years. We observed that 65.2% of patients had MDR-TB, 19.6% had Pre-XDR, 14.1% had RR-TB, and 1.1% had XDR-TB. We identified three main lineages, with Lineage 4 being the most common (81.52%), followed by Lineage 5 (14.13%) and Lineage 2 (3.26%). The dominant genotypes were Cameroon, LAM, Harleem, West Africa 1b, and Beijing, accounting for 47.82%, 19.56%, 17.39%, 6.5%, and 4.3% of cases, respectively.

Conclusion Our study reveals a high proportion of Pre-XDR patients, underscoring the need to enhance laboratory capacities to monitor Pre-XDR and XDR-TB patients. This is the first detection of Lineage 2, the most virulent TB strain in Gabon, Further studies are needed to investigate the transmission dynamics of the Lineage 2 TB strain in Gabon. TB programs should prioritize the effective and rational use of second-line drugs for newly diagnosed MDR-TB patients to prevent the emergence of Pre-XDR/XDR-TB strains.

PA-193 SIMPLE IMAGING SYSTEM FOR OPTICAL LABEL-FREE IDENTIFICATION OF BACTERIAL CLINICAL ISOLATES IN LOW-RESOURCE SETTINGS (LRS)

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Background Only 1.3% of the sub-Saharan African diagnostic laboratories are performing clinical bacteriology. To improve this, diagnostic tools in LRS should be simple, affordable and maintenance-friendly, in contrast with the expensive machinery used in high-income countries, such as mass spectrometer for identification. Lensfree imaging is a label-free identification technique that can be performed directly on colonies growing on agar plates, with low-cost instrumentation.

Methods We report here the very first clinical assay of a wide-field lensfree imaging device, namely 24mm x 36mm, for identification down to species. Considering this large field of view, several hundreds of colonies can be analysed simultaneously. A database of over 250 clinical bacterial isolates was collected at LHUB-ULB, gathering respiratory (20% of isolates), urine/genital tract (20%) and skin/wound (20%) samples, as well as positive blood cultures (40%). Partially coherent light emitting diodes (wavelengths 550nm and 940nm) illuminated microbial cultures growing on Mueller Hinton agar at 36°C. Clinical isolates were labelled through MALDI-TOF mass spectroscopy. To optimize supervised learning, various deep learning models, pre-trained or not, were developed and compared.

Results Over 11.000 colonies were collected in the database that focused on 5 species (Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus, Staphylococcus epidermidis). From these, different deep learning models were trained with at least 1800 samples per species. As a result, the algorithms yielded unambiguous identification of each species, with at least 90% accuracy.

Conclusion This very first database paves the way towards a future imaging device for the diagnosis of bloodstream infections in LRS, within the SIMBLE project. As a second stage, a second database is to be acquired, in Africa, on positive blood cultures.

PA-201 SPECIES IDENTIFICATION AND DRUG SUSCEPTIBILITY TESTING OF NON-TUBERCULOUS MYCOBACTERIA ISOLATED AMONG PRESUMPTIVE TUBERCULOSIS PATIENTS IN LAMBARÉNÉ, GABON

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Background Non-tuberculous mycobacteria are increasingly recognised as causative agents of opportunistic and device-associated infections in humans. In Gabon, data is scarce, as species identification and drug susceptibility are not performed in most laboratories. The objectives of our study were to identify the relative frequencies of non-tuberculous mycobacteria species circulating and to determine their genotypic susceptibility pattern regarding the antibiotics most commonly used to treat NTM infections among presumptive tuberculosis patients.

Methods This cross-sectional prospective study was conducted at the CERMEL TB laboratory from January 2020 to December 2022 to generate drug susceptibility data on NTM species identified from presumptive TB patient specimen sent to the National TB Reference Laboratory. The drug susceptibility to macrolides and aminoglycosides and the NTM subspecies identification were performed using the genotype NTM-DR kit.

Results Among 524 culture-positive specimen, 146 (28%) were NTM. The predominant group was Mycobacterium avium complex, MAC 80/146 (54.8%), of which M. intracellular 53/146 (36.3%) and M. avium 27/146 (18.5%)); followed by Mycobacterium abscessus complex, MABC 38/146 (26.0%), of which M. abscessus subsp. abscessus 20/146 (13.6%); M. abscessus subsp. massiliense 10/146 (7.0%); and M. abscessus subsp. bolletii 8/146 (5.4%)). All MAC were genotypically fully susceptible to macrolides and aminoglycosides. All five isolates of MABC showed polymorphisms both of the erm (41) and rrl genes, both coding for macrolide resistance.

Conclusion All MAC isolates were fully susceptible to macrolides and aminoglycosides, thus confirming their role in NTM treatment. However, resistance-conferring polymorphisms indicate limited susceptibility of M. abscessus complex isolates against both drug classes; requiring further investigation to comprehensively determine M. abscessus drug susceptibility. The study results presented here shall guide clinicians to better manage treatment. Routine susceptibility testing is not available.