A Bayesian molecular clock analysis was performed with BEAST using the isolation date of each genome as a calibrator. The colored strip showed the most frequent clones. The red dot shows a major event of divergence in 2008.

**Conclusion.** The ChC clone remains the most prevalent MRSA in Chile. However, our data is consistent with the evolution of this clone and a progressive replacement of ST105 and ST12 genetic lineages.

**Disclosures.** Lorena Diaz, PhD; Nothing to disclose

**References**

1. Praska J, Arias CA, Gasson M, et al: Enterococcal resistance and risk of false negative results. J Clin Microbiol 1992;30:508-510.

667. Next Generation Sequencing of Microbial Cell Free DNA in the Diagnosis and Treatment of Infectious Disease in Children: When Does the Result Justify the Cost?

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**Session:** P-30. Diagnostics: Typing/sequencing

**Background.** Pathogen testing using next-generation sequencing of microbial cell-free DNA (NGS cfDNA) is a promising diagnostic tool to identify pathogens that might not be detected using conventional lab evaluation. Considering the cost of this test, it is important to determine when it is most useful to the plan of care (POC).

**Methods.** In this retrospective study, we collected data from the medical charts of 50 consecutive NGS cfDNA tests in a free-standing children’s hospital. We evaluated patients for demographics, underlying conditions, diagnosis at time of testing, conventional laboratory testing and timing, medical treatment, and NGS cfDNA test results for clinical relevance or false negative results compared to conventional testing. The primary goal was to identify patients for whom the NGS cfDNA testing affected the POC. Charts were reviewed, and determinations regarding whether the result influenced the POC were confirmed by a provider.

**Results.** We were unable to differentiate patients with clinically valuable NGS cfDNA results (Fig 1 & 2). Among those with NGS cfDNA results valuable to the POC (n=22), both negative and positive testing guided POC (12 valuable negative vs. 9 diagnostic cases). In the total sample, 5 cases (10%) had a clinically relevant pathogen identified through conventional testing, but not through NGS cfDNA and 2 cases had antimicrobial resistance on culture, which is not detected by NGS cfDNA.

**Conclusion.** While we did not find a specific clinical profile for NGS cfDNA use, positive results were essential to the diagnosis in 18% of cases with otherwise negative laboratory evaluation for the pathogen identified in NGS cfDNA. Negative tests affected the POC in 26% of cases by avoiding unnecessary antimicrobials in high risk immunocompromised patients and patients that presented with low-risk of infection, but unclear disease process.

Caution must be exercised with reliance on this test with respect to antimicrobial resistance and risk of false negative results.

**Disclosures.** All Authors: No reported disclosures

668. Restricting Ordering of Multiplex Gastrointestinal Panel Improves Test Utilization

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**Session:** P-30. Diagnostics: Typing/sequencing

**Background.** The multiplex gastrointestinal pathogen panel (GIP) is a convenient and quick diagnostic test for determining the infectious etiology of diarrhea. It identifies several of the most common pathogens associated with gastroenteritis. However, it is expensive, and test results may not impact care, given that several of the pathogens in the panel are managed expectantly. We describe our experience with a diagnostic stewardship initiative to resolve the overuse of this testing method.

**Methods.** We performed a pre/post study of GIPs ordered for inpatients 18 years old and older from December 19, 2018, to December 18, 2020, at Mayo Clinic hospital in Rochester, Minnesota. GIP orders for inpatients were limited to the first 72 hours of hospitalization starting December 19, 2019. Orders after 72 hours were encouraged to be changed to C. difficile NAAT testing or sent to an infectious disease provider to override on a case-by-case basis. Our hospitals used BioFire FilmArray Gastrointestinal Panel (BioFire Diagnostics, Salt Lake City, Utah).

**Results.** A total of 2,641 GIPs were performed during the study period. There were 1,568 GIPs (3.3/100 hospitalizations) in the pre-intervention period compared to 1,073 (2.6/100 hospitalizations) post-intervention, representing a drop of 21.2%. The most common pathogen detected was C. difficile (toxin A/B) (48.8%, n=402), followed by norovirus (17.5%, n=144). The overall test positivity rate was 27.9% (n=736). The test positivity rate decreased 1.8% from 28.6% (n=448) to 26.8% (n=288) after the restriction (p=0.33). The proportions of C. difficile among all pathogens detected increased from 48.5% to 49.7% (p=0.67).
Conclusion. Our study showed that restricting the ordering of GIP to the first 72 hours of hospitalization and directing providers to standalone *C. difficile* NAA testing resulted in a reduction of GIPs performed. There were marginal changes in the test positivity rate of GIP. A limitation of our study is that the timing of post-intervention coincided with the COVID-19 pandemic, which had unpredictable effects on hospital practice and patient admissions. Ideally, future quality improvement projects should increase the test positivity of pathogens other than *C. difficile* while lowering the GIP use in diagnosing *C. difficile* colitis.

Disclosures. John C. O’Horo, Sr., MD, MPH, Bates College and Elsevier Inc (Consultant)

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| Pathogen | Pre-intervention (a %) | Post-intervention (b %) | Change | p value |
|----------|-------------------------|-------------------------|--------|---------|
| Bacteria |                         |                         |        |         |
| Clostridium difficile (total & A) | 23 (15.18) | 14 (15.25) | 0.11 | 0.94 |
| Enteroaggregative Escherichia coli | 16 (1.92) | 5 (6.47) | -4.55 | 0.12 |
| Enteropathogenic E. coli | 39 (1.76) | 32 (2.95) | 0.78 | 0.29 |
| Enteroinvasive E. coli | 9 (0.51) | 5 (0.29) | 0.22 | 0.37 |
| Staphylococcus epidermidis | 10 (0.44) | 6 (0.56) | 0.08 | 0.80 |
| Staphylococcus aureus | 6 (0.80) | - | - | - |
| Pleurococcus stipitisidis | - | - | - | - |
| Streptococcus | 10 (0.44) | 5 (0.47) | 0.37 | 0.56 |
| Viruses |                         |                         |        |         |
| Adenovirus (FDV41) | 2 (0.13) | 1 (0.09) | -0.04 | 0.8 |
| Astrovirus | 4 (0.26) | 5 (0.28) | 0.02 | 0.9 |
| Norovirus GI/II/III | 74 (4.72) | 70 (6.12) | 0.60 | 0.04 |
| Rotavirus A | 21 (1.34) | - | - | - |
| Sipovirus (II, IV, and V) | 10 (0.56) | 9 (0.54) | 0.2 | 0.55 |
| Parasites |                         |                         |        |         |
| Cryptosporidium | 6 (0.30) | 6 (0.35) | 0.15 | 0.32 |
| Cryptosporidium parvum | 0.26 | 2 (0.19) | 0.07 | 0.72 |
| Entamoeba histolytica | 4 (0.26) | 5 (0.28) | 0.02 | 0.9 |
| Giardia lamblia | 4 (0.26) | 3 (0.28) | 0.02 | 0.9 |

Abundance of bacteria and fungi detected on plasma mcf-DNA-seq test. Data classified by organism and level of immunosuppression. Abundance is expressed in microbial cell free DNA per microliter. Warmer colors towards red represent higher abundance.

Figure 1. Bacteria abundance from date of symptom onset.