Congenital cytomegalovirus (cCMV) infection is the most common cause of non-genetic sensorineural hearing loss in infancy. Screening of newborns for cCMV infection has been performed utilizing saliva due to ease of collection and high sensitivity. Positive saliva screens for CMV DNA by polymerase chain reaction (PCR) testing has been reported to occur secondary to breast milk feeding without signifying congenital infection. The NICUs of Nationwide Children’s Hospital recently began universal saliva screening of all admissions. We report 3 neonates whose saliva CMV screen was positive yet the urine CMV PCR test was negative in order to inform CMV screening strategies.

Methods. Retrospective review of the electronic health records of neonates admitted to the neonatal intensive unit (NICU) at Nationwide Children’s Hospital, Columbus, OH who had CMV detected by PCR from saliva specimens but not from urine. Pertinent demographic and clinical data were obtained.

Results. Three female neonates had a positive saliva CMV DNA PCR test but urine CMV PCR was negative. The first infant (gestational age [GA] 34 weeks, birth weight [BW] 1790 Grams) was a monochorionic diamionic twin gestation and born vaginally with unknown duration of rupture of membranes (ROM). At 16 days of age, the infant had a positive saliva CMV PCR but a negative urine CMV PCR test. The infant received maternal milk. The twin’s CMV PCR tests of saliva and urine were negative. The second infant (GA 38 weeks, BW 2952 grams) was born vaginally after 9 hours of ROM. On the first day of age, the infant had a positive saliva CMV PCR test that was followed by a negative urine CMV PCR on the third day of age. The infant had not been breastfed. The third infant (GA 33 weeks, BW 1762 grams) was born by C-section delivery with ROM at delivery. Saliva CMV PCR test was positive on the second day of age but urine PCR was negative twice (days 3 and 7). All 3 infants had no signs or symptoms of CMV infection and passed the newborn hearing screen.

Conclusion. Testing of saliva for CMV DNA by PCR is not always confirmatory for cCMV infection as contamination of saliva specimens with CMV could result from exposure to maternal milk and possibly vaginal secretions. Definitive diagnosis of CMV infection requires additional confirmatory testing preferably with urine.

Disclosures. All authors: No reported disclosures.
Background. There is limited data on the indirect and non-medical costs associated with congenital cytomegalovirus (CMV). Attempts to predict the economic impact of disease often rely on secondary analyses of large private databases, and may not capture the full spectrum of a disease. The granularity of billing codes in the Electronic Medical Record (EMR) make it possible to track health outcomes over time, however, with over 80,000 unique codes in ICD-10, selecting the appropriate codes requires specific content knowledge and can lead to bias in categorization. The Systematized Nomenclature of Medicine—Clinical Terms (SNOMED-CT)® provides physicians a tool to find specific ICD-10 on the basis of semantic terms. These terms can be used to build disease state-specific clusters of ICD-10 codes by which to study the economic impact of any disease, including this potentially devastating congenital infection.

Methods. Using a series of data parsing and processing scripts written in SAS V9.4 ( Cary, NC), we extracted the diagnosis codes for 190 patients seen in our Congenital Cytomegalovirus Clinic at Texas Children’s Hospital in Houston, Texas. This data were consolidated into a relational database of clinical information. Through a second program we developed, clusters of ICD-10 codes were imputed from the SNOMED-CT® on the basis of semantic terms associated with CMV (e.g., “hearing problem,” “developmental disability,” “neurological problem”).

Results. A total of 190 patients have been seen in our clinic with an ICD-10 diagnosis of CMV infection, 144 of these had cCMV, and 102 of these were born after 1/1/2008 (the inception date of our EMR). 40% of these patients were Caucasian (21%), Hispanic, and 25% African American. 54 (53%) had hearing deficits, 17 (16%) had hearing aids, and 55 (54%) had developmental abnormalities. The average time (in years) to development of specific deficits are shown in Figure 1.

Conclusion. The spectrum of disease of CMV is broad and has been well studied in the past. The EMR gives us the potential to further study this disease in finer detail and identify rates of disease progression by mining the ICD-10 codes associated with these patients throughout time. These results should prove invaluable for generating cost-models for the economic impact of CMV.

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2339. Clostridioides difficile: Impact of Active Screening of Asymptomatic Carriers and Testing Stewardship

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Background. C. difficile infection is a significant cause of mortality and morbidity worldwide. The emergence of C. difficile infection with hypervirulent (‘‘tonic’’) C. difficile has been associated with a tendency towards increased morbidity and mortality compared with prior C. difficile infection. The introduction of non-subtyping diagnostic testing has significantly reduced the number of patients who are treated with empiric therapy for C. difficile infection.

Methods. This retrospective cohort was performed in a 600-bed hospital in Milwaukee, WI, from January 1, 2016 to March 31, 2018. All clinical C. difficile tests included nucleic acid amplification (NAAT; Xpert C. difficile, Cepheid). On February 2017, all NAAT+ tests had toxin (tox) checked (Quick check complete, Alere). Testing algorithm (Figure 1) started mid 2016 until now. Screening phases included: Phase 1 (September 2016–May 2017): C. difficile screening cultures in units shared with units not placed in electronic medical records (EMR). Patients placed on enteric precautions (gown, gloves, hand hygiene). Phase 2 (May 2017–January 2018): C. difficile screening (NAAT) performed on admission and weekly thereafter, results placed in EMR, NAAT+ patients placed on enteric precautions. Phase 3 (January 2018–present): C. difficile screening (NAAT) on admission, results placed in EMR, NAAT+ patients placed on enteric precautions. Federal reporting changed to only reporting NAAT+ tox. Tests (NAAT+, NAAT+ tox, and NAAT+ tox+) were analyzed using Poisson regression offsetting for log of patient-days using SAS, v9.4.

Results. Hospital-wide C. difficile tests decreased from 21 to 10.9 tests per 1,000 patient-days (P < 0.0001; Figure 2). This effect was seen in heme-onc units (41 ± 15.7; P < 0.0001; Figure 3) and in all other units (18.9 ± 9.9; P < 0.0001). All NAAT+ results decreased from 2.99 to 1.94 per 1,000 patient-days hospital wide (P = 0.0001) and unchanged in heme-onc units (4.6 ± 3.7; P = 0.05). NAAT+ tox results remained unchanged hospital wide and in heme-onc units (0.8 ± 0.7 and 1.1 ± 1.2, respectively).