

**P0915**

**Poster Session III**

**Recent advances in molecular diagnosis of *M. tuberculosis***

**EVALUATION OF A NEW REVERSE HYBRIDIZATION-BASED MOLECULAR METHOD FOR DETECTING FIRST- AND SECOND-LINE DRUG RESISTANCE IN MYCOBACTERIUM TUBERCULOSIS IN CLINICAL SAMPLES**

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**Objectives:** Drug resistant tuberculosis (TB) is a global threat. Conventional methods to detect drug resistance require several weeks for *Mycobacterium tuberculosis* culture, identification and drug susceptibility testing (DST). New molecular methods are needed for the rapid detection of drug resistance. The objective of this study is to evaluate a rapid molecular method based on reverse hybridization with specific probes to detect *M. tuberculosis* and resistance to first-line drugs (isoniazid [INH], rifampicin [RIF], streptomycin [STR] and ethambutol [EMB]) and second-line drugs (fluoroquinolones [FQ], kanamycin, amikacin and capreomycin [KM/AM/CM]) directly on clinical samples.

**Methods:** Sixty-five clinical samples corresponding to 32 patients were retrospectively selected. The reverse hybridization-based method AID TB Resistance (AID Diagnostika, Alemania) was performed to detect resistance to first- and second-line drugs in *M. tuberculosis*. This system consists on PCR amplification and reverse hybridization on probes bound to nitrocellulose strips in order to detect *M. tuberculosis* complex and mutations associated to drug resistance. The genotypic results obtained by this method were compared to phenotypic results obtained by BACTEC 460TB or MGIT960. Discordant results between both methods were analyzed by alternative molecular methods (GenoType MTBDR<sub>plus</sub>, GenoType MTBDR<sub>s</sub>/ [Hain Lifescience, Alemania] and/or pyrosequencing).

**Results:** Sensitivity values comparing the results obtained by both AID TB Resistance and BACTEC 460TB/MGIT to detect resistance to INH, RIF, STR, EMB, FQ y KM/AM/CM were 97.8% (45/46), 100% (43/43), 100% (22/22), 60.0% (21/35), 33.3% (2/6) and 100% (17/17), respectively. Specificity values obtained for this same set of drugs were 100% (14/14), 100% (17/17), 96.6% (28/29), 91.7% (22/24), 98.1% (52/53) y 100% (34/34), respectively. The global concordance rate between both AID TB Resistance and BACTEC 460TB/MGIT to detect resistance to INH, RIF, STR, EMB, FQ y KM/AM/CM were 98.3% (59/60), 100% (60/60), 98.0% (50/51), 72.9% (43/59), 91.5% (54/59) y 100% (51/51), respectively. For the discordant results obtained between both AID TB Resistance and BACTEC 460TB/MGIT, alternative molecular methods confirmed the genotypic result in all the cases, with the exception of a sample identified as FQ heteroresistant by AID TB Resistance but detected as sensitive by the alternative molecular methods. Alternative molecular methods do not detect STR resistance.

**Conclusions:** The reverse hybridization-based AID TB Resistance is useful for the rapid detection of drug resistance in clinical samples and for a initial therapeutic approach. Nevertheless, for a correct management of drug resistant tuberculosis patients, the results should be confirmed by a phenotypic method.