The emergence and spread of drug-resistant Tuberculosis (TB) is a major public health threat. TB resistance originates in the course of treatment due to genomic mutations in *Mycobacterium tuberculosis* (MTB). An increase in new cases with drug-resistant TB could be an indicator of high levels of circulating resistant strains. This study was conducted to determine the occurrence and frequency of genomic mutations that mediate Isoniazid (INH) and Rifampicin (RIF) resistance among isolates from untreated TB cases in urban Blantyre, Malawi.

Methods

A cross-sectional retrospective study was conducted on a panel of 141 (n=141) MTB clinical isolates recovered between June 2010 and January 2012 from ≥ 2+ Ziehl-Neelsen smear positive new pulmonary-TB patients with no history of treatment. Frozen isolates were revived using the BACTEC MGIT detection system. DNA was extracted using GenoLyse DNA extraction kit and detection of genomic mutations was carried out using the GenoType MTBDRplus Ver 2.0 assay.

Results

Out of the 141 isolates studied, 3 (2.1%) were found carrying mutations in the katG gene that confer resistance to Isoniazid (INH). No mutations were detected in the inhA promoter region gene that confer weak INH resistance or in the rpoB gene that confer Rifampicin resistance. All katG mutant genes had a S315T1 single point mutation, a genomic alteration that mediates high INH resistance.

Introduction

Tuberculosis (TB) is an important global infectious disease that kills more than 1.2 million people annually. This is largely attributed to HIV co-infection and most important, the emergence of drug-resistant TB. Isoniazid (INH) and Rifampicin (RIF) forms the backbone of the first-line TB treatment. TB that is resistant to both drugs (referred to as Multidrug-resistant TB, MDR-TB) is usually associated with poor prognosis and increased mortality. More than 600,000 cases of MDR-TB are reported annually. Genomic mutations in *Mycobacterium tuberculosis* (MTB) mediate resistance. More than 96% of RIF resistant MTB possess a genetic mutation in the rpoB gene at codon positions 531, 526 and 516 located within the 81-bp core region (Rifampicin Resistance Determining Region, RRDR) spanning codons 507-533. The molecular basis of INH resistance involves mutations in more than one gene with the most mutations occurring in the katG gene on codon 315 (>70%) and within the promoter region of inhA gene (15-35%). Mutations in the katG gene are relatively more common and usually the first to occur. It is estimated that more than 90% of RIF-resistant MTB isolates are also resistant to INH, making RIF resistance a surrogate marker for MDR-TB diagnosis.

Active surveillance and screening for drug-resistant TB, early isolation and management of confirmed cases are key steps in the fight against the spread of drug-resistant TB. TB remains a serious health problem in Malawi. However, low levels of drug-resistant MTB have been reported. A 2012 phenotypic culture-based large-scale survey in several districts of Malawi indicated MDR-TB levels of <0.4% among new TB cases and 4.8% among previously treated patients (J. Mpunga, personal communication, August, 2012). While phenotypic studies may still provide useful data, they are time-consuming and may be misinterpreted in cases where susceptible MTB and resistant MTB co-exist in the same patient (Heteroresistance). There is currently no evidence of the existence of transferable genetic elements (such as plasmids) between strains of MTB. Thus, indicating that drug resistance in MTB is solely mediated by chromosomal mutations and that the presence of such mutations in MTB strains from treatment naïve TB patients would indicate a direct person-to-person transmission.

In this study, we screened MTB strains isolated from treatment naïve pulmonary-TB (PTB) patients living in urban Blantyre, Malawi, to determine the occurrence and frequency of genomic mutations that confer resistance to
INH and RIF using the GenoTypeMTBDRplus Version 2.0. The GenoTypeMTBDRplus is a molecular assay designed to detect common genetic mutations associated with resistance to RIF and INH.\textsuperscript{11,23,31,32}

### Materials And Methods

#### Study isolates

All MTB isolates (n = 159) used in this study were obtained from the frozen culture collections of Dr. Derek Sloan from the Malawi Liverpool Wellcome Trust. Isolates were recovered from treatment naïve patients with PTB, living in urban Blantyre, Malawi, between June 2010 and January 2012 and were identified using Ziehl-Neelsen (Z-N) microscopy at Queen Elizabeth Central Hospital (Q.E.C.H) Laboratory in Blantyre, Malawi. Specimens with 2+ or 3+ Z-N result were cultured in Mycobacterial growth indicator tubes (MGIT) on a BACTEC MGIT automated Mycobacterial detection system (Becton Dickinson, New Jersey, USA) and were stored in cryovials at -80°C in 30% glycerol. A fixed sample size of 159 MTB isolates was the biggest available.

#### Ethical Issues

Ethical approval for this study was obtained from the University of Malawi, College of Medicine Research Ethics Committee (COMREC). All MTB clinical isolates were numerically coded and delinked from patient identifiers and no patient information was accessible. Therefore, informed consent was not required for this study.

#### Reviving frozen Mycobacterium tuberculosis isolates

During this study, all frozen isolates were revived and analyzed at Malawi Liverpool Wellcome Trust/College of Medicine (MLWT/CoM) TB Research Laboratory at the College of Medicine, Blantyre, Malawi. All specimen handling and manipulations were performed in a Class II safety cabinet in a Bio-safety level-2 (BSL-2) laboratory. During revival process, isolates were thawed at room temperature for one hour and then a 0.5 ml aliquot of the sample was inoculated into MGIT, prepared for each isolate by adding 0.8 ml oleic acid-albumin-dextrose-catalase (OADC)-PANTA (Becton Dickinson, New Jersey, USA). The tubes were then incubated at 37°C for 6 - 7 days in an automated BACTEC MGIT960 (Becton Dickinson, New Jersey, USA) device and were identified using Ziehl-Neelsen (Z-N) microscopy at Queen Elizabeth Central Hospital (Q.E.C.H) Laboratory in Blantyre, Malawi. Specimens with 2+ or 3+ Z-N result were cultured in Mycobacterial growth indicator tubes (MGIT) on a BACTEC MGIT automated Mycobacterial detection system (Becton Dickinson, New Jersey, USA) and were stored in cryovials at -80°C in 30% glycerol. A fixed sample size of 159 MTB isolates was the biggest available.

DNA extraction was done using GenoLyse DNA extraction Kit Ver 1.0 (Hain Lifesciences, Nehren, Germany) attached on an interpretation worksheet. Lane A: negative control containing amplification mix A and B. Lane G: Negative control containing Genolysy DNA extraction kit. Lane 10: katG (MUT 1) genomic mutation indicating a S315T1 amino acid change. Lane 11: katG (MUT 1) genomic mutation indicating a S315T1 genomic mutation detected/AGC→ACC (Serine→Threonine).

### Table 1: Revived M. tuberculosis isolates (n=159).

| GenoTypeMTBDRplus Strip Interpretation | Number of M. tuberculosis isolates | % |
|---------------------------------------|-----------------------------------|---|
| V in all katG WT                      | 138                               |   |
| V in all katG MUT                     |                                   |   |
| Δ in all katG MUT                     |                                   |   |
| Δ in all inhA WT                      | 141                               |   |
| V in all inhA MUT                     |                                   |   |
| No Mutation detected                 |                                   |   |
| No Mutation detected                 |                                   |   |
| No Mutation detected                 |                                   |   |

| Drugs | Gene | Number of isolates | GenoTypeMTBDRplus Strip Interpretation | Mutation detected | % mutation detected |
|-------|------|--------------------|----------------------------------------|-------------------|---------------------|
| INH   | katG | 3                  | VkatG WT1                              | S315T1 genomic mutation detected/AGC→ACC (Serine→Threonine) | 2.1 |
|       |      |                    | ΔkatG MUT1                             |                   |                     |
|       |      |                    | VkatG MUT2                             |                   |                     |
|       |      | 138                | ΔkatG WT1                              |                   |                     |
|       |      |                    | V in all katG MUT                      |                   |                     |
|       | inhA | 141                | Δ in all inhA WT                       |                   |                     |
|       |      |                    | V in all inhA MUT                      |                   |                     |
|       |      | 141                | Δ in all rpoB WT                       |                   |                     |
|       |      |                    | V in all rpoB MUT                      |                   |                     |
|       | rpoB |                    |                                       |                   |                     |

\(\nabla\), absence of band; \(\Delta\), presence of band; MUT, mutant; WT, wild-type.

### Table 2: Detected genomic mutations that confer INH and RIF resistance using (n=141) (see Fig.1 for Interpretation)

| TB drugs | Gene | Number of isolates | GenoTypeMTBDRplus Strip Interpretation | Mutation detected | % mutation detected |
|----------|------|--------------------|----------------------------------------|-------------------|---------------------|
| INH      | katG | 3                  | VkatG WT1                              | S315T1 genomic mutation detected/AGC→ACC (Serine→Threonine) | 2.1 |
|          |      |                    | ΔkatG MUT1                             |                   |                     |
|          |      |                    | VkatG MUT2                             |                   |                     |
|          |      | 138                | ΔkatG WT1                              |                   |                     |
|          |      |                    | V in all katG MUT                      |                   |                     |
|          | inhA | 141                | Δ in all inhA WT                       |                   |                     |
|          |      |                    | V in all inhA MUT                      |                   |                     |
|          | rpoB | 141                | Δ in all rpoB WT                       |                   |                     |
|          |      |                    | V in all rpoB MUT                      |                   |                     |

\(\nabla\), absence of band; \(\Delta\), presence of band; MUT, mutant; WT, wild-type.

### Molecular assay

The GenoTypeMTBDRplus Ver 2.0 (Hain Lifesciences, Nehren, Germany) was used to detect MTB drug-resistant
related chromosomal point-mutations within the katG, inhA promoter, and rpoB genes. The GenoTypeMTBDRplus employs a multiplex PCR during which katG, inhA, rpoB genes are amplified using biotin-labeled primers and the resulting amplicons are hybridized to DNA probes bound to a membrane. During PCR, a total amplification volume of 50 µl comprising of 10 µl amplification mix-A, 35 µl amplification mix-B and 5 µl template DNA was prepared according to the manufacturer’s recommendations.33 The amplification protocol was optimized and consisted of 15 min initial denaturation at 95°C, 10 cycles; 95°C for 30 sec and 65°C for 2 min, and then 20 cycles; 95°C for 25 sec, 50°C for 40 sec, and 70°C for 40 sec, and the final cycle at 70°C for 8 min.

Reverse hybridization of biotin-labeled amplicons to membrane-bound probes on the strip was performed manually at 45°C using a shaking water bath and this consisted of the addition of conjugate and substrate to detect visible band patterns as recommended by the manufacturer. After several washing steps, the membrane-strips were allowed to dry. The membrane-bound DNA included the following probes: one katG wildtype (WT) probe; two katG mutant (MUT) probes (S315T1 and S315T2); four rpoB MUT probes (D516V, H526Y, H526D, and S531L); two inhA WT probes and four inhA MUT probes (C15T, A16G, T8C, and T8A) (Figure 1). All results were interpreted according to the manufacturer’s instructions. The absence of mutation was defined as hybridization (indicated by the presence of a colored band) to all the WT probes and no hybridization to the MUT probes. The presence of mutation was defined as the absence of hybridization on any one of the WT probe, with or without hybridization on the corresponding MUT probe (Figure 1).

**Data analysis**

Simple data summaries and descriptive statistics including proportions and percentages were used to present the occurrence and frequency of genomic mutations conferring resistance to rifampicin or isoniazid or to both drugs among the studied MTB isolates.

**Results**

A total of 141 MTB isolates recovered from treatment naïve pulmonary TB patients were screened to determine the occurrence and frequency of genomic mutations within the katG, inhA promoter region and rpoB genes. Out of the 141 MTB isolates studied, gene mutation was only confirmed for the katG gene. No mutations in inhA promoter region and rpoB gene were detected in any of the isolates (Table 2). Since no MTB isolate carried both INH and RIF resistant genes, no MDR-MTB were detected. As for the frequency of katG genetic mutation, only 3 out of the 141 MTB (2.1%) possessed a katG mutant gene. All katG mutations were S315T1, a AGC-to-ACC (Ser → Thr) point mutation (Table 2). All of the katG mutations detected at wild-type probes were also observed at the corresponding mutant probes.

**Discussion**

The emergence of drug-resistant TB is a major threat to TB treatment and eradication. The consequences of the rise of TB drug-resistance in Malawi, a country with a high burden of HIV and poverty, would be extremely devastating. Active screening for drug-resistant TB and early management of cases is therefore important. The geographical distribution of genomic mutations, that are associated with TB drug-

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Malawi. The characterization and distribution of specific types of genomic mutations that mediate resistance in MTB could be important for optimization of the diagnosis, treatment, and prevention of drug-resistant TB. Low levels of circulating drug-resistant MTB isolates evidently indicate remarkable efforts by the National TB control program in the fight against TB in Malawi.

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