Tuberculosis (TB) is the most common opportunistic infection in human immunodeficiency virus (HIV)-infected patients and the emergence of drug-resistant tuberculosis (DR-TB) is a growing problem in resource-limited settings. Adequate infrastructure for testing drug sensitivity and sufficient evidence of first-line resistance are currently unavailable in Nigeria. We collected sputum samples from HIV-infected patients enrolled in the Harvard PEPFAR/APIN Plus program over 12 months at two PEPFAR antiretroviral therapy (ART) clinics in the southwest and north central regions in Nigeria. Smear-positive sputum samples were submitted for GenoType MTBDRplus testing (n = 415); mutations were confirmed through sequencing. Our results show high rates of DR-TB in Nigerian HIV-infected individuals (7.0% for rifampin [RIF] and 9.3% for RIF or isoniazid [INH]). Total RIF resistance indicative of MDR-TB in treatment-naive patients was 5.52%, far exceeding the World Health Organization predictions (0 to 4.3%). RIF resistance was found in 6/213 (2.8%) cases, INH resistance was found in 3/215 (1.4%) cases, and MDR-TB was found in 8/223 (3.6%) cases. We found significantly different amounts of DR-TB by location (18.18% in the south versus 3.91% in the north central region [P < 0.01]). Furthermore, RIF resistance was genetically distinct, suggesting possible location-specific strains are responsible for the transmission of drug resistance (P < 0.04). Finally, GenoType MTBDRplus correctly identified the drug-resistant samples compared to sequencing in 96.8% of cases. We found that total DR-TB in HIV-infection is high and that transmission of drug-resistant TB in HIV-infected patients in Nigeria is higher than predicted.

The conventional methods of drug resistance testing involve growth of Mycobacterium tuberculosis on liquid or solid culture medium (35). Culture methods are costly and time-consuming, thus limiting both utility for patient care and likelihood of timely treatment. Recently, several new commercial tests have been described that identify MDR-TB based on the genetic sequence; one is a line probe assay named GenoType MTBDRplus, which diagnoses TB and identifies drug resistance. It specifically examines samples for classic genetic mutations that confer resistance to both INH and RIF. Due to the reported efficiency and low cost of this test, it represents an alternative to conventional drug sensitivity testing through culture. The test has been successfully used in several locations worldwide with high sensitivity rates for RIF (>95.5%) and INH (>81.8%) resistance (2, 4, 15, 17, 21, 23) and 100% specificity (2, 4, 15, 17, 21, 23). The GenoType MTBDRplus test is also reliable as a method for surveillance of drug resistance (26). The surveillance and monitoring of both INH- and RIF-resistant M. tuberculosis is not only beneficial for an individual patient but also for the HIV-infected population as a whole, since they are more susceptible to M. tuberculosis infection (10). Implementation of the GenoType
### MATERIALS AND METHODS

Two geographically distinct locations in Nigeria were chosen, the Nigerian Institute for Medical Research (NIMR) in Lagos and the Jos University Teaching Hospital (JUTH), located in the southwestern and northern central zones of the country, respectively. NIMR data were collected from June 2009 to June 2010, and JUTH data were collected between August 2009 and November 2010. The ethical approval was obtained from the institutional review boards at NIMR, JUTH, and Harvard School of Public Health (approval 16430-103).

At regular clinic visits, HIV-infected patients were screened for symptoms of pulmonary TB, including chest pain, cough lasting more than 2 weeks, fever, night sweats, and weight loss. Upon identification, patients were asked to participate in the study and provided written informed consent. Consent was obtained from the participants, and the study was conducted according to the guidelines of the ethical committee of each center. The tests strips were decontaminated using the modified Petroff method and stained directly for acid-fast bacilli (AFB) using the Ziehl-Neelsen method (20).

Patients with AFB-positive samples were enrolled in the study for a 12-month period.

Samples identified as sputum smear positive (SS⁺) for AFB were included in the study. Crude DNA extraction was performed on site, followed by PCR and hybridization on test strips, according to the GenoType MTBDRplus (Hain Lifesciences, Nehren, Germany) protocol (11). Isolated DNA was stored at −20°C until the genotypic resistance testing was performed. GenoType MTBDRplus test instructions were followed for M. tuberculosis DNA amplification and hybridization (11). The tests strips were scored for resistance based on the presence of a mutant strain or the absence of wild-type DNA.

**Multiplex-nested PCR and DNA sequencing of resistance genes.** Samples diagnosed as resistant with the GenoType MTBDRplus test and 16 susceptible samples from the same cohort were sequenced. Portions (5 to 10 μl) of crude lysate were used to amplify the four resistance-conferring genes (rpoB, katG, the inhA promoter, and the oxyR-ahpC intergenic regulatory region) using a multiplex PCR. The PCR was established using 1× KOD polymerase buffer, 0.2 mM deoxynucleoside triphosphate (each), 1.5 mM MgSO₄, 5% dimethyl sulfoxide, 100 nM concentrations of each primer, and 1% KOD Hot Start polymerase (Toyobo, Osaka, Japan). Cycling consisted of 1 cycle of 3 min at 95°C, followed by 25 cycles of 20 s at 95°C, 10 s at 63°C, and 15 s at 72°C, and then 1 cycle of 2 min at 72°C. A nested PCR was performed individually on each gene using 5 to 10 μl of the multiplex sample. The reagent concentrations were identical to the multiplex PCR, except that 200 nM inner primer was used. The nested PCR protocol consisted of 1 cycle of 3 min at 95°C, followed by 30 cycles of 20 s at 95°C and 10 to 15 s of annealing/extension at various temperatures (rpoB and inhA, 10 s for 60°C; katG, 10 s for 65°C; oxyR-ahpC, 10 s for 62°C; and 5 s for 72°C).

The nested PCR products were then separated through electrophoresis on a 2% NuSieve (Lonza, Rockland, ME) agarose gel. The bands of the appropriate sizes were excised and purified from the gel using a MiniElute kit (Qiagen, Hilden, Germany) according to the manufacturer’s protocol. After the PCR fragment concentrations were evaluated using a Quanti-IT Picogreen (Invitrogen, Carlsbad, CA), 10 ng of the DNA was used for sequencing with a BigDye Terminator (v1.1; Applied Biosystems, Carlsbad, CA) cycle sequencing kit on an Applied Biosystems 3100 sequencing instrument. Primers used for sequencing were the inner primers of the multiplex-nested PCR, except for the inhA promoter region that used separate primers (see Table S1 in the supplemental material).

**Data analysis.** Experimentally obtained sequences were aligned with the known genetic sequence of a susceptible M. tuberculosis strain H37Rv using Lasergene (DNASTar, Madison, WI) and examined for previously reported resistance associated mutations. The sequence consensus of each sample was compared to the GenoType MTBDRplus results to assess the two genotypic evaluations of resistance. Groups of resistant samples were compared using the Fisher exact test, while patient characteristics at study entry were compared using the chi-square or Wilcoxon rank-sum test as appropriate. Significance threshold was set to \( P < 0.05 \).

### Results

A total of 940 patients presented with signs and symptoms of TB, while 535 had at least one AFB⁺ sputum. Of 415 available patient samples that were tested with GenoType MTBDRplus, genes representative of RIF susceptibility could be evaluated for 213 cases, INH susceptibility for 215 cases, and MDR-TB for 223 cases. RIF resistance with the GenoType MTBDRplus test was evaluated with the hybridized band profile of the rpoB gene, while INH was evaluated by hybridization to the katG open reading frame and the inhA promoter sequence. When we compared patients by site, there were no statistically significant differences in age (median, 36 years; \( P = 0.72 \), evidence of previous TB treatment (JUTH, \( n = 37 \); NIMR, \( n = 17 \) [\( P = 0.17 \)], or the percentages of female patients with 53.7% at JUTH and 64.4% at NIMR (\( P = 0.11 \)). There were differences in time from symptom onset to clinic presentation (4 weeks at JUTH versus 3 weeks at NIMR; \( P < 0.01 \) (Table 1).

A greater number of resistant samples were observed at NIMR (\( n = 14 \)) than at JUTH (\( n = 5 \) (\( P = 0.001 \)). The percentage of resistant samples for each drug, but not for both (MDR-TB), demonstrated significantly higher rates of resistance at NIMR com-

---

**Table 1: Patient characteristics at study entry by site location**

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>NIMR (n = 90)</th>
<th>JUTH (n = 134)</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Previous TB treatment</td>
<td>17</td>
<td>37</td>
<td>0.13</td>
</tr>
<tr>
<td>Median age in yrs (IQR)</td>
<td>35.62 (29.4–43.3)</td>
<td>35.99 (30.8–42.6)</td>
<td>0.72</td>
</tr>
<tr>
<td>Gender</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Female</td>
<td>58</td>
<td>72</td>
<td>0.11</td>
</tr>
<tr>
<td>Male</td>
<td>32</td>
<td>62</td>
<td></td>
</tr>
<tr>
<td>Median no. of wks (IQR) between symptom onset and clinic presentation, no. of observations</td>
<td>3 (2–3), 86</td>
<td>4 (3–8), 123</td>
<td>&lt;0.01</td>
</tr>
</tbody>
</table>

a NIMR, Lagos state, South-west region; JUTH, Plateau state, North-central region. Data refer to numbers of patients except as noted in column 1. IQR, interquartile range.

b Data available for a subset of patients.
pared to JUTH (Table 2). Fifty-four patients had previous exposure to TB treatment, while 170 were treatment naive. The stratification based on patient’s prior treatment status showed no significant differences between the prevalence of drug resistance in naive versus pretreated patients (Table 3).

All of the polymorphisms found with the GenoType MTBDRplus test, the codons they identify, and the numbers of samples with each profile by location are listed in Table 4. The GenoType MTBDRplus resistance profile for RIF differed by study site, where rpoB mutations from JUTH samples were predominantly found in codons 526 to 529 (wt2), while the NIMR samples showed mutations in codons 530 to 533 (wt3) (LG7 excluded, $P = 0.04$). Genotype resistance profiles also indicate that mutations conferring INH resistance in Nigeria occur at a similar rate in the inhA promoter and the katG S315T region, in contrast to previous reports (3, 14, 16). Furthermore, all of the mutations found in katG were the same point mutation, S315T1, and the inhA promoter was mutated at the C−15T position.

Using the multiplex/nested PCR technique, we amplified and sequenced most of the resistant samples (exceptions included LG12, LG13, and LG14), as well as 16 susceptible samples directly from sputum, to examine exact mutations found in resistance conferring genes. The GenoType MTBDRplus susceptible samples showed no polymorphisms previously reported to be associated with resistance (Table 4). Interestingly, each of the three samples from JUTH with a mutation in codon 526 of the rpoB gene had a different point substitution responsible for resistance. The most common mutation spanning the rpoBwt2 codon in NIMR samples was S315L.

Only 2 of the 16 resistant samples (LG7 and LG4) and none of 16 susceptible samples had discordant results obtained from the GenoType MTBDRplus test and sequencing. Sample LG7 was still resistant to RIF, and one of the three mutations indicated by GenoType MTBDRplus was concordant (rpoBwt4 D516A). Instead of the mutations in the rpoBmut1 or rpoBmut2 region, a mutation was observed in the rpoBmut2 region L511P.

In addition, although sample LG7 exhibited no mutations conferring INH resistance in the katG or inhA promoter regions, it was the only sample that had a C→T substitution at location −25 (in relation to the ahpC transcription start) of the oxyR-ahpC regulatory region, previously described only in inhA resistant strains (14, 16, 25). Therefore, LG7 was not misdiagnosed for RIF resistance, but potential inhA resistance could have been missed by not including the oxyR-ahpC regulatory region in the assay.

Sample LG4 was designated as INH resistant by the GenoType MTBDRplus test but was not confirmed by sequencing; instead, the sample appeared to be susceptible according to its sequence analysis. With LG4 identified as susceptible, INH resistance still differed significantly by site (NIMR INH resistance = 9.4% [P < 0.03] versus JUTH; NIMR any resistance = 16.9% [P < 0.01] versus JUTH). There was not a significant difference in any resistance, including INH between treatment-naive and experienced individuals.

In total, 1 of 31 sequenced samples (3.2%) did not confirm the resistance diagnosis obtained with the GenoType MTBDRplus; therefore, the concordance rate for DR-TB diagnosis was 96.8% (oxyR-ahpC promoter region excluded). We sequenced a total of 93 regions (rpoB, katG, and inhA) that are analyzed by the GenoType MTBDRplus test. GenoType MTBDRplus misidentified only four mutations and was therefore 95.7% specific.

**DISCUSSION**

In Nigeria, HIV/TB coinfection rates are as high as 30% in antiretroviral therapy (ART) clinic settings, and the national prevalence of MDR-TB is unknown. Our results show high rates of transmitted drug-resistant TB (5.5%), inferred by rates of rifampin resistance in treatment-naive patients. This rate exceeds the upper limit of the WHO MDR-TB models (4.3%). Furthermore, AFB sputum smears, using the Ziehl-Neelsen stain, lack sensitivity in identifying TB cases, and some cases of *M. tuberculosis* infection could have been missed. Since resistant bacteria are more likely to be less fit than sensitive bacteria (1, 8, 9, 30) and therefore cause paucibacillary disease, our results may represent an underestimate of drug resistance. This indicates that transmission of drug-resistant TB is a more serious problem than previously anticipated.

The GenoType MTBDRplus test correctly identified mutations with a high concordance rate. In recent literature, the gene-based identification of MDR-TB has gained prominence. The GeneXpert MTB/RIF is considered an appropriate new technology for diagnosing both TB and rifampin drug resistance. Although both GeneXpert and GenoType MTBDRplus work on a similar principle—gene amplification and subsequent hybridization—GeneXpert MTB/RIF does not examine INH resistance. Mutational analysis of INH resistance is more complex than RIF because it requires evaluating more genes. Furthermore, the genotypic analysis of rpoB for RIF resistance is thought to be sufficient for evaluating the public health threat of drug-resistant TB. However, recent reports indicate that this remains controversial (29). In our study, we observed 1.4% INH monoresistance and 2.8% RIF monoresistance, highlighting the importance of evaluating both drug susceptibilities. Although one case of INH resistance was incorrectly identified with GenoType MTBDRplus, the inclusion of inhA and katG mutation analysis in this test correctly identified three INH-resistant, RIF-susceptible strains. This is particularly important in HIV-prevalent settings where INH prophylaxis is"
being considered. Such preventative measures might not be effective and could increase the rates of INH resistance, exacerbating the diagnostic challenges for MDR-TB. Furthermore, misdiagnosing patients as MDR-TB when they are only Rif mono-resistant would lead to inappropriate second-line treatment, when such treatment in resource-limited settings is already limited.

The baseline characteristics of age, gender, and prior treatment status of patients did not show major site differences, indicating that the sites were comparable. Although the duration of symptoms prior to clinic visit differed, this difference might be due to the fact that patients visiting the clinic in Jos traveled longer distances and therefore were at a disadvantage to be adherent to clinic visits. In these two geographically distinct study populations, a significantly higher number of drug-resistant TB was found in Lagos compared to Jos. Transmission of drug-resistant TB in Lagos is further suggested by the fact that 9 of 13 patients with drug-resistant TB were treatment-naive (versus 2/5 in Jos). An alternative explanation is that the M. tuberculosis strains differed by location and therefore did their transmission and/or mutation rates. Although we were not able to evaluate the M. tuberculosis strains or their characteristics in the present study, the mutations in the rpoB gene are suggestive of such differences. All of the Jos mutations in the rpoB gene were distinct, implying that they were acquired through separate mutagenesis events, whereas most of the Lagos strains had the same mutation (S531L) belonging to a potentially more transmissible strain.

In summary, our study demonstrated high rates of drug-resistant TB in HIV-infected patients. We also showed that the cost-effective GenoType MTBDRplus test correctly identified resistance-conferring mutations in the majority of samples examined (95.7%). Although our sample size was small, this is the first multisite study of MDR-TB in HIV-infected population in Nigeria. Consistent with WHO recommendations, our results support the urgent need for systematic drug resistance testing in all HIV-infected patients with symptoms suggestive of TB.

ACKNOWLEDGMENTS

We are deeply grateful to the patients for their willingness to participate in this study. Furthermore, we thank the clinical and laboratory staff of the NIMR and JUTH APIN Plus clinics. We especially thank Rosemary Adu, Favor Olatunbasun, Godwin Imade, Moses Adie, Nwanneka Tochukwu, Lauretta Efere, Peter Nwadike, Tope Abiodun, and Eucharia Obihide.

This study was funded in part by the U.S. Department of Health and Human Services, Health Resources, and Services Administration (U51HA02522-01-01). Research support to L.D. was provided by the Zlatko and Balokovic Scholarship, the Uwe Brinkmann Traveling Grant, and a Harvard University Science and Engineering Committee Scholarship.

The contents are solely the responsibility of the authors and do not represent the official views of the funding institutions.

REFERENCES


