APFID
ASIA PACIFIC FOUNDATION FOR INFECTIOUS DISEASES
ANSORP
ASIAN NETWORK FOR SURVEILLANCE OF RESISTANT PATHOGENS

Monthly Newsletter
February 2014

ANSORP *NOW*

CONTENTS :

Dear ANSORP Investigators

Greetings from Seoul !
I hope all ANSORP investigators are doing well.

This is the 2014 February issue of ANSORP NOW. It provides update information and current status of ANSORP activities. "ANSORP NOW" is a monthly newsletter, delivered to all ANSORP investigators by e-mail and website of APFID (www.apfid.org).

Please read this ANSORP NOW carefully to update our international collaboration. If you have any ideas, opinions, or issues that can be shared with other ANSORP investigators, please send us e-mails or FAX.

I always appreciate your active participation in the ANSORP activities.

Jae-Hoon Song, MD, PhD
Organizer, ANSORP
Founder & Chairman, APFID

Report of the APEC Health Working Group meeting in Ningbo, China

The APEC Health Working Group (HWG) meeting was held in Ningbo, China from February 23-24, 2014. Dr. So Hyun Kim, ANSORP Project Manage, attended the HWG meeting to present the completion report of the APEC project entitled ***"Enhancing health security in APEC – International campaign program to control antimicrobial resistance in the Asia-Pacific",*** which was approved by APEC in 2012. We have developed the campaign program named as "Campaign 4" to increase awareness on antimicrobial resistance (AMR) and promote appropriate use of antibiotics for control and prevention of AMR in the Asian region.

Based on the successful completion of the study, we also proposed a new project entitle ***"Enhancing health security in APEC – Implementation of international campaign program to control antimicrobial resistance in the Asia-Pacific"*** to get APEC's support. APEC member economies actively supports the project. The international campaign, "Campaign 4", will be implemented in Asia from this year.

Contact Information

Jae-Hoon Song, MD, PhD
Organizer, ANSORP / Chairman, APFID
Samsung Medical Center
Tel: 82-2-3410-0320, FAX: 82-2-3410-0041
E-mail: ansorp@gmail.com or
songjh@skku.edu

Doo Ryeon Chung, MD, PhD
Coordinator, ANSORP
Samsung Medical Center
Tel: 82-2-3410-0323, FAX: 82-2-3410-0041
E-mail: iddrchung@gmail.com or
drchung@skku.edu

So Hyun Kim, DVM, PhD
Project Manager, ANSORP
Asia Pacific Foundation for Infectious Diseases
Tel: 82-2-3410-6826, FAX: 82-2-3410-6667
E-mail: shkim@ansorp.org or
shkim.ansorp@gmail.com

Interesting papers

Surveillance for antimicrobial drug resistance in under-resourced countries

Emerg Infect Dis. 2014 Mar;20(3):434-41

Vernet G, Mary C, Altmann DM, Doumbo O, Morpeth S, Bhutta ZA, Klugman KP.

ABSTRACT

Antimicrobial drug resistance is usually not monitored in under-resourced countries because they lack surveillance networks, laboratory capacity, and appropriate diagnostics. This accelerating problem accounts for substantial number of excess deaths, especially among infants. Infections particularly affected by antimicrobial drug resistance include tuberculosis, malaria, severe acute respiratory infections, and sepsis caused by gram-negative bacteria. Nonetheless, mapping antimicrobial drug resistance is feasible in under-resourced countries, and lessons can be learned from previous successful efforts. Specimen shipping conditions, data standardization, absence of contamination, and adequate diagnostics must be ensured. As a first step toward solving this problem, we propose that a road map be created at the international level to strengthen antimicrobial resistance surveillance in under-resourced countries. This effort should include a research agenda; a map of existing networks and recommendations to unite them; and a communication plan for national, regional, and international organizations and funding agencies.

Rationale for eliminating Staphylococcus breakpoints for beta-lactam agents other than penicillin, oxacillin or cefoxitin, and ceftaroline

Clin Infect Dis. 2014 Jan 22 [Epub ahead of print]

Dien Bard J, Hindler JA, Gold HS, Limbago B.

ABSTRACT

Due to the ongoing concern about the reliability of Staphylococcus breakpoints (interpretive criteria) for other beta-lactam agents, the Clinical and Laboratory Standards Institute (CLSI) recently approved the elimination of all breakpoints for anti-staphylococcal beta-lactams except for penicillin, oxacillin or cefoxitin, and ceftaroline. Routine testing of penicillin and oxacillin or cefoxitin should be used to infer susceptibility for all beta-lactams with approved clinical indications for staphylococcal infections. It is critical for laboratories to reject requests for susceptibility testing of other beta-lactams against staphylococci and to indicate that susceptibility to these agents can be predicted from the penicillin and oxacillin or cefoxitin results. This article reviews beta-lactam resistance mechanisms in staphylococci, current antimicrobial susceptibility testing and reporting recommendations for beta-lactams and staphylococci, microbiologic data and clinical data supporting the elimination of staphylococcal breakpoints for other beta-lactam agents.

Evolution of methicillin-resistant *Staphylococcus aureus* towards increasing resistance

J Antimicrob Chemother. 2014 Mar;69(3):616-22

Strommenger B, Bartels MD, Kurt K, Layer F, Rohde SM, Boye K, Westh H, Witte W, De Lencastre H, Nübel U.

ABSTRACT

OBJECTIVES : To elucidate the evolutionary history of *Staphylococcus aureus* clonal complex (CC) 8, which encompasses several globally distributed epidemic lineages, including hospital-associated methicillin-resistant *S. aureus* (MRSA) and the highly prevalent community-associated MRSA clone USA300.

METHODS : We reconstructed the phylogeny of *S. aureus* CC8 by mutation discovery at 112 genetic housekeeping loci from each of 174 isolates, sampled on five continents between 1957 and 2008. The distribution of antimicrobial resistance traits and of diverse mobile genetic elements was investigated in relation to the isolates' phylogeny.

RESULTS : Our analyses revealed the existence of nine phylogenetic clades within CC8. We identified at least eight independent events of methicillin resistance acquisition in CC8 and dated the origin of a methicillin-resistant progenitor of the notorious USA300 clone to the mid-1970s. Of the *S. aureus* isolates in our collection, 88% carried plasmidic rep gene sequences, with up to five different rep genes in individual isolates and a total of eight rep families. Mapping the plasmid content onto the isolates' phylogeny illustrated the stable carriage over decades of some plasmids and the more volatile nature of others. Strikingly, we observed trends of increasing antibiotic resistance during the evolution of several lineages, including USA300.

CONCLUSIONS We propose a model for the evolution of *S. aureus* CC8, involving a split into at least nine phylogenetic lineages and a subsequent series of acquisitions and losses of mobile genetic elements that carry diverse virulence and antimicrobial resistance traits. The evolution of MRSA USA300 towards resistance to additional antibiotic classes is of major concern.

If you need PDF version of the papers, please contact ANSORP Project Manager (Dr. So Hyun Kim, shkim@ansorp.org).

We always appreciate your active contribution to ANSORP activities.
If you have any questions, or issues that can be shared with other ANSORP investigators, please let us know them at any time.