration with the United States Botanic Garden.

The subject for the Symposium was developed by Elizabeth Zimmer of the Smithsonian Institution and her former colleague Jeff Bennetzen at the University of Georgia. Both felt that the museum and the public would benefit from presentations highlighting how genomics has changed plant science, what genomics can do to aid research and conservation at the museum, and the challenges that remain concerning the discovery and application of genomic data. The symposium was convened by Zimmer, who noted that the explosive growth in genomics research has the potential to help scientists working at the National Museum of Natural History and that the public needed to be better informed about this work.

Before the seven invited speakers presented their talks, Laurence Dorr awarded the Eighth José Cuatrecasas Medal for Excellence in Tropical Botany to Norris H. Williams from the Florida Museum of Natural History and the University of Florida in Gainesville. Williams is an expert of Orchidaceae systematics and

evolution, with particular emphasis on Neotropical groups. Accepting the award on Williams' behalf was Douglas S. Jones, Director of the Florida Museum of Natural History. Jones read a letter of acceptance from Williams in which Williams highlighted his long relationship with the Smithsonian Institution, including the time in 1972 he met Cuatrecasas during his postdoctoral research associate years at NMNH.

The first speaker was Kenneth Wurdack of the National Museum of Natural History, with a talk titled "Phylogenomics and the End of Incongruence?" Wurdack began by introducing the basic premise of genomics – what type of data is collected, from where and how – and discussed how genomics may come to radically alter the way relationships among species are inferred in modern phylogenetic systematics. Genomics can be broadly defined as the large-scale collection of sequence data from DNA. In the case of systematic studies, it means we can collect DNA sequence data from all genes for a species, while doing so for multiple species simultaneously. First generation genome sequencers (notably 454 sequencing) collect millions of very short DNA sequences (25-50 nucleotides in length), each from a random portion of the genome. The challenge then is to assemble these minute sequences in the correct order. Second generation genome

sequencers have begun to collect longer sequence reads (>400 nucleotides in length) from each of the millions of

reads, making assembly into a continuous chromosome easier and more accurate.

Third generation sequencers offer the promise of ever longer sequence reads for more segments, making the sequence coverage for the genome easier and more accurate. And while cost currently remains prohibitive, accessibility is expected to improve.

Genomics can change the way phylogenetics is conducted in two major ways. Typically in modern systematic studies, a choice between more samples versus more data per sample is demanded. Genomics offers the promise of having both. By dramatically accelerating the speed at which data is collected, more data per sample is readily obtained, and as cost declines, more samples can be subjected to genomic level sequencing. Wurdack used his own work as a reference, noting that a published 13 gene phylogeny of the Malpighiales had more data than most published phylogenies, yet retained a number of unresolved nodes. He also noted that taxa whose affiliations were not previously known with certainty still were not assigned to resolved clades with much certainty. Thus genome scale data is likely the most robust way to resolve difficult



Smithsonian
Botanical Symposium

Continued on page 12

Pedro Acevedo traveled to Acre, Brazil (1/28 – 2/23) to join a botanical expedition financed by the Flora of Acre Project (Universidade Federal do Acre and the New York Botanical Garden).

Walter Adey traveled to Gloucester Point, Virginia (1/5 – 1/7; 1/14 – 1/16) to attend meetings at the Virginia Institute of Marine Science at the College of William & Mary.

Christian Feuillet traveled to St. Louis, Missouri (2/9 – 2/10) to visit with several times co-author John MacDougal and work on the *Dilkea* (Passifloraceae) collections at the Missouri Botanical Garden; to Paris, France (2/18 – 2/26) to look for specimens of *Dilkea* at the Museum of Natural History in Paris and to work on the revision of a paper in preparation; and to French Guiana (3/1 – 3/24) to work in the collections at the Institut de Recherche pour le Developpement (IRD), Herbar de Guyane and to search for *Passiflora* in the wild with a team of scientists and amateurs.

Vicki Funk traveled to Merida, Mexico (1/5 – 1/12) to attend the meeting of the International Biogeography Society where she completed her term as President of the organization; and to Montreal, Canada (2/1 – 2/4) to work with colleagues on the data from the Biological

Diversity of the Guiana Shield and to plan for the next meeting of The International Compositae Alliance.

W. John Kress traveled to Stockholm, Sweden (2/9 – 2/12) to give an invited lecture on DNA barcoding to the Royal Swedish Academy of Sciences; to Cambridge, Massachusetts (2/23 – 2/25) to deliver an invited talk to the Department of Organismic and Evolutionary Biology at Harvard University; and to the Dominican Republic and Puerto Rico (3/13 – 3/26) with post-doctoral student **Silvana Marten-Rodriguez** to conduct field work on *Heliconia* and hummingbirds.

Mark and Diane Littler traveled to Atlanta, Georgia (3/12 – 3/15) to give a presentation entitled “Health of Coral Reefs: Measuring Dominances of Benthic Indicator Groups and Calculating Top-down/Bottom-up Tipping Points,” at the American Academy of Underwater Sciences 27th Scientific Diving Symposium.

Rusty Russell traveled to Riverside County, California (3/27 – 4/4) with a team of Earthwatch volunteers to work with the Bureau of Land Management and the University of California Natural Reserve System in assessing the floristic history of desert canyons in the western Colorado Desert.

Laurence Skog traveled to Sarasota, Florida (1/25 – 2/1) to work in the collections at Marie Selby Botanical Gardens and work with staff of the Gesneriad Research Center based at Selby.

Robert Soreng traveled to Ottawa, Canada (2/23 – 2/29) to work on *Poa* and give a presentation on Steppe vegetation and culture in Kyrgyz Republic at the Canadian Museum of Nature.

Alain Touwaide traveled to Victoria, Canada (2/1 – 3/1; 3/6 – 3/21) with **Emanuela Appetiti** to present lectures and teach classes on the history of medicine in the Mediterranean at the University of Victoria; to Chicago, Illinois (2/13 – 2/15) with Appetiti to attend the annual meeting of the American Association for the Advancement of Science; and to Chicago, Illinois (3/25 – 3/27) to chair a session at the Annual Meeting of the Association for Asian Studies.

Jun Wen traveled to Merida, Mexico (1/8 – 1/13) to attend the International Biogeography Society meeting, where she co-organized a symposium on Asian-American biogeographic disjunctions; and to Raleigh, North Carolina (3/20 – 3/22) to participate in graduate student recruitment activities and discuss collaborations with colleagues at North Carolina State University.

Kenneth Wurdack traveled to Cambridge, Massachusetts (1/14) to obtain a loan of amber orchid fossil at Harvard University for the 2009 exhibit “Orchids Through Darwin’s Eyes.”

Elizabeth Zimmer traveled to Baltimore, Maryland (2/24) to give a talk on “Plant Molecular Systematics and Evolution” at Johns Hopkins University.



The Plant Press

Reu Series - Vol. 12 - No. 2

Chair of Botany

Warren L. Wagner
(wagnerw@si.edu)

EDITORIAL STAFF

Editor

Gary Krupnick
(krupnickg@si.edu)

News Contacts

MaryAnn Apicelli, Robert Faden, Ellen Farr, Shirley Maina, Rusty Russell, Alice Tangerini, and Elizabeth Zimmer

The Plant Press is a quarterly publication provided free of charge. If you would like to be added to the mailing list, please contact Dr. Gary Krupnick at: Department of Botany, Smithsonian Institution, PO Box 37012, NMNH MRC-166, Washington, DC 20013-7012, or by E-mail: krupnickg@si.edu.

Web site: <http://botany.si.edu/>

Visitors

Lei Xie, Beijing Institute of Botany, China; *Clematis* (Ranunculaceae) and *Circaea* (Onagraceae) (1/2/07-1/2/09).

Blanca Leon, Universidad Nacional Mayor de San Marcos, Lima, Peru; Peruvian *Tillandsia* (Bromeliaceae) and flora (10/18/07-10/18/09).

Lu Jin-Mei, Kunming Institute of Botany, China; *Adiantum* (Adiantaceae) (2/1/08-1/31/09).

Rong Li, Kunming Institute of Botany, China; Asian *Schefflera* (Araliaceae) (2/15/08-2/14/09).

Athena Tellis, Thomas Jefferson High School for Science and Technology; *Magnolia* (Magnoliaceae) (6/30/08-2/28/09).

Mauricio Diazgranados, St. Louis University; Asteraceae (12/17/08-1/7/09).

Nadia Roque, Universidade Federal da Bahia, Salvador, Bahia, Brazil; *Gochnatia* (Asteraceae) (12/29/08-1/6/09).

Ze-long Nie, Kunming Institute, China; Eastern Himalayan plants (1/5-3/12).

Rodney Dever, West Virginia University; *Allium* (Liliaceae) (1/6).

Kerrie Kyde, Maryland Department of Natural Resources; *Oplismenus* (Poaceae) (1/9).

Paul Berry, University of Michigan; *Croton* and *Euphorbia* (Euphorbiaceae) (1/12-1/13).

Past, Present, and Future

Thirty-six years ago the Department of Botany started a newsletter called *Botanical News*. With the fourth issue the name changed to the current *Plant Press*, provided by departing Botany staff member, Charley Potter, who later transferred from Botany to the Mammals Division of the Department of Vertebrate Zoology (where he has been ever since). Thanks Charley for name! Through the years *The Plant Press* has documented the travels, visitors, meetings, and other activities of the department as well as provides novel content on a variety of topics.

This issue of *The Plant Press* continues to emphasize the activities of the Department and the visitors to the United States National Herbarium. We focus on our annual Smithsonian Botanical Symposium. This year the Symposium covered the timely topic of plant genomics. It was a very successful meeting with good participation and a fine slate of presenters. We owe our thanks to Jeff Bennetzen for initially contacting Liz Zimmer with the idea of this year's symposium topic and for successfully obtaining funding from the National Science Foundation. We also continue to have the great funding support from the U.S. Botanic Garden and the Cuatrecasas Family Foundation.

Also featured in this issue are two current Cuatrecasas Fellows, Amalia Diaz, who is visiting from Colombia to study the Eriocaulaceae, and Ya-Yi Huang from the New York Botanical Garden studying Lecythidaceae. The Cuatrecasas Family Foundation with their continued annual and increasing support has made it possible to continue to expand the activities supported by the endowment, including the annual symposium, fellowships, and archiving and digitizing the José Cuatrecasas collections and images.

On another note, I am particularly pleased to announce an initiative involving several of the researchers in the Department and elsewhere in the Smithsonian Institution: The Pacific Science Initiative (PRI). Scholars from across the Institution, with our external partners, are working to integrate what we do so that we can ask questions with the depth and breadth to match that of our study area, the Pacific. We plan to use our results to increase our knowledge of the biota

and peoples of the Pacific and plug significant gaps.

One of the projects "Team Pacific" is developing is a scientific meeting, "Evolution of Pacific Island Biota," to be held at the University of Hawaii, Honolulu from 20-22 May 2010. This meeting will be a three-day, stand-alone meeting designed to bring together a diverse international group of experts and students to examine the biogeography and evolution of terrestrial, near-shore, and freshwater biota from across the tree-of-life, including humans, which are distributed across Pacific islands. There will be a variety of ways to participate in the meeting, including public lectures, invited presentations, contributed papers, poster and discussion sessions, as well as pre- and post-meeting fieldtrips and workshops. The meeting will be organized around several themes and questions, and it will focus on both empirical studies and methods for analyzing biogeographical data, including:

- What phylogeographic patterns are found in the Pacific Islands?
- Do Pacific Islands act as sources for dispersal to other areas?
- Do fossil data change our interpretation of evolution and biogeography of the Pacific Islands?
- What are the evolutionary patterns of community assembly?
- Do Pacific biogeographic patterns track the geologic or human history of the area?
- How do data from biogeography and evolution inform conservation efforts?

We have already sent out an email announcing the meeting to those in our database of researchers working in Pacific islands. This database, however, is certainly incomplete so if you or your colleagues are interested in participating in the meeting please contact the program coordinator, Danica T. Harbaugh, at harbaughd@si.edu. Comments on the program should be sent to me at wagnerw@si.edu. A website is currently in development.

W. L. Wagner

**Chair
With
A
View**

**Warren
L.
Wagner**



Carlos Moura, Independent researcher; Volunteer interview (1/16).

Laura Lagomarsino, University of California Berkeley; *Heliconia* (Heliconiaceae) (1/21-3/20).

Yong Jiang Zhang, Institute of Animal and Plant Quarantine, Chinese Academy of Inspection and Quarantine, Beijing; Plant DNA Barcoding (1/21-4/24).

James Beck, Duke University; *Astroblepis* (Pteridaceae) (1/27).

Robynn Shannon, Wesleyan University; Plant reproductive biology (1/28).

Koos Roux, South African National Biodiversity Institute, Claremont, South Africa; South African pteridophytes (1/28-1/29).

Zhumei Ren, Shanxi University, China; Coevolution of gallnut aphids and host plant based on DNA sequences (2/1/09-1/31/10).

Cameron Brooks, University of New Hampshire, Shoals Marine Laboratory; Coralline microscopy (2/2-3/2).

Tingshuang Yi, Kunming Institute of Botany, China; *Osmorhiza* (Umbelliferae) (2/2-5/2).

Chris Frye, Maryland Department of Natural Resources; *Bromus* (Poaceae), *Dryopteris* (Dryopteridaceae) and *Pycnanthemum* (Labiatae) (2/10).

Continued on page 5

Staff Research & Activities

Robert Faden was part of the organizing committee of the Potomac Valley Chapter of the North American Rock Garden Society which hosted the Eastern Winter Study Weekend. The meeting was held in Reston, Virginia, 30 January to 1 February. Audrey Faden, a Smithsonian Behind-the-Scenes Volunteer, also participated in the organization of the meeting. Along with Greenhouse Manager **Mike Bordelon**, she gave a talk on gravel gardens that focused on the garden that Bordelon installed around the Botany Research Greenhouse in Suitland, Maryland.

In March, **Christian Feuillet** visited French Guiana to search for *Passiflora* in the wild. His team collected a few specimens for herbarium collections and some for cultivation, for a total of 31 *Passiflora* and one *Dilkea*, including cuttings of three specimens that may prove to be new species.

Mark and Diane Littler recently attended the American Academy of Underwater Sciences 27th Scientific Diving Symposium in Atlanta, Georgia, 7-12 March, where they presented "Health of Coral Reefs: Measuring Benthic Indicator Groups and Calculating Tipping Points." The presentation outlined a model for assessing the health and resiliencies of coral reef ecosystems and used their recent survey and assessment of Bonaire, Netherlands Antilles (funded by Conservation International) as a test case. The Littlers were surprised and pleased when Caren Eckrich, Assistant Director of the Council on International Educational Exchange Research Station, Bonaire, stood and congratulated them on their report, which was used by the Bonaire National Marine Park Authority (STINAPA) to secure a mandate and funding (from the Dutch government) for tertiary treatment of wastewaters entering the ocean.

Rusty Russell participated in Smithsonian Citizen Science Week (April 5-10) in Riverside, California. The Riverside Metropolitan Museum, a Smithsonian Affiliate, organized numerous public activities

around a workshop entitled "The Record of Southern California Biodiversity, and a Role for Citizen Science." This workshop, organized and convened by Rusty Russell and James Bryant, Natural History Curator at RMM, assembled more than 40 professionals from over 22 public and private institutions throughout the state.

Alice Tangerini participated (for the second year in a row) in the "Big Draw" event at North Chevy Chase Elementary School in Chevy Chase, Maryland, on February 25. Organized by elementary school teacher, Jackie Moore, the "Big Draw" is an interactive series of classes given by local artists from private studios and by staff from museums at the Smithsonian Institution. Each artist had a 45 minute class with 20 to 30 students from the 4th and 5th grades. Tangerini gave an introductory explanation of botany, botanists and how artists work with the scientists. She then gave a demonstration of drawing from herbarium specimens. Each student then had a chance to make their own "scientific illustration" with black fine point markers using samples of drawings that Tangerini provided. The local *Montgomery County Gazette* ran a piece on the "Big Draw" and featured a picture of Tangerini with her students.

Tangerini was part of an Artist Research Fellowship Panel Review Committee who selects the recipients for the 2009 Artist Research Fellowship. Organized by Jane Milosch, curator at the Renwick Gallery, the program is a pan-Institutional initiative that seeks to encourage artists outside the Smithsonian to interact with staff on art related projects. Collaboration on research topics of interest to both the artist and the Smithsonian scholars is one of the main objectives. On 4 March an all day panel review took place where a final 10 artists were selected from 63 applicants. Tangerini was the only scientific illustrator on the panel which afforded her a slightly different perspective on the applicants than the rest of the panel.

On March 14 Tangerini participated in the American Association of University Women's annual Career Day for Middle School Girls held at Fairfax High School in Fairfax, Virginia. During the program women in the science fields present talks about their careers to three classes of 7th and 8th grade girls. Tangerini gave a presentation about how a plant travels from

field to herbarium and finally to publication.

On 4 March, **Alain Touwaide** delivered two talks in the Washington, D.C. area: "Health and Healing from the Mediterranean Tradition" at the National Institutes of Health, and "Ancient Drug Lore for the Future?" at the Cosmos Club.

Recipients of the Jose Cuatrecasas Award Visit NMNH

Amalia Diaz, a researcher from the Humboldt Institute in Bogotá, Colombia, visited the U.S. National Herbarium during the month of March, for the "Eriocaulaceae of Colombia" project. The main goal of her research visit was to revise the collection of Eriocaulaceae as a source of information for a final and official checklist of the Eriocaulaceae of Colombia. Eriocaulaceae is a primarily pantropical family with a few species in temperate regions. It consists of 11 genera and 1,200 species, although the species number is uncertain and can vary from 700 – 1,440. There are nine genera in northern South America: *Actinocephalus* (Koern.) Sano, *Blastocaulon* Ruhl., *Eriocaulon* L., *Leiothrix* Ruhl., *Paepalanthus* Kunth, *Philodice* Mart., *Rondonanthus* Herzog, *Syngonanthus* Ruhl., and *Tonina* Aubl. In Colombia, the Eriocaulaceae exhibit a disjunct distribution which is very interesting from a biogeographical point of view,



Amalia Diaz

since there is a group of plants growing on savannas and lowlands which belong to an extension of the Guiana Shield and another group of plants in the high Andean páramos of the three cordilleras, with these Andean ecosystems much younger than Guiana Shield. During her visit she found approximately 400 specimens of Eriocaulaceae collected in Colombian páramos and lowlands by José Cuatrecasas, José Celestino Mutis, Richard Evans Schultes, among others, as well as 21 types, which she recorded in the checklist. She also found very interesting records of Ericaulaceae in páramos from Peru, Venezuela and Ecuador, which can be a good source of information for furthering knowledge of the flora of the high Andean ecosystems. She contributed to the identification of the Eriocaulaceae collections of the Plants of the Guiana Shield project and made some additional updates to the presence in Colombia of certain species reported in the *Checklist of the Plants of the Guiana Shield*.

Ya-Yi Huang, a Ph.D. graduate student at the City University of New York and the New York Botanical Garden, visited the U.S. National Herbarium from 23 to 27 March 2009, to study specimens of Neotropical Lecythidaceae. Her research focuses on the genera *Bertholletia*, *Corythoiphora*, *Eschweilera* and *Lecythis*. These four genera all possess zygomorphic androecia and are closely related. During her five-day visit, she annotated three species of *Allantoma* (*A. decandra* (Ducke) S. A. Mori, Y.-Y. Huang & Prance, *A. integrifolia* (Ducke) S. A. Mori, Y.-Y. Huang & Prance, and *A. pluriflora* S. A. Mori, Y.-Y. Huang & Prance), which were included in *Cariniana* Casaretto in the most recent monograph (Prance & Mori, 1979) and were transferred to the genus *Allantoma* Miers in 2008 (Huang et al.). She also went through all specimens of *Corythoiphora* and *Lecythis*, and most specimens of *Eschweilera*. Huang recorded morphological characters such as leaf venation patterns, midrib pubescence, punctuation, papillae on the abaxial leaf surface, calyx orientation, calyx imbrication, and presence of style etc, for her phylogenetic analysis. The result will be compared and eventually combined with her molecular phylogeny. In addition, Huang databased the coordinates of the specimens and georeferenced the speci-

mens without coordinates. The herbarium records will be used for species distribution mapping and modeling using the computer programs AcrGIS and Maxent. These records combined with environmental factors such as rainfall, temperature, and elevation etc, will help fill the gap due to incomplete collection and predict areas of potential new populations.



Ya-Yi Huang

Visitors

Continued from page 3

Wesley Knapp, Maryland Natural Heritage Program and Delaware State University; *Juncus* (Juncaceae) and *Rhynchospora* (Cyperaceae) (2/10).

Joe Hereford, University of Maryland; Rubiaceae (2/18).

Jose Mauricio Bonifacio, Herbario Bernardo Rosengurt, Montevideo, Uruguay; Asteraceae (2/18-3/20).

Tatyana Livshultz, Academy of Natural Sciences Philadelphia; Herbarium management (2/19).

Nina Alexeeva, Komarov Botanical Institute, St. Petersburg, Russia; Iridaceae (2/20; 3/2-3/4).

Fabian Michelangeli, New York Botanical Garden; Melastomataceae (2/23-2/24).

Carmen Amalia Diaz-Pena, Humboldt Institute, Bogota, Colombia; Colombian Eriocaulaceae (3/1-4/1).

Tieyao Tu, Chinese Academy of Sciences; *Bauhinia* (Leguminosae-Caesalpinioideae)

and *Typha* (Typhaceae) (3/1-7/31).

Pingting Chen, Central China Agricultural University; Vitaceae (3/1/09-2/28/10).

Ihsan Al-Shehbaz, Missouri Botanical Garden; Brassicaceae (3/12-3/13).

Eric Christenson, Independent researcher; *Maxillaria* (Orchidaceae) (3/12-3/14).

John R. Clark, Marie Selby Botanical Gardens; Hawaiian *Cyrtandra* (Gesneriaceae) (3/16-3/20).

Eric Roalson, Washington State University; Hawaiian *Cyrtandra* (Gesneriaceae) (3/17-3/19).

Fred Barrie, Missouri Botanical Garden and Field Museum; Flora Mesoamericana Gesneriaceae (3/17-3/31).

Richard Mack, Washington State University; Asian Bambusoideae (Poaceae) (3/19-3/20).

William and Margaret Dix, Universidad del Valle de Guatemala, Guatemala City; Central American Orchidaceae and Bromeliaceae (3/19-4/7).

Eva Gonzales, Appalachian State University; *Uniola paniculata* (Poaceae) (3/20).

Jerry (Arnold) Tiehm, University of Nevada; Great Basin flora (3/23-3/25).

Ya-Yi Huang, New York Botanical Garden; Neotropical Lecythidaceae (3/23-3/27).

German Muttoni, Herbario Bernardo Rosengurt, Montevideo, Uruguay; Asteraceae (3/23-4/5).

Raluca Kogalniceanu, Alexandru Ioan Cuza University of Iasi, Romania; Archaeobotany (3/30).

David Monsees, Monsees Consulting LLC, Washington, DC; Archaeobotany (3/30).

Alexandru Morintz, Vasile Pârvan Institute of Archaeology, Romania; Archaeobotany (3/30).

Bertil Nordenstam, Swedish Museum of Natural History, Stockholm; *Nordenstamia* and Tribe Senecioneae (Asteraceae) (3/31-4/1).

Collecting Sapindaceae in Acre, Brazil

During February 2009, **Pedro Acevedo** traveled to the state of Acre, Brazil, to join a botanical expedition financed by the Flora of Acre Project (Universidade Federal do Acre and the New York Botanical Garden). The expedition consisted of two Melastomataceae specialists, Renato Goldenberg from Universidade Federal do Paraná and Fabian Michelangeli from the New York Botanical Garden; two local botanists, Edilson Oliveira and Flavio Obermuller; an undergraduate student, Herison Medeiro; and Acevedo as the liana and Sapindaceae specialist.

The expedition targeted the least botanically explored area in the entire state of Acre, where there is substantial forest left. The team flew from Rio Branco to Jordao where they hired a 25-foot boat for use as a floating laboratory and hotel. They then traveled downstream along Taruaca River until reaching Taruaca, 200 kilometers and about 10 days later.

During their journey they stopped at interesting forested sites daily collecting all fertile plant species with which they came into contact. Overall the team collected over 600 numbers with several duplicates. Acevedo collected more than 100 Sapindaceae species, some of which

represent new records for Brazil or for the state of Acre. As a result, he was able to add six species of Sapindaceae to the checklist of Acre. The material was pressed in alcohol and processed upon their return to the Universidade Federal do Acre in Rio Branco. Duplicates will soon arrive to all participating institutions.

After the expedition Acevedo spent two additional weeks in the Rio Branco region. The first week he taught a mini-class on Sapindaceae taxonomy and phylogeny to a group of students from Universidade Federal do Acre. The second week was devoted to further explorations in the seasonally flooded forest along Andira River.



Global Plants Initiative

By *Shruti Dube*

Global Plants Initiative (GPI) is an international partnership of herbaria

working to create a coordinated database of information and images of plants from around the world. With support from the Mellon Foundation, partner organizations capture data and create high resolution digital images of type specimens from their collections. The goal of the GPI project (formerly called the Latin American Plant Initiative – LAPI) is a self-sustaining resource that an international community of scholars can access via the World Wide Web. The repository of images and data is hosted by Aluka (<http://www.aluka.org>), a not-for-profit initiative with a mission to create a digital library of scholarly resources from and about the developing world, as an aid for research and teaching worldwide. Aluka is already hosting a similar repository for African plant type specimens.

Under the guidance of Collections Manager **Rusty Russell**, the staff for this project is progressing well in this effort. **Shruti Dube**, who serves as Project Manager, has been working for the Department of Botany for over two years now. She plays a key role in managing all areas of this project, including locating and extracting type specimens from the general herbarium, digital scanning and photography of extracted specimens, quality checking of images, electronic cataloging, and facilitating the transfer of specimen metadata to Aluka. She manages the combined efforts of a team composed of several hard-working individuals:

- **Natasha Crump** has participated in a couple Department projects over the past three year, most recently in the repair and conservation of the gymnosperm collection;
- **Vinita Gowda** has worked part-time while she successfully pursued her Ph.D.;
- **Ingrid Lin**, as she has done for more than five years, handles all the digital photography for this project;
- **Janet Kline**, a volunteer, has been assisting in Department activities for more than a year and graces the scanning machine on Monday;
- **Elsbeth Kursh** finished her Masters in Museum Studies at the George Washington University and worked with Cathy Hawks on preparing objects for the “Written in Bone” exhibit;
- **Emily Robinson** recently finished a stint with the Latin American and



Students from Universidade Federal do Acre that participated in Pedro Acevedo's (bottom right) Sapindaceae mini-class.



Shruti Dube prepares a plant specimen to be digitized.

Caribbean Collections Management Training Program; and,

- **Karen Roberts** splits her time between this project and her work in Paleobiology before a planned return to Australia this fall.

Critical to this process, and to ensure the integrity and relevance of our Type Register, **John Boggan** has provided considerable assistance with the checking and verifying of types before they are processed into the Type Collection.

A strong botanical background and good management skills have supported Dube's efforts to increase the rate at which types are being located, processed and digitized. Under her management, the GPI team has successfully exceeded every monthly target for productivity. They have completely canvassed over 91 higher plant families, including Euphorbiaceae, Rosaceae, and Chenopodiaceae. Three very large families, Rubiaceae, Melastomataceae and Fabaceae, are currently being checked. With an efficient workflow process, Team GPI has digitized more than 29,000 type specimens employing two Herb Scans and one high-end digital camera setup. Each month, more than 1,800 images and data are transmitted to Aluka (now JSTOR). Continued support from the Mellon Foundation and significant in-kind support from the Smithsonian Institution should help us realize a fully digitized

Type Register of more than 115,000 verified type specimens by the end of 2010.

Pancake-Seagrass Formations: Alien Crop Circles in the Sea?

Mark and Diane Littler and their colleague Ned Smith have reported on mys-

terious pancake-like patterns, resembling flattened circular nests of drifting seagrass blades, from Florida Bay, USA. The 2,072-km² bay, with its vast mangrove, seagrass and coral-reef habitats, interacts importantly with the entire Florida Keys and Coral Reef Tract. The drifting fragments, consisting mostly of the shoal grass *Halodule wrightii* (Cymodoceaceae), are exceptional because they can maintain viability for up to 4 weeks. Interestingly, such extraordinary mosaic patterns of pancake-seagrass rafts are previously unreported, but consistently originate in the western region of Florida Bay under light wind and wave conditions.

To date, the Littlers have no evidence identifying the mechanisms responsible for the circular patterns, but the patterns do appear to be analogous to cold-water pancake-ice formations (see http://en.wikipedia.org/wiki/Pancake_ice) in respect to how they take shape. As in pancake-ice, the patterns are posited to be sculpted by the bumping action of adjacent clumps, in conjunction with the nature of the curved crescent-shaped individual blades. The initial stages of formation seem to develop from a tendency for the buoyant blades to be shuffled inward to coalesce as overlapping/interlocking concentric rings, with the mean pancake diameter being 18 cm $\pm$ 4 SD. The possibility that the pancakes are rolled into shape by tidal-current shear has also been suggested.



Overview of a large floating pancake-seagrass raft comprised of nest-like circular clumps (~18 cm in diameter).

Publications

- Appetiti, E.** 2009. Smithsonian Institution and the US Exploring Expeditions, or: how the Nation's Attic was created. *J. Wash. Acad. Sci.* 95(1): 35-45.
- Bagatini, M.D., T.G. Vasconcelos, **H.D. Laughinghouse**, A.F. Martins and S.B. Tedesco. 2009. Biomonitoring hospital effluents by the *Allium cepa* L. test. 2009. *Bull. Environ. Contam. Tox.* 82: 590-592.
- Boggan, J.K., L.E. Skog** and E.H. Roalson. 2008. A review of the neotropical genera *Amalophyllon*, *Niphaea*, and *Phinaea* (Gesneriaceae - Gloxinieae). *Selbyana* 29(2): 157-176.
- Carvalho, L.R., F. Pipole, V.R. Werner, **H.D. Laughinghouse IV**, A.C.M. Camargo, M. Rangel, K. Konno and C.L. Sant'Anna. 2008. A toxic cyanobacterial bloom in an urban coastal lake, Rio Grande do Sul. *Brazilian J. Microbiol.* 39: 761-769.
- Costa, R.C.L., A.K.S. Lobato, C.F. Oliveira Neto, P.S.P. Maia, G.A.R. Alves and **H.D. Laughinghouse**. 2008. Biochemical and physiological responses in two *Vigna uguiculata* (L.) Walp. cultivars under water stress. *J. Agron.* 7(1): 98-101.
- Davidse, G., **R.J. Soreng** and **P.M. Peterson**. 2009. *Agrostopoa* (Poaceae, Pooideae, Poeae, Poinae), a new genus with three species from Colombia. *Novon* 23(1): 32-40.
- Dorr, L.J.** 2009. Review of: Two Journeys: Six Years in Siberia and Six Hours in Alaska. *Taxon* 58(1): 237-238.
- Fachinetto, J.M., **H.D. Laughinghouse IV**, A.C.F. Silva and S. Tedesco. 2008. Variability of the chromosomal number and meiotic behavior in populations of *Bidens pilosa* L. (Asteraceae) from southern Brazil. *Caryologia* 61(2): 164-169.
- Faden, R.B.** 2008. New species of *Commelina* (Commelinaceae) from East and South-Central Africa. *Novon* 18(4): 469-479.
- Harbaugh, D.T., **W.L. Wagner**, G.J. Allan and **E.A. Zimmer**. 2009. The Hawaiian Archipelago is a stepping stone for dispersal in the Pacific: an example from the plant genus *Melicope* (Rutaceae). *J. Biogeogr.* 36(2): 230-241.
- Harbaugh, D.T., **W.L. Wagner**, D.M. Percy, H.F. James and R.C. Fleischer. 2009. Genetic structure of the polymorphic *Metrosideros* (Myrtaceae) complex in the Hawaiian islands using nuclear microsatellite data. *PLoS ONE* 4(3): e4698.
- Hollowell, T.H.** 2009. Plant community structure, fire disturbance, and recovery in mangrove swamps of the Waini Peninsula, Guyana. *Contrib. Study Biol. Divers.* 3: 1-166.
- Lobato, A.K.S., C.F. Oliveira Neto, R.C.L. Costa, B.G. Santos Filho, F.K.S. Silva, F.J.R. Cruz, A.C.S. Abboud and **H.D. Laughinghouse**. 2008. Germination of *Sorghum* under the influences of water restriction and temperature. *Agr. J.* 3(3): 220-224.
- Lobato, A.K.S., C.F. Oliveira Neto, R.C.L. Costa, B.G. Santos Filho, F.K.S. Silva, F.J.R. Cruz and **H.D. Laughinghouse IV**. 2008. Biochemical and physiological behavior of *Vigna uguiculata* (L.) Walp. under water stress during the vegetative stage. *Asian J. Plant Sci.* 7(1): 44-49.
- Lubini, G., J.M. Fachinetto, **H.D. Laughinghouse IV**, J.T. Paranhos, A.C.F. Silva and S.B. Tedesco. 2008. Extracts effecting mitotic division in root tip meristematic cells. *Biologia* 63(5): 647-651.
- Luebert, F., **J. Wen** and M.O. Dillon. 2009. Systematic placement and biogeographical relationships of the monotypic genera *Gypothamnium* and *Oxyphyllum* (Asteraceae: Mutisioidae) from the Atacama Desert. *Bot. J. Linn. Soc.* 159: 3251.
- Olkoski, D., **H.D. Laughinghouse IV**, A.C.F. Silva and S. Tedesco. 2008. Meiotic analysis of the germplasm of three medicinal species from the Asteraceae family. *Ciênc. Rural* 38(6): 1777-1780.
- Simmons, R.H., **M.T. Strong** and J.M. Parrish. 2008. Noteworthy collections: Virginia. *Castanea* 73(4): 328-332.
- Touwaide, A. 2008. 72 entries (from "Agathinos of Sparta" to "Zenon of Laodikeia"), approximately 88 pp. In P. Keyser and G. Irby-Massie, eds. *Encyclopedia of Ancient Natural Scientists: The Greek Tradition and its Many Heirs*. Routledge, London and New York.
- Verbruggen, H., M. Ashworth, S.T. LoDuca, C. Vlaeminck, E. Cocquyt, T. Sauvage, F.W. Zechman, **D.S. Littler**, **M.M. Littler**, F. Leliaert and O. De Clerck. 2009. A multi-locus time-calibrated phylogeny of the siphonous green algae. *Mol. Phylogenet. Evol.* 50(3): 642-653.
- Wagner, W.L.** and P.C. Hoch. 2009. Nomenclatural corrections in Onagraceae. *Novon* 19(1): 130-132.
- Wen, J.**, Y. Zhu, C. Lee, E. Widjaja and L.G. Saw. 2008. Evolutionary relationships of Araliaceae in the Malesian region: a preliminary analysis. Materials and methods. *Acta Bot. Yunnan.* 30: 391-399.



Smithsonian Botanical Symposium

Williams Receives Eighth Cuatrecasas Medal

The Department of Botany and the United States National Herbarium present this annual award to a botanist and scholar of international stature who has contributed significantly to advancing the field of tropical botany. The José Cuatrecasas Medal for Excellence in Tropical Botany is named in honor of Dr. José Cuatrecasas (1903-1996), a pioneering botanist and taxonomist who spent nearly a half-century working in the Smithsonian Institution's Department of Botany. Cuatrecasas devoted his career to plant exploration in tropical South America and this award serves to keep vibrant the accomplishments and memory of this outstanding scientist.

The winner of this prestigious award is selected by a committee made up of four botanists on the staff of the Department in consultation with other plant scientists outside of the Smithsonian Institution. Nominations for the Medal are accepted from all scientists in the Botany Department. The award consists of a bronze medal bearing an image of José Cuatrecasas on the front with the recipient's name and date of presentation on the back. Highlights from past presentations to the recipients are available on the Symposium Archives at <<http://botany.si.edu/cuatrecasas/cuatrecasasMedal.cfm>>.

Norris H. Williams of the Florida Museum of Natural History and the University of Florida in Gainesville is the eighth recipient of the José Cuatrecasas Medal for Excellence in Tropical Botany. Williams' area of expertise is on Neotropical Orchidaceae. His work on orchid molecular phylogenetics, the chemistry of floral fragrances, and pollination biology of orchids has given us a better understanding of the evolution of these plants and their insect pollinators.

Williams received a B.S. from the University of Alabama in Tuscaloosa with

a major in Biology in 1964 and an M.S. from the same university in the same field in 1967. In 1964-1965 he held a Woodrow Wilson Fellowship at Washington University in St. Louis. He received his Ph.D. from the University of Miami in 1971. After graduation he held a series of postdoctoral positions—at the University of Miami; in the Department of Botany of the National Museum of Natural History, Smithsonian Institution; and at the Fairchild Tropical Garden in Coral Gables, Florida. In 1973 he secured an appointment as an Assistant Professor of Biology at Florida State University in Tallahassee. Promoted to Associate Professor, he remained at FSU until 1981, when he moved to Gainesville. Currently, he has a joint appointment at the Florida Museum of Natural History and University of Flor-

ida where he is a Professor of Botany. He served as Chairman of the Department of Natural Sciences of the Florida Museum of Natural History for almost ten years.

Williams is author or co-author of almost 100 papers. His current research focuses on the molecular systematics of *Maxillaria* and its relatives, and the molecular systematics of the subtribe Oncidiinae (Orchidaceae). His field work has taken him to Central America (notably Panama), the Caribbean, and South America (Colombia, the Guianas, Ecuador, Bolivia, and Argentina). He is an Honorary Life Member of the American Orchid Society, and has received the President's Medal of the University of Costa Rica and the Lankester Prize for pioneering work on the ecology, evolution, phylogeny, and systematics of orchids.



Norris H. Williams received the 2009 José Cuatrecasas Medal for Excellence in Tropical Botany.

Abstracts from the Speakers at the Smithsonian Botanical Symposium

The eighth annual Smithsonian Botanical Symposium was held 27-28 March 2009. The symposium, "Genes, Genomics, and Genome Evolution in Plants," explored the results of current studies on plant genes and genomes, especially as they apply to fundamental questions in evolutionary biology, crop improvement and ecosystem sustenance in rapidly changing environments. Below are the speakers' abstracts from the papers that were presented.

Kenneth Wurdack Smithsonian Institution

"Phylogenomics and the End of Incongruence?"

The future of molecular systematics seems to lie in amassing ever larger datasets with more genes and more taxa in pursuit of more robust trees. Such a "total evidence" approach shows promise for resolving deeper nodes, placing difficult taxa (e.g., parasitic plants), and resolving challenging rapid radiations (i.e., Malpighiales or Saxifragales). Furthermore, genome-scale data do provide a powerful tool towards realizing these goals by providing the vast quantity of characters needed and enabling gene choices better tailored to the problems addressed. However, both complexity and the risk of systematic errors grow rapidly with such large datasets. For instance, individual gene trees can conflict which presents an opportunity to explore its causes (i.e., horizontal gene transfer), although some consider such incongruence to be a nuisance that is preferably avoided through better experimental design (i.e., better gene selection or methods of analysis). There are certain challenges and opportunities emerging with regard to the types of evolutionary questions that can be addressed with genomic data and its use in phylogenetic inference.

Jill Preston University of Kansas

"Importance of Multigene Transcription Factor Families for Flower Develop-



Chair of the Department of Botany Warren L. Wagner (left) with the speakers of the 2009 Smithsonian Botanical Symposium: Bob Jansen, Jill Preston, Susan McCouch, Ken Wurdack, Gerry Tuskan, Liz Zimmer (Symposium Convener), Rob DeSalle, and Jeff Bennetzen. (Photo by Donald Hurlbert)

ment and Its Diversification"

Inflorescences and flowers vary greatly in both architecture and identity, suggesting repeated evolutionary modifications to a shared ancestral ground plan. In model organisms, such as *Arabidopsis thaliana* and *Antirrhinum majus*, the genetic basis of floral development is fairly well understood. However, less is known about similar pathways in morphologically divergent species. Theoretical and empirical studies suggest that gene duplications may be important for the evolution of plant form, since relaxed selection following gene doubling may allow functional divergence of one or both genes, commonly distinguished as non-, sub- or neo-functionalization. Here, I present two studies examining the evolution of genes from multigene families, and their possible roles in diversification of floral form. The first examines the role of duplicated *API/FUL* MADS-box genes in the evolution of Poaceae flowers (spikelets) and the second determines the role of TCP- and MYB-family transcription factors in evolution of petal symmetry and stamen number in Veronicaceae.

Bob Jansen University of Texas

"Comparative Plastid Genomics Resolves Phylogenetic Relationships

among Major Angiosperm Lineages and Reveals Genome-scale Evolutionary Patterns"

Currently there are 149 plastid genome sequences available on GenBank with 93 of these from angiosperms. The genomic data has provided a wealth of new data for resolving phylogenetic relationships among the major clades of angiosperms and for improving our understanding of genome evolution. Phylogenetic analyses of a data set that includes 81 genes from all available angiosperm genomes provide excellent resolution and support for resolving relationships among the major clades. This includes: confirmation that *Amborella* is the earliest diverging lineage of angiosperms; resolution of the placement of Chloranthales sister to magnoliids; placement of Chloranthales/magnoliids clade sister to a strongly supported eudicot/monocot clade; placement of *Ceratophyllum* sister to eudicots; and placement of Caryophyllales sister to asterids. Genomic-wide comparisons across angiosperms identified a strong positive correlation between rates of nucleotide substitutions and genomic rearrangements. Comparisons of genome organization of Geraniaceae identified extensive rearrangements, including large expansions/contractions of the inverted repeat and numerous gene order changes.

These rearrangements are associated with dispersed repeats, suggesting that they may play an important role in genomic rearrangements. Comparisons of rates of sequence evolution among protein-coding genes in Geraniaceae and Poaceae identify extensive rate heterogeneity among lineages and genes but the overall pattern in these two families is distinct. In Geraniaceae, rapid rate accelerations occur both on the branch leading to the family as well as the internal branches, whereas in Poaceae rate acceleration is restricted to the branch leading to the family. In both groups accelerated substitution rates are associated with only certain functional groups of genes.

Rob DeSalle

American Museum of Natural History

“Are Whole Genomes the Way to Go?”

Genome level information and high throughput methods have opened a new phase of modern systematics. Some unanswered questions and difficulties have surfaced as a result of incorporating data from high throughput methods that require immediate attention. One question that always arises is “how much?” Another question that is very persistent with genome level information concerns the problem of incongruence and how to treat incongruent information in systemat-

ics. Using several examples from the tree of life the question of “how much” and the problem of incongruence will be examined from a genomic perspective. The utility of a fully fleshed out tree of life for determining function in an evolutionary context will also be discussed.

Gerry Tuskan

Oak Ridge National Laboratory

“The Entangled History of *Populus* and Humans – Genomics, Accelerated Domestication and Napoleon”

From origin myths onto the Roman Empire, Davy Crockett, the minuteman missiles and through to modern biofuels development *Populus* has shared a common history with humans. As one of the fastest growing woody perennial plants, one which can be easily clonally propagated through the use of unrooted lateral branches, *Populus* has been used to provide shade, demarcate roadway, control soil erosion, and provide fiber for pulp, paper, veneer, and bioenergy feedstocks. The domestication process however has been erratic and slow due to the large size and delayed reproductive habit of this woody perennial tree. Modern genomics tools and approaches are being brought to bear on the efforts to accelerate the domestication process in *Populus*. The genome of *Populus trichocarpa* was sequenced,



Gerry Tuskan

assembled, and annotated in 2006 through an international effort that included over 250 scientists from over 20 countries. The assembled genome contains 45,500 predicted gene models and revealed a recent whole-genome duplication that suggested the molecular clock in *Populus* is ticking at one sixth the rate seen in herbaceous annual plants such as *Arabidopsis*. Utilizing this information has made it possible to refine genetic maps, improve candidate gene isolation through QTL analyses and association genetics, and test hypotheses on accelerated domestication. Candidate genes related to drought tolerance, crown architecture, cell wall chemistry and disease resistance are currently being evaluated in greenhouse and field trials.

Susan McCouch

Cornell University

“Gene Flow and Genetic Isolation during Crop Evolution”

Knowledge about the structure and evolutionary history of naturally occurring variation in crops and their wild relatives provides a road map for understanding domestication and new opportunities for utilizing novel alleles in crop improvement. Domesticated Asian rice (*Oryza sativa* L.) is comprised of five, well-differentiated subpopulations that evolved from a common, out-crossing wild ancestor, *O. rufipogon*. We seek to



Liz Zimmer, Symposium Convener, welcomes the audience to the eighth annual Smithsonian Botanical Symposium. (Photo by Elaine Haug)

Continued on page 12

Abstracts

Continued from page 11

understand the evolutionary forces that acted on this tropical ancestor to generate the subpopulation structure of modern *O. sativa*. Using recently isolated domestication genes, we trace the evolutionary history of alleles that both define and transcend the deep population subdivisions of domesticated rice. Documented patterns of allele-sharing and dispersal suggest a complex pattern of gene flow and genetic exchange coupled with an increase in genetic isolation reinforced by inbreeding. Understanding the biological, social and cultural dynamics of these opposing processes challenges existing models of crop domestication and provides a framework for conserving, characterizing and utilizing wild and exotic germplasm in crop improvement.

Jeff Bennetzen

University of Georgia

“Leveraging Evolutionary Genomics for Crop Improvement in Sub-Saharan Africa”

The genomes of most plants are large, and quite complex. The average flowering



Jeff Bennetzen

plant genome, for instance, is twice the size of the human genome. Much of the DNA within these plant chromosomes is comprised of transposable elements that have expanded and rearranged their host genomes at an exceptional rate. Afloat in these seas of repetitive DNA are the gene islands that actually determine plant development, physiology and adaptability. A few angiosperm (flowering plant) genomes have been sequenced, and several more are in the works. With this sequence information, the genes that specify the common properties of angiosperms (like photosynthesis, root development and seed production) are being identified. Most exciting, the genes responsible for the differences in plant biology that make each species unique are also under investigation, both at the level of their functions and in their modes of evolution. We are now attempting to use this information, extracted largely by comparative genomics, to accelerate the improvement of crops like tef millet that are vital to millions of Africans, but have been largely ignored by most scientists in advanced research environments. Because so few plant species have been investigated at the molecular and genomic level, surprises abound, but comparative genomics provides a framework whereby such novel observations are being integrated and utilized for the study and improvement of any targeted crop.

Symposium

Continued from page 1

relationships by freeing scientists to compile consensus phylogenies across many genes. Wurdack further noted that more genes alone would not magically solve all the challenges in molecular systematics, as when different genes suggest different species relationships, as well as the computational challenge of analyzing these huge datasets. But the advent of genomics should be regarded as a powerful tool that will help biologists and particularly systematists make better sense of the world.

The next speaker was Jill Preston, a postdoctoral fellow currently at University of Kansas. Preston, who works on floral development, outlined current advances in the genetic basis of floral development, expanding on the classical model of 3-gene interaction first elucidated by Elliot Meyerowitz and colleagues. Preston described her work investigating how gene duplication events in targeted gene families may have allowed for the acquisition of novel genetic behaviors that result in new floral architectures. Because much of what is known about floral development comes from *Arabidopsis*, it is important to begin to look at alternate floral morphologies and examine the mechanisms that underlie their differences. Preston described work in two highly divergent floral morphologies, the small and non-showy grass spikelet and a showy orna-

Acknowledgements

The success of the Symposium was due to the significant time and efforts of the following people:

Organizers

- Jeff Bennetzen
- Laurence Dorr
- Ellen Farr
- Vicki Funk
- W. John Kress
- Gary Krupnick
- Sue Lutz
- Warren L. Wagner
- Jun Wen
- Kenneth Wurdack
- Elizabeth Zimmer

Support

- Mary Ann Apicelli
- Patricia Davis

Photographer

- Elaine Haug

And many others who had helped in a myriad number of ways.

mental snapdragon (*Anarrhinum*). In both cases, changes in the regulation of genes produces much of the morphological differentiation we see among floral types. Changes in the expression of transcription factors and their targets, both temporal and spatial, can be readily diagnosed through the tools of genomics and will offer researchers new avenues for continued diagnosis of the molecular basis for the floral diversity that enthalls all lovers of plants.

Following Preston was Bob Jansen from the University of Texas. Jansen's talk was the perfect compliment to the topic of genomic analyses as he presented results using the complete sequence of plant chloroplasts to reconstruct molecular plant phylogenies. Genomic studies will likely produce data sets of comparative data structure that Jansen presented, and he illuminated how powerful the use of these large data sets are when evaluating deep and complex phylogenies. His results from 93 angiosperm taxa demonstrated *Amborella* as the unquestioned basal angiosperm, but also noted that within the phylogenetic tree, discordances could also be observed, particularly with regard to Poaceae and Geraniaceae. These two clades could be recognized as being different from other angiosperm clades due to dramatic differences in the rates of evolutionary change along branch lengths leading to those clades, which were well supported by the chloroplast genomic scale data. The discordance of the two taxa suggests novel episodes in evolution for these clades, which may correspond to a rapid expansion of the clade (Poaceae) and intrinsic structural rearrangements that have accelerated sequence evolution (Geraniaceae). The ability to robustly

Sponsors of the 8th Smithsonian Botanical Symposium

- Cuatrecasas Family Foundation
- National Museum of Natural History
 - Department of Botany
 - Office of the Associate Director for Research and Collections
- National Science Foundation
- United States Botanic Garden



Douglas Jones (center), Director of the Florida Museum of Natural History, accepts the 2009 José Cuatrecasas Medal for Excellence in Tropical Botany on the behalf on Norris H. Williams from Warren Wagner, Chair of the Department of Botany (left) and Laurence J. Dorr, Chair of the Award Committee (right). Photo by Donald Hurlbert.

reconstruct these complex relationships empowers us to identify the exceptional clades which in turn allows us to better investigate evolutionary mechanisms underlying evolutionary diversification.

Following Jensen was Rob DeSalle from the American Museum of Natural History in New York, who bravely acknowledged his role as lone zoologist at a botanical symposium. His talk, titled "Are Whole Genomes the Way to Go?," considered in more quantitative detail what the consequences of the massive amounts of genomic data will be for phylogenetics. While it is easy to assume that more data will resolve all uncertainties in phylogenetics, DeSalle challenged that notion, suggesting that it will not be a trivial plug-and-play outcome to just add more data and expect better results in all cases. Serious issues, including how to root complex clades, how to manage inclusion or exclusion of contradictory data, and questions about orthology with genomic data were all touched on. DeSalle described specifically how estimation of orthology will be a challenge, but also suggested it is superable. He demonstrated his model, Orthology ID, as a step toward addressing that challenge. Two other sig-

nificant challenges to phylogenomics were addressed—lineage sorting and horizontal gene transfer—with the former compounded when tree roots are ambiguous and the latter estimated from *Drosophila* as far less common than some predict. In the end, the process of assimilating the very large quantities of data used in phylogenomics will require the right balance of care to ensure proper assessment of orthology and homology while maximizing the speed to annotate and align data.

The next speaker, Gerald Tuscan from the Oak Ridge National Laboratory, gave a compelling account of how modern genomic tools are accelerating plant breeding in poplar (*Populus tremuloides*). Only a handful of plant species have had their genomes completely sequenced, poplar being one. Exactly how the genome sequence can be used to assist in plant breeding was the focus of his talk. Tuscan prefaced his talk with an excellent history of the early cultivation of poplar during the Napoleonic wars of 18th century Europe, due to its ease in propagation and rapid growth rate. Those same characters mean the species is still relevant today and increasingly so for use in biofuels. Avail-

Continued on page 14

Symposium

Continued from page 13

ability of the genome sequence means that marker assisted breeding can be accelerated through the availability of thousands of SNP and SSR markers associated with functional traits via QTL or association analyses. Because poplar is a tree and may require a decade per generation, identification of very narrow gene regions or genes that improve growth rate, or that change the crown structure to make the plants shorter and wider can be selected early and standardized. Tuscan noted that even in poplar where the genome sequence is very complete, gaps in the genome sequence remain, largely due to repeated elements. They represent ongoing challenges for annotation and assembly of genome sequences even under ideal conditions. However, the rapid progress in cultivar development for this long-lived species has been greatly accelerated and is a keystone example of how genomics can lead to tangible improvements in applied biology.

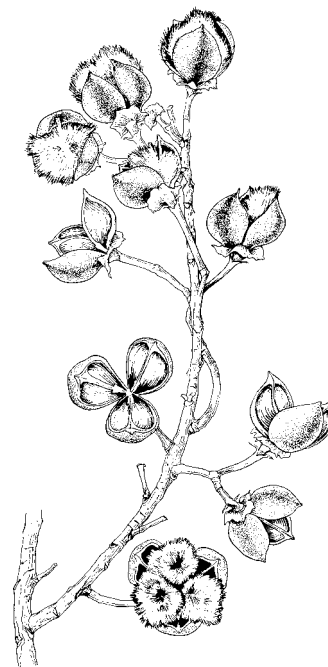
Following Tuscan was Susan McCouch from Cornell University, who described the history and challenges of rice domestication. McCouch's talk covered the subjects of population genetics and phylogenetics, and suggested how genomics may further assist in both crop breeding and in reconstructing the history of this critical species. McCouch outlined the five basic varieties of *Oryza sativa*: *indica*, *aus*, *tropical japonica*, *temperate japonica* and *basmati*. Each of these varieties was observed to be a genetically distinct sub-population, likely with different historical origins. McCouch gave an example of how genomic data makes a significant difference in rice breeding, outlining how a color mutation that makes rice red is physically linked on chromosome 7 with the gene that controls shattering. Since early shattering of the rice panicle can lead to massive crop losses, identification of the molecular basis affects rice bowls worldwide. Using genetic tools, McCouch demonstrated that two mutations associated with *indica* and *japonica* varieties suppress shattering, and investigated the origins of the two alleles which informed as to the origins of the cultivars in China and India, respectively. The identification of the genes controlling shattering in different varieties represents a powerful tool

in marker assisted selection, and points the way forward for use of genome-wide marker data in similar challenges.

The final speaker in the symposium was Jeff Bennetzen from the University of Georgia, who sought to place genomic advances in the context of improving lives, not just in advancing knowledge. However, Bennetzen also regaled the audience with details of the magnitude of evolutionary change prompted by transposable-elements which has been detected only through massive amounts of genome level sequencing. Particularly in grasses, the genomes have been revealed to be islands of genes afloat in a sea of inactive transposable elements. Upwards of 80% of the maize genome is derived from transposable elements – many of which have been mistaken as novel plant genes. The dramatic flux in genome content – almost entirely of TEs – exemplified by *Oryza sativa* whose genome appears to have grown by 3% even though 300 megabases of DNA have been lost in the last two million years. Transposable elements are also seen to acquire exons and gene-promotor sequences and then reposition them in different genetic contexts, potentially as a rapid accelerator of genome evolution and developmental function. His dramatic presentation was capped by going beyond statistics to note that for many farmers around the world, available crop species are in dire need of advanced breeding to improve productivity, disease- and pest-resistance, and adaptation to changing climates. In these cases, knowledge of gene function in related crop species investigated through genomics represents a change capable of greatly accelerating breeding practices.

Following Bennetzen's presentation, Zimmer provided concluding remarks noting the importance of genomics in the identification of genomic rearrangements, the importance of those structural changes in development and evolution, and the need to categorize genetic changes to fully implement genomic data within the context of phylogenomics. Department of Botany Chair Warren Wagner followed Zimmer, thanking the audience who gleefully adjourned to the museum's latest orchid show, "Orchids Through Darwin's Eyes," for a reception and discussion followed by a sumptuous dinner in the museum's rotunda where food and food for thought was enjoyed by all.

Next year, the Ninth Annual Smithsonian Botanical Symposium will focus on marine plants. The date of the Symposium is tentatively set for 16-17 April 2010. All are invited to attend.



Supplementary Symposium Links on the Web

The Web site to the 8th Annual Smithsonian Botanical Symposium <<http://botany.si.edu/sbs/>> has many links and documents related to the conference. Included on the Web site is the full program, abstracts of the talks, links related to the speaker's presentations, and selected images from the various events. A digital video recording of the presentations will be posted soon. Additional items related to the Symposium can be added to the list of links and documents by sending an e-mail to sbs@si.edu.

The Symposium archive pages <<http://botany.si.edu/events/sbsarchives/>> also includes programs, abstracts and images from the past six symposia: "Linnaean Taxonomy in the 21st Century" (2001); "The Convention on Biological Diversity" (2002); "Botanical Frontiers in South-east Asia" (2003); "Botanical Progress, Horticultural Innovations, and Cultural Changes" (2004); "The Future of Floras: New Frameworks, New Technologies, New Uses" (2005); "Island Archipelagos: Cauldrons of Evolution" (2006); and, "Partners in Evolution: Interactions, Adaptations, and Speciation" (2008).

Additional Scenes from the 8th Annual Smithsonian Botanical Symposium



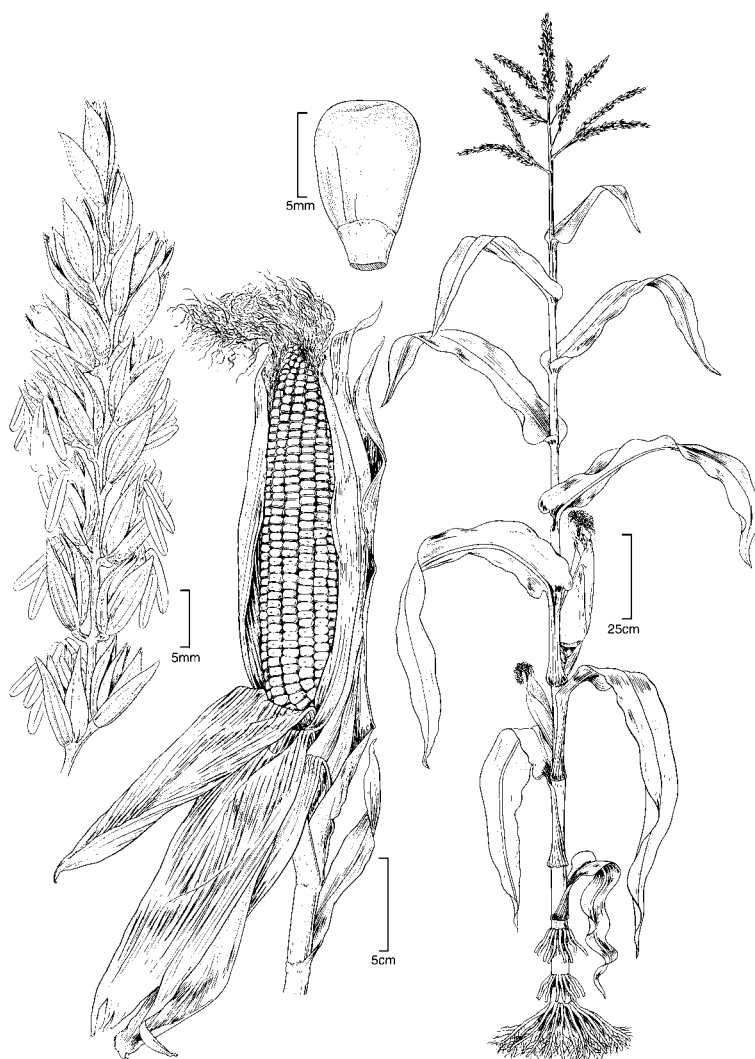
Clockwise (from top left): Participants of the Symposium enjoy lunch above the Rotunda of the Museum; engaging in conversation during the reception in the exhibition "Orchids Through Darwin's Eyes," Friday night's opening reception at the U.S. Botanic Garden; a table of guests at the Symposium Banquet; and *Cymbidium iridioides* on display during the reception in the orchid exhibit. (All photos by Elaine Haug)



Art by Alice Tangerini

***Zea mays* L.**

Several presentations at the eighth annual Smithsonian Botanical Symposium highlighted current genomic research of domesticated maize, rice, and poplar. These illustrations of *Zea mays* were drawn for a traveling panel exhibit, "Listening to the Prairie," prepared by the Office of Public Programs and designed by the Office of Exhibits at the National Museum of Natural History. The exhibit opened at NMNH in November 2000, and traveled as part of the American Library Association tour in May 2001. The drawing images were scanned and etched into acrylic panels along with drawings of big bluestem (*Andropogon gerardii*) for a section of the exhibit titled, "Amber Waves of Grain." Tangerini sketched the *Zea mays* from living plants on site at the Beltsville Agricultural Research Center in Beltsville, Maryland, with help from U.S. Department of Agriculture researcher, Mark Davis.



Smithsonian
National Museum of Natural History

Department of Botany
PO Box 37012
NMNH, MRC-166
Washington DC 20013-7012

Official Business
Penalty for Private Use \$300