and the adequacy of the above regimen was tested. An adequate regimen was one that met the WHO criteria of a minimum of 4 effective drugs. All drugs were weighted equally. Results: Of 491 isolates, 259 (52%) were Rif-resistant. The derivation and validation cohorts had similar drug susceptibilities (Figure 1).

A prescription with the above 5 drugs would result in 132 (51%) patients being treated with at least 4 effective drugs, and 209 (81%) being treated with a minimum of 3 effective drugs. Conclusion: Prescribing the 5 most susceptible drugs failed to provide an effective regimen for almost half of our cohort. In the absence of line probe assays, we recommend the addition of drugs such as cycloserine or linezolid (untested here) for empiric treatment, while awaiting results of cultures and susceptibility tests.

PA1907

Interpretation of indeterminate Rif-susceptibility results obtained by rapid molecular diagnostics test

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XpertMTB/RIF is a rapid molecular diagnostic tool detecting MTB and Rif-susceptibility within two hours. However, indeterminate Rif-susceptibility results occur and cause uncertainty about clinical judgment. Objective: To evaluate the level of indeterminate Rif-susceptibility results by XpertMTB/RIF, to assess the Rif-susceptibility of such strains and to determine the method that should be used for reference. Methods: Sputum from patients with TB diagnosed in Azerbaijani prisons during 2013-2015 were directly examined by XpertMTB/RIF. Strains with indeterminate Rif-susceptibility results were examined with MGIT-based DST and rpoB sequencing. For comparison, frozen MGIT cultures collected from patients' diagnosis were subjected to measure the MICs using OADC contained Middlebrook 7H9. Direct DNA sequencing of quinolone resistance-determining regions (QRDRs) were performed using a IS6110 aimed Amplicor® kit. There were 101 positive, 212 negative and 14 inconclusive (contaminated) results for Lowenstein Jensen; the MODS/PCR approach returned 127 positive and 200 negative results (estimated time to result 7 days) and zero (0) had indeterminate RIF-susceptibility results, respectively (p=0.009). MGIT results indicated full concordance with sequencing among the samples showing indeterminate Rif-susceptibility results by XpertMTB/RIF.

Table 1. Xpert MTB/RIF Rif-susceptibility results of the patients with tuberculosis diagnosed in the penitentiary system of Azerbaijan, 2013-2015 (n=575). Comparison between direct analysis of the sputum and the frozen MGIT cultures collected at patients' diagnosis.

<table>
<thead>
<tr>
<th>Rif-susceptible</th>
<th>Rif resistant</th>
<th>Rif indeterminate</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Applied directly to sputum</td>
<td>114 (74.7)</td>
<td>37 (25.3)</td>
<td>151 (100)</td>
</tr>
<tr>
<td>Applied to culture</td>
<td>181 (76)</td>
<td>52 (24)</td>
<td>233 (100)</td>
</tr>
<tr>
<td>Total</td>
<td>395 (70)</td>
<td>89 (15)</td>
<td>484 (85)</td>
</tr>
</tbody>
</table>

PA1908

Rapid detection of mycobacterium tuberculosis from MODS culture by PCR

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Introduction: Cultures are currently the mainstay of tuberculosis diagnosis but high sensitivity comes at the cost of late results. Time to result could be improved by combining liquid media cultures and molecular methods. Aim To develop a fast culture method combining MODS cultures and mycobacterial PCR identification Methods DNA was extracted after 3, 4 and 5 days of incubation using a MODS approach on 88 high tuberculosis suspicion samples; day 4 and 5 returned the same yield – day 4 was considered the optimum approach. A total of 327 high suspicion samples (sputum and bronchial washing) were cultured on both Lowenstein Jensen and MODS. Mycobacterial DNA was extracted in day 4 and 5 and PCR was performed using a IS6110 aimed GenProbe® kit. There were 101 positive, 212 negative and 14 inconclusive (contaminated) results for Lowenstein Jensen; the MODS/PCR approach returned 127 positive and 200 negative results (estimated time to result 7 days) to a sensibility of 99%, specificity 89%, positive predictive value 81%. Conclusion A MODS/PCR hybrid method is feasible and has the potential of returning microbiological results 20 sooner as compared to solid media cultures, some false positive results are to be expected.

PA1909

MIC and gyrA/B genetic analyses of fluoroquinolones against mycobacterium tuberculosis isolated in Japan

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Background: The caution of strain of DNA gyrase causes fluoroquinolone resistances to Mycobacterium tuberculosis (Mtb). The aim of this study was to evaluate the interrelations of minimum inhibitory concentrations (MICs) of Sifaloxacin (STFX), Moxifloxacin (MFLX), Levofloxacin (LVFX) and Ciprofloxacin (CPFX), and the mutations in the gyrA/B genes in Mtb. Methods: A total of 109 clinical Mtb isolates including 73 multi-drug resistant (MDR) strains were subjected to measure the MICs using OADC contained Middlebrook 7H9. Direct DNA sequencing of quinolone resistance-determining regions (QRDRs) were performed. Results: MIC50 and MIC90 of STFX, MFLX, LVFX and CPFX were 0.06µg/ml, 0.25µg/ml, 0.5µg/ml, 0.5µg/ml and 0.4µg/ml, 8µg/ml, 8µg/ml, 8µg/ml, respectively. Eighty (7%) and 37 (34%) strains had mutations in gyrB and gyrA. The mutant patterns were D94G, D94A, A90V, D94H, D94N and G88A in gyrA, and A53V, A53T, E540D, R485C, D500A, I552S and D577A in gyrB. The MICs were significantly higher.

Figure 1. Positive probability value of rifampicin resistance in 2014 and 2015 cohorts.