

# ANSORP NOW

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## Dear ANSORP Investigators

Greetings from Seoul !

I hope all ANSORP investigators are doing well and wish you and your family the New Year filled with joy and happiness.



This is the **2013 March 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](http://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

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## ISAAR 2013

March 13-15, 2013  
Kuala Lumpur Convention Centre  
Kuala Lumpur, Malaysia



## Thank you for your participation & contribution!

On behalf of the Organizing Committee of the 9th International Symposium on Antimicrobial Agents and Resistance (ISAAR 2013), we would like to extend our deepest gratitude and sincere appreciation for your valuable contribution and support to ISAAR 2013 in conjunction with APEC symposium held in Kuala Lumpur, Malaysia, March 13-15, 2013.

It was our great honor to host such a prestigious congress. We are very proud that ISAAR 2013 had been able to provide valuable academic discussions as well as to develop mutual friendship and professional network among the participants.

Thank you again for your leadership and sincere support !



## Minutes of 9th Investigator Meeting of ANSORP

It was our great pleasure to have ANSORP principal investigators in KL, Malaysia for the 9th Investigator Meeting of ANSORP.

ANSORP, which is the Asia's first multinational collaborative study group for research on infectious diseases and antimicrobial resistance, has been carrying out multinational surveillance studies and related international activities since 1996. Thanks to your continuing contribution and strong leadership, ANSORP has been successfully growing and has completed many international projects on infectious diseases and antimicrobial resistance.

In addition to these international surveillance studies and research activities, ANSORP will do more active role in control and prevention of antimicrobial resistance in the Asian region. In collaboration with APEC, Asia Pacific Foundation for Infectious Diseases (APFID) will launch a new international campaign for control of antimicrobial resistance in the Asian region from this year. ANSORP will obviously be a major infrastructure to implement this international campaign in Asia. We are quite sure that these projects will be of great help to all countries in the Asian region to control and prevent antimicrobial resistance in the future. We hope that all ANSORP investigators can actively join these projects. In addition, ANSORP will have an opportunity to work with WHO and WPRO for control and prevention of antimicrobial resistance.

We always appreciate your leadership and sincere support that has made this group alive and successful. We are quite sure that our friendship and collaboration will be stronger and more productive in the future and will contribute to improve the public health in the region.



ANSORP will perform the following three projects from 2013, including studies proposed by ANSORP investigators, which shows diversity of ANSORP studies and suggests future model of ANSORP studies.

- A prospective, hospital-based, multicenter surveillance on antimicrobial resistance and serotypes of *Streptococcus pneumoniae* in hospitalized patients over 50 years with invasive pneumococcal diseases or pneumonia in Asia (PI : Jae-Hoon Song, Korea ; sponsored by Pfizer)
- A multicenter, multinational serosurvey study for pertussis among children 10-18 years old in Asia (PI : Cheng-Hsun Chiu, Taiwan & Yae-Jean Kim, Korea ; sponsored by Sanofi-Pasteur)
- Capacity assessment of antimicrobial stewardship in the Asia Pacific (PI : David Lye & Li Yang Hsu, Singapore ; possibly sponsored by APFID)

Additionally, other possible future ANSORP studies such as surveillance studies on Gram negatives, *Clostridium difficile* infections, antimicrobial resistance of *Mycoplasma pneumoniae*, community-acquired methicillin-resistant *Staphylococcus aureus* (CA-MRSA), correlation between antibiotic prescription and resistance, etc., have been discussed at the ANSORP meeting.

APFID will launch a new international campaign, **Campaign 4** (tentative) for control of antimicrobial resistance in the Asian region by increasing awareness of antimicrobial resistance and preventing abuse or misuse of antibiotics in the region.

When **Campaign 4** is implemented in Asian countries, professional society and government of each Asian country will be the host of this campaign program in collaboration with APFID and international organizations such as APEC and possibly WPRO.

We will provide more details about this international campaign program and ask for ANSORP investigators' opinion.



## Interesting papers

### Investigation of antibiotic resistance in the genomic era of multidrug-resistant Gram-negative bacilli, especially *Enterobacteriaceae*, *Pseudomonas* and *Acinetobacter*

*Expert Rev Anti Infect Ther.* 2013 Mar;11(3):277-296

Diene SM, Rolain JM

#### **ABSTRACT**

The increase and spread of multidrug-resistant (MDR) Gram-negative bacteria, including *Enterobacteriaceae*, *Pseudomonas* and *Acinetobacter* species, have become major concerns worldwide. Although the frequent misuse of antibiotic drugs has greatly contributed to worldwide antibiotic resistance by causing a large dispersal of resistance determinants, recent studies demonstrate that these resistance determinants could have emerged from ancient or environmental sources. Moreover, during the last 10 years, we have been witnessing the emergence and development of technologies for high-throughput sequencing, coinciding with an exponential increase in the number of bacterial genomes sequenced. These sequencing technologies allow a complete study of MDR bacterial genomes and are the best way to investigate the genetic determinants of antimicrobial resistance. Accordingly, studies using genome sequencing to decipher resistance determinants in *Enterobacteriaceae*, *Pseudomonas* and *Acinetobacter* species have demonstrated several advantages including, among others: an exhaustive identification of resistance determinants from any clinical, epidemiological or environmental MDR bacterium; identification of the acquisition mechanisms for resistance determinants exchanged between bacterial species through mobile genetic elements and elucidation and understanding, in record time (less than 1 week), of some critical or epidemic events caused by particular pathogenic bacteria. Therefore, it is clear today that the bacterial genome sequencing approach has revolutionized all fields of scientific research and represents a powerful tool to explore the world of microorganisms.

### The role of the natural environment in the emergence of antibiotic resistance in gram-negative bacteria

*Lancet Infect Dis.* 2013 Feb;13(2):155-165

Wellington EM, Boxall AB, Cross P, Feil EJ, Gaze WH, Hawkey PM, Johnson-Rollings AS, Jones DL, Lee NM, Otten W, Thomas CM, Williams AP

#### **ABSTRACT**

During the past 10 years, multidrug-resistant Gram-negative *Enterobacteriaceae* have become a substantial challenge to infection control. It has been suggested by clinicians that the effectiveness of antibiotics is in such rapid decline that, depending on the pathogen concerned, their future utility can be measured in decades or even years. Unless the rise in antibiotic resistance can be reversed, we can expect to see a substantial rise in incurable infection and fatality in both developed and developing regions. Antibiotic resistance develops through complex interactions, with resistance arising by de-novo mutation under clinical antibiotic selection or frequently by acquisition of mobile genes that have evolved over time in bacteria in the environment. The reservoir of resistance genes in the environment is due to a mix of naturally occurring resistance and those present in animal and human waste and the selective effects of pollutants, which can co-select for mobile genetic elements carrying multiple resistant genes. Less attention has been given to how anthropogenic activity might be causing evolution of antibiotic resistance in the environment. Although the economics of the pharmaceutical industry continue to restrict investment in novel biomedical responses, action must be taken to avoid the conjunction of factors that promote evolution and spread of antibiotic resistance.

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