VBI e_Connections

VBI Hosts International Alpha-Proteobacteria Symposium

VBI hosted an international symposium on April 26-29 at the VBI Conference Center. The "International Symposium on the Comparative Biology of the Alpha-Proteobacteria" brought together experts from around the world to present and discuss some of the very latest research and findings on the alpha-proteobacteria. Alpha-proteobacteria are diverse organisms that have successfully adopted different lifestyle and energy-yielding strategies throughout the course of evolution. The symposium included over 30 presentations spanning topics such as metabolism, intracellular lifestyle, the genomics of development of the alpha-proteobacteria, and evolutionary biology.

Siv Andersson, professor in Molecular Evolution and head of the Department of Evolution, Genomics and Systematics at Uppsala University, Sweden, was the keynote speaker on the first day of the symposium. Andersson's work on the alpha-proteobacteria has achieved widespread recognition by the scientific community. In 1998, she was group leader of the genome sequencing project for the typhus pathogen, the first alpha-proteobacterial genome to be fully sequenced.

During her presentation, Andersson modestly described her first choice of genome sequencing project as fortuitous. It turns out that the typhus pathogen, *Rickettsia prowazeki,* has the smallest genome in the Rickettsiales, which makes it a good choice for this type of work. To date, more than 40 alpha-proteobacterial genomes have been fully sequenced and more are in progress.

Andersson remarked: "The alpha-proteobacteria show a tenfold difference in the size of their genomes as well as an amazing variation in lifestyles. You can find alpha-proteobacteria in organisms as wide-ranging as amoebae, insects, plants, mice, cats and humans. As proteobacteria have evolved into organisms closely associated with their human hosts, there has been a tremendous reduction in the size of the genome." She added: "We want to know why this reduction has taken place. An ideal way to do this is to study how the bacterial genome has evolved over time and determine what specific changes have occurred at the different stages of evolution."

Dr. Siv Andersson

To do so, Andersson's group performs experimental research, develops bioinformatics tools, and analyzes microbial genomes. "One thing that's clear is that the lifestyles of these diverse organisms have exerted a major impact on the genomic evolution of the alpha-proteobacteria," she remarked.

At the three-day symposium, scientists were able to hear about the evolution of chronic infection strategies in the alpha-proteobacteria, how these organisms have adapted to lifestyles in different hosts, such as insects and arthropods, as well as the different molecular strategies that have been used for the invasion of host cells and survival once invasion has been completed.

"The first edition of the symposium was extremely well received," said Bruno Sobral, executive and scientific director of VBI. "We're already talking about a follow-up meeting that will build further on the success of the International Symposium on the Comparative Biology of the Alpha-Proteobacteria."

Alpha-proteobacteria at a glance

- One of the most abundant bacterial groups in the environment
- Pathogens of humans and domestic animals as well as insects and plant hosts
- Inhabit diverse ecological niches such as water, soil, intracellular and free-living environments
- Excellent model system for the study of the evolution of different bacterial genomes of different sizes
- Lifestyle has exerted a major impact on the genomic evolution of the alpha-proteobacteria

Gene expression studies on a single cell shed light on parasite

Beth Kirkpatrick, University of Vermont, and Dr. Bill Petri, University of Virginia Health System, are pictured together with children being monitored or treated for amebiasis at a field site in Dhaka, Bangladesh.

VBI's Core Laboratory Facility has succeeded in amplifying the RNA from a single cell of the amebic dysentery-causing parasite *Entamoeba histolytica*. The RNA was applied to a custom-made *Entamoeba* Affymetrix array for gene expression analysis. Professor William A. Petri, chief of the Division of Infectious Diseases and International Health at the University of Virginia Health System, remarked: "We were able to capture a single trophozoite, the feeding stage of the parasite, by state-of-the-art microdissection. The VBI team was able to define the gene expression pattern from this single cell using NuGEN's Ovation™ technology as a highly sensitive amplification step followed by analysis on the custom-made *Entamoeba histolytica* Affymetrix chip."

Clive Evans, manager of the Core Laboratory Facility at VBI, commented: "This is one example of how we work closely with our customers to find the most effective and efficient solution for their research needs." Professor Petri concluded: "By adopting this collaborative approach, we obtained a crucial piece of information about the expression of a transmembrane kinase gene family, namely that more than one kinase enzyme is expressed in a cell. This has important implications for the biology of the parasite."

About the Core Computational Facility

The Core Computational Facility (CCF) provides high-performance computing resources to assist researchers in the study of large-scale biological systems that involve genes, proteins, and their interactions, as well as metabolic networks (systems biology).

The services offered by the CCF include:
- Computational processing
- Compound services (web applications, analysis web services)
- Database and system administration
- Data storage and backup

For more information, please consult: www.vbi.vt.edu

Guy Cormier joins Core Computational Facility as Chief Information Officer

VBI has named Guy Cormier as Chief Information Officer. Dr. Cormier will serve as a member of the senior management team with direct responsibility for operations, resources and strategic development of the Core Computational Facility (CCF) as well as Information Technology support for VBI. Cormier joins VBI from the University of Puerto Rico System where he was director of the High Performance Computing facility (HPCf). The HPCf, which Cormier founded in 1997, provides computing infrastructure and technical resources to the research community of the 11 campuses in the University of Puerto Rico educational system. Since 1998, Cormier has been leading the development of the Internet2 project for Puerto Rico.
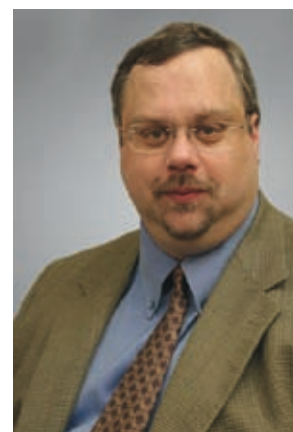
Dr. Guy Cormier

Cormier holds a Ph.D. in Chemistry from Concordia University, Montréal, Québec, Canada, and a B.Sc. (honors) degree in Chemistry from the Université du Québec à Montréal. From 1995-1997, he was a visiting scholar at the Chemistry Department, University of Cambridge, England, where he focused on using Molecular Dynamics modeling to investigate the glass transition phenomenon in silicon- and silica-based materials. From 1994-1995, Cormier carried out postdoctoral research at the Physics Department, Università degli Studi di Padova, Italy.

Dr. Zhangjun Fei

Tomato Metabolite Database

Dr. Zhangjun Fei, a senior bioinformatics scientist in VBI's Cyberinfrastructure Group, is developing a database and computational tools to help scientists learn more about how certain genes in tomatoes affect the crop's flavor and nutritional value. The Tomato Metabolite Database will be used to store a wide range of information and data about tomato, including microarray and metabolite profiling data as well as information on metabolic pathways. This resource will be used to identify key genes involved in the synthesis of essential metabolites that impact tomato flavor and the quality of its nutrients.

Source: Supercomputingonline.com

Orion and VBI Sign Diagnostic-Development Deal for Viral Pathogens

VBI and Orion Integrated Biosciences plan to co-develop new diagnostic methods for viral pathogens, the partners said. Under the agreement, VBI will integrate data on encephalic and hemorrhagic viruses from its PathPort project into Orion's integrated computational analysis system. "The lack of diagnostic tools that can integrate and analyze molecular surveillance data is a major gap in disease prevention and the development of countermeasure responses," said Oswald Crasta, director of bioinformatics for VBI's Cyberinfrastructure Group. VBI's PathPort platform includes pathogens with the potential use as biological weapons, according to the statement. New York-based Orion Integrated Biosciences is a drug-discovery and viral disease detection

shop, focusing on the development of antiviral agents and devices that can recognize lethal pathogens in medical and military settings.

Source: GenomeWeb News

Calendar of VBI Sponsored Events

• October 28-31: 9th Annual Computational Genomics Conference

www.conted.vt.edu/genomics

VBI Scientific Publications

VMD: a community annotation database for oomycetes and microbial genomes.

Tripathy S, Pandey VN, Fang B, Salas F, Tyler BM.

Nucleic Acids Res. 2006 Jan 1: 34 (Database issue): D379-81.

Researchers at VBI have launched a publicly available microbial database to host a range of microbial genome sequences. The VBI Microbial Database (VMD) contains genome sequence and annotation data for the plant pathogens *Phytophthora sojae* and *Phytophthora ramorum*. The purpose of the database is to make widely available to researchers the recently completed genome sequences of these pathogens as well as powerful analytical tools in one integrated resource. The database was featured in the NetWatch section of *Science* magazine: *Science*, volume 311, no. 5768, 24 March 2006, page 1685

A high throughput targeted gene disruption method for *Alternaria brassicicola* functional genomics using linear minimal element (LME) constructs.

Cho Y, Davis JW, Kim KH, Wang J, Sun QH, Cramer RA Jr, Lawrence CB.

Mol Plant Microbe Interact. 2006 Jan: 19(1): 7-15.

Researchers at VBI, Colorado State University and Duke University Medical Center have developed a new method to determine gene function on a genome-wide scale in the fungal pathogen *Alternaria brassicicola*. *A. brassicicola*, which causes black spot disease in cultivated Brassica, is a destructive fungus that may lead to considerable leaf loss in economically important crops including canola, cabbage, and broccoli.

Genomic methods that allow the disruption of several thousand genes are needed because they allow high-throughput identification of genes and gene function. Associate Professor Christopher Lawrence of VBI, the director of the project and one of the authors of the study, remarked: "The development of this protocol is timely as the genome sequence of *A. brassicicola* is scheduled for completion in 2006. We now have in our hands a versatile method that will allow us to dissect the pathogen's nucleotide sequence information and establish the function of many of the individual genes in this filamentous fungus."

Interview with Lee Falin

Lee Falin is a student in Virginia Tech's Genetics, Bioinformatics, and Computational Biology (GBCB) graduate program and a graduate programming assistant in the research group of Brett Tyler, professor at VBI and the Department of Plant Pathology, Physiology and Weed Science at Virginia Tech.

"I've been working on a lot of Perl scripts and PHP applications for data visualization of genomic data. The largest project that I have been involved with is the VBI Microbial Database under the direction of Dr. Tripathy and Dr. Tyler of VBI".

What kinds of skills do you bring to VBI and the GBCB program?

I worked for several years as a software developer in the telecommunications industry using a variety of programming languages, but I mainly developed software for the Microsoft platform. I received a premier technical certification from Microsoft, the Microsoft Certified Solution Developer certification, which qualified me to develop full-scale enterprise solutions using Microsoft technologies. Later, a friend introduced me to the Macintosh and I found it to be an ideal platform for software development. In my spare time, I started a small business developing commercial applications for the Mac. It was a lot of fun, but sales were nowhere near good enough to support a family and I began to reconsider my options.

What sparked your interest in bioinformatics?

My wife bought me a copy of Richard Bolles' book, "What Color Is Your Parachute?" which includes tests to help identify personal strengths, interests and career possibilities. One of my previous experiences in software development that I most enjoyed was when I was called upon to develop and teach short training courses for the other programmers in my department. Teaching these courses was as enjoyable as the actual software development itself. We decided that I should finish my undergraduate degree and then continue on to graduate school. Bioinformatics is where all of my interests overlapped.

Why did you join Virginia Tech's GBCB program?

I had the opportunity to work as a programming assistant with Dr. Sucheta Tripathy and Dr. Brett Tyler at VBI for a few months. I was fascinated by the work that they were doing and by the immediate impact that their work could have. The GBCB program seemed a logical step to take.

What kind of projects are you involved with at VBI?

Right now I work on several different projects as needs arise within our research group. I've been working on a lot of Perl scripts and PHP applications for data visualization of genomic data. The largest project that I have been involved with is the VBI Microbial Database under the direction of Dr. Tripathy and Dr. Tyler. The database has been featured in *Science* and contains completed genome sequences and annotation data for the plant pathogens *Phytophthora sojae* and *Phytophthora ramorum*. It also includes analytical tools to help researchers extract specific types of information relevant to their work.

How would you describe the hands-on training offered through the GBCB program?

It has been wonderful to not only hear about research but to be a part of it. The people in my reseach group are great at helping me understand the relevance of different principles as they come up.

How is the GBCB program preparing you for a future in the bioinformatics field?

One of the things that I most enjoy about the GBCB program is the seminar series. The seminars feature guest speakers from various departments at Virginia Tech and other universities. It is really helpful to learn what is going on in the forefront of the field. It helps you to get a better feel for what direction your own research might take.

What advice would you give to students interested in the bioinformatics field?

Before you enter the program, I would recommend learning some statistics. Every paper I read or presentation I attend, whether it relates to computational or traditional lab experiments, is heavily immersed in statistical data. Statistics permeate every aspect of bioinformatics. If I could change anything about my past coursework, I would have taken additional courses in statistics. After you enter the program, don't be discouraged by what you don't understand. In the first few meetings and seminars that I attended, I spent most of the time writing notes on what I didn't know so that I could make reference to them later. Now my notes are getting shorter.

What are your future plans?

The driving force that caused me to return to graduate school was my enjoyment of teaching. The more time that I spend at VBI, the more interested I become in continual learning and research. Eventually, I would like to conduct my own research as well as spend a significant amount of time teaching. I'm particularly interested in the areas of discrete modeling, host-pathogen interactions, and data visualization.

Virginia Tech's Ph.D. program in Genetics, Bioinformatics, and Computational Biology (GBCB)

- Encompasses applications of molecular biology, genomics, mathematics, statistics, and computer sciences to all areas of the life sciences
- Combines discipline-specific and cross-disciplinary course work, encourages a multidisciplinary research environment
- Allows students to work with faculty from many departments and colleges at Virginia Tech
- Tailored to students' individual background

For more information about the GBCB program, please visit www.grads.vt.edu/academics/programs/gbcb