of agreement are included, the number rises to 98.2–99.4% agreement. Using CHROM for presumptive identification of pure or predominant organisms, UCA was in agreement with manual identification in 251 of 272 cultures (92.3%). Of the 21 discrepant organisms, 19 were classified as “other” by manual reading but were identified as specific organisms by UCA. Definitive organism identification was not performed.

UCA was able to accurately categorize bacterial growth into five semi-quantitative categories using five media types. Pure and predominant uropathogens were accurately identified from CHROM using UCA. The use of UCA software application may enable laboratories to save time screening urine cultures by allowing more efficient use of technologist time.
and clinical utility of a method for rapid microorganism identification from blood and sterile site fluid enrichment cultures using matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) in a high-throughput regional microbiology laboratory.

**Methods.** A drop of blood or fluid from cultures flagging positive was inoculated onto chocolate agar and incubated until MALDI-TOF MS analysis 5–6 hours later. Results obtained with conventional overnight incubation were used as controls. The number of isolates reliably and correctly identified, and recommendations for changes to clinical management were recorded. A pilot study was undertaken to demonstrate feasibility using a cut-off score of ≥2.0, following which the method was integrated into the laboratory workflow using a cut-off score of ≥1.7 (identification to genus level) because patient management can often be altered with this degree of accuracy.

**Results.** In the pilot study, 154/210 blood cultures (73.3%) were reliably identified (score ≥2.0) and, of these, 151 (98.1%) were correctly identified. The operational study included 144 blood cultures and 14 sterile site fluid enrichment cultures. 121 (76.6%) were reliably identified (score ≥1.7) and, of these, 117 (96.7%) were correctly identified. Four isolates (2.5%) were yeast, 104 (65.8%) were Gram-positive bacteria and 50 (31.6%) were Gram-negative bacteria. 78 of the 104 bacteria (75.0%) were correctly identified. The median score for Gram-positives was 1.89 (IQR 0.36). For Gram-negatives, 47 of the 50 isolates (94.0%) were correctly identified. The median score for Gram-negatives was 2.29 (IQR 0.14). No yeasts were reliably identified. Recommendations for changes to clinical management were made for seven (3.8%) and nine patients (6.0%) in the pilot study and operational study, respectively. The method was easily integrated into the laboratory workflow and did not require additional staff.

**Conclusion.** We build on previous work by providing a simple method for rapid micro-organism identification which allows easy integration into a busy laboratory, and which improves clinical management.

**Figure 1:** Correlation between findings of MALDI-TOF MS and SDS-PAGE. A) CPCR strain with expression of OmpA (orange arrow) and porin (purple arrow). B) NCPCR strain with expression of OmpA (orange arrow) and absence of porins.

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

**2155. Accelerated Confirmation of Porin Loss in Carbapenem-Resistant Enterobacteriales: A MALDI-TOF Mass Spectrometry-Based Approach**

**Background.** The accurate identification of carbapenem resistance mechanisms is decisive for the appropriate selection of antibiotic regimens. Numerous methods can detect carbapenemase-producing carbapenem-resistant bacteria (CPCR). However, non-CPCR (NCPCR) are routinely assumed to display porin loss as a diagnosis of exclusion. No further confirmatory tests are performed since the gold standard (sodium dodecylsulfate polyacrylamide gel electrophoresis, SDS–PAGE) is laborious and time consuming. We propose a test for rapid and easy detection of porin loss by matrix-assisted laser desorption/ionization-time of-flight mass spectrometry (MALDI-TOF MS).

**Methods.** Clinical meropenem-resistant Enterobacteriales strains (10 CPCR, 10 NCPCR) and control strains recommended by EUCAST (5 carbapenemase-producing, one with porin loss, one-negative control) were analyzed. Membrane proteins were extracted by successive centrifugation of bacterial suspensions (McFarland 0.5) and addition of ethanol, formic acid and acetonitrile. MALDI-TOF MS of the protein extracts was performed on a 96-spot target (Bruker Daltonics, Germany). Peaks between 35 and 40 kDa were analyzed for the presence of porins and compared with the bands observed in the SDS-PAGE of the protein extracts.

**Results.** Within the molecular weight range of 35–40 kDa, the MALDI-TOF MS-based method revealed peaks in all CPCR isolates corresponding to those observed in the carbapenemase-producing control strains. In contrast, the control strain with porin loss as well as all NCPCR isolates showed a lower quantity of peaks in this range. All peaks observed correlated with the bands observed in the SDS-PAGE of the protein extracts at the corresponding molecular weight (Figure 1).

**Conclusion.** Yielding results that reliably correspond to the current gold standard, we propose a method for accelerated detection of porin loss as an alternative to the diagnosis of exclusion usually made in routine settings. With a processing time of approximately 20 minutes, the method can be easily implemented in the clinical setting. Applying this MALDI-TOF MS-based approach, valuable information will be provided about a resistance mechanism that otherwise remains unexplained.

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

**2156. To Evaluate the Role of Kit-Based Loop-Mediated Isothermal Amplification (TB-LAMP) Assay in the Diagnosis of Tubercular Lymphadenitis**

**Background.** Tuberculosis (TB) is the leading cause of death as a single infectious agent worldwide. In 2017, there were an estimated 1.3 million TB deaths among HIV-negative people and 300,000 deaths among HIV-positive people. The rapid and accurate diagnosis of TB in lymphnode specimens remains a challenging task today. In 2016, World Health Organization endorsed a commercial molecular assay, the LoopAMP™ Mycobacterium tuberculosis complex (MTBC) detection kit (Eiken Chemical Company, Tokyo, Japan), which uses loop-mediated isothermal amplification (LAMP) for sputum samples only. No prospective studies on LAMP in diagnosis of Tubercular Lymphadenitis in adults have been done yet.

**Methods.** A prospective observational study with a total of 70 lymph-node aspirate specimens from suspected cases of Tubercular Lymphadenitis with age >18 years were selected and subjected to Ziehl-Neelsen staining, LAMP and culture in mycobacterial growth indicator tube (MGIT960). The immunochromatographic test was used to confirm MTB complex (MTBC) in culture positive samples and phenotypic drug susceptibility testing was done using MGIT-960. The composite reference standard (CRS) used in the study includes symptoms, radiological evidence and follow-up of 2 months. 2 x 2 tables were made and Sensitivity, Specificity, PPV, NPV of TB-LAMP were calculated with respect to AFB smear and composite reference standard (CRS).

**Results.** LAMP assay was able to detect MTBC in 34.3% (24/70) of lymph-node specimens. Sensitivity and specificity of the assay were 100% and 69.7%, respectively; considering smear as gold standard. On comparing with CRS, the assay showed 100% sensitivity and 100% specificity in the diagnosis of MTBC.