



# Chemical and Biological Defense Technology Watch Newsletter

*In Support of the Joint Science & Technology Office  
for Chemical and Biological Defense*

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## Special points of interest:

- In the News
- Website Reviews
- Biodetection
- Researcher of the Month
- Feature Article
- Upcoming and Past Events
- Conference Reviews
- Employee Corner
- Kudos

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From America's  
Father of Science & Technology,  
*Benjamin Franklin:*

"A slip of the foot you may soon  
recover, but a slip of the tongue  
you may never get over."

"An investment in knowledge  
always pays the best interest."



Caption from *The Pennsylvania Gazette*,  
May 9, 1754

## Greetings

This quarter's CB Defense Technology Watch Newsletter, a product from the A&AS Research & Analysis Group, features disruptive technologies and efforts to understand biological pathogens, biotechnology and nanotechnology, along with information about the scientists who are contributing unique and powerful methods for defense. We hope you find the newsletter useful to the planning and execution of your respective capability areas and programs. As always your comments and/or recommendations are welcome. Please refer any communications to [j.alvelo@ngc.com](mailto:j.alvelo@ngc.com).

## In the News

### *Invisibility Cloak-The Advent of the "Stealth Predator"*

On October 19, 2006 Science Express announced the first working "invisibility cloak" created by a team of researchers led by the Duke University's Pratt School of Engineering, including Professor David R. Smith and cloak designer, David Schurig. The "invisibility cloak" deflects microwave beams so they flow around a "hidden" object inside with little distortion, making it appear almost as if nothing were there at all.

The "metamaterials" used in the "cloaking device" are made of artificial composites that can be made to interact with electromagnetic waves in ways that natural materials cannot. These materials are precisely arranged in a series of concentric circles that confer specific electromagnetic properties.

#### Reference:

<http://www.pratt.duke.edu/news/?id=792>

For more information  
about the Duke University

Engineering project visit  
[http://www.ee.duke.edu/~drsmith/neg\\_ref\\_home.htm](http://www.ee.duke.edu/~drsmith/neg_ref_home.htm).

### *New Theory Explains En- hanced Superconductivity in Nanowires*

University of Illinois physics professor Alexey Bezyradin and his research group have studied the effect of applying a magnetic field to ultra-narrow superconducting nanowires. His research team discovered that magnetic fields can enhance the critical current in superconducting wires with very small diameters. By applying a microscopic theory proposed by U. of Illinois physics professor Paul Goldbart, this curious phenomenon was able to be explained as reported in the Sept. 29 issue of Physical Review Letters.

Goldbart's postdoctoral researcher Tzu-Chieh Wei and graduate student David Pekker proposed that the enhancement observed by Bezyradin's group was due to magnetic moments in the wires. "Even though the two ef-

fects - magnetic fields and magnetic moments - work separately to diminish superconductivity, together one effect weakens the other, leading to an enhancement of the superconducting properties, at least until very large fields are applied," Goldbart said.

The collaborating groups proposed that exposure of the wires to oxygen in the atmosphere causes magnetic moments to form on the wire surfaces. Generally, the moments weaken the superconductivity, but in this case, the magnetic field inhibits their ability to do this because so many atoms lie near the surface, where the magnetic moments form.

#### References:

- (1) <http://www.physorg.com/news80397248.html>
- (2) <http://nanotechwire.com/news.asp?nid=3906>
- (3) <http://www.engr.uiuc.edu/news/index.php?xid=068909120700>

## Websites of Interest



Subscription to the *Nature* Podcast is free. To register for the free service go to <http://www.nature.com/nature/podcasts/rss/nature.xml>

The top five science “blogs” suggested by *Nature* are

<http://scienceblogs.com/pharyngula/>

<http://www.pandasthumb.org/>

<http://www.realclimate.org/>

<http://cosmicvariance.com/>

<http://scienceblogs.com/scientificactivist>

Genome projects of the Department of Energy may be found at <http://genomics.energy.gov/>

The NIH has instituted a Mouse Knockout Project for understanding genes related to humans disease. More information may be found at <http://www.genome.gov/19517927>

For *Systems Biology*, the Institute for Systems Biology

([http://www.systemsbiology.org/Resources\\_and\\_Development/Downloadable\\_Software](http://www.systemsbiology.org/Resources_and_Development/Downloadable_Software))

has several websites of interest:

**SEAMLESS DATABASE AND SOFTWARE INTEGRATION FRAMEWORK**

<http://gaggle.systemsbiology.org/>

**DATA MANAGEMENT**

The Systems Biology Experiment Analysis Management System (SBEAMS): <http://www.sbeams.org/>

**DATA GENERATION SOFTWARE**

ISB proteomics pipeline: <http://www.proteomecenter.org/software.php>  
<http://sashimi.sourceforge.net/>  
<http://peptideprophet.sourceforge.net/>  
<http://proteinprophet.sourceforge.net/>  
ISB microArray pipeline:  
<http://db.systemsbiology.net/software/ArrayProcess/>  
<http://db.systemsbiology.net/software/VERAandSAM/>

For biologists and historians, the complete works of Charles Darwin have been made available online at <http://www.darwin-online.org.uk/>



## Biodetection

### *Defective Interfering Influenza A Virus: Flu Symptom Reduction to Vaccination*

*Sharon Shields, Ph.D.*

Professor Nigel J. Dimmock at the University of Warwick has been working for the last decade on an approach to fighting the flu virus with the flu virus, specifically a defective interfering virus. Influenza A is a RNA virus comprising eight individual segments. As early as the 1950's it was shown that the flu virus often generates particles with large deletions of genomic RNA during replication. Some of these defective particles, depending on the deletion site, can then interfere with replication of infectious virus.

Dr. Dimmock designed an Influenza A virus retaining the native 3' and 5' termini with a large deletion, approximately 80% of the genome, in the central domain. Maintaining the 3' and 5' termini is important for replication, transcription and packaging; however, without the central region, the viral particle cannot replicate by itself because it cannot synthesize the proteins necessary for reproduction. However, it can begin to reproduce when an infectious virus from the

same family enters the cell, providing the missing proteins. Initially there are fewer defective virus particles present compared to the infectious strain. Yet, because the genome is much smaller in the defective virus, it replicates at a much faster rate than the infectious virus and results in a “crowding out” of the infectious agent. It is then thought that while the interference reduces or inhibits flu symptoms, there is time for the body's immune system to develop a response to the infectious pathogen making the pathogen more like a vaccine than a virulent pathogen.

Up until recent studies by Dimmock, there has been little success extending this defective interfering virus concept from proven antiviral activity in vitro to in vivo systems. However, the recent study evaluated the defective interfering Influenza A virus in the ferret and found that it nearly eliminated clinical signs of illness at the time of infection and protected the animal from subsequent challenges of influenza virus. They also

demonstrated the defective interfering virus protected the animals from other subtypes of the Influenza A virus including H3N8 and H3N2.

#### References

1. Mann, A., Marriott, A.C., Balasingam, S., Lambkin, R., Oxford, J.S., and Dimmock, N.J. (2006). Interfering vaccine (defective interfering influenza A virus) protects ferrets from influenza, and allows them to develop solid immunity to reinfection. *Vaccine* 24, 4290-4296.
2. Dimmock, N.J., and Marriott, A.C. (2006). In vivo antiviral activity: defective interfering virus protects better against virulent Influenza A virus than avirulent virus. *Journal of General Virology* 87, 1259-1265.
3. Noble, S., McLain, L., and Dimmock, N.J. (2004). Interfering vaccine: a novel antiviral that converts a potentially virulent infection into one that is subclinical and immunizing. *Vaccine* 22, 3018-3025.

# Investigators of the Month:

## Kevin P. O'Connell, Ph.D. and Alexander Sulakvelidze, Ph.D.



Dr. Kevin P. O'Connell's research interests are focused in three areas: 1) the development of new simulants for bacterial and viral threat agents that will be usable from lab bench to field test, new real-time assays to detect threat agent genetic signatures, and 3) genetic characterization of *Ricinus communis*, the

castor plant and source of the toxin ricin. He has also recently begun collaborating on work to redefine the phylogenetic relationships among strains of *Yersinia pestis*, and consults with the US Army Corps of Engineers on biotechnology applications for soil stabilization. His research experience also includes studies of prokaryotic gene expression, biosensor characterization, and practical applications of molecular biology in biological defense.

Dr. O'Connell serves as adjunct assistant professor in the departments of Pharmacology and Epidemiology at the University of Maryland School of Medicine, lecturing on topics from the pharmacology of antibiotics to molecular biology and bacterial genetics. He has presented his work in biological defense research at several national, international, university and other professional settings. Since 2002, Dr. O'Connell has been a review panelist for the Force Protection session of the biannual Army Science Conference.

Dr. O'Connell is an author on over 40 peer-reviewed scientific journal articles, Army technical reports, book chapters, abstracts, and other articles. He is currently serving a three-year term on the editorial board of the ASM journal Applied and Environmental Microbiology, and is an *ad hoc* grant reviewer for the Army Research Office. He is a co-inventor on eight patents and pending patent applications. Before joining government service, Dr. O'Connell received postdoctoral training at the NSF Center for Microbial Ecology at Michigan State University, the University of Maryland School of Medicine, and was a NRC Research Fellow at ECBC. He received MS and Ph.D. degrees in Bacteriology from the University of Wisconsin-Madison, and his BS degree in Biology from MIT.



Dr. Alexander Sulakvelidze is currently Associate Professor of Epidemiology and Preventive Medicine at the University of Maryland School of Medicine. He is also Chief Science Officer of Intralytix, Inc., a biotechnology company based in Baltimore, Maryland with a focus on the use of bacteriophages as antimicrobial agents in the food safety

and medical fields. His research interests are in the broad areas of emerging infectious diseases, molecular epidemiology, pathogenesis of diseases caused by bacterial enteric pathogens, bacterial toxins, and phage therapy. One of the major focuses in Dr. Sulakvelidze's research are studies of the potential usefulness of bacteriophages in preventing and treating infectious diseases caused by multidrug resistant bacteria. Dr. Sulakvelidze has published extensively on the subject of phage therapy, and he is the author of one issued and several pending patents related to that field. He also co-edited (with Dr. Elizabeth Kutter) a major book about bacteriophages. Dr. Sulakvelidze's phage therapy research has been featured in several magazines and newspapers (including the Los Angeles Times, ASM News, Genetic Engineering News, Washington Techway, US News & World Report, Newsweek, Science, Smithsonian, and Wired), and in various radio programs and television documentaries (including National Public Radio's Science Friday and Tributaries programs, BBC Radio and Voice of America radio programs, and a BBC Horizon television documentary about phage therapy).

Dr. Sulakvelidze serves as an *ad hoc* reviewer on such journals as Antimicrobial Agents and Chemotherapy, Applied and Environmental Microbiology, Clinical and Experimental Dermatology, FEMS Immunology and Medical Microbiology, Food Microbiology, and the Journal of Clinical Microbiology, and for several funding agencies, including the Binational Agricultural Research and Development Fund, Civilian Research and Development Foundation, International Science and Technology Center, and National Institutes of Health.

Dr. Alexander "Sandro" Sulakvelidze, a naturalized US citizen, received his formal training in microbiology in the former Soviet Union, including a B.A. from Tbilisi State University, a Ph.D. from Tbilisi State Medical University, and specialized training at the Engelhard Institute of Molecular Biology, Russian Academy of Sciences, Moscow, Russia, and the University of Maryland School of Medicine, Baltimore, Maryland, USA.

# Phylogenetic analysis of FSU *Yersinia pestis* Strains

Kevin P. O'Connell , Ph.D. and Alexander Sulakvelidze, Ph.D.

## Principal Investigators:

Kevin P. O'Connell, Ph.D., US Army Edgewood Chemical Biological Center, Bldg E3831  
5183 Blackhawk Rd., AMSRD-ECB-RT-BM, Aberdeen Proving Ground, MD 21010  
Tel 410-436-5999; Fax 410-436-6536; [kevin.oconnell1@us.army.mil](mailto:kevin.oconnell1@us.army.mil)

Alexander Sulakvelidze, Ph.D., Assoc. Professor, Dept of Epidemiology, University of Maryland Medical School; 10 S. Pine Street, MSTF Building, Rm. 9-34-D, Baltimore, MD 21201  
Tel 410-706-4587; Fax 410-706-4581; [asulakve@epi.umaryland.edu](mailto:asulakve@epi.umaryland.edu)

**Introduction.** *Yersinia pestis* is the bacterial pathogen that causes plague, a disease that has repeatedly ravaged humanity over the last several millennia (Perry and Fetherston 1997). Combating this pathogen, whether emerging from natural reservoirs or intentionally disseminated by malefactors, requires a detailed understanding of its biology (host-pathogen interactions) at the molecular level. It also requires an understanding of the genetic and biochemical diversity of the species, so that assays for the rapid detection of *Y. pestis* will include all members of the species, while screening out members of closely related species that do not cause plague.

Overall, *Y. pestis* is comprised of strains that are considered by many investigators to be very closely related, based on both biochemical and genetic studies. However, the most recent methods for strain discrimination have not been applied to *Y. pestis* isolated from the Caucasus region of the former Soviet Union. This region is believed to harbor some of the oldest and potentially most varied populations of *Y. pestis*. The potential availability of *Y. pestis* strains from the FSU to adversaries of the United States emphasizes the importance of understanding the diversity of *Y. pestis* and the potential difficulties of identifying any given isolate during an attack. Scientists in the Republic of Georgia, funded by the Cooperative Threat Reduction program at DTRA, are providing a collection of FSU *Y. pestis*, and new isolates may arise from field work over the funded three year period.

Because the design of assays depends on a detailed understanding of how well-conserved potential target signatures are among members of the species, we are characterizing this collection of heretofore unavailable *Y. pestis* strains both genetically and biochemically. The data obtained will be immediately useful to biodefense workers assessing the ability of assays to identify all strains of *Y. pestis* that may be encountered following an intentional release.

**Study goals.** The specific objectives in our analysis of the biochemistry and genetics of strains of *Y. pestis* isolated in the former Soviet Union (FSU) are to answer two pressing questions: first, are existing methods for detecting and identifying *Y. pestis* (primarily PCR) sufficiently robust to identify all members of what is likely to be a highly diverse *Y. pestis* population? Second, is the genetic diversity of *Y. pestis* as reported in the peer-reviewed literature an accurate reflection of biochemical differences as evidenced in the composition of membrane lipids (fatty acids)?

The answers to these questions may have profound implications for *Yersinia* species and strain identification. Assays for the detection of *Y. pestis* have been developed using information derived from a limited number of strains known to be fairly homogeneous in nature. It is believed by experts in the biology of *Y. pestis* that the diversity of this species in nature is greatest in parts of the former Soviet Union. The characterization of a collection of such strains are providing the background information necessary to determine whether existing assays are sufficient, and if not, then the data required to improve their design. We are answering the questions posed above by applying four state-of-the-art methodologies to a population of *Y. pestis* strains isolated in the FSU and comparing the results to those obtained using strains from better-characterized populations. The resulting data will provide valuable background for assay designers, for medical microbiologists, and for basic microbial scientists concerned with the evolution and speciation of mammalian pathogens.

**Historical perspective.** During the last two millennia, epidemics of plague have occurred in 5- to 12-year cycles grouped in 3 pandemics (Figure 1). The 3<sup>rd</sup> pandemic, which is currently ongoing, started in 1855 in the Yunnan region of China and spread to Hong Kong, India (where it killed an estimated 12.5 million people during 1898-1918), Africa, South and North America, and much of the rest of the world. Although *Y. pestis* was endemic in many countries of Europe and Asia for several centuries, it was not introduced into the United States

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until the turn of the 20<sup>th</sup> century, when it entered through the port of San Francisco (pandemic 3, Figure 1). After its entry, *Y. pestis* caused hundreds of deaths, with the last major American outbreak of plague occurring in Los Angeles in 1924 - 1925. Because of the relatively recent introduction of *Y. pestis* into this country, the genetic and phenotypic diversity of American *Y. pestis* isolates is relatively restricted, compared to *Y. pestis* strains from Central and Eastern Asia. Indeed, most of the characterized American strains have been reported to be fairly homogeneous (reviewed by Anisimov *et al.*; 2002). In the United States and much of the developed world, the genetic organization, virulence mechanisms, and life cycle of *Y. pestis* have been primarily studied using a few such genetically homogeneous *Y. pestis* strains. Molecular analyses of these strains have been unable to distinguish strain differences sufficient to allow determinations of genetic relatedness.

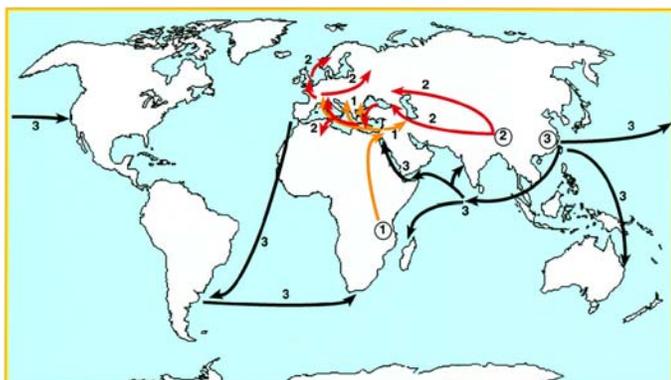


Fig. 1. Routes followed by the three plague pandemic waves, labeled 1, 2, and 3. Circled numbers indicate the regions thought to be the origins of these pandemic waves. (from Achtman *et al.* 1999)

To gain a better understanding of the evolutionary relatedness of *Y. pestis* strains and their origins from ancestral *Yersinia*, this project is using a collection of strains most likely to harbor genetic variability because of the antiquity of the population, and its location on the geographic “crossroads” across which the three global pandemics have swept between Asia and Europe (note the density of “pathways” of plague transmission in the Caucasus region in Figure 1). *Y. pestis* likely has been endemic in the Caucasus region of southwest Asia likely its emergence as a distinct bacterial species.

**Molecular typing of *Y. pestis*—state of the art.** Several molecular typing methods have been used to determine the genetic relatedness of various *Y. pestis* strains. Although those approaches usually have worked well for most of the *Yersinia* species, their applicability or value for typing *Y. pestis* remains problematic. In general, these methods discriminate among the three biovars of *Y.*

*pestis*, but either cannot differentiate individual strains, or provide data insufficient to establish the extent of genetic relatedness among *Y. pestis* strains. Attempts to apply still other molecular genetic methods (PCR based on the chromosomal location of certain genetic elements, or the analysis of variable number tandem repeats (VNTRs)) also failed to provide the needed resolving power.

**New genetic approaches.** While sequencing entire genomes of bacteria is the ultimate approach for delineating their genetic relatedness, both the sequencing of large numbers of genomes and the analysis of such large datasets is still impractical. However, sequencing a single gene also is not optimal. Using a technique that allows sequence-based analysis of several genes simultaneously is providing a balance between sequence-based resolution and technical feasibility. This approach (multilocus sequence typing; MLST) (Maiden *et al.* 1998), differentiates among genotypes in which variations accumulate relatively slowly. MLST has been used to study *Y. pestis* (Achtman *et al.*, 1999), but flaws in early work suggest new approaches to conduct an MLST study that will shed light on an ancient and diverse population of strains. Such ancient endemic populations are more likely to be the reservoir from which future pandemics are more likely to arise, rather than from the homogeneous populations that have been more thoroughly studied to date. *Y. pestis* strains from endemic foci of plague in the FSU are more genetically heterogeneous than the strains used in the above-referenced study. Thus, we are examining genetically and biochemically strains isolated from several endemic foci of plague in former Soviet Georgia (Figure 2). Our targets for MLST will be both



Figure 2. Locations of endemic plague foci in countries of the former Soviet Union, Caucasus region.

“housekeeping” genes (those that encode essential cellular functions) and virulence genes. Virulence genes are likely to exhibit more genetic variability, because evolutionary pressures against the maintenance of mutations are presumed to be lower than that for housekeeping

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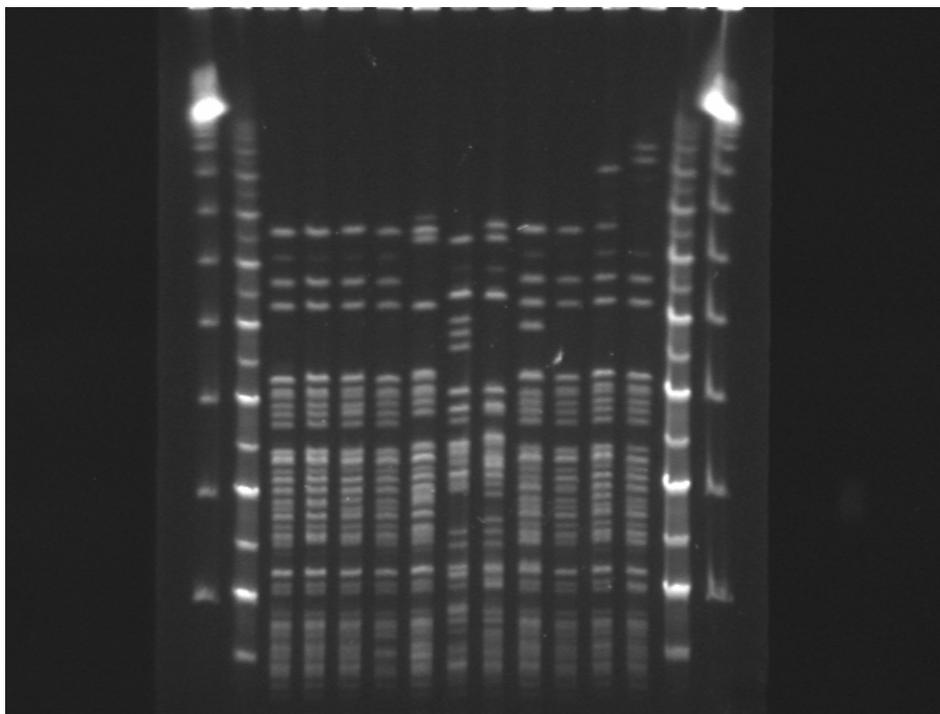


Figure 3. Whole genome fragments following digestion by *Ascl* and separation by pulsed field gel electrophoresis. Lanes (left to right) 1 & 15, I ladder pulsed field gel size markers; lanes 2 & 14, midrange II pulsed field gel size markers; lane 3, *Y. pestis* strain 3082G; lane 4, 1954; lane 5, 3758; lane 6, 3768; lane 7, C1522; lane 8, C2614; lane 9, C790; lane

genes. We have completed an initial survey of seven housekeeping genes, a 16S rRNA gene, and four virulence genes (data not shown), whose sequences are now being analyzed using standard bioinformatics tools that convert raw sequence divergence data and make estimates of strain-strain relationships based on statistical models. The data from this MLST study is being compared with whole-genome restriction digest assays (“PFGE”, or pulsed field gel electrophoresis), a method that provides DNA “fingerprints” based on the location of certain short repeated sequences scattered around the microbial genome (Fig. 1, 2). Later in our study, we will be using two additional approaches, subtractive hybridization and microarray analysis, to further hone the ability to distinguish among strains rapidly, and detect genes whose presence, absence, or sequence diversity may indicate the severity of disease each strain may cause.

**Biochemical diversity of *Y. pestis*.** In addition to genetic characterization by MLST, we are also examining the use of fatty acid methyl ester (FAME) analysis as a tool for the identification of *Y. pestis*. FAME is based on the observation that lipid membrane composition is characteristic of individual bacterial species. Commercial systems exist for performing FAME, and it is a standard

method for identifying pathogens in the clinical setting. However, FAME signatures have not received much attention from the biodetection community and represent a class of non-protein, non-nucleic acid signature molecules that deserve additional attention. A single report of a FAME analysis of *Y. pestis* strains reported that *Y. pestis* strains were highly homogeneous in their membrane fatty acid composition (Leclercq et al. 2000). However, only 29 strains were analyzed, and only one of these was isolated in the FSU (a single strain from Kurdistan). We will determine the FAME profiles for a number of strains of N. American, Asian, and Georgian origin, and compare them to existing FAME data libraries for *Y. pestis* in order to test two hypotheses: first, that genetic variability in *Y. pestis* is reflected in FAME profiles, and second, that existing FAME data for *Y. pestis* is sufficiently robust to identify *Y. pestis* isolated from a distinct, diverse, and previously uncharacterized population. This information will provide additional evidence supporting or rejecting the hypotheses that strains of *Y. pestis* originating in the Caucasus form a distinct, discernible population of this pathogen, and that this population of *Y. pestis* is among the oldest on Earth (Anisimov et al. 2004, and references therein).

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**Summary.** The basic science of *Y. pestis* molecular biology has potential impacts for both “non-medical” and medical issues in biological defense. Having a good understanding of the genetic, biochemical, and virulence trait differences among *Y. pestis* strains is of critical importance during the development of advanced tools and strategies to detect possible *Y. pestis*-related bioterrorism attacks in the United States or elsewhere. For example, *Y. pestis* strains harboring altered, or undescribed variants of, virulence markers may be undetected by modern state-of-the-art approaches. Such “undetectable” strains, if used during bioterrorism attacks, could cause many casualties before the nature of the threat was determined. Medically, antibiotic therapy could be complicated if some unusual (i.e., not commonly found in North American *Y. pestis* strains) antibiotic resistance genes are encoded by plasmid(s) known to exist in some FSU strains, but that are not well characterized in the West. Moreover, *Y. pestis* vaccines currently under development in the United States and Western Europe are based primarily on antigens expressed by non-FSU isolates, and it will be important to ascertain whether such vaccines would adequately protect against *Y. pestis* strains with different antigenic compositions.

A major goal of this study is the discovery of genetic and biochemical signatures both sufficiently distinct to allow the precise identification of individual strains, and sufficiently robust to ensure the positive ID of a much greater variety of strains as a member of *Y. pestis*. The biochemical data we obtain will also determine the usefulness of FAME analysis as a method for the identification of *Y. pestis*. As a necessary by-product, this work will also shed light on the evolutionary history and relationships among *Y. pestis* populations and allow us to determine the relationship between genetic and biochemical diversity in a species of particular interest. This work is supported by the DTRA CB Physical Science and Technology Group. The project is also supported by the DTRA Biological Weapons Proliferation Prevention Program (Cooperative Threat Reduction), which supports work in the Sulakvelidze lab, as well as colleagues at the Republic of Georgia’s National Center for Disease Control (NCDC). —O’Connell and Sulakvelidze

“A major goal of this study is the discovery of genetic and biochemical signatures both sufficiently distinct to allow the precise identification of individual strains ...”

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# Disruptive Technologies

Joseph O. Anderson, Ph.D.

AS&S Research and Analysis Group

A disruptive technology or disruptive innovation is a new technological innovation, product, or service that eventually overturns the existing dominant technology or product in the market.<sup>1</sup> Disruptive innovations can be broadly classified into lower-end and new-market disruptive innovations. A new-market disruptive innovation is often aimed at non-consumption, whereas a lower-end disruptive innovation is aimed at main stream customers who were ignored by established companies. Sometimes, a disruptive technology comes to dominate an existing market by either filling a role in a new market that the older technology could not fill (as more expensive, lower capacity but smaller-sized hard disks did for newly developed notebook computers in the 1980s) or by successively moving up-market through performance improvements until finally displacing the market incumbents (as digital photography has begun to replace film photography). By contrast, "sustaining technology or innovation" refers to the successive incremental improvements to performance that market incumbents incorporate into their existing product. The term disruptive technology was coined by Clayton M. Christensen and described in his 1997 book *The Innovator's Dilemma*. In his sequel, *The Innovator's Solution*, Christensen replaced the term with the term disruptive innovation because he recognized that few technologies are intrinsically disruptive or sustaining in character. It is strategy that creates the disruptive impact. This term has now reached the point of excessive usage in industry. It is preferred by those who market and sell new products, but rarely used by those who actually invent them, who generally find it undignified and arrogant to claim that their new idea will revolutionize the world.

John C. Dvorak adds to Christensen's description. Dvorak states that a disruptive technology is defined as a low-performance, less expensive technology that enters a heated-up scene where the established technology is outpacing people's ability to adapt to it.<sup>2</sup> The new technology gains a foothold, continues to improve, and then bumps the older, once-better technology into oblivion. Dvorak adds that the problem is that there is

not one example of this ever happening. There is no such thing as a disruptive technology. There are inventions and new ideas, many of which fail while others succeed. That's it. This concept only services venture capitalists who need a new term for the PowerPoint show to sucker investors.

Joab Jackson states that disruptive technologies often come from outside the mainstream.<sup>3</sup> Owners of established technologies tend to focus on making incremental improvements to their own products, avoiding the potential threat to their own businesses. Systems integrators, which profit by bringing innovation to their customers, must keep track of movements outside established markets. Something such as the personal computer or the Internet is always just around the corner. Jackson continues by adding that now is the time to prepare for two coming disruptors: open-source software and nanotechnology, two potentially disruptive technologies watched closely by integrators. Each holds the promise of radically changing the landscape of information technology.

The National Defense Industrial Association in coordination with the Office of the Director, Defense Research & Engineering conducted its 3rd Annual Disruptive Technology Conference, titled, *Seeking the Capability Before the Capability is the Surprise*, in September 2006. The conference provided a forum for the interchange of ideas among subject matter experts in government and industry to examine commercial industry and military sponsored science and technology. The conference promoted collaboration between the commercial sector and traditional DoD industry, specifically to identify lower-cost commercial technology products that result in high-end military capability. When coupled with a DoD boost, commercial-off-the-shelf technologies may provide an enhanced capability to the warfighter and ultimately make DoD rethink how the military should fight.

Dr. Ruth David is Chair for the Committee on Defense Intelligence Agency Technology Forecasts and Reviews. This committee was asked to produce a report, based on its discussions with the intelligence community, that discusses capabilities upon which U.S. warfighters are de-

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and to identify the potential for adversaries to threaten those capabilities through the exploitation of evolving technologies. She highlighted several of the committee's findings at the conference.<sup>4</sup>

1. *There is a multitude of evolving technologies for which advances are being driven by the nongovernmental, global, scientific and technical communities. Recommendation: establish an ongoing collaborative relationship with scientific and technical communities in the industrial and academic sectors.*

2. *New intelligence indicators are likely to be needed to provide technology warning for the diverse spectrum of evolving technologies that are being driven by commercial forces in the global marketplace. Recommendation: establish, maintain, and systematically analyze a comprehensive array of indicators pertaining to globalization and commercialization of science and technology to complement and focus intelligence collection and analysis.*

3. *The landscape of potentially important evolving technologies is both vast and diverse.*

Vice Director for Force Structure Resource and Assessment, J-8, Major General Michael A. Vane describes disruptive in the following manner. Disruptive may be challenges from state and non-state actors who employ technologies and capabilities (such as biotechnology, cyber and space operations, or directed energy weapons) in new ways to counter

military advantages the United States currently enjoys.<sup>5</sup> These disruptive challenges may come from adversaries who develop and use break through technologies to negate current U.S. advantages in key operational domains. Dual use civilian technologies, especially information technologies, high-resolution imagery and global positioning systems are widely available. These relatively low cost, commercially available technologies will improve the disruptive and destructive capabilities of a wide range of state and non-state actors.

In summary, disruptive technology lacks refinement, often has performance problems, appeals to a limited audience, and may not yet have a proven practical application.<sup>6</sup> More than likely, large corporations are more prone to work with sustaining technologies. They excel at knowing their market, staying close to their customers, and having a mechanism in place to develop existing technology. Conversely, they have trouble capitalizing on the potential efficiencies, cost-savings, or new marketing opportunities created by low-margin disruptive technologies. It is not unusual for a big corporation or superpower to dismiss the value of a disruptive technology because it does not reinforce current established goals. Meanwhile, as a disruptive technology matures, gains a larger audience and marketshare, it has the potential to blindside and threaten the status quo.

*Recommendation: Adopt a capabilities-based framework within which to identify and assess potential technology-based threats.*

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For a detailed trip report with analysis and recommendations, please contact Dr. Joseph O. Anderson at [joseph.anderson@ngc.com](mailto:joseph.anderson@ngc.com)

— Joseph O. Anderson, Ph.D.

# Upcoming and Past Events

## Upcoming Events

*Nanomanufacturing Workshop*  
October 17-19, 2006  
Gaithersburg, MD.

*2<sup>nd</sup> National Conf on Environmental Sampling and Detection for Bio-Threat Agents*  
October 25-27, 2006  
Brooklyn, New York.

*10th Annual Small Business Conference*  
Theme: "Army & Small Business: Partners for Success"  
Event #7430  
November 1-2, 2006  
Hilton McLean Tysons Corner  
POC: Carissa Mirasol, Meeting Planner, cmirasol@ndia.org or (703) 247-2588

*6th Annual CMMI® Technology Conference and User Group*  
"The Role of CMMI® in Facilitating Program Performance in Large Scale Systems with Complex Teaming Arrangements"  
Event #7110  
November 13-16, 2006  
Location: Hyatt Regency Tech Center Denver  
POC: Meredith Geary, Meeting Planner, mgeary@ndia.org or (703) 247-9476

*NanoBioTech World Congress*  
Boston, MA  
Nov 16-17, 2006  
<http://www.selectbiosciences.com/conferences/nanobiotech2006/>

*10th MIT-LL Bio-Chem Defense Systems Workshop*  
Nov 29-30, 2006  
Cambridge, MA.

## Conference Reviews

*The Future of Biodetection Systems Workshop*

Santa Fe, NM  
September 26-27, 2006

Sponsored by the Los Alamos National Laboratory (LANL), the Future of Biodetection Systems Workshop was held in Santa Fe, NM. In attendance, representing DTRA CB S&T, were Dr. Sharon Shields. 125-150 scientists from DOE weapons laboratories (LLNL, LANL, SNL), DOD, DHS, several academics and private/public companies attended the workshop. Approximately half of the attendees were LANL scientists and/or LANL collaborators.

The purpose of the meeting was to bring together the national security stakeholders and biodetection researchers to discuss current state-of-the-art technology, identify characteristics of an ideal biological detector, assess the technical gaps between current and future biosensors, and define a research and development plan.

LANL's stated motivation in organizing the workshop was to identify technologies for sensor based systems that are more portable, faster, less expensive, and rely on fewer resources. Dr. Jose Olivares opened the workshop with a half hour presentation describing attributes of sensors and detectors including nonspecific and specific detectors. Examples of nonspecific detectors include stand off technologies such as IR or LIDAR and spectroscopic point detectors such as raman, UV, fluorescence. Examples of Specific detection and identification systems are sequence based detectors using DNA or RNA signatures, structure based detectors utilizing immunoassay type

detection schemes, biological function based detectors utilizing cells, and chemical based detectors that measure mass/size and/or chemical functionality. Keynote speakers for the two day workshop were selected based on their experience in dealing with the six primary components to of detection sensors or systems including sampling techniques and challenges, spectroscopy based detection, signal transduction, ligand design, DNA technologies and systems Integration. Below is a brief summary of each presentation.

*Topic 1: Challenges of Sampling for Biodetection Systems*

Dr. Gary Long, Vice President of TetraCore, Inc. focused on the challenges of sampling and sample preparation for environmental and clinical/veterinary molecular diagnostics via immuno or PCR based diagnostics. He addressed the commercially available assays and described the diagnostic process in the following manner:

**Specimen Acquisition → Processing or Sample Preparation → Analysis**

The primary challenge for PCR and immuno based diagnostics are the first two steps with then number of technologies for analysis rather small. The combination of sample matrix (swabs, air filters, water, soil, food, blood, saliva, etc.) and the amount of target in such matrices is generally very minute relative to the mass of sample matrix and interferences. In all analyses there is often a trade off between sensitivity and the time and cost required for sample preparation. For example, PCR analysis of a diluted sample only versus a sample that has been carefully prepared to open spores and remove PCR inhibitors will, in general, be less sensitive, yet cost and time of analysis is significantly reduced. Conversely, sampling

*Continued on page 11*

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Strategies of large matrix quantities for a small amount of target are neither predictable nor uniform.

Several questions were asked of the speaker. One asked for his opinion on the use of microfluidics to automate sample preparation and detection.

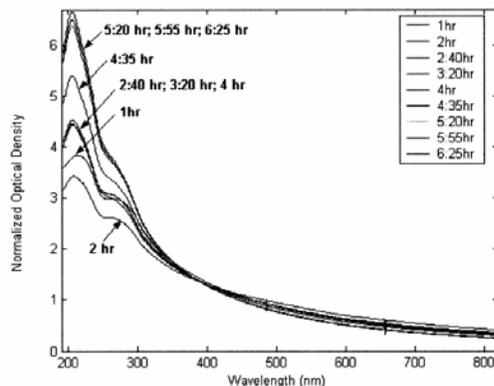
Dr. Long's paraphrased response - clearly, having microfluidics for automation may be useful, but the microfluidics must be more functional than just a device to move a solution from point A to point B, they have to be functional. That is, the microfluidic devices must perform sample preparation routines such as rinsing, beating, extracting DNA, etc and deliver the sample to the detector. Provided such a technical solution to sample preparation exists, sample acquisition and sampling strategies will remain a challenge. How does one display a mL or more of sample to the microfluidic device and speed up the process at the same time?

### Topic 2: Spectroscopy Systems

Dr. Luis H. Garcia-Rubio, Professor at the University of South Florida, provided a brief overview of spectroscopic systems and described their advantages, disadvantages and advances for biodetection systems. He followed the overview with a description of his biophotonic technology using fiber optic spectroscopic methods. He presented several medical applications using FTIR and UV-Vis spectroscopy using fiber optics. One particular interesting application was the use of this technology to monitor a fetus's O<sub>2</sub> levels during in fetal surgery.

For environmental applications, Dr. Garcia-Rubio presented a UV-Vis spectroscopic method to identify bacteria suspended in media. While the medical applications were designed for specificity, *i.e.*, monitoring a specific chemical, the environmental sampling examples were designed to be non-specific, *i.e.*, characterizing the broad phenotypic characteristics associated with whole organisms. Multi-wavelength UV-Vis spectroscopy combines light absorption and light scat-

tering information which is dependent upon the size, shape and optical properties of the bacteria. The figure below [1] contains overlays (*i.e.*, data were collected independently) of normalized UV-Vis spectra intensities for different *E. coli* growth stages.



With pure bacterial cultures, Dr. Garcia-Rubio claimed the ability to differentiate *E. coli* strains and differentiate different growth stages of a given strain. This statement was followed with the claim that this tool will be useful for fielded biodetection systems because the measurements are very precise. This broad extrapolation from differentiation of bacterial strains and their growth stages in a lab setting with pure cultures to field detection brought great criticism from the audience for the following reasons: a) experimental variability and reproducibility not demonstrated, b) biological variability of the same organism in different preps, c) all the data shown were on pure cultures, not mixtures. The technology may be one tool for biodetection and provide one piece of information to a system of detection schemes, but the claims that this technology will identify an organism is a long way from reality.

It is my opinion that this concept, however, could benefit from materials development approaches that provide some selection criteria or reaction chemistry (*e.g.*, in situ separations) to integrate some specificity such as separating gram-positive from gram negative bacteria on the fly and prior to analysis.

### Topic 3: Systems Integration

Systems integration refers not only to deploying multiple sensors in many locations acquiring multidimensional data about the threat, it also refers to integration of various phases of predicting and responding to the threat:

**Pre-attack (intelligence and threat assessment) → Trans-attack (environmental surveillance, ideally pre-symptomatic disease detection) → Post-attack (Medical surveillance, decon, sampling, law enforcement/forensics).**

Dr. Cullin concluded by describing the need to increase the density of detection systems in the field which necessitates the detectors and/or samplers must be cheap, provide multidimensional data (perhaps incorporating less specific information such as spectroscopy based systems), fast, rapidly feed information back to a central command post for data fusion of disparate information, and have a false positive rate of 10<sup>-6</sup> or better. Dr. Cullin also raised the hypothesis that since chemical and biological agents are designed to attack humans, perhaps an alternative or at least parallel effort at monitoring the human and animal population for infection could be an added component of the system.

### Topic 4: Overview of DNA Technologies

Dr. Stephen Apatow of the Humanitarian Resource Institute was the plenary speaker for this session. He did not discuss DNA technologies at all. Rather, he described the efforts of his non-profit company and the need to get cheap and fast assays out into the field to monitor veterinary and human disease at the global level. He spent ample time criticizing the FDA and USDA for their slow response to approving DNA PCR assays for diagnostics.

Continued from page 11

of diseases such as Bird Flu, West Nile Virus, SARS, FMD, etc. His final conclusion, an obvious one, was that we need low cost, fieldable detection technology, yet he provided no insight into the current technology used, let alone what the technology of the future may look like.

#### Topic 5: Ligand Based Technologies for Biodetection

Dr. Brian Kay, Professor at the University of Illinois at Chicago began by stating that the biodefense community needs “smart molecules (materials)” in addition to the hardware and software associated with detection systems in order to enhance specificity and selectivity of detection. Essentially, the idea of this “smart molecule” or ligand based approach is synonymous with immunoassays for detection; however, instead of an antibody, the ligand is a small molecule, aptamer, or peptide designed to bind with significant affinity and specificity to a given target. Dr. Kay’s presentation focused on combinatorial chemistry synthesis of peptides that bind to active sites on proteins. Several of the applications were biological in nature, e.g., finding peptides to interfere with protein-protein interactions to alter cellular function. Other applications were process in nature, *i.e.*, finding peptides for affinity purification of proteins from cellular systems.

(Comment/Analysis: There was nothing new in Dr. Kay’s presentation, but it was a solid explanation of current approaches to ligand based efforts for selective, or immunoassay-like sensor design. His presentation completely focused on combinatorial chemical synthesis and high throughput screening selection for biologically active ligands. This is primarily a result of method development for the pharmaceutical industry; however, it is not necessary to identify only biologically active molecules for sensor development. In fact, it might be useful to have ligands that bind specifically to denatured or functionally non-active proteins. This ability could certainly

simplify sample preparation for immunoassays. In addition, the examples discussed focused on known target proteins with no discussion of the use of combinatorial chemistry for molecular discovery of new targets - a chemical genomics approach. Perhaps combining non-specific spectroscopy methods and specific “smart molecule” detection schemes would be a useful pursuit. For example, if by developing a material that segregates lipids, or hydrophobic cellular components from the soluble carbohydrate and protein classes, the spectroscopic systems can provide greater specificity without the need for developing highly specific ligands to a specific target. In other words, arrays of materials that can perform an in situ and rapid separation of bulk sample that describes different aspects of the chemistry and/or biology of a given sample. While it won’t necessarily identify a specific antigen, it can provide more chemical detail than mere spectroscopic analysis yet less specific information than a protein-ligand binding event).

#### Topic 6: Signal Transduction - Examples from nature

Dr. Larry Sklar, Professor at the University of New Mexico, was the last speaker. The presentation began with a description of cellular principles of signaling:

1. Senses use arrays or “antennae” that
  - a) optimize collection
  - b) optimize discrimination
  - c) are extremely rapid
2. Highlights
  - a) Eye - 1 photon
  - b) Ear - 20 mPascal
  - c) Nose - ~ 300 olfactory sensor to form a network that determine/differentiate 104 odors
  - d) Taste - 5 types of sensors that network to differentiate hundreds of tastes
3. Recognition Principles
  - a) Redundant - chemicals and proteins that have opposing activities, e.g., adrenaline
  - b) Diversity - a biological system can

have different recognition principles

- c) Valency - different biophysical principles

The primary example that Dr. Sklar used to demonstrate how rapid the cascade of molecular events occurs was the photoreceptor response of the human eye. He posed the following questions: How fast is the inactivating chemistry? (How fast does darkness register when one closes their eyes?) How fast is the activating biochemistry? (How fast does one register light when eyes open?) How rapid is adaptation? (How long does it take for eyes to adapt to a dark room?) What is the range of adaptation? The inactivating and activating signal transduction is immediate while adaptation takes several minutes. The cascade of molecular events that occur in the “blink of an eye”, or nanoseconds, include:

- light absorption by *cis*-retinal bound to a protein, called opsin, in the retina induces *cis*-retinal to isomerize to *trans*-retinal (*cis*-retinal-opsin complex is called rhodopsin)
- *trans*-retinal does not fit into the pocket of opsin which forces the protein to change conformation
- Opsin changes shape to accommodate *trans*-retinal, and goes through several intermediate structures, but the structure is energetically unfavorable so *trans*-retinal is eventually expelled from the protein
- One of the intermediate structures, Metarhodopsin, activates the enzyme transducin.
- Transducin binds to and activates the enzyme phosphodiesterase.
- Phosphodiesterase catalyzes hydrolysis of cyclic GMP (cyclic GMP is required to keep Na<sup>+</sup> channels in the plasma membrane open and degradation of GMP allows Na<sup>+</sup> to build up on the outside of the plasma membrane creating a large charge difference across the membrane and this charge difference is the electrical impulse down to the nerve cell).

Continued from page 12

(Comments: This presentation was truly fascinating. The ability to harness the chemical reactions and molecular interactions that result in a sensitive and specific sensing event with more environmentally robust multifunctional materials would truly revolutionize biological or chemical detection. Note this cannot be done without a team of multidisciplinary scientists).—Sharon Shields, Ph.D.

For a detailed trip report with analysis and recommendations, please contact Sharon Shields at Sharon.Shields@ngc.com

### **Analysis/ Recommendations:**

There were no revolutionary ideas forthcoming from this workshop. Maybe the question we should be asking has nothing to do with detection or technology or sensors per say, but rather...How do we know what we don't know? Will we identify an unknown threat and rapidly? If we attempt to answer these questions, we will have to move away from standard DNA signatures (3-5 from each "known" organism) and immunoassays designed to detect a specific protein from a known organism. If we can identify an unknown then surely the known will also be detected. Perhaps then, the process will lend itself to development of revolutionary technology.

### **The Fiber Society 2006 Fall Annual Meeting and Technical Conference**

October 10-12, 2006  
Knoxville, Tennessee

The three-day meeting was attended by Mr. Jeff Owens, DTRA CB S&T and Dr. Eugenia Posey-Marcos, AS&S Support to DTRA CB S&T, along with representatives from the U.S. Air Force, U.S. Army, academia, and industry. The program chair, Dr. Gajanan Bhat, from the University of Tennessee, presented the opening remarks along with Dr. Phil Gibson, U.S. Army Soldier Center, Natick, MA,, and Dr. Way Kao, the Dean of the College of Engineering, University of Tennessee. The opening plenary talk was given by Wesley Hoffman, U.S. Air Force Research Laboratory on "How Well Does Carbon Handle Stress?" The importance of carbon fiber as structural components of aircraft was discussed as well as the shortage of carbon fiber. Oakridge National Laboratories are working on ways to make better and cheaper carbon fibers and have one of the only projects on this endeavor.

Morning session topics dealt with high-performance fibers, moderated by Andy Campbell, Sunoco Chemicals, with an adjacent session on fiber assemblies, moderated by Rakesh Gupta, from the Eastman Chemical Company. One of the presentations was on polymer nanocomposites fibers and the processes, structure and applications as discussed by Dr. A. Ajji from the Industrials Materials Institute of the National Research Council of Canada. The research of PET nanocomposites materials as potential biomaterials for load bearing bone applications of the orthopaedic/dental implant field was presented. The compatibility with fibroblast cell culture was demonstrated and suggest potential use of certain PET composites as load-bearing bone biomaterials.

Dr. Richard Gregory, from Old Dominion University, Norfolk, VA presented "Electroactive and Photonic All-Organic Polymers for Fiber Based SMART Materials". His discussion dealt with conductive polymers and t

why photonic plastics were important for use in chemical sensors, RF tags, antistatic properties, and energy storage. He envisioned "optical computers" in the near future.

Researchers from the Ecole Nationale Supérieure des Industries textiles de Mulhouse spoke on textile heart valve prosthesis, which offered low bending stiffness for good fatigue resistance and durability, and good orthotropical traction stiffness, essential for bearing the diastolic membrane stress.

Other topics were on fiber formation and fabrics and modeling, moderated by Dr. Phil Gibson, from the U.S. Army Soldier Center, Natick.

A special tribute was given to honor Professor J.E. Spruiell. His former graduate students, now well established in industry and academic positions, came from all over the world and presented their fiber/ engineering research. Among Dr. Spruiell's former students were Dr. Miko Cakmak, from the University of Akron, speaking on Structural Hierarchy Developed in Polypropylene/Clay Melt Spun Fibers; Dr. Rajen Patel from Dow Plastics on Thermal Bonding of Polyolefin Fibers; Dr. Pankaj Gupta from the Virginia Polytechnic Institute and State University speaking on Superparamagnetic Flexible Substrates Based on Submicron Electrospun Estane Fibers Containing MnZnFe-Ni Nanoparticles; Dr. Kyung-Ju Choi from AAF International on Morphological Investigation of Fibrous Materials by Multiaxially Stretched Films; and Dr. Jack Zhou, from Ethicon, Inc. on Fibrous Form of Bioabsorbable Polymers in Surgical Applications.

An extremely useful computer modeling project was presented by Dr. Colby C. Swan from the University of Iowa depicting a clothing modeling framework for uniform and armor system design to study the effects of clothing on a wearer's physical performance capabilities, quantifying the mechanical interactions between a given uniform or body armor system design and a specific wearer performing defined physical tasks. Dr. Swan's

Continued from page 14

research went beyond “digital human modeling” that is used in the automotive industry. His research incorporates the use of mathematical projections of human motion (kinematics). Eventually these data will be integrated with structural and thermal performance data of the materials and components used in the uniforms. Dr. Swan’s research is part of the Virtual Soldier Research (VSR) Team at the University of Iowa who conducts research in the following areas: Human Modeling and simulation, Dynamic Simulation, Virtual Reality, Biomechanics, Control, Multi-Objective Optimization, Clothing, Human Performance Measures, Electromyography, Artificial Intelligence, Human Kinematics and Dynamics, Physiology, Muscle Modeling, Hand modeling, Posture and Motion Prediction, Motion Capture, and Real-Time Visualization. The digital human model is called Santos™. (See corresponding video at <http://www.exn.ca/dailyplanet/view.asp?date=12/2/2005>)

Dr. Youqi Wang from Kansas State University presented research on “Ballistic Penetration Simulation of Textile Fabrics. Her project is a collaborative effort with Bryan Cheeseman at the U.S. Army Research Laboratory in Aberdeen, Maryland. Ballistic penetration resistance is determined by fabric topology, yarn structures, fiber strength and modulus and yarn-to-yarn and fiber-to-fiber frictions. This research is based on an explicit digital element approach. See Figure 1 below.

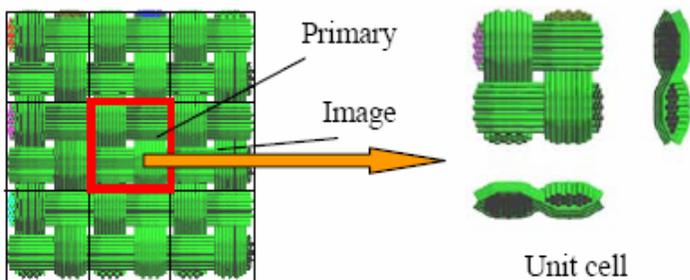


Figure 1 Generation of Textile Fabric Unit Cell

A fiber is first modeled as a digital chain. Then a yarn is modeled from an assembly of digital chains, followed by the generation of a textile fabric using a “dynamic relaxation approach” to develop a detailed fabric geometry. Then the explicit digital element approach is used to simulate ballistic penetration of textile fabrics. If the friction coefficient is small, the bullet penetrates through fabric by pushing fibers aside, called “wedge out”. The greater the friction coefficient, the greater the penetration resistance. The bullet penetrates fabrics due to fiber failure. By varying types of fibers, the yarn structures and fabric geometry, better resistance to bullet penetration can be achieved. Then a fabric could be optimally designed.

M.M. Hossain from Swiss Materials Science & Technology, St. Gallen, Switzerland presented “Plasma Surface Modification of Textiles.” Surface wettability is a very important property of textiles and can be improved by incorporation of hydrophilic groups such as -OH, -COOH, -C=O on the surface using non-polymer forming gases. Polar group addition improved soil resistance and alevel dyeing as well.

In addition to talks about various fibers and applications, new kinds of spinning techniques were discussed. Dr. Soumayjit Sarkar’s (from the Virginia Commonwealth University in Richmond) presentation was on polymer nanofibers produced by electrospinning. This laboratory has developed a new method for making highly

aligned arrays of polymer nanofibers by using “biased AC electrospinning” to deposit aligned arrays of polymer nanofibers onto virtually any substrate and without the need for an external “lens” electrode. Dr. Michael Jaffe from the New Jersey Institute of Technology presented a mathematical model of the electrospinning process for both process control and property prediction. Other talks presented ways to improved fabrics through coatings and or chemical treatments.

Several talks from Clemson University dealt with polymer materials for light-emitting and photovoltaic applications. Polymer light emitting diodes have grown in importance because of their high efficiencies, low power consumption and ease of fabrications for use in such items as electrochromic devices, especially for high resolution display devices.

The concluding talk by Dr. Lynn Penn from the University of Kentucky was on polymer brushes for creating fiber surfaces of controlled structure. Such brushes could trap or release designated species, such as chemical or biological agents, and would be useful in filtering applications.

Throughout the conference issues of “scaling up” novel techniques and ways to meet industrial-based production challenges were discussed.

– Eugenia L. Posey-Marcos, Ph.D.

#### **Recommendations:**

Fiber research today is more than “textile-based” and encompasses “material sciences, biotechnology, physics and chemistry.” Thus, continued participation in and study of this discipline is necessary to meet DoD mission challenges.

For a detailed trip report with analysis and recommendations, please contact Dr. Eugenia Posey-Marcos at [eugenia.posey-marcos@ngc.com](mailto:eugenia.posey-marcos@ngc.com)

## A Personal Account: China's Coming of Age-- Factors Which May Lead China to Become a Technological Competitor

Jessica Miller, AS&S Research and Analysis Group



Jessica Miller in Hong Kong

This past August I traveled to China for two weeks to complete the capstone course of my MBA program. Having never been to a country so far east, I had no real idea of what to expect. I was curious if Chinese citizens would have the same guarded attitude towards Americans as their government projected. My experience during the two weeks left me understanding a great deal more about the weakness of the Chinese government and the power of the Chinese people.

Although there is a thin crust of government-imposed communism across the country, and many of the elderly still hold fast to the Confucian principles, capitalism is in the heart of the Chinese people. I had the opportunity to converse with several Chinese government officials which gave a stark contrast to the average citizens I talked to on the streets. I met with a Beijing Olympic committee official and the President of the Free Trade Zone, both members of the Communist Party. Their answers to our questions were very politically correct, never quite giving us enough to make a judgment. On the other hand, a store clerk and a car salesman I spoke to were both completely open about their opinions of not only their fondness of America and Europe, but also their opinion of their own government, which basically came down to: as long as they didn't attract too much attention, they could do whatever they wished in terms

of the "grey market" (designer knock-offs, bootleg DVDs, etc).

I feel the Chinese government has not necessarily overlooked their populations desire to become more friendly with the west, although politically and ideologically they may feel constrained. These grey markets seem far too large and public for them NOT to notice. More specifically, I feel they allow the grey markets to stay open as it supports many citizens who might otherwise be unemployed and dependent on the social system. In addition, recent actions by the government to help satisfy China's desperate need for skilled workers (millers, welders, artisans, etc) I believe will have an incredible impact on China's technology growth.

Chinese officials announced that the central government planned to invest Rmb10B (about 1.3BUSD) in the infrastructure of vocational education over the next five years and local governments shall spend more than Rmb20B in the initiative. This effort hopes to grow a new population of skilled workers from the more rural/agricultural sectors. I see this as having a huge impact on the financial growth of the country. In essence, this move could raise the general financial well being of the entire country.

*How?* Many of the young Chinese professionals of today are children of skilled workers who had the opportunity to move to the cities. The most fortunate of children were allowed access to the city school systems. My belief is that the same will slowly occur with the new influx of skilled workers. As more skilled workers are educated and drawn to the cities to fill the vast vacancies, their children will be born in the cities, allowing some of them access to better schools and universities. This, to me, mirrors the movement decades ago in the US when we became a less agriculturally focused society.

*So why does this matter so much when considering China's development of technology?* Everything. More education means more innovation. This and China's recent entrance into the WTO will have a profound effect on their status around the world. I read an article shortly before my trip that suggested in the next

two decades, China will become the largest buying power in the world followed closely by India. Their massive populations combined with increased stability, prosperity, education, and connections with the rest of the world will give them a significant advantage over many other developing countries. Possibly becoming a contender for the world super power position currently being held by the US. It may seem far fetched, but I think a dismissive attitude by America and Europe could result in being blindsided.

I am by no means an expert, but I know what I saw. China is thirsty for knowledge and technology, and hungry for the wealth and prosperity that accompanies success. The people of China not only recognize the opportunities of stronger western/global relations, but they embrace the essence of capitalism at its best. This is why China has the opportunity to move forward and become a formidable technologically advanced nation. What this all means in terms of national security is yet to be seen. I feel it will depend heavily on China's ability to meet WTO requirements on corruption, legal protection, and trade barriers, and the rest of the world's attitude towards their growth. —Jessica Miller



Shanghai



Shanghai Bridge



Shanghai at Night



Beijing Street



Jessica at the Great Wall of China



Temple of Heaven-Beijing, China



Western Culture meets the East



*In Support of  
the Joint Science & Technology Office  
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A&AS Research and Analysis Group

**Editorial Staff:**

Mr. Jose I. Alvelo, Editor

Dr. Eugenia L. Posey-Marcos

Dr. Joseph D. Anderson

Dr. Sharon J. Shields

8211 Terminal Road, Suite 210

Lorton, VA 22079-1421

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## Kudos

Congratulations to the new 2006 Nobel Prize winners in Medicine and Physiology, Dr. Andrew Fire and Dr. Craig Mello, for their discovery of RNA interference - gene silencing by double-stranded RNA and for Dr. Roger Kornberg, the 2006 Nobel Prize Winner in Chemistry, for his studies of the molecular basis of eukaryotic transcription.



Dr. Andrew Fire  
Stanford University  
School of Medicine



Dr. Craig Mello  
University of Massachusetts  
Medical School



Dr. Roger Kornberg  
Stanford University