|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Case ID | Preexisting antibiotic resistant mutations(WGS) | Preexisting antibiotic resistant phenotype(MGIT) | Antibiotic  resistant mutations emerged in MDR-TB(Month, % genetic variant ) | Emerging antibiotic resistant phenotype(Month) | Other mutations(Month, % genetic variant) | *M. tuberculosis*sub-lineage | Lineage specific SNP | Treatment regimen |
| Pt072 | ***katG S315T******rpsL K43R******embB M306I*** | **INH****STR** | ***rpoB H445Y*****(1M, 2M > 90%, 5M = 74%)** | **RIF****(1M, 2M, 5M)**  |  | 2.2.1.1 | *embB (D534D)* | 2RHZE/6HE |
| Pt078 | ***rpsA* V260I*****pncA* C14R** | **INH****STR** | ***rpoB* H445Y****(5M = 66%, 8M > 90%)** | **RIF****(5M, 8M)** | *Rv1444c* (M109V): hypothetical protein, (5M = 62%, 8M > 90%)*Rv3806c* (I162L)*, ubiA\** (8M > 90%) | 1.1 | *Rv3915* (L352L) | 2SRHZ/RHZ/5HE |
| Pt080 | ***katG* S315T*****rpsL* K88R** | **INH****STR** | ***rpoB* H445Y** **(8M = 70%)** | **RIF****(8M)** |  | 2.2.1 | *Rv0697* (L268L) | 2SHRZ/6HE |
| Pt102 | ***katG* S315T*****rpsL* K43R** | **INH****STR** | ***rpoB* S450L****(1M =10%, 12M, 18M > 90%)** | **RIF****(12M, 18M)** | *Rv2472* (C84R)Hypothetical protein,(0M = 73%, 12M, 18M >90%) | 2.2.1.1 | *embB* (D534D) | 2RHZE/6HE |
| Pt108 | ***katG* S315T*****rpsL* K43R** | **INH****STR** | ***rpoB* D435V****(2M = 76%, 8M,12M,****18M, 24M > 90%)*****embB* M306V (8M,12M, 18M , 24M >90%)** | **RIF****(2M, 8M, 12M, 18M, 24M)****EMB****(8M, 12M)** |  | 2.2.1 | *Rv0697* (L268L) | 2SRHZ/6HE |
| Pt152 | ***fabG1* C-15T*****rpsL* K88R** | **INH****STR** | ***rpoB* D435V (24M > 90%)** | **RIF****(24M)** |  | 4.5 | *Rv1524* (P344P) | 2SHZR/6HE |
| Patients with intermediate SNPs difference  |  |
| Pt061 | ***katG S315T******embB M306I******rpsL K43R*** | **INH****STR** | ***rpoB* S450L(2M = 20%)** | **RIF****(2M)** | NADH pyrophosphatase*nudC P239R* (0M= 80%, 2M >90%) | 2.2 | *Rv2231c* (A205A) | 2SHRZ/6HE |
| Pt079 | ***katG S315T******rpsL K43R*** | **INH****STR** | ***rpoB H445P* (1M = 77%) *rpoB S450L* (8M > 90%)*, embB Q497R* (8M = 88%)** | **RIF****(1M, 8M)****EMB****(8M)** |  | 2.2.1.1 | *embB (D534D)* | 2SRHZ/6HE |
|  |  |  |  |  |  |  |  |  |

**Table 1. Emergence of genetic variants in *de novo* and intermediate emergence of MDR-TB isolates.**

\*ubiA – gene involved in *M. tuberculosis* cell wall biosynthesis and ethambutol resistance

% - Percentage of reads with genetic variant compared to wild type reference.

Bold sections highlight patient code, preexisting and emerging antibiotic resistant variants and phenotypes.