sis of reads from next-generation sequencing of total RNA extracted from CSF. We interpreted differentially expressed genes using pathway analysis by open-source Reactome software.

Results: TBM was unmasked by ART initiation within 90 days prior to diagnosis in 17% (68/412) of the cohort. In this group, patients with inflammatory CSF had double the 14-day mortality of those without CNS inflammation (8/29 vs 5/39, Relative Risk 2.2, 95%CI, 0.8 to 5.9) despite similar baseline disease, a relationship not observed in ART-naïve or long-term ART cases of TBM. CSF RNA sequencing of nine cases each of inflammatory and non-inflammatory ART-associated TBM showed that those with CSF inflammation had upregulation of genes in pathways involved in signaling by interferon-gamma, Interleukin-12, and neutrophils.

Conclusions: This study suggests two distinct populations of ART-associated TBM patients exist: one with a paucity of CNS inflammation and relatively good prognosis, and one with significant CNS inflammation and poor prognosis. While the former group might be heterogeneous and include patients with other CNS infections or pathologies, the latter group could represent unmasking TBM-IRIS and is characterized by a host response with upregulated interferon and neutrophil pathways.

LB-2082-21 Assessment of whole genome sequencing technology applied to drug-resistant tuberculosis diagnosis

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Background: The constant rise and global spreading of drug-resistant tuberculosis is a major threat to Global Health. Drug susceptibility testing (DST) is the reference method for the diagnosis of resistances in Mycobacterium tuberculosis. However, this technique has significant drawbacks such as the requirement of complex infrastructure and expertise, a long period to obtain results and low accuracy and reproducibility for certain first-line drugs. In recent years, Whole Genome Sequencing (WGS) of Mycobacterium tuberculosis has emerged as a fast and reliable tool to predict the drug susceptibility profile of the bacteria.

Methods: We have performed a retrospective study of 735 isolates belonging to the Valencia Region (Spain) to assess the performance of WGS resistance prediction in a low burden setting. We compared our bioinformatics prediction with the phenotypic DST data to obtain the sensitivity and specificity. Additionally, we re-tested the clinical isolates with discordant DST-WGS results using the REMA assay.

Results: The results reveal a sensitivity of 85%, 73.3%, 50% and 52.38% for isoniazid, rifampicin, ethambutol and pyrazinamide respectively, and specificities ranging from 98.8% to 99.6%. The re-test data support a higher reliability of the WGS resistance prediction compared to the DST method but also highlight the necessity of expanding our catalogue of resistance-associated mutations.

First-line drug	Resistant strains using DST	Resistant strains using WGS	Sensitivity	Specificity	Positive Predictive Value	Negative Predictive Value	Accuracy	Cohen's kappa
Isoniazid	40	39	85.00%	99.39%	89.47%	99.09%	98.57%	0.864
Rifampicin	15	14	73.33%	99.56%	78.57%	99.42%	99.00%	0.753
Ethambutol	12	10	50.00%	99.41%	60.00%	99.12%	98.56%	0.538
Pyrazinamide	21	20	52.38%	98.81%	57.89%	98.51%	97.40%	0.537

[Table.]

Conclusions: Our results suggest that WGS predicts drug susceptibility profile better than DST when the bacteria possess a common associated-resistance mutation. However, we need to expand our catalogue of rare mutations to improve our prediction analysis in terms of sensitivity. Our data also support the use of more than one critical concentration in DST, because the current breakpoints sometimes do not correspond with the clinical outcome. In conclusion, WGS is a promising tool to diagnosis first-line drug susceptibility that could be faster and more reliable than DST and would allow a better tailoring of treatments.

LB-2115-21 Personalized adherence management in TB: using AI to schedule targeted interventions

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Background: This work addresses challenges in tuberculosis (TB) medication adherence for drug-sensitive patients in India. For support, patients are assigned a community health worker (CHW) who helps manage their adherence via basic monitoring and intervention. However, the CHW may manage as many as 200 patients simultaneously, making it challenging to target interventions to patients who need it most each day. Thus, we design an artificial intelligence (AI)-based system which learns to make intervention recommendations based on available resources and individual patient responsiveness to interventions over time.

Methods: We model the task as follows: Each day, each of N patients may or may not adhere to medication with some patient-specific probability. Due to limited resources, a CHW may only call k of those N patients