Background. Little is known as to how hospital C. difficile infection (CDI) may impact nursing home (NH) CDI, or how patient transfers may modify this relationship. This study aims to examine a possible association between hospital and NH CDI rates, and whether NH CDI rates are influenced by patient transfers from hospital to NH.

Methods. Patient transfers among the 5 hospitals and 34 NHs in Monroe County, NY were identified from the Minimum Data Set (MDS) 3.0 and Medicare Provider Analysis and Review files for 2011–13, and aggregated to the NH level. NH and hospital CDI rates were obtained from Emerging Infections Program CDI population surveillance and National Healthcare Safety Network data, respectively. Multivariate negative binomial regression models of the association between hospital CDI rate (weighted by hospital-to-NH transfers/overall transfers among hospitals and NHs) and NH CDI rate, controlling for NH covariates from NH Compare and the Online Survey, Certification, and Reporting files. Patient transfer networks between hospitals and NHs were constructed, and basic network analysis of transfer patterns was conducted to confirm contributing factors to NH CDI rates from the multivariate model.

Results. When weighted hospital CDI rate increased by 1%, NH CDI rate increased by 18% (P = 0.016). Antibiotic and feeding tube prevalence were associated with a 4% and 8% increase in NH CDI rate, respectively (P≤0.014). Network analysis confirmed multivariate results and detected hospital-NH pairs with high edge weights (number of transfers) where NHs receiving patients from hospitals with high CDI rates had higher CDI rates. Network clustering methods were used to identify 2 sub-networks within overall annual networks and clusters of hospital-NH pairs targeted for intervention.

Conclusion. Hospital CDI rate, adjusting for patient transfers, is associated with higher NH CDI rates in multivariate and network analyses, suggesting that NHs with a large inflow of patients from hospitals may need to implement stricter infection prevention practices to reduce transmission among residents. By identifying regional sub-networks, network analysis can also be used to actively manage facility CDI and prevent spread to other healthcare facilities.

Disclosures. All authors: No reported disclosures.

1311. Risk factors for Clostridium difficile infection in C. difficile colonized ICU patients

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Background. Clostridium difficile is a major cause of healthcare-associated infections leading to significant morbidity and mortality; however, data-driven interventions to decrease C. difficile infections (CDI) are lacking due to an incomplete understanding of disease transmission and risk factors. Asymptomatic C. difficile carriers may be an important source of nosocomial transmission and disease but few studies have examined colonized patients who later develop CDI. We describe risk factors for the development of CDI in a critical care population screened for C. difficile colonization.

Methods. All patients admitted to our medical or trauma ICUs were screened for toxigenic C. difficile by PCR via rectal swab. Collected patients were placed in contact enteric precautions for their entire hospitalization and monitored for signs and symptoms of CDI. Retrospective chart review assessed risk factors associated with development of CDI.

Results. 868 rectal swabs were collected from 4/01/16 to 10/31/16. 40 patients were colonized with C. difficile on ICU admission and 20 developed symptomatic CDI (Table 1). Risk factors for CDI in colonized patients include enteral feeding and exposure to antibiotics (Table 2).

Conclusion. 50% of C. difficile colonized ICU patients progressed to symptomatic CDI during their hospitalization. Antibiotic use was a significant risk factor for CDI. C. difficile carriers may be a particularly vulnerable population for CDI, warranting further investigation for early identification of colonized patients and strategies for infection prevention.

Table 1 – Patient Demographics

| Risk Factor | CDI (N = 20) | No CDI (N = 20) | p-value |
|-------------|-------------|-------------|--------|
| Mean Age    | 52.8 (20–88) | 51.9 (18–90) | 0.76   |
| Sex         |             |             |        |
| Female      | 6 (30)      | 10 (50)     | 0.20   |
| Male        | 14 (70)     | 10 (50)     |        |
| Race        |             |             |        |
| White       | 15 (75)     | 15 (75)     | 0.44   |
| Black       | 1 (5)       | 3 (15)      |        |
| Asian       | 4 (20)      | 2 (10)      |        |
| Comorbidities |           |             |        |
| DM          | 7 (35)      | 7 (35)      | 1.00   |
| Immuno compromised | 3 (15) | 10 (50) | 0.63 |
| ESRD        | 4 (20)      | 6 (30)      | 0.47   |
| From SNF/LTC | 1 (5)       | 3 (15)      | 0.29   |
| Past Hospitalization | 8 (40) | 15 (75) | 0.03 |
| CDI History | 0 (0)       | 2 (10)      | 0.15   |

Table 2 – CDI Risk Factors in C. difficile colonized ICU patients

| Risk Factor | CDI N = 20 (%) | No CDI N = 20 (%) | p-value |
|-------------|---------------|-----------------|--------|
| Enteral Feeding | 10 (50) | 2 (10) | <0.01 |
| Abdominal Surgery | 4 (20) | 1 (5) | 0.15 |
| PPI/H2 Blocker | 9 (45) | 8 (40) | 0.75 |
| Antibiotics | None | 2 (10) | <0.01 |
|             | 1 class      | 3 (15) | 0.23   |
|             | 2+ classes   | 15 (75) | 5 (25) | <0.01 |

Disclosures. F. C. Fang, BioFire: Collaborator; Consultant and Scientific Advisor, Consulting fee, Research support and Speaker honorarium; Cepheid: Collaborator, Consultant and Scientific Advisor, Consulting fee, Educational grant, Research support and Speaker honorarium.

1312. Use of Electronic Data to Identify Risk Factors Associated with Clostridium difficile Infection (CDI) and to Develop CDI Risk Scores

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Background. Clostridium difficile is a major cause of severe diarrhea in the U.S. We described characteristics of Kaiser Permanente Northern California (KPNC) members with C. difficile infection (CDI), identified risk factors associated with CDI, and developed risk scores to predict who may develop CDI.

Methods. Retrospective cohort study with all KPNC members ≥18 years old from May 2011 to July 2014 comparing demographic and clinical characteristics for those with and without lab-confirmed incident CDI. We included CDI risk factors in logistic regression models to estimate the risk of developing future CDI after an Identification Recruitment Date (IRD), a time when an individual might be a good candidate for a C. difficile vaccine clinical trial. Two risk score models were created and cross validated (70% of the data used for development and 30% for testing).

Results. During the study period, there were 9,986 CDI cases and 2,230,354 members without CDI. CDI cases tended to be >65 years old (59% vs. 21%), female (61% vs. 53%), and white race (70% vs. 53%), with more hospitalizations (42% vs. 3%), emergency room visits (51% vs. 14%), and skilled nursing facility stays (25% vs. 6.6%) in the year prior to CDI compared with members without CDI. At least 10 office visits within the prior year (53% vs. 16%), use of antibiotics in last 12 weeks (81% vs. 11%), proton pump inhibitors in the last year (36% vs. 7%), and multiple medical conditions within the prior year (eg, chronic kidney disease, congestive heart failure, and pneumonia) were important risk factors for CDI. Using a hospital discharge event as the IRD, our risk score model yielded excellent performance in predicting the likelihood of developing CDI in the subsequent 31–365 days (C-statistic of 0.851). Using a random date as the IRD, our model also predicted CDI risk in the subsequent 1–30 days (C-statistic 0.658) and 31–365 days (C-statistic 0.722) reasonably well.

Conclusion. CDI can be predicted by increasing age, medications, comorbidities and office visits, exposure, particularly ≥10 office visits, hospitalizations, infections and nursing stays in the prior year and recent antibiotics. Such risk factors can be used to identify high-risk populations for C. difficile vaccine clinical studies.

Disclosures. H. Yu, Pfizer, Inc.: Employee, Salary; B. Cai, Pfizer, Inc.: Employee; R. McCaffrey, BS: Employee, Salary; E. Gonzalez, MS: Employee, Salary; J. Lawrence, PhD: Employee, Salary; N. P. Klein, GSK: Investigator, Grant recipient; sanofi pasteur: Investigator, Grant recipient; Merck & Co: Investigator, Grant recipient; MedImmune: Investigator, Grant recipient; Protein Sciences: Investigator, Grant recipient; Pfizer: Investigator, Grant recipient.

1313. A data-driven approach to predict daily risk of Clostridium difficile infection at two large academic health centers

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