



ANSORP NOW

CONTENTS:

- 1. Current status of ANSORP studies
- 2. Publication of APFID in June 2014
- 3. Interesting papers

Dear ANSORP Investigators

Greetings from Seoul!

I hope all ANSORP investigators are doing well.

This is the 2014 June 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.

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Current status of ANSORP studies

 A prospective, hospital-based, multicenter surveillance on antimicrobial resistance and serotypes of *S. 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. Only some centers in Korea and Thailand have started case enrollment while invitation of centers which are willing to join the study and IRB approval process in some centers are in progress in the other countries.

• 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/areas (Korea, China, Japan, Taiwan, Thailand, Sri Lanka, and India) are participating in the study. Investigators have enrolled about 70 cases (37% of target enrollment) so far and plan to complete case enrollment by the end of this year. The interim report will be presented at the ANSORP meeting which will be held in May 2015 in Korea.

• 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 (ASP) in hospitals in Asian countries has been conducting from May. The results of the survey may provide valuable information about ASP in the Asian region.

Publication of APFID in June 2014

Prevalence of isolates of *Streptococcus pneumoniae* putative serotype 6E in South Korea

J Clin Microbiol. 2014 Jun;52(6):2096-9

Baek JY, Park IH, Song JH, Ko KS

ABSTRACT

The prevalence of serogroup 6 among 1,206 *Streptococcus pneumoniae* clinical isolates collected from Korean hospitals over three periods (1996 to 2001, 2004 to 2006, and 2008 to 2009) was investigated.

Interesting papers

Evidence for soft selective sweeps in the evolution of pneumococcal multidrug-resistance and vaccine escape

Genome Biol Evol. 2014 Jun 10. [Epub ahead of print]

Croucher NJ, Chewapreecha C, Hanage WP, Harris SR, McGee L, van der Linden M, Song JH, Ko KS, de Lencastre H, Turner C, Yang F, Sá-Leão R, Beall B, Klugman KP, Parkhill J, Turner P, Bentley SD.

ABSTRACT

The multidrug-resistant Streptococcus pneumoniae Taiwan19F-14, or PMEN14, clone was first observed with a 19F serotype, which is targeted by the heptavalent polysaccharide conjugate vaccine (PCV7). However, 'vaccine escape' PMEN14 isolates with a 19A serotype became an increasingly important cause of disease post-PCV7. Whole genome sequencing was used to characterise the recent evolution 173 pneumococci of, or related to, PMEN14. This suggested PMEN14 is a single lineage that originated in the late 1980s in parallel with the acquisition of multiple resistances by close relatives. One of the four detected serotype switches to 19A generated representatives of the sequence type (ST) 320 isolates that have been highly successful post-PCV7. A second produced an ST236 19A genotype with reduced resistance to β-lactams owing to alteration of pbp1a and pbp2x sequences through the same recombination that caused the change in serotype. A third, which generated a mosaic capsule biosynthesis locus, resulted in serotype 19A ST271 isolates. The rapid diversification through homologous recombination seen in the global collection was similarly observed in the absence of vaccination in isolates from the Maela refugee camp in Thailand. This sample also allowed variation to be observed within carriage through longitudinal sampling. This suggests some pneumococcal genotypes generate a pool of standing variation that is sufficiently extensive to result in 'soft' selective sweeps: the emergence of multiple related mutants in parallel upon a change in selection pressure, such as vaccine introduction. The subsequent competition between these mutants makes this phenomenon difficult to detect without deep sampling of individual lineages.

The number of serogroup 6 isolates increased from 9.7 to 17.5% over the three periods. While the proportion of serotype 6A and 6D isolates increased significantly, that of serotype 6B isolates decreased. Twenty-four isolates (2.0%) were typed as the recently identified putative serotype 6E or genetic variants of serotype 6B. The results suggest that the lack of change in frequency of serotype 6B, in spite of the introduction of the PCV7 vaccine as seen in previous studies in South Korea, might be due mainly to the improper inclusion of putative serotype 6E in serotype 6B. All but three serotype 6E isolates belonged to CC90, indicating their clonal expansion.

New epidemiology of S. aureus infection in Asia

Clin Microbiol Infect. 2014 Jun 2. [Epub ahead of print]

Chen CJ, Huang YC.

ABSTRACT

Asia was not only the most populous region in the world but inappropriate therapy, including self-medication with overthe-counter antimicrobial agents, was also a common behavior against infectious diseases. The high antibiotic selective pressure in the overcrowded inhabitants created an environment suitable for the rapid development and efficient spreading of numerous multidrug-resistant pathogens. Indeed, Asia was among the regions with the highest prevalence of healthcare-associated (HA)-methicillin-resistant Staphylococcus aureus (MRSA) and community-associated (CA)-MRSA in the world. Most of the hospitals in Asia were endemic for multidrug-resistant MRSA, with a ratio estimated from 28% (in Hong Kong and Indonesia) to >70% (in Korea) among all clinical S. aureus isolates in early 2010s. The strains with reduced susceptibility or highly resistant to glycopeptides were also increasingly identified in the past few years. In contrast, the rate of MRSA among CA S. aureus infection in Asian countries varied markedly, from <5% to >35%. Two pandemic HA-MRSA clones, namely multilocus sequence type (ST) 239 and ST5, were disseminated internationally in Asia, while the molecular epidemiology of CA-MRSA in Asia was characterized by clonal heterogeneity, similar to that in Europe. In this review, the epidemiology of S. aureus in both the healthcare facilities and communities in Asia are addressed, with emphasis on the prevalence, clonal structure and antibiotic resistant profiles of the MRSA strains. The novel MRSA strains from livestock animals have been considered a public health threat in western countries. The emerging livestock-associated MRSA in Asia are also included in this review.

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