

Conclusion. MRSA colonization is associated with increased risk of NH transfer following hospital admission. Additionally, acquisition of MRSA seems to result in a slightly elevated risk of NH transfer compared with those who are colonized at the time of hospital admission.

Disclosures. All authors: No reported disclosures.

2182. Molecular Epidemiology of Community-Associated and Hospital-associated Methicillin-resistant *Staphylococcus aureus* in a Japanese University Hospital

Naokatsu Fukukawa, RN, MMS^{1,2}; Yuki Uehara, MD, PhD^{1,3}; Takashi Sasaki, DVM, PhD^{1,4}; Masayoshi Chonan, MT⁵; Ayako Nakamura, PhD⁵; Shigeki Misawa, PhD⁵; Naomi Komatsuzaki, RN, CICN⁶; Satoshi Hori, MD, PhD^{1,6}; Akimichi Ohsaka, MD, PhD^{5,7} and Keiichi Hiramatsu, MD, PhD^{1,1}.¹Department of Infection Control Science, Juntendo University Graduate School of Medicine, Tokyo, Japan,²Department of Nursing, Kyorin University Hospital, Tokyo, Japan, ³Department of General Medicine, Juntendo University Faculty of Medicine, Tokyo, Japan, ⁴Animal Research Center, Sapporo Medical University School of Medicine, Sapporo, Japan, ⁵Department of Clinical Laboratory, Juntendo University Hospital, Tokyo, Japan, ⁶Infection Control Office, Juntendo University Hospital, Tokyo, Japan, ⁷Department of Transfusion Medicine and Stem Cell Regulation, Juntendo University Faculty of Medicine, Tokyo, Japan

Session: 242. HAI: MRSA, MSSA, and Other Gram-positives

Saturday, October 7, 2017: 12:30 PM

Background. Community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) has been reported in healthcare facilities worldwide. But details of CA-MRSA in Japanese healthcare facilities are rarely reported. The aims of this study are to know the distribution of CA-MRSA and healthcare-associated MRSA (HA-MRSA) with detailed molecular typing, and to assess the efficacy of infection control practice in a Japanese hospital.

Methods. From July to October in 2015, first MRSA isolate from each patient was collected in Juntendo University Hospital, Tokyo, Japan. MRSA strains were categorized as CA-MRSA and HA-MRSA according to the clinical definition of CDC. Detection of toxin genes and SCCmec typing were performed by PCR. Genetic relatedness among isolates was determined by pulsed-field gel electrophoresis (PFGE). Multilocus sequence typing was performed using whole genome sequencing data.

Results. A total of 102 MRSA strains were collected in the study period, and categorized as 34 CA-MRSA (33.3 %) and 68 HA-MRSA (66.7 %), respectively. Among the 73 strains isolated from hospitalized patients, 10 were CA-MRSA (13.7 %). Whereas among the 29 strains isolated in clinic, 5 were HA-MRSA (17.2 %). Three major types were as follows: ST8-SCCmec IV ($n = 26$, 25.5 %; CA: HA= 10: 16), ST5-SCCmec IIa ($n = 17$, 16.7 %, CA: HA= 5: 12), and ST1-SCCmec IVa ($n = 13$, 12.7 %, CA: HA= 6: 7). Among ST8-SCCmec IV strains, SCCmec IVI, originally reported in Japanese CA-MRSA, was found both in CA-MRSA and HA-MRSA ($n = 11$, 10.8 %, CA: HA= 5: 6). Only one ST772-SCCmec V strain carried Panton-Valentine leukocidin (PVL) gene. Two ST765-SCCmec IIa strains in CCU, 2 ST765-SCCmec IIa strains in general ward, and 6 ST2764-SCCmec IVa strains in NICU showed genetic relatedness by PFGE, respectively. Especially, ST2764-SCCmec IVa was a clone originally reported as HA-MRSA in another Juntendo-affiliated hospital.

Conclusion. CA-MRSA and HA-MRSA were comparably found both in hospital and clinic. Unique Japanese clones were found in this study, but it seemed impossible to distinguish CA-MRSA and HA-MRSA simply by ST-SCCmec typing. In contrast, transmission of MRSA rarely happened in hospital. This heterogenous population structure of MRSA suggested that conventional HA-MRSA had lost its predominance by sufficient infection control, resulting in relative increase of CA-MRSA in hospital environment.

Disclosures. All authors: No reported disclosures.

2183. Post-intervention Survey on Scaling Back Contact Precautions for MRSA and VRE

Kay Negishi, MD¹; Carolyn Fisher, PhD² and Lou Ann Bruno-Murtha, DO³; ¹Internal Medicine, Cambridge Health Alliance, Cambridge, Massachusetts, ²Institute for Community Health, Malden, Massachusetts, ³Cambridge Health Alliance, Cambridge, Massachusetts

Session: 242. HAI: MRSA, MSSA, and Other Gram-positives

Saturday, October 7, 2017: 12:30 PM

Background. In December 2014, Cambridge Health Alliance (CHA) discontinued contact precautions (CPs) for methicillin-resistant *Staphylococcus aureus* (MRSA) and vancomycin-resistant Enterococci (VRE) based on lack of evidence showing that CPs decrease the rate of transmission of these organisms in endemic settings. There is evidence that patient isolation may cause harm. We surveyed staff's beliefs, comfort, knowledge, and practices surrounding hand hygiene, standard precautions (SPs), and CPs. The goal was to shed light on knowledge gaps, misconceptions, or practice inconsistencies.

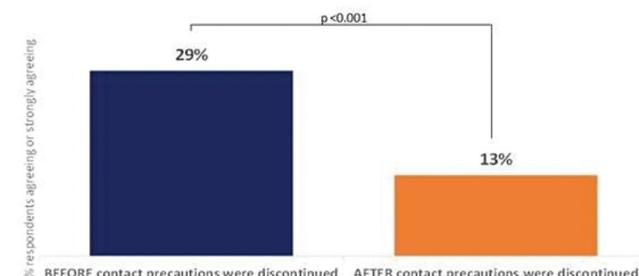
Methods. A ten-minute, 38-question English anonymous online survey was designed, piloted in three successive iterations, and deployed in February 2017 to staff who perform clinical work in two inpatient and three emergency departments at a safety-net organization. Four email reminders were sent. 100 respondents were randomly selected to receive a \$10 cafeteria gift card. Data were obtained and analyzed via Google tools.

Results. Among 1804 providers, 202 (11%) completed the survey. 90% of respondents recognize unclean hands are the main route of cross-transmission. Most (54%) incorrectly believe VRE requires CPs, and over a third (38%) for MRSA. Half are comfortable caring for MRSA/VRE patients without CPs. While 29% reported previously spending less time with isolated MRSA/ VRE patients than non-isolated patients, significantly fewer are spending less time with these patients since the change (13%, $P < 0.001$; see graph). 43% agree that their job efficiency has improved.

Conclusion. Staff understand the importance of hand hygiene in preventing cross-transmission. Misconceptions over CP and SP persist, indicating a need for further education. The majority of respondents are pleased with the change. Staff are spending more time with patients who were previously isolated. There are varying beliefs across professional roles, which are also reflected in the Beth Israel Deaconess Medical Center's (BIDMC) survey conducted within a year of their intervention. More CHA trainees agree that CP prevent cross-transmission than BIDMC trainees, although two-thirds of them were not at CHA during the change implementation, suggesting the need for reinforcing rationale for new hires.

"Due to the time required to don gowns and gloves, I visit(ed) patients with MRSA and/ or VRE less frequently than I would (have) otherwise"

(n=187)



Disclosures. All authors: No reported disclosures.

2184. Systemic Analysis of the *mecA* Gene Using a Bioinformatics Tool

Shin-Yi Tsai, MD^{1,2,3}; Fu-Chieh Chang, MT⁴; Kevin Sheng-Kai Ma, MD¹; Cheng-Wei Hsu, MD¹; Po-Ya Tung, MD^{1,3}; Yan-Jiun Hung, MD^{1,3}; Yi-Ting Chou, MT¹ and Chien-Feng Kuo, MD⁵. ¹Department of Laboratory Medicine, Mackay Memorial Hospital, Taipei, Taiwan, ²Johns Hopkins University, Baltimore, MD, ³Department of Medicine, Mackay Medical College, New Taipei City, Taiwan, ⁴Infection control center, Mackay Memorial Hospital, Taipei, Taiwan, ⁵Department of Infectious Disease, Mackay Memorial Hospital, Taipei, Taiwan

Session: 242. HAI: MRSA, MSSA, and Other Gram-positives

Saturday, October 7, 2017: 12:30 PM

Background. The *mecA* gene, carried by methicillin-resistant *Staphylococcus aureus* (MRSA), allows the bacterium to promote bacterial resistance to antibiotics such as methicillin, penicillin, and other penicillin-like antibiotics. Our objectives are to use a bioinformatics tool to analyze the sequence of the *mecA* gene, which is spread on the SCCmec genetic element, and to investigate the relationship between each *mecA* gene.

Methods. From 2008 to 2016, we collected 229 MRSA from bacteremia; we extracted DNA from the MRSA and designed specific primers to target *mecA* using PCR. The primer used are listed in *mec A-1*(5'-GGGATCATAGCGTCATTATT-3') and *mec A-2*(5'-AACGATTGTGACAGATAGCC-3'). We determined whether the *mecA* gene was present by using electrophoresis and then sequenced the MRSA samples in which it was present. The POWER tool was employed to analyze the *mecA* gene and compile a pedigree chart.

Results. Using the sequencing data, we created an MRSA database, and the BLAST findings demonstrated that most of the *mecA* genes were similar, with over 95% identified. The pedigree chart illustrates that there are four groups of *mecA* genes, and these groups were found to be not differentiated between the sources of the MRSA, whether from communities or hospital association infections.

Conclusion. Our findings indicate that even though there were four groups with ancestors in the pedigree chart, no significant difference was found between MRSA from community- and hospital-associated infections. We plan to collect more MRSA samples for analysis and investigate the differences between MRSA groups and MRSA from various geographical regions.

Disclosures. All authors: No reported disclosures.

2185. Impact of Antibiotic Treatment on the Burden of Nasal *Staphylococcus aureus* (SA) Among Hospitalized Veterans

Anubhav Kanwar, MD¹; Jennifer L. Cadnum, BS²; Annette Jencson, BS, MT, CIC³; Christina Piedrahita, BS⁴ and Curtis Donskey, MD⁵; ¹Medicine, Division of Infectious Diseases and HIV Medicine, Case Western Reserve University School of Medicine/UH Cleveland Medical Center, Cleveland, Ohio, ²Geriatric Research Education and Clinical Center, Louis Stokes Cleveland VA Medical Center, Cleveland, Ohio, ³Research Service, Cleveland VA Medical Center, Cleveland, Ohio,