Conclusions. A simple score (CRD-45 TB-score) based on 4 clinical variables was highly predictive for the in-house mortality in patients with tuberculosis from this cohort. Generability of this score to predict in-house morbidity of patients with tuberculosis should be prospectively evaluated in a larger multicenter cohort.
Key words: tuberculosis, in-hospital death, risk evaluation, CRD-45 TB-score

103. COMPARISON OF MOLECULAR DRUG RESISTANCE TESTING AND PHENOTYPIC DRUGRESISTANCE TESTING IN MULTI- AND EXTENSIVELY DRUG-RESISTANT TUBERCULOSIS

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Introduction. For the treatment of MDR and XDR tuberculosis, it is important to select the most suitable drug regimen. The resistance testing procedure should be as fast and accurate as possible. Within the framework of personalized medicine, the most suitable therapy approach for the individual patient should be found. With the faster available information from a new form of susceptibility testing, the best regimen could be created in a shorter period of time and the appropriate therapy for the patient could be initiated.
Aim of the study. With our study we want to compare the genotypic drug resistance testing with phenotypic drug resistance testing. It will demonstrate to what extent the measured resistance results overlap and where there may be differences.
Materials and methods. We compared the utility of genotypic DST assays with phenotypic DST (pDST) using Bactec 960 MGIT or Löwenstein-Jensen to construct M/XDR-TB treatment regimens for a cohort of 25 consecutive M/XDR-TB patients and 15 possible anti-TB drugs. Genotypic DST results from Cepheid GeneXpert MTB/RIF (Xpert) and line probe assays (LPAs; Hain GenoType MTBDRplus 2.0 and MTBDRsl 2.0) and whole-genome sequencing (WGS) were translated into individual algorithm-derived treatment regimens for each patient. We further analyzed if discrepancies between the various methods were due to flaws in the genotypic or phenotypic test using MIC results.
Results. Compared with pDST, the average agreement in the number of drugs prescribed in genotypic regimens ranged from just 49% (95% confidence interval [CI], 39 to 59%) for Xpert and 63% (95% CI, 56 to 70%) for LPAs to 93% (95% CI, 88 to 98%) for WGS. Only the WGS regimens did not contain any drugs to which pDST showed resistance. Importantly, MIC testing revealed that pDST likely underestimated the true rate of resistance for key drugs (rifampin, levofloxacin, moxifloxacin, and kanamycin) because critical concentrations (CCs) were too high.
Conclusions. With the analysis of the genome, even in M/XDR strains with complex resistance patterns it is possible to characterize these resistances. The procedure is fast and the results are very similar to those of phenotypic testing. Only for some drugs, the susceptibility test has to be carried out phenotypically in order to compile the final regimes.
Key words: Mycobacterium tuberculosis; drug resistance testing; molecular genetics

104. ADDITIONAL SECOND LINE TB DRUG RESISTANCE IN HIGH BURDEN MDR TB SETTING

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