Monthly Newsletter
January 2014

ANSORP *NOW*

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Dear ANSORP Investigators

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

This is the 2014 January 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

Current status 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)
  - The study has been started since Dec 2013 (Nov 2012 in Korea) and is supposed to be completed by Nov 2015.
  - Seven countries (Korea, China, Indonesia, Malaysia, Philippines, Singapore, and Thailand) are participating in the study.
- A multicenter, multinational serosurvey study for pertussis among children 10-18 years old in Asia
  (PIs : Cheng-Hsun Chiu, Taiwan & Yae-Jean Kim, Korea ;
  sponsored by Sanofi-Pasteur)
  - The study has been started since Oct 2013 and is supposed to be competed by Sep 2015.
  - Ten centers in seven countries (Korea, China, Japan, Taiwan, Thailand, Sri Lanka, and India) are participating in the study.
- Capacity assessment of antimicrobial stewardship in the Asia Pacific
  (PI : David Lye & Li Yang Hsu, Singapore ; sponsored by APFID)
  - Online questionnaire survey on antimicrobial stewardship in hospitals in Asian countries (including both ANSORP centers and non-ANSORP centers) will be performed soon.

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Publication of ANSORP in December 2013

Risk factors for levofloxacin-nonsusceptible *Streptococcus pneumoniae* in community-acquired pneumococcal pneumonia: a nested case-control study.

Eur J Clin Microbiol Infect Dis. 2014 Jan;33(1):55-9

Kang CI, Song JH, Kim SH, Chung DR, Peck KR, So TM, Hsueh PR; ANSORP Study Group

ABSTRACT

This study was performed to evaluate the clinical features of community-onset levofloxacin-nonsusceptible pneumococcal pneumonia and to identify risk factors for levofloxacin resistance. Using the database of a surveillance study of community-acquired pneumococcal infections in Asian countries, we conducted a nested case-control study to identify risk factors for levofloxacin-nonsusceptible *S. pneumoniae* in community-acquired pneumonia in adults. Of 981 patients with pneumococcal pneumonia, 46 (4.7 %) had levofloxacin-nonsusceptible *S. pneumoniae*, of whom 39 evaluable cases were included in the analysis. All cases were from Korea, Taiwan, and Hong Kong. Among patients with levofloxacin-susceptible *S. pneumoniae*, 490 controls were selected based on patient country.

Of the 39 cases of levofloxacin-nonsusceptible pneumococcal pneumonia, 23 (59.0 %) were classified as healthcare-associated, while 164 (33.5 %) of the 490 controls of levofloxacin-susceptible *S. pneumoniae* (P = 0.001) were classified as healthcare-associated. Multivariate analysis showed that previous treatment with fluoroquinolones, cerebrovascular disease, and healthcare-associated infection were significantly associated with levofloxacin-nonsusceptible pneumococcal pneumonia (all P < 0.05). Levofloxacin-nonsusceptible pneumococci pose an important new public health threat in our region, and more information on the emergence and spread of these resistant strains will be necessary to prevent spread throughout the population.

Interesting papers

In vivo evolution of antimicrobial resistance in a series of *Staphylococcus aureus* patient isolates: the entire picture or a cautionary tale?

J Antimicrob Chemother. 2014 Feb;69(2):363-7

van Hal SJ, Steen JA, Espedido BA, Grimmond SM, Cooper MA, Holden MT, Bentley SD, Gosbell IB, Jensen SO.

ABSTRACT

OBJECTIVES: To obtain an expanded understanding of antibiotic resistance evolution in vivo, particularly in the context of vancomycin exposure.

METHODS: The whole genomes of six consecutive methicillin-resistant Staphylococcus aureus blood culture isolates (ST239-MRSA-III) from a single patient exposed to various antimicrobials (over a 77 day period) were sequenced and analysed.

RESULTS: Variant analysis revealed the existence of non-susceptible sub-populations derived from a common susceptible ancestor, with the predominant circulating clone(s) selected for by type and duration of antimicrobial exposure.

CONCLUSIONS: This study highlights the dynamic nature of bacterial evolution and that non-susceptible sub-populations can emerge from clouds of variation upon antimicrobial exposure. Diagnostically, this has direct implications for sample selection when using whole-genome sequencing as a tool to guide clinical therapy. In the context of bacteraemia, deep sequencing of bacterial DNA directly from patient blood samples would avoid culture 'bias' and identify mutations associated with circulating non-susceptible sub-populations, some of which may confer cross-resistance to alternate therapies.

Methicillin-resistant *Staphylococcus aureus*: An evolving pathogen

Clin Infect Dis. 2014 Jan;58 Suppl 1:S10-9

Stryjewski ME, Corey GR.

ABSTRACT

The horizontal transmission of methicillin resistance to *Staphylococcus aureus* (MRSA) in hospital and community settings, and growing prevalence of these strains, presents a significant clinical challenge to the management of serious infections worldwide. While infection control initiatives have stemmed the rising prevalence, MRSA remains a significant pathogen. More recently, evidence that MRSA is becoming resistant to glycopeptides and newer therapies raises concern about the use of these therapies in clinical practice. Vancomycin resistance has become evident in select clinical settings through rising MICs, growing awareness of heteroresistance, and emergence of intermediate-resistant and fully resistant strains. While resistance to linezolid and daptomycin remains low overall, point mutations leading to resistance have been described for linezolid, and horizontal transmission of cfr-mediated resistance to linezolid has been reported in clinical isolates. These resistance trends for newer therapies highlight the ongoing need for new and more potent antimicrobial therapies.

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.