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e_Connections

In This Issue

Wells reveals the depth of human ancestry

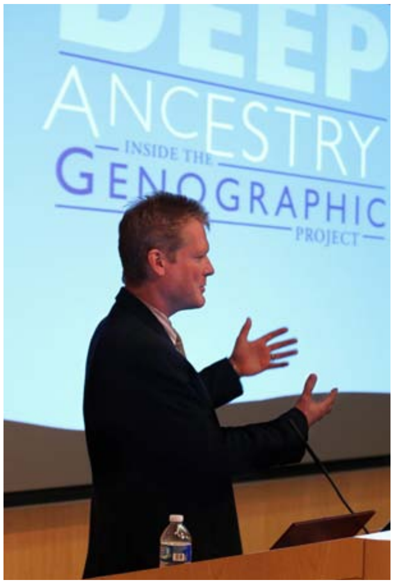
Spencer Wells, a leading population geneticist, National Geographic Explorer-in-Residence, and Frank H.T. Rhodes Professor at Cornell University, revealed his thoughts on the depth of human ancestry at a recent keynote lecture at the Virginia Bioinformatics Institute's Conference Center. The lecture, which took place on October 7, was part of the 10-year anniversary celebration of the Institute.

Wells received his Ph.D. in biology from Harvard University in 1994 and was a postdoctoral fellow at Stanford University's School of Medicine. An interest in the study of genetic diversity in populations blossomed into a personal quest to learn more about early human migration. In 1996, Wells began his field studies in human population genetics with a survey of Central Asia. This work helped to advance the understanding of the Y chromosome, the male sex-determining chromosome found in most mammals, and its role in tracing ancestral human migration.

Today, Wells devotes much of his time to communicating his scientific discoveries through books and film. In his lecture, Wells explained the origins of the Genographic Project, which has led him and his team to over 36 countries across the globe. The project is an effort to analyze DNA from people from around the world to learn more about the history of human migration. Said Wells, "The questions we are interested in are related to origin and journey. Are we all related? If so, how closely? How did we come to occupy every corner of the globe?"

According to Wells, the question of origin is a question of genealogy or how the line of descent of humans today can be traced from a common ancestor. "Our understandings of genetics and developments in molecular biology have given us access to a molecular clock that allows us to look at human evolution in a way that complements the approach of paleontologists and others. It allows us to count backwards in time and build a wider picture of our human ancestry."

By looking at mitochondrial DNA and the genetic makeup of the Y chromosome, the work suggests that all humans alive today are likely descended from one man, Y-chromosomal Adam, who lived in Africa 60,000-90,000 years ago.



The Genographic Project is also revealing how populations have migrated within and out of Africa to colonize the planet in a very short space of time. Said Wells, "Through the Genographic Project, we have collected 65 000 samples from indigenous and traditional groups across the globe. Analysis is underway of the data and the first scientific publications have already appeared or are coming out right now." *

The public can also play a part by ordering non-medical testing kits and helping to trace their own ancestral migrations. Money raised from the sale of these test kits is used to support not-for-profit projects around the globe that help to give back to indigenous communities.

Concluded Wells: "What is becoming clear from our studies is the indelible imprint that climate change can have on the migration of populations. Climate change appears to have been a big driving factor for the exodus of populations from Africa to the rest of the world via the Saharan gateway, events that are deep in our human ancestry. In a very short period of time, occurrences like Hurricane Katrina can have a huge impact on the migration of populations." He added, "Much remains to be discovered but we are catching a fascinating glimpse of our deep ancestry and learning more about what it means to be human." ■

* Behar DM, Rosset S, Blue-Smith J, Balanovsky O, Tzur S, et al. 2007 The Genographic Project Public Participation Mitochondrial DNA Database. *PLoS Genetics* **3**(6): e104. doi:10.1371/journal.pgen.0030104.

Photos: Dr. Spencer Wells during his presentation at the Virginia Bioinformatics Institute's Conference Center illumina®

Photo: Illumina Genome Analyzer *II*x at VBI's Core Laboratory Facility

VBI launches Data Analysis Core

The Virginia Bioinformatics Institute (VBI) at Virginia Tech recently launched a new core facility that provides state-of-the-art data analysis support for biologically related research. The Data Analysis Core (DAC) is a dedicated multi-user resource that provides state-of-the-art data analysis assistance for biologically related research. The DAC was created to remove data analysis as an obstacle for highly complex and data-intensive experiments, the type of experiments required to solve modern problems in life science research.

VBI's new Data Analysis complements the services offered by the recently expanded Core Laboratory and Computational Facilities (www.vbi.vt.edu/clf and www.vbi.vt.edu/ccf) that offer state-of-the-art laboratory technologies and computational infrastructure.

DAC services range from training and self-serve workstations preloaded with necessary software to full service project support. Next generation sequencing projects include the analysis, assembly, and annotation of genomic sequence information including protein function prediction, variant/allele discovery, and expression analysis (CHIP-seq, RNA-seq, DNA-reseq, SNP-seq, and others). For gene expression (Affymetrix or custom), DAC offers statistical expression analysis, normalization, quality analysis, filtering customized to the experimental design, hierarchical clustering, and, when appropriate, function analysis. Custom array design for both oligonucleotide and proteomics arrays as well as target design for deep sequencing experiments are also available. For proteomics, offerings include statistical expression analysis, pathway and GO analysis. All services result in manuscript-ready figures and text.

Further details are available at https://www.vbi.vt.edu/dac

Industrial Affiliates Program hits the ground running

A new program at the Virginia Bioinformatics Institute (VBI) at Virgina Tech aims to bridge the gap between industry and university research. The institute's Industrial Affiliates Program is designed to facilitate strong cooperative relationships and partnerships, as well as research and information exchange opportunities, with industry.

The financial assistance provided by industry partners will help advance the work at VBI that spans four program areas - network dynamics and simulation science and policy informatics, cyberinfrastructure, biosystems, and medical informatics and systems.

The Industrial Affiliates Program offers companies two levels of sponsorship to support VBI research. The Gold Partner membership is available for companies seeking to better understand how research at VBI can impact their business. For an annual gift of $25,000, Gold Partners receive access to non-proprietary information produced by the institute, opportunities to visit VBI's facilities and participate in discussions with faculty members and students involving research activities, and access to VBI events held at the institute's 189-seat conference center and other meeting spaces. In addition, members at this level of sponsorship may submit research suggestions to the Research Advisory Panel, which recommends the research scope for the institute, and attend the annual meeting of the VBI Futures Roundtable, a group created to discuss the strategic goals of the institute's scientific program, as well as the implementation of these goals and related scientific and logistical issues.

For an annual contribution of $50,000, Platinum Partner membership is designed for companies seeking access to intellectual property generated by VBI faculty members. Partners at this membership level receive all of the benefits of the Gold Partner membership, as well as early licensing access to confidential research information prior to public disclosure and a seat on the Research Advisory Panel with the opportunity to provide input on the selection of annual VBI research program projects. In addition, Platinum Partners can earmark up to 80 percent of the their annual gift to support a graduate student fellowship to explore a research area relevant to the institute's strategic plan.

Further details on the program and contact information are available at https://www.vbi.vt.edu/technology_development

Marathe receives Research Excellence Award

Dr. Madhav Marathe

Madhav Marathe, Deputy Director of the Network Dynamics and Simulation Science Laboratory at VBI, received the Research Excellence Award at the Institute's 10-year anniversary event for his outstanding contributions to the scientific output of VBI.

Barrett and Marathe invited to roundtable on science and technology in India

Chris Barrett, Director of the Network Dynamics and Simulation Science Laboratory (NDSSL) at the Virginia Bioinformatics Institute (VBI), and VBI Professor Madhav Marathe, Deputy Director of NDSSL, were recently invited to attend the *4th IndoUS Science and Technology Roundtable* in Bangalore, India. The meeting, which took place on September 21-23, was sponsored by the Office of Naval Research Global and organized by the National Institute of Advanced Studies (NIAS) on the campus of the Indian Institute of Science, Bangalore, India. The focus of the meeting encompassed the cognitive sciences and power and energy. In the session on cognitive sciences, NDSSL gave two presentations entitled "From desktops to clouds: Pervasive informatics for network, behavioral and social sciences" and "Interaction-based modeling of population dynamics and socio-behavioral processes."

First Genomic Map of the Domesticated Turkey

PLoS BIOLOGY

U.S. Department of Agriculture researchers and their university colleagues have sequenced the majority of the genome of *Meleagris gallopavo*, the domesticated turkey, creating the first-ever turkey genome map.

The nearly complete map could help growers to more efficiently produce bigger, meatier turkeys. The research is reported today in *PLoS Biology*, an online journal of the Public Library of Science.

The research was a partnership led by Curtis Van Tassell and Julie A. Long with the USDA's Agricultural Research Service; Otto Folkerts and Rami Dalloul of the Virginia Bioinformatics Institute at Virginia Tech (VBI); and Steven L. Salzberg of the University of Maryland's Center for Bioinformatics and Computational Biology, at College Park.

Source: Abridged from USAgNet, September 8, 2010.

VBI Launches Affiliates Program with More Corporate Research Partners in Mind

Dr. Stan Hefta

Eager to attract more corporate research partners, the Virginia Bioinformatics Institute at Virginia Tech has launched a program designed to develop new academic-industry partnerships, as well as new opportunities for research and information exchange.

The VBI Industrial Affiliates Program allows businesses to help the bioinformatics institute by advancing its work in its four research programs — network dynamics and simulation science and policy informatics; cyberinfrastructure; biosystems; and medical informatics and systems.

"Right now, we have one active member, and are in the final stages of negotiating with a handful of others," Stan Hefta, director of the industrial affiliates program, told GenomeWeb Daily News. "The partners tend to be both biotech companies as well as large pharmaceutical companies."

Source: Abridged from GenomeWeb News, Sept. 14, 2010.

VBI Scientific Publications

The BioPAX community standard for pathway data sharing. Demir E, Cary MP, Paley S et al (2010) *Nature Biotechnology* **28**: 935-842.

Bruno Sobral, Director of the Cyberinfrastructure Division at the Virginia Bioinformatics Institute, and Harsha Rajasimha, currently Senior Lead Bioinformatics Programmer and Analyst at information technology service provider Digicon, contributed to a community-wide effort to define standards for biological pathway data. A paper describing the standardized language BioPAX was published in the journal *Nature Biotechnology* in September. BioPAX helps overcome incompatibility problems between different data storage formats that have hindered the sharing and analysis of digital representations of biological pathways.

The human-bacterial pathogen protein interaction networks of *Bacillus anthracis*, *Francisella tularensis*, and *Yersinia pestis*. Dyer M, Neff C, Dufford M, Rivera CG, Shattuck D, Bassaganya-Riera J, Murali TM, Sobral B (2010) *PLoS One* **5**(8): e12089.

Researchers from the Virginia Bioinformatics Institute, the Department of Computer Science at Virginia Tech, and Myriad Genetics have published the first extensive protein interaction network for three deadly pathogens and their human hosts. *Bacillus anthracis*, *Francisella tularensis*, and *Yersinia pestis* are bacterial pathogens that can cause anthrax, pneumonia, and bubonic plague, respectively. They are included in the National Institutes of Health's Category A priority list as pathogens that might be used as biological weapons. The study identified more than 8000 human-pathogen protein interactions collectively for the three pathogens, which is the first large-scale protein interaction map for three respiratory bacterial pathogens and their human host. ■

Virginia Bioinformatics Institute celebrates ten-year anniversary

Photo: Dr. Tracy Wilkins addressing VBI's ten-year anniversary guests.

Further information on VBI's ten-year anniversary is available at www.vbi.vt.edu/anniversary/

The Virginia Bioinformatics Institute (VBI) at Virginia Tech celebrated its 10th anniversary on October 7, 2010, with a day of scientific talks, building tours, an art exhibition, and poster sessions, including a keynote lecture by renowned population geneticist and anthropologist Spencer Wells.

The day's events began with an honorary talk from Tracy Wilkins, Chairman of TECHLAB Inc. and one of the key leaders in the early development of the institute. Tracy Wilkins outlined the first steps in the path to create VBI, from a white paper arguing the merits of biotechnology to the opening of the first laboratories in the Corporate Research Center. Wilkins gave a sense of some of the personal feelings as well as commitment and perseverance that were needed to kick-start what was an ambitious undertaking for all involved. He also emphasized that much research remains to be done and that VBI was well positioned to make major contributions in the years ahead.

In the inaugural Bruno Sobral Lectureship, named after VBI's founding executive director, Spencer Wells, a leading population geneticist, National Geographic Explorer-in-Residence, and Frank H.T. Rhodes Professor at Cornell University, revealed his thoughts on the depth of human ancestry. Wells devotes much of his time to communicating his scientific discoveries through books and film. In his lecture, he explained the origins of the Genographic Project, which has led him and his team to over 36 countries across the globe. The project is an effort to analyze DNA from people from around the world to learn more about the history of human migration. Said Wells, "The questions we are interested in are related to origin and journey. Are we all related? If so, how closely? How did we come to occupy every corner of the globe?" Wells went on to give a fascinating glimpse of the deep ancestry of humans and explained how this work is helping to explain what it means to be human today.

Additional talks by Dr. Stan Hefta, VBI Executive Director Harold "Skip" Garner, Dr. Chris Barrett, and Dr. Rebecca Will spotlighted the four program areas that contribute to VBI's research interests: Biosystems; Medical Informatics and Systems; Network Dynamics and Simulation Science and Policy Informatics; and Cyberinfrastructure. These talks were followed by presentations from Cynda Johnson, President and Dean of the Virginia Tech Carilion School of Medicine, and Michael Friedlander, Founding Executive Director of the Virginia Tech Carilion Research Institute.

In addition to scientific talks, visitors were able to take part in tours of the VBI building and view art exhibitions and poster sessions. Linda Correll, Associate Director, Facilities Management at VBI, Susan Huckle, Laboratory Operations Assistant and Technical Writer, and Darleen Baker, Project Coordinator at VBI, were judged winners of the art show, each receiving Genographic Project DNA testing kits. David Ball, postdoctoral associate in Live Cell Imaging, and Matt Lux, doctoral student in the Genetics, Bioinformatics, and Computational Biology program at Virginia Tech and SMART Scholar for the Edgewood Chemical Biological Center, both of whom are affiliated to Dr. Jean Peccoud's laboratory at VBI, received Dell laptop computers for their contributions to the graduate and postdoctoral scientific poster session.

Earlier in the day Madhav Marathe, Deputy Director of the Network Dynamics and Simulation Science Laboratory at VBI, was announced as the recipient of the Research Excellence Award for his outstanding contributions to the scientific output of the institute. ■

VBI e_Connections is a quarterly publication of the Virginia Bioinformatics Institute produced by the Public Relations team. The newsletter includes feature articles, technology updates as well as interviews that may be of interest to VBI's audiences. Contributions are welcomed. Please direct submissions to newsletter-editor@vbi.vt.edu. Newsletter team: Susan Bland: Editor; Barry Whyte: Editor.

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