5 February 2009

This supplement has been prepared to present scientific and technical news items that may be of more interest to technical personnel at RDT&E activities and the labs, or the medics rather than the broader readership of the basic CB Daily. Due to the nature of the material, the articles, if available online, are usually only available through subscription services thus making specific links generally unavailable. Thus, usually only the bibliographic citation is available for use by an activity's technical library.

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Chem-Bio News- S&T Edition

1. BLUE LIGHT DESTROYS TWO MRSA STRAINS: *"Two common strains of methicillin-resistant Staphylococcus aureus (MRSA) were virtually eradicated in the laboratory by exposing them to a wavelength of blue light, in a process called photo-irradiation that is described in a paper published online ahead of print in Photomedicine and Laser Surgery."*

2. IDENTIFICATION OF MELIOIDOSIS OUTBREAK BY MULTILOCUS VARIABLE NUMBER TANDEM REPEAT ANALYSIS: *"We developed a simplified 4-locus multilocus variable number tandem repeat analysis (MLVA-4) for rapid typing and compared results with PFGE and MLST for a large number of well-characterized B. pseudomallei isolates."*

3. COMPARATIVE GENOMICS REVEALS MOLECULAR EVOLUTION OF Q FEVER PATHOGEN: *"Scientists from the National Institute of Allergy and Infectious Diseases, Texas A&M Health Center, and the Virginia Bioinformatics Institute at Virginia Tech have uncovered genetic clues about why some strains of the pathogen Coxiella burnetii are more virulent than others."*

4. GLUTATHIONE PROVIDES A SOURCE OF CYSTEINE ESSENTIAL FOR INTRACELLULAR MULTIPLICATION OF FRANCISELLA TULARENSIS: *"Thus, the capacity this intracellular bacterial pathogen has evolved to utilize the available GSH, as a source of cysteine in the host cytosol, constitutes a paradigm of bacteria–host adaptation."*

5. GENOME-SCALE RECONSTRUCTION OF THE METABOLIC NETWORK IN YERSINIA PESTIS, STRAIN 91001: *"Here, we report the first genome-scale metabolic model of Yersinia pestis biovar Mediaevalis based both on its recently annotated genome, and physiological and biochemical data from the literature."*

6. RESEARCHERS FIND ENZYME UNIQUE TO TULAREMIA ORGANISM: *"Karl Klose, director of the South Texas Center for Emerging Infectious Diseases (STCEID) at the University of Texas at San Antonio (UTSA), says his lab collaborated with researchers at the Burnham Institute for Medical Research, The University of Texas Southwestern Medical Center at Dallas and Thomas Jefferson University in a study that discovered that Francisella*

tularensis makes an essential metabolic molecule, nicotinamide adenine dinucleotide (NAD), using a different process and different enzyme from all other living organisms."

7. COMPACT BIOSENSOR FOR WIDE-RANGING APPLICATIONS: *"Scientists at the Naval Research Laboratory (NRL) are partnering with industry to develop a sensor system for biomolecules that could make a significant contribution to a variety of fields such as healthcare, veterinary diagnostics, food safety, environmental testing, and national security."*

8. DETECTION OF NOVEL SARS-LIKE AND OTHER CORONAVIRUSES IN BATS FROM KENYA: *"The frequency and diversity of CoV detections in bats, now in multiple continents, demonstrate that bats are likely an important source for introduction into other species globally."*

CB Daily Report

Chem-Bio News

BLUE LIGHT DESTROYS TWO MRSA STRAINS
Infection Control Today Magazine
January 29, 2009

"Two common strains of methicillin-resistant Staphylococcus aureus (MRSA) were virtually eradicated in the laboratory by exposing them to a wavelength of blue light, in a process called photo-irradiation that is described in a paper published online ahead of print in Photomedicine and Laser Surgery. The article will appear in the April 2009 issue (Vol. 27, No. 2) of the peer-reviewed journal published by Mary Ann Liebert, Inc.

Antibiotic-resistant bacterial infections represent an important and increasing public health threat. At present, fewer than 5 percent of staphylococcal strains are susceptible to penicillin, while approximately 40 percent to 50 percent of Staph aureus isolated have developed resistance to newer semisynthetic antibiotics such as methicillin as well.

Chukuka S. Enwemeka, Deborah Williams, Sombiri K. Enwemeka, Steve Hollosi, and David Yens from the New York Institute of Technology had previously demonstrated that photo-irradiation using 405-nm light destroys MRSA strains grown in culture. In the current study, "Blue 470-nm Light Kills Methicillin-Resistant Staphylococcus aureus (MRSA) in Vitro," the authors exposed bacterial colonies of MRSA to various doses of 470-nm light, which emits no UV radiation."

The full article can be found at: http://www.infectioncontroltoday.com/hotnews/blue-light-destroys-mrsa.html

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IDENTIFICATION OF MELIOIDOSIS OUTBREAK BY MULTILOCUS VARIABLE NUMBER TANDEM REPEAT ANALYSIS

By Bart J. Currie, Asha Haslem, Talima Pearson, Heidie Hornstra, Benjamin Leadem, Mark Mayo, Daniel Gal, Linda Ward, Daniel Godoy, Brian G. Spratt, and Paul Keim
Emerging Infectious Diseases
February 2, 2009

"Endemic melioidosis is caused by genetically diverse Burkholderia pseudomallei strains. However, clonal outbreaks (multiple cases caused by 1 strain) have occurred, such as from contaminated potable water. B. pseudomallei is designated a group B bioterrorism agent, which necessitates rapidly recognizing point-source outbreaks. Pulsed-field gel electrophoresis (PFGE) and multilocus sequence typing (MLST) can identify genetically related isolates, but results take several days to obtain. We developed a simplified 4-locus multilocus variable number tandem repeat analysis (MLVA-4) for rapid typing and compared results with PFGE and MLST for a large number of well-characterized B. pseudomallei isolates. MLVA-4 compared favorably with MLST and PFGE for the same isolates; it discriminated between 65 multilocus sequence types and showed relatedness between epidemiologically linked isolates from outbreak clusters and between isolates from individual patients. MLVA-4 can establish or refute that a clonal outbreak of melioidosis has occurred within 8 hours of receipt of bacterial strains."

The full article can be found at: http://www.cdc.gov/eid/content/15/2/169.htm

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COMPARATIVE GENOMICS REVEALS MOLECULAR EVOLUTION OF Q FEVER PATHOGEN

Infection Control Today Magazine
February 2, 2009

"Scientists from the National Institute of Allergy and Infectious Diseases, Texas A&M Health Center, and the Virginia Bioinformatics Institute at Virginia Tech have uncovered genetic clues about why some strains of the pathogen Coxiella burnetii are more virulent than others.

The researchers compared the sequences of four different strains of C. burnetii, an intracellular bacterium that can cause acute and chronic Q fever in humans, to build up a comprehensive picture of the genetic architecture and content of the different genomes. The scientists examined C. burnetii strains of differing virulence to unveil clues on the genetic features associated with pathogenicity."

"Dr. Robert Heinzen, head of the Coxiella Pathogenesis Section at the National Institute of Allergy and Infectious Disease, remarked, "Our results suggest that mobile genetic elements have played a major role in the evolution and function of the C. burnetii genome. Recombination between insertion sequence elements or jumping genes appears to have brought about large-scale generation of non-functional genes, a change that may be associated with a more pathogenic lifestyle."

The full article can be found at: http://www.infectioncontroltoday.com/hotnews/evolution-of-q-fever-pathogen.html

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GLUTATHIONE PROVIDES A SOURCE OF CYSTEINE ESSENTIAL FOR INTRACELLULAR MULTIPLICATION OF FRANCISELLA TULARENSIS

Khaled Alkhuder, Karin L. Meibom, Iharilalao Dubail, Marion Dupuis, Alain Charbit
PLoS Pathogens
February 3, 2009

"Abstract

Francisella tularensis is a highly infectious bacterium causing the zoonotic disease tularemia. Its ability to multiply and survive in macrophages is critical for its virulence. By screening a bank of HimarFT transposon mutants of the F. tularensis live vaccine strain (LVS) to isolate intracellular growth-deficient mutants, we selected one mutant in a gene encoding a putative γ-glutamyl transpeptidase (GGT). This gene (FTL_0766) was hence designated ggt. The mutant strain showed impaired intracellular multiplication and was strongly attenuated for virulence in mice. Here we present evidence that the GGT activity of F. tularensis allows utilization of glutathione (GSH, γ-glutamyl-cysteinyl-glycine) and γ-glutamyl-cysteine dipeptide as cysteine sources to ensure intracellular growth. This is the first demonstration of the essential role of a nutrient acquisition system in the intracellular multiplication of F. tularensis. GSH is the most abundant source of cysteine in the host cytosol. Thus, the capacity this intracellular bacterial pathogen has evolved to utilize the available GSH, as a source of cysteine in the host cytosol, constitutes a paradigm of bacteria–host adaptation.

Author Summary

The role of nutrient acquisition systems in survival and multiplication of intracellular bacterial pathogens within infected cells is yet poorly understood. The data presented here suggest that Francisella tularensis, a highly infectious facultative intracellular bacterium, is capable of utilizing glutathione (GSH) and γ–glutamyl-cysteine peptides present in the cytosol of infected host cells. An in vitro negative selection method, based on the use of a bacteriostatic antibiotic, to recover intracellular growth mutants directly from a pool of mutants, allowed us to select one mutant in a gene encoding a γ-glutamyl transpeptidase (GGT). The mutant strain showed impaired intracellular multiplication and was strongly attenuated for virulence in mice. The cleavage of these cysteine-containing peptides by GGT activity provides thus the essential source of cysteine required for intracellular multiplication. The capacity F. tularensis has evolved to utilize GSH, the most abundant source of cysteine in the host cytosol, constitutes a model of bacterial adaptation to intracellular lifestyle."

The full article can be found at: http://www.plospathogens.org/article/info%3Adoi%2F10.1371%2Fjournal.ppat.1000284;jsessionid=A2C076E5D3B54FB6205C0F3489E5A811

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GENOME-SCALE RECONSTRUCTION OF THE METABOLIC NETWORK IN YERSINIA PESTIS, STRAIN 91001
By Ali Navid and Eivind Almaas
Molecular BioSystems
January 26, 2009

“Here, we report the first genome-scale metabolic model of Yersinia pestis biovar Mediaevalis based both on its recently annotated genome, and physiological and biochemical data from the literature. Our model demonstrates excellent agreement with Y. pestis known metabolic needs and capabilities. Since Y. pestis is a meiotrophic organism, we have developed CryptFind, a systematic approach to identify all candidate cryptic genes responsible for known and theoretical meiotrophic phenomena. In addition to uncovering every known cryptic gene for Y. pestis, our analysis of the rhamnose fermentation pathway suggests that betB is the responsible cryptic gene.

Despite all of our medical advances, we still do not have a vaccine for bubonic plague. Recent discoveries of antibiotic resistant strains of Yersinia pestis coupled with the threat of plague being used as a bioterrorism weapon compel us to develop new tools for studying the physiology of this deadly pathogen. Using our theoretical model, we can study the cells phenotypic behavior under different circumstances and identify metabolic weaknesses that may be harnessed for the development of therapeutics. Additionally, the automatic identification of cryptic genes expands the usage of genomic data for pharmaceutical purposes.”

The full article can be found at: http://www.rsc.org/delivery/_ArticleLinking/DisplayHTMLArticleforfree.cfm?JournalCode=MB&Year=2009&ManuscriptID=b818710j&Iss=Advance_Article

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RESEARCHERS FIND ENZYME UNIQUE TO TULAREMIA ORGANISM
Infection Control Today Magazine
February 3, 2009

“Karl Klose, director of the South Texas Center for Emerging Infectious Diseases (STCEID) at the University of Texas at San Antonio (UTSA), says his lab collaborated with researchers at the Burnham Institute for Medical Research, The University of Texas Southwestern Medical Center at Dallas and Thomas Jefferson University in a study that discovered that Francisella tularensis makes an essential metabolic molecule, nicotinamide adenine dinucleotide (NAD), using a different process and different enzyme from all other living organisms.”

“"There is a 'conventional' way to make NAD, nicotinamide adenine dinucleotide, in all living organisms studied thus far, ranging from bacteria to humans," said Klose, whose lab studies

the genetics behind the virulence of F. tularensis. "Our study uncovered that Francisella makes NAD in a very unique way, using the enzyme nicotinamide mononucleotide synthetase, or NMS. The findings offer us a possible target for the development of therapeutics against tularemia."

The full article can be found at: http://www.infectioncontroltoday.com/hotnews/tularemia-organism-enzyme.html

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COMPACT BIOSENSOR FOR WIDE-RANGING APPLICATIONS
Medical News Today
February 4, 2009

“Scientists at the Naval Research Laboratory (NRL) are partnering with industry to develop a sensor system for biomolecules that could make a significant contribution to a variety of fields such as healthcare, veterinary diagnostics, food safety, environmental testing, and national security. NRL has developed a highly sensitive, portable biosensor system called the compact Bead Array Sensor System (cBASS®). This innovative instrument utilizes a special integrated sensor chip, called the Bead ARray Counter (BARC®), which contains an embedded array of giant magnetoresistive sensors. With 64, 200 µm diameter sensors on the chip, BARC® has the potential to detect 64 different target analytes.”

“Dr. Baselt looked specifically at a type of GMR [giant magnetoresistance] called multilayer GMR in which the resistance of two thin antiferromagnetically exchange-coupled layers, separated by a thin non-magnetic conducting layer, can be altered by changing the moments of the ferromagnetic layers from anti-parallel to parallel. This change decreases the spin-dependent interfacial scattering of charge carriers resulting in a decrease in the resistance of the GMR material. Dr. Baselt realized this very sensitive phenomenon could have potential in the development of sensors for biological materials which are naturally biochemically specific, but are not usually magnetic. By attaching tiny paramagnetic particles to biomolecules, such as proteins or single-stranded DNA, scientists could then perform standard sandwich-type immuno or nucleic acid hybridization assays over the GMR sensors. The GMR sensors, each covered with complementary protein or single-stranded DNA (the "probe"), could then detect the magnetically labeled biomolecules (the "target") the assays were designed to identify.”

The full article can be found at: http://www.medicalnewstoday.com/articles/137819.php

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DETECTION OF NOVEL SARS-LIKE AND OTHER CORONAVIRUSES IN BATS FROM KENYA
By Tong S, Conrardy C, Ruone S, Kuzmin IV, Guo X, Tao Y, et al.
Emerging Infectious Diseases

March 2009

"These data demonstrate that the CoV diversity in bats previously detected in Asia, Europe, and North America is also present, possibly to a greater extent, in Africa. The extent of this diversity among CoVs may be shown more clearly through additional studies in bats, and increased demonstration of CoV diversity in bats may require a reconsideration of how they should be grouped. The frequency and diversity of CoV detections in bats, now in multiple continents, demonstrate that bats are likely an important source for introduction into other species globally. Understanding the extent and diversity of CoV infection in bats provides a foundation for detecting new disease introductions that may, like SARS, present a public health threat."

The full article can be found at: http://www.cdc.gov/eid/content/15/3/pdfs/08-1013.pdf

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Steve Tesko: Steve.Tesko@anser.org

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