

horizontal measures and a change of the environmental disinfectant from a quaternary ammonium compound to a peroxide-based product; we wanted to understand whether patient-to-patient spread was occurring or the environment was the major contributor. **Methods:** We submitted all the 15 isolates from clinical samples for WGS and phylogenetic analysis; along with operation theater (OT) and ICU environment random swabs for metagenomic analysis. DNA sample QC DNA extraction was done using a Qiagen QiAmp DNA mini kit (cat. no. 51306). The DNA samples were subjected to QIAXPERT and Qubit for quantifying the amount of DNA in the extracted sample. Also, the 260/280-nm ratio was examined for the purity of the same. They were also subjected for agarose gel electrophoresis. For the DNA library prep protocol, whole-genome libraries were prepared from 21 samples using NEBNext Ultra IITM DNA Library Prep Kit (Cat. No: E7645L). The adapter sequences were added to the ends of DNA fragments to generate paired-end libraries. The resulting adaptor-ligated libraries were purified and index tags were added by amplification, followed by purification. Libraries were assessed to check the quality and quantity using Agilent 2200 Tape station (cat. no. 3-PM 863NA). For the sequencing protocol, prepared libraries were quantified using Qubit High Sensitivity reagent. The obtained libraries were diluted to final concentration of 2 nm in 10  $\mu$ L and were subjected to cluster amplification. Once the cluster generation was completed, the flow cells were loaded on to the sequencer. Sequencing was carried out in Hi Seq X10 to generate 2X150-bp sequence reads at >100X sequencing depth (~1.5 Gb). A minimum of 75% of the sequenced bases were of Q30 value. Sequenced data were processed to generate FASTQ files and were uploaded on the FTP server for download and secondary data analysis. **Results:** Overall, 2% of the DNA from the OT and SICU environment showed *Candida auris*. The phylogenetic analysis confirmed 2 different clusters. Furthermore, 13 of the clinical isolates belonged to the same cluster, confirming that patient-to-patient transmission had occurred, which was subsequently confirmed by line listing the patients. **Conclusions:** *Candida auris* can efficiently spread from patient to patient, resulting in outbreaks. It can also persist in the healthcare environment causing ongoing propagation of these outbreaks.

**Funding:** None

**Disclosures:** None

Doi:10.1017/ice.2020.965

#### Presentation Type:

Poster Presentation

#### Pilot Point-Prevalence Survey for Healthcare-Associated Infections in Long-Term Care Hospitals, South Korea, 2018

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**Background:** Recently, healthcare-associated infections (HAIs) in long-term care hospitals (LTCHs) have markedly increased, but no infection control policy has been established in South Korea. We investigated the current HAI surveillance system and executed a point-prevalence pilot study in LTCHs. **Methods:** HAIs were defined by newly established surveillance manual based on McGeer criteria revised in 2012. Three LTCHs in Seoul and

Gyeonggi province were voluntarily recruited, and data were collected from up to 50 patients who were hospitalized on August 1. The medical records from September to November 2018 were retrospectively reviewed by a charge nurse for infection control per each hospitals after 1 day of training specific for LTCH surveillance. All data were reviewed by a senior researcher visiting onsite. **Results:** The participating hospitals had  $272.33 \pm 111.01$  beds. Only 1 hospital had an onsite microbiological laboratory. In total, 156 patients were enrolled and 5 HAIs were detected, for a prevalence rate of 3.2%. The average patient age was  $79.04 \pm 9.92$  years. The HAIs included 2 urinary tract infections, skin and soft-tissue infection, low respiratory infection, and conjunctivitis. **Conclusions:** This is the first survey of HAI in LTCHs in South Korea. The 3.2% prevalence rate is lower than those from previous reports from the European Union or the United States. This study supports the development of a national HAI surveillance and infection control system in LTCHs, although implementation may be limited due to the lack of laboratory support and infection control infrastructure in Korea.

**Funding:** None

**Disclosures:** None

Doi:10.1017/ice.2020.966

#### Presentation Type:

Poster Presentation

#### Pilot Survey for National Point Prevalence Study of Healthcare-Associated Infections in Acute-Care Hospitals in South Korea

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**Background:** The Korean National Healthcare-Associated Infections Surveillance System (KONIS) was established to conduct nationwide surveillance of device-associated healthcare-associated infections (HAIs) and surgical site infections annually in 2006. However, no surveillance on overall HAIs has been conducted. **Objective:** We conducted a point-prevalence survey of total HAIs to estimate the incidence rate of HAIs in acute-care hospitals in South Korea. **Methods:** We defined HAIs according to KONIS and NHSN criteria. In total, 29 acute-care hospitals including 9 tertiary-care hospitals (TCHs) and 20 secondary-care hospitals (SCHs) were recruited as representing the population of every metropolitan city and province in South Korea. Patients who stayed at the hospitals on August 1, 2018, were randomly selected: 100 for SCHs and 200 for TCHs. Their medical records were retrospectively reviewed for HAIs according to the NHSN criteria by the infection control nurses (ICNs) from each hospital. A web-based data collection and analysis program was developed, and participating ICNs were educated in a 1-day training course with pre- and postevaluations. They received continuous feedback of input data and questions through the web-based system during the study. To generate estimates of the incidence rate of HAIs, we converted prevalence to incidence using the formula of Rhame and Sudderth. **Results:** Of 4,296 patients, 133 had  $\geq 1$  HAI (3.1%). In total, 141 HAIs were identified: gastrointestinal infections ( $n = 30$ , 21.3%), bloodstream infections ( $n = 30$ , 21.3%), pneumonia ( $n = 29$ , 20.6%), urinary tract infection ( $n = 26$ , 18.4%). Among the gastrointestinal infections, *C. difficile* infections were the most common (17.7%). Device-associated infections accounted for 34.8% of all HAIs. The overall incidence of HAIs in TCHs was 4.39%, which was a higher incidence than SCHs (3.76%). Intensive care units had 12.6% of HAIs, whereas general wards had 3.4%. HAI incidences were 5.7%, 2.8%, and 2.3%, respectively, for each of the medical wards, surgical wards, and pediatric wards. The 3 most common pathogens were *Escherichia coli*, *Acinetobacter baumannii*, and *Enterococcus faecium*.