information on financial cost (direct and indirect) and turnaround time (TAT) for NGS results.

Results. A total of 33 clinical specimens from 25 patients were sent for NGS. The majority of specimens comprised joint tissue/fluid, organ tissue and CSF.

Concordance occurred between SOC and NGS testing in 75.8% (25/33) of samples; of those, 88% excluded infection. NGS identified a pathogen in 20% (5/25) patients in which concomitant SOC testing was negative. A subsequent change in antimicrobial management occurred in 16% (4/25) of patients. The mean TAT was 14 days and average cost per specimen was $821.52 (range: $573-$1590).

Table 1. Pathogens identified by NGS with negative traditional microbiological test results

Table 1. Organisms identified by NGS with negative SOC
Gordonia sputi
Bartonella species
Corynebacterium species
Streptococcus agalactiae

Figure 1. Distribution of specimen site (in %) sent for NGS

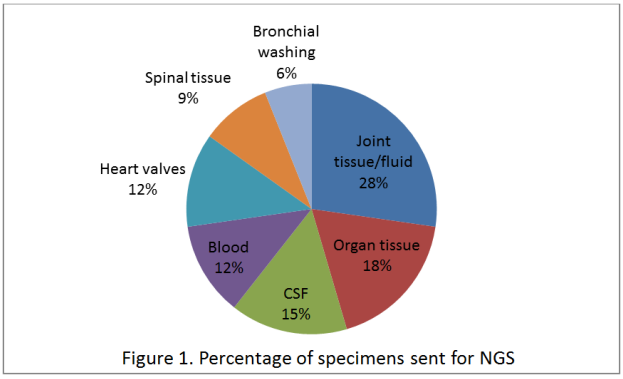


Figure 1. Percentage of specimens sent for NGS

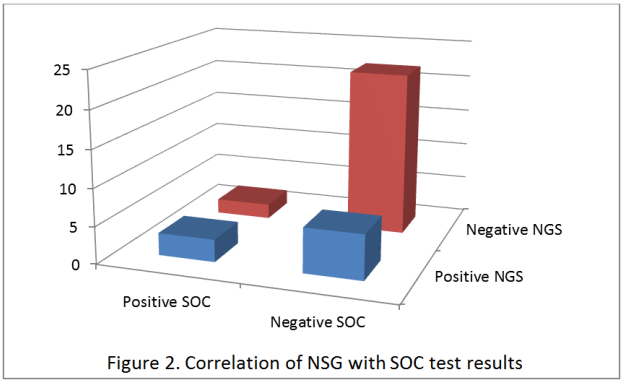


Figure 2. Correlation of NSG with SOC test results

Conclusion. NGS can provide additional diagnostic sensitivity in infectious diseases, which at our institution identified a new pathogen in 20% and a resultant treatment change in 16% of our patients. This testing may also allow physicians to reaffirm the absence of an infection diagnosis. A larger NGS testing population may reveal more significant benefits. While the attributable cost of NGS was substantial, it should be measured against the costs of administration of unnecessary antibiotics, inaccurate diagnosis, and adverse patient outcomes that may result from SOC testing alone. Considering its financial cost and extended TAT, in-house NGS testing may be warranted to facilitate a higher volume of testing.

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

666. Molecular Epidemiology of Methicillin-Resistant *Staphylococcus aureus* in Chile between 1999-2018

Jose RW. Martínez, BSc, MSc[1]; Maria Spencer, BSc, MSc[1]; Lina M. Rivas, MS[1]; Rafael Rios, MSc[2]; Lorena Diaz, PhD [2]; Lorena Diaz, PhD [2]; Jinnethe Reyes, MSc, PhD[3]; Paul J. Planet, MD, PhD[4]; Patricia Garcia, M.D.[5]; Cesar A. Arias, M.D., MSc, Ph.D., FIDSA[6]; Jose Munita, MD[1]; [1]Genomics & Resistant Microbes (GeRM), Instituto de Ciencias e Innovación en Medicina, Facultad de Medicina Clínica Alemana, Universidad del Desarrollo, Chile; Millennium Initiative for Collaborative Research on Bacterial Resistance (MICROB-R), Santiago, Region Metropolitana, Chile; [2]Universidad El Bosque, Bogota, Distrito Capital de Bogota, Colombia; [3]Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, Bogota, Colombia, Bogota, Distrito Capital de Bogota, Colombia; [4]Children's Hospital of Philadelphia/UPenn, Philadelphia, Pennsylvania; [5]Pontificia Universidad Catolica de Chile, Santiago, Region Metropolitana, Chile; [6]CARMiG, UTHealth and Center for Infectious Diseases, UTHealth School of Public Health, Houston, TX; Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, BOG, COL, Houston, Texas

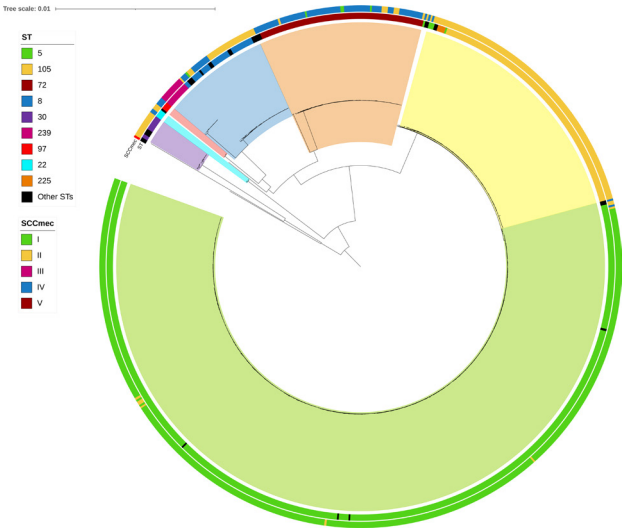
Session: P-30. Diagnostics: Typing/sequencing

Background. The global spread of methicillin-resistant *Staphylococcus aureus* (MRSA) is associated with distinct genetic lineages that predominate in specific geographical regions. Available evidence suggests the Chilean-Cordobes clone (ChC), an ST5-SCC*mec*I lineage, has largely predominated in Chilean hospitals since its first description in the late 1990's. Although the circulation of other MRSA lineages, including community-associated clones, has been well documented, the dynamics of clonal replacement over time has not been explored. Therefore, we aimed to study the molecular epidemiology and dynamics of clonal replacement using a large collection of clinical MRSA strains recovered from Chile during the last two decades.

Methods. We used whole-genome sequencing (WGS) and core-based phylogenomic analysis to identify genetic lineages and explore their relationship in 798 MRSA isolates obtained between 1999-2018 from two tertiary-care Chilean hospitals.

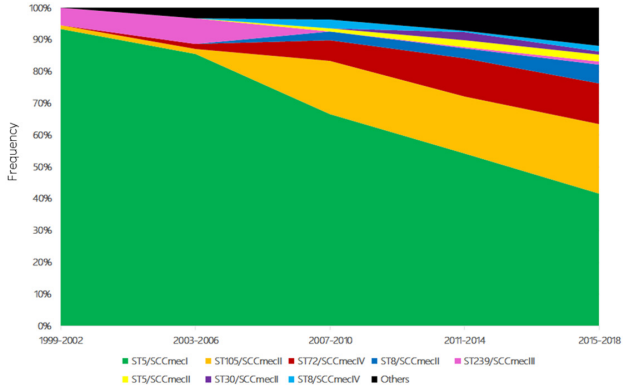
Results. Overall, the most frequently identified clones were the ST5-SCC*mec*I ChC (n=476, 60%), followed by ST105-SCC*mec*II (n=119, 15%), ST72-SCC*mec*IV (n=74, 9%), and ST8-SCC*mec*II (n=26, 3%). Phylogenomic reconstruction demonstrated 7 major clades: Clade I (CC30); Clade II (CC22); Clade III (CC97); Clade IV (CC8); Clade V (ST72); Clade VI (CC5/ST225 and ST105) and Clade VII (CC5/ST5-SCC*mec*I) (Fig. 1). The ChC clone remained the most frequent MRSA lineage throughout the study period (Fig. 2). However, its relative abundance decreased from >90% of isolates in 1999 to ca. 40% in 2018. This decrease began around 2005 and was associated with a progressive expansion of the ST105-SCC*mec*II and ST72-SCC*mec*IV lineages (Fig. 2). A Bayesian molecular clock analysis established the most recent common ancestor in 1964 (95% HPD interval=1961.975-1966.218) and corroborated a CC5 expansion event starting in Chile in 1999 (Fig. 3). Interestingly, our analyses revealed two branches within the ST5-SCC*mec*I lineage: one predominating in 1999-2006, and a more recent branch (related to the ST105-SCC*mec*II clone) that emerged around 2008.

Figure 1. Core genome phylogenomic reconstruction of the 798 MRSA isolates.



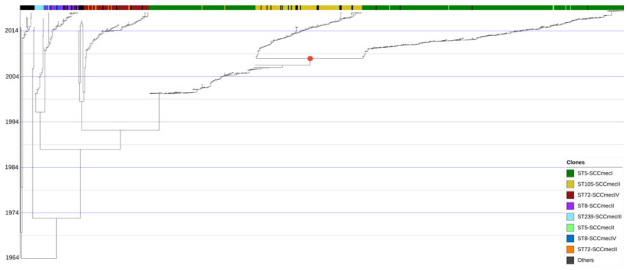
The seven major clades are represented by colored sections. The Clade I (purple section) was composed of isolates belonging to the CC30. Clade II (cyan section) includes four isolates of CC22. Clade III (red section) is composed of isolates of CC97. Clade IV (blue section) grouped isolates of different ST239 and ST8, belonging to the CC8. Clade V (orange section) includes isolates of ST72. Clade VI (yellow section) includes isolates of ST225 and ST105, both belonging to CC5. Clade VII (green section) is mostly composed of isolates of ST5-SCCmecI. The inner ring shows the ST of the isolates; the external ring shows the staphylococcal chromosomal cassette mec (SCCmec) type.

Figure 2. Relative frequency of MRSA clones from 1999 to 2018.



The genomes were grouped according to their isolation dates. Most frequent MRSA clones are represented by colored sections.

Figure 3. Maximum clade credibility tree from the molecular clock analysis of the 798 MRSA genomes.



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 with ST105 and ST72 genetic lineages.

Disclosures. **Lorena Diaz, PhD** , Nothing to disclose **Cesar A. Arias, M.D., MSc, Ph.D., FIDSA**, **Entasis Therapeutics** (Grant/Research Support)**MeMed Diagnostics** (Grant/Research Support)**Merk** (Grant/Research Support)

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?

Rachel Downey Quick, MSN, RN, CNS[1]; Kelli A. Martinez, MD[2]; Susan M. Russo, MSN, APRN, CPNP-PC[1]; Sarah E. McGwier, MSN, APRN, CPNP-PC[3]; Rachel A. Quirt, MSN, APRN, CPNP-PC[3]; Sarmistha Bhaduri. Hauger, MD[4]; Mariosl Fernandez, MD[4]; Donald Murphey, MD[5]; [1]Dell Children's Medical Group, Austin, TX; [2]Dell Medical School at the University of Texas at Austin, Austin, TX; [3]Dell Children's Medical Group, Autsin, TX; [4]Dell Children's Medical Center, University of Texas at Austin Dell Medical School, Austin, TX; [5]Dell Children's Medical Center; University of Texas at Austin Dell Medical School, Austin, TX

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).

Figure 1. Unit of admission among cases

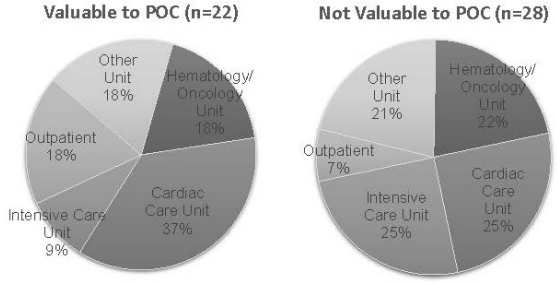
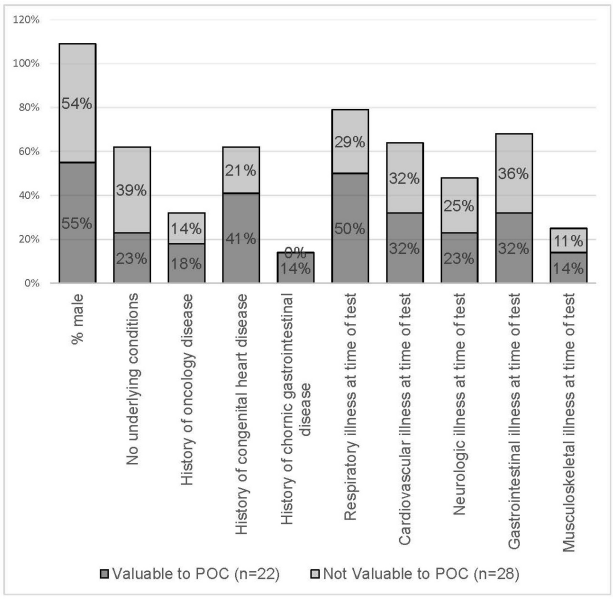


Figure 2. Patient characteristics in cases determined to be valuable and not valuable to the plan of care (POC)



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 (13 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

Don Bambino Geno Tai, MD, MBA[1]; Anisha Misra, PhD[1]; Priya Sampathkumar, MD[1]; John C. O'Horo, Sr., MD, MPH[1]; [1]Mayo Clinic, Rochester, Minnesota

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 *Clostridioides 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 proportion of *C. difficile* among all pathogens detected increased from 48.5% to 49.7% (*p*=0.67).