



e_Connections

feature

technology

in the news

interview

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Newsletter of the Virginia Bioinformatics Institute at Virginia Tech

Chinese scientists visit VBI

Virginia Bioinformatics Institute Professor Brett Tyler recently welcomed a six-member delegation of plant pathologists from Northwest Agricultural and Forestry University in Yangling, China to VBI as part of a program to increase awareness of research, education, and cooperative extension activities at Virginia Tech and foster new collaboration projects.

The visit was coordinated by Tyler and Weixing Shan, co-leader of the delegation and a professor at Northwest Agricultural and Forestry University. A former postdoctoral researcher in Tyler's research group, Shan has a research interest in molecular genetics of oomycete pathogens. In addition to Shan, other visiting members of the delegation included:

- Professor Yunfeng Wu – leader of the delegation and a virologist focused on insect-transmitted viruses and the exploration of plant metabolites inhibiting viruses.
- Professor Guangyu Sun – interested in mycology and fungal disease of fruit trees; uses molecular genetic methods to identify fungi in the sooty blotch and flyspeck complex on apples.
- Professor Qing Ma – investigates ultrastructure of wheat cultivars with high-temperature and slow-rusting resistance to stripe rust, *Puccinia striiformis*; the function of the cytoskeleton in the resistance of wheat against stripe rust; apple post-harvest disease control; and induced resistance.
- Professor Jinxue Jing – interested in the genetics of stripe rust resistance in wheat, including the introduction of novel resistance genes from distant cereal species.
- Professor Baotong Wang – research in cereal disease management.

The group received a tour of VBI facilities, which included the Core Computational Facility's data center, the Core Laboratory Facility, and various research labs, and met with several faculty members at VBI, including Executive and Scientific Director Bruno Sobral, to discuss research



Left to right: Baotong Wang, Guangyu Sun, Qing Ma, Jinxue Jing, Brett Tyler, Weixing Shan and Yunfeng Wu

collaboration opportunities. They also met with Virginia Tech faculty members and administrators from departments and units within the university's College of Agriculture and Life Sciences, including Crop and Soil Environmental Sciences; Plant Pathology, Physiology, and Weed Science; and the Virginia Agricultural Experiment Station. While visiting VBI, the group participated in a videoconference with Virginia Tech Associate Professor of Plant Pathology Chuanxue Hong who works at the university's Hampton Roads Agricultural Research and Extension Center.

The visit supports the university's international vision, which is outlined in Virginia Tech's International Strategic Plan, to promote collaboration with colleagues from around the globe and establish international partnerships that are strategically important to the university.

"We were very pleased to welcome the visiting scientists from Northwest Agricultural and Forestry University," said Sobral. "With our transdisciplinary approach to science, both national and international collaborations are critical to our success as an institute. We had productive conversations with the delegation and look forward to establishing joint research initiatives in the future. We are also exploring ways in which students can benefit from the research strengths of both institutions."

Northwest Agricultural and Forestry University was founded in 1934 as the first high-level institution for modern agricultural education in northwest China. With a goal of expanding international collaboration and exchange in education, science, and technology, the university currently has cooperative relations with over 50 universities and research institutes around the world.

In This Issue

Chinese scientists visit VBI....1

Technology Focus.....2

VBI in the News.....3

VBI Scientific Publications.....3

Linda Correll.....4

Tools for the Rosaceae genomics community



A recent paper published in the journal *Plant Physiology* provides a comprehensive overview of the genomics tools and resources available for the rapidly growing Rosaceae scientific community.[‡] Rosaceae is an economically important group of plants that comprises more than 3000 species including strawberry, apple, peach and pear. Members of this plant family provide high-value nutritional foods and they are also the source of other desirable aesthetic and industrial products.

Modern breeding programs have produced numerous cultivars that play a significant role in commercial agricultural markets in the United States and around the world. In recent years, a global community of Rosaceae scientists has arisen that is benefiting from collaborative efforts designed to develop genetic and genomic resources for representative crops in this family such as apple, peach and strawberry. These crops are emerging as attractive organisms for functional genomics studies due to the availability of resources like expressed sequence tags, bacterial artificial chromosome libraries,

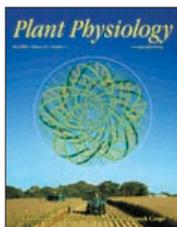
physical and genetic maps, molecular markers, genetic transformation protocols and bioinformatic tools.

In the past few years, for example, researchers at the Virginia Bioinformatics Institute and the Department of Horticulture in the College of Agriculture and Life Sciences at Virginia Tech have developed new procedures for the efficient transfer of specific DNA sequences into the genome of the woodland strawberry *Fragaria vesca*. They have also developed tools for reverse and forward engineering genetics in this plant. Due to the small size of its genome, short reproductive cycle and small plant size, *F. vesca* is an ideal model system for genomic studies in commercial strawberry. Developments like high throughput transformation make the Rosaceae attractive as model systems for genomics research.

Vladimir Shulaev, Associate Professor at the Virginia Bioinformatics Institute, remarked: “The review article has been compiled by some of the leading practitioners in Rosaceae genomics. It serves as a synopsis of the resources and initiatives of the Rosaceae community, covers recent developments in Rosaceae genomics, and summarizes plans to apply newly accumulated knowledge and resources toward breeding and crop improvement.”

High throughput sequencing technologies, methods for quantitative gene expression analyses and novel phenotyping platforms are also under development. Researchers looking to study the crop species in the Rosaceae family are well positioned to benefit from these emerging technologies as well as the considerable genomics tools and resources already available for the Rosaceae community.

[‡]Multiple models for Rosaceae genomics. *Plant Physiology* 2008 May 16 doi: 10.1104/pp.107.115618 PMID: 18487361



Selected genomic features of the three Rosaceae model plants *Malus xdomestica* (apple), *Prunus persica* (peach) and *Fragaria vesca* (woodland strawberry)

The table is an excerpt from the following publication: Shulaev V, Korban SS, Sosinski B, Abbott AG, Aldwinckle HS, Folta KM, Iezzoni A, Main D, Arus P, Dandekar AM, Lewers K, Brown SK, Davis TM, Gardiner SE, Potter D, Veilleux RE (2008) Multiple models for Rosaceae genomics. *Plant Physiology*. In press. PMID: 18487361.

Feature	<i>Malus xdomestica</i>	<i>Prunus persica</i>	<i>Fragaria vesca</i>
Genome size (Mbp/C)	750	280	206
Chromosome number (2n)	2n=2x=34 (sometriploid cultivars)	2n-2x=16	2n=2x=14
Transformation	Tissue culture	Tissue culture	Tissue culture
Transformation efficiency (%)	80	<1	100
Expressed Sequence Tags	>300,000	85,340	>45,000
Genome sequence	Mid-2008	End of 2008	~1%
Physical map	Yes	Yes	In progress
Linkage maps	Yes	Yes	Yes



Joshua Shallom

Shallom is invited to Idexx Laboratories

Joshua Shallom, computational biologist in the PATRIC group, was invited to present a seminar at Idexx Laboratories in Portland, Maine on April 11, 2008. His presentation, "Bioinformatics data and tools used to identify outer membrane/secreted proteins in Gram-negative bacteria: *Rickettsia conorii* as a model

organism" described the PATRIC curation of Gram-negative bacteria as well as the pipeline developed to predict potential outer membrane/secreted proteins. Idexx Laboratories, Inc. is a worldwide leader in the development and commercialization of innovative technology-based products and services for veterinary, food and water applications.

Barrett attends board meeting and ceremony in Italy

VBI Professor Chris Barrett attended a meeting of the Institute for Scientific Interchange (ISI) Foundation's Scientific Advisory Board in Turin, Italy on April 13-21. Barrett serves as a member of the board for the foundation, which has a mission of promoting scientific cooperation at the highest degree of quality both in terms of creativity and of novelty. He also attended the ceremony for the award of the Lagrange-CRT Foundation Prize on April 18 in Turin. The prize, which aims at promoting research activities on complex systems, is awarded every year to two researchers.

Eubank speaks at conference on complex systems

VBI Professor Stephen Eubank gave an invited presentation titled "A Data-driven Epidemiological Model" at the General Integration of the Applications of Complexity in Science (GIACS) Conference in Palermo, Italy on April 7-10. The goal of the conference is to discuss problems of data collection, data mining, data dissemination and data sharing for research projects dealing with complex systems

VBI e_Connections

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.

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Madhav Marathe

Marathe gives two invited presentations in India

In February, VBI Professor Madhav Marathe gave two invited presentations in India. He presented a talk titled "Building Virtual Cities: Computational Aspects of Modeling Large Societal Infrastructure Systems" at the Indian Institute of Technology in Bombay. He also visited the National Institute of Virology in Pune, where he gave

a presentation titled "Computational Epidemiology: An Interaction Based Approach."

Tyler and group members attend molecular genetics conference

VBI Professor Brett Tyler and research group members Shiv Kale, Sucheta Tripathy, Biao Gu and Marcus Chibucos attended the 2008 Oomycete Molecular Genetics Conference in Birnam, Scotland on May 6-8. Tyler and Kale gave talks on the mechanisms by which oomycetes (fungus-like plant pathogens related to marine algae) cause disease on soybean plants, while Tripathy, Chibucos and Gu presented posters. Tyler is also coordinator of the Oomycete Molecular Genetics Research Collaboration Network, which sponsored the conference.

VBI Scientific Publications

Genome sequence of *Brucella abortus* vaccine strain S19 compared to virulent strains yields candidate virulence genes

Crasta OR, Folkerts O, Fei Z, Mane SP, Evans C, Martino-Catt S, Bricker B, Yu G, Du L, Sobral BW

PLoS ONE 2008 **3**(5): e2193

Researchers from the Virginia Bioinformatics Institute and the National Animal Disease Center in Ames, Iowa, along with collaborators at 454 Life Sciences, have applied pyrosequencing technology together with conventional sequencing to rapidly and comprehensively determine the complete genome sequence of the attenuated *Brucella abortus* vaccine strain S19, which has been used as a vaccine strain in vaccination of cattle against brucellosis for six decades. Despite many studies, the physiological and molecular mechanisms causing the attenuation are not known. The main goal of this study was to identify candidate virulence genes by systematic comparative analysis of the attenuated strain with the published genome sequences of two virulent and closely related strains of *B. abortus*, 9-941 and 2308. By making these comparisons, the researchers discovered a group of 24 genes that are linked to virulence.



Linda Correll

While the concept of team science is a way of life at the Virginia Bioinformatics Institute (VBI) at Virginia Tech, many logistical issues arise when scientists from different disciplines work together under the same roof. With 40 shared laboratory spaces, proper management and coordination is necessary to ensure projects run smoothly, which is where Linda Correll and her team come in.

“It’s our job to keep this place humming,” explains Correll, VBI’s laboratory facilities and resource manager. A self-proclaimed problem solver by nature, her group’s responsibility is just that – to assist with the Institute’s lab-related issues. From equipment training to service contracts, budget creation to proper chemical disposal, Correll and her group, which consists of Wilson Barnes, Susan Huckle, and Sheryl Locascio, are available to assist with any laboratory needs.

“What we really are is a resource for people at VBI,” Correll says. “We help with equipment needs, provide advice, and help answer procedural questions. There is definitely a major ‘fix-it’ component to my job.”

By leading the Institute’s Shared Laboratory Resource program, Correll handles many of the day-to-day tasks needed to keep the labs operating

Getting the job done

Linda Correll, laboratory facilities and resource manager at VBI, directs the Shared Laboratory Facilities program for the institute’s multi-user environment. Here she describes some of the day-to-day tasks needed to keep VBI labs operating at full steam.

“I’ve seen her negotiation and communication skills utilized to smooth ruffled feathers, drive hard bargains and address core issues to get things done—all with the utmost respect and good cheer in dealing with others.”

Susan Huckle, laboratory operations assistant and technical writer, VBI

smoothly, allowing the Principal Investigators and their teams to focus on research. In addition, the shared resource program provides shared equipment for the laboratories, such as centrifuges, spectrometers, and incubators, saving resources and eliminating equipment duplication for all of the research groups. Correll and her team are also responsible for overseeing VBI’s growth chamber facilities. These duties make customer service an important component of Correll’s position.

“Each Principal Investigator, each student, each growth chamber customer—they’re all clients,” she explains. “It’s a real people job that requires working cooperatively with many different personalities.”

Correll’s work also extends across the Virginia Tech campus. She has been an instrumental member of the university’s Laboratory Employee Professional Development Network (LEPDN), which helps all university employees working in laboratory and field research and instructional lab units to identify and promote opportunities for professional development. Correll has also been involved in the creation of university-wide laboratory policies and procedures. When she saw a need at VBI for a standard policy for autoclave use, only to discover that the university had no such policy in place, her team pursued the issue. After meeting periodically in

the fall of 2007 with representatives from Virginia Tech’s Environmental Health and Safety Services (EHSS), the two groups helped create the university’s Autoclave Use and Verification Program, which establishes requirements for decontaminating potentially infectious materials and other biohazardous waste before disposal to ensure the decontamination process is completed using standard procedures.

Correll is currently working to establish an electronic laboratory management system, which would be available to all laboratory managers on campus to help organize documentation and create an online tracking system. Her goal is to establish a pilot program at VBI that will eventually be adopted by the university.

Correll’s dedication to VBI and the university community hasn’t gone unnoticed. She recently received the 2008 Virginia Tech Staff Leadership Award in recognition of her strong leadership qualities. “Linda brings several unique and valuable abilities to her managerial role at VBI,” explains Huckle, a laboratory operations assistant and technical writer on Correll’s team. “I’ve seen her negotiation and communication skills utilized to smooth ruffled feathers, drive hard bargains and address core issues to get things done—all with the utmost respect and good cheer in dealing with others.”