

Final Abstract Number: 46.008  
 Session: Emerging Infectious Diseases  
 Date: Friday, June 15, 2012  
 Time: 12:45-14:15  
 Room: Poster & Exhibition Area

### Superantigens gene profile and *emm* typing of *Streptococcus pyogenes* at a tertiary care hospital of north India

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**Background:** The incidence and severity of invasive group A streptococcal infection demonstrate great variability over time, which at least, in part, seems to be related to group A streptococcal type distribution among the human population. Further, emerging resistance to major antibiotics is of great concern. In view of this, we conducted a Superantigens gene profile and *emm* typing of GAS infections at a tertiary care hospital of north India.

**Methods:** Molecular epidemiological study of Group A Streptococcus (GAS) was done at a tertiary care hospital of north India from Jan 2009 – Jan 2012. The confirmation of identity was done by the Vitek 2 identification cards and group A antigen detection by kit based agglutination. Antibiotic sensitivity was done for 10 selected antibiotics and the MIC was compared by CLSI guidelines. Detection of 11 Superantigen genes and 1 resistance gene was done by PCR. Further typing of *emm* type was done by conventional sequencing method.

**Results:** A total of 180 strains of streptococcus were collected and 135 were identified as GAS. None of the isolates were resistance to Penicillin, ampicillin, vancomycin, linezolid and ceftriaxone. A total of 69% and 38% isolates were resistant to tetracycline and erythromycin respectively. However, a lower resistance pattern of 6%, 3% and 2% were seen in ciprofloxacin, levofloxacin, and clindamycin respectively. Out of 11 superantigens gene; *Spe B, Z, F, G* was present in between 92–86%; the prevalence of *Spe C, M, h, J* ranged between 22–27% and very low prevalence were observed for *Spe A, I* and *Ssa* gene. Further *erm B* gene were positive for 40% in GAS isolates. *Emm* type101 was most prevalent in GAS isolates followed by *emm 110* and *emm 92*.

**Conclusion:** The study shows the isolation rate of GAS was 75%, with high exotoxins and resistance genes which may result in more resistant and virulent strains. GAS vaccine coverage and control of GAS infections will need to take these factors and strain differences into consideration.

<http://dx.doi.org/10.1016/j.ijid.2012.05.880>

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### Detection of new flavivirus from *Aedes* mosquito in South Korea, 2011

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**Background:** As an early warning system for Japanese encephalitis (JE) a nation-wide surveillance program, JE Epidemic Forecast Program (JE-EFP), has been implemented since 1976 in Korea. The program consists of monitoring vector abundance, virus detection from mosquitoes, and pig surveillance as well as laboratory diagnosis. While JE has been well controlled with very low incidence, surveillance of other introducible flaviviruses was implemented in 2011.

**Methods:** Mosquitoes were caught on a weekly basis by the staff of National Quarantine Station (NQS, Busan, Gunsan, Masan, Incheon airport, and Jeju) in 17 sites, of which 12 sites were located near the harbor and 5 ones were at the international airport. Pooled mosquitoes (up to 50 mosquitoes in a pool) were subjected to the real-time RT-PCR optimized for detecting JE virus (JEV), dengue virus (DENV), West Nile virus (WNV), and yellow fever virus (YFV) in a single reaction.

**Results:** Only mosquito species known as vector of JEV, DENV, and WNV were tested by real-time RT-PCR and virus isolation. About 90,000 mosquitoes were collected during the surveillance in 2011. Overall, *Cx.tritaeniorhynchus* was the most abundant species (81.4%) followed by *Cx.pipiens* (13.7%), *Aedes vexans* (4.7%), and *Aedes albopictus* (0.2%). Thirteen mosquito pools were positive for RT-PCR and sequencing analysis revealed two JEV (genotype 1), one Chaoyang virus (first reported in China in 2008), and 10 new flaviviruses which have not been reported previously. The unidentified flaviviruses were detected in *Ae. albopictus* from May to Sep in Jeju, Masan, and Tonyoung provinces. No virus was isolated from cell culture using C6/36 and BHK-21 cell lines.

**Conclusion:** We detected three kinds of district mosquito-borne flaviviruses which was not previously reported in Korea. Little is known about these viruses such as distribution range, natural cycle and possibility of human infection. So, continuous surveillance covering whole country range need to be implemented, which will help health authority do adequate risk assessment and prepare effective control measures.

<http://dx.doi.org/10.1016/j.ijid.2012.05.881>