

***atpE* Mutation in *Mycobacterium tuberculosis* Not Always Predictive of Bedaquiline Treatment Failure**

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We report the emergence of an *atpE* mutation in a clinical *Mycobacterium tuberculosis* strain. Genotypic and phenotypic bedaquiline susceptibility testing displayed variable results over time and ultimately were not predictive of treatment outcome. This observation highlights the limits of current genotypic and phenotypic methods for detection of bedaquiline resistance.

Bedaquiline is one of the core drugs used to treat multidrug-resistant (MDR) tuberculosis (TB) and extensively drug-resistant TB (XDR TB) (1). Bedaquiline resistance is now part of the revised definition of XDR TB, and its incidence is rising alarmingly (2,3). Resistance to bedaquiline is mainly caused by mutations in *Rv0678* (*mmpR*), which encodes the repressor of the efflux pump MmpL5–MmpS5, usually leading to low-level resistance (4). Conversely, mutations in *atpE*, which encodes the target of bedaquiline, the c subunit of the ATP synthase, are rarely described in clinical strains (5) and are associated with high increase of MICs (4). Mutations in *pepQ* and *Rv1979c* are also reported, but their effect on bedaquiline susceptibility is unclear. We report a case of an *atpE* mutation in a bedaquiline-resistant clinical strain of *Mycobacterium tuberculosis* and discuss the performances of current methods for susceptibility testing (Appendix, <https://wwwnc.cdc.gov/EID/article/28/5/21-2517-App1.pdf>) and their clinical implications (6).

A 32-year-old man from Georgia received a diagnosis of bilateral cavitary lung MDR TB upon his

arrival in France in January 2020. Three consecutive treatment regimens of bedaquiline and clofazimine had failed. A fourth regimen combining bedaquiline, linezolid, cycloserine, clofazimine, delamanid, and amoxicillin/clavulanate + meropenem was initiated on arrival.

The first isolate from January 2020 (S1) was bedaquiline-resistant with a MIC one dilution above the breakpoint (MIC = 2 mg/L) and clofazimine-susceptible with a MIC close to the breakpoint (MIC = 1 mg/L). We detected 2 deletions (P129fs [15%] and G66fs [54%]) in *Rv0678* (Figure).

At the end of March 2020, cycloserine was withdrawn because of phenotypic resistance, and bedaquiline, which had been stopped 1 month earlier, was resumed; the patient underwent a lobectomy. One month after, sputum microscopic examination and culture were still positive. The second isolate (S2) from April 2020 had an increased bedaquiline MIC (4 mg/L) but clofazimine MIC remained unchanged (1 mg/L). No mutation in *Rv0678* was detected, but we observed an AtpE I66M (63%) substitution (Figure).

Two months later in June, the patient was sputum smear-negative but remained culture positive. Isolate S3 was susceptible to bedaquiline (MIC = 0.5 mg/L) and clofazimine resistant (MIC = 2 mg/L). A deletion was found in *Rv0678* different from those identified in S1: deletion at position 293 (N98fs) (97%), whereas no mutation was identified in *atpE* (Figure). Verapamil and ethionamide were added and amoxicillin-clavulanate + meropenem was stopped. Finally, samples from September 2020 were culture negative, with regression of pulmonary lesions. The outcome was classified as treatment success in February 2021 after 13 months of treatment and was still favorable as of December 2021.

All 3 isolates shared the same spoligotype (SIT1) (Beijing lineage) and displayed only 3 single-nucleotide variants (SNVs) of difference by pairwise comparison. The SNVs were all nonsynonymous. Two SNVs were only recovered in strain S2, 1 corresponding to the AtpE: I66M substitution and 1 located in *Rv0243* (L136P substitution) encoding the acetyl-CoA acyltransferase FadA2 and probably implicated in lipid degradation. One SNV was only found in S1 in *Rv3909* (M683L substitution), encoding a protein of unknown function. No mutations were observed in *pepQ*, its promoter, or in *Rv1979c* (7).

As this case illustrates, identifying bedaquiline resistance in the laboratory and its effects on patient management appear complex. Over a 6-month period, we tested 3 *M. tuberculosis* isolates with different genotypic and phenotypic patterns regarding

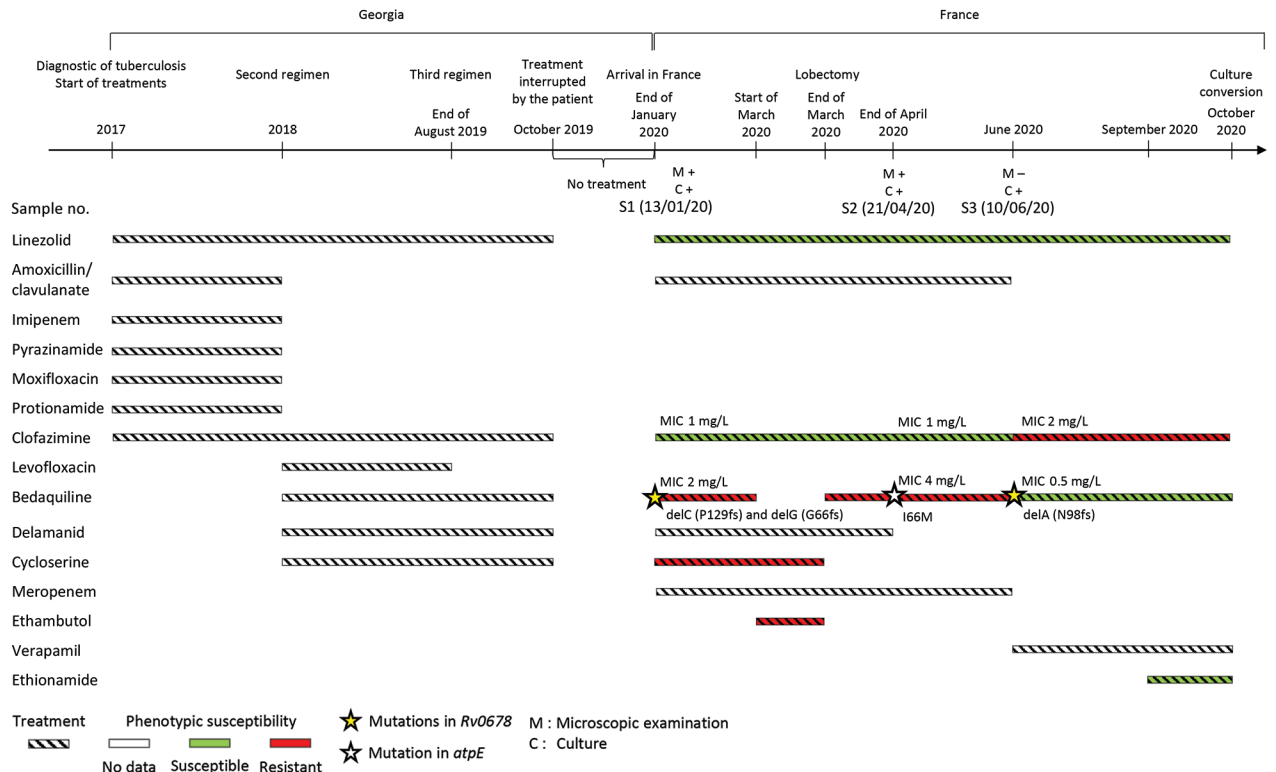


Figure. Timeline of treatment regimen and microbiologic data for patient with multidrug-resistant tuberculosis before and after his arrival in France from Georgia. Timeline for each antibiotic indicates treatment (striped), phenotypic resistance (red), and susceptibility (green), as indicated in patient records. M, microscopic examination; C, culture.

bedaquiline, exhibiting various MIC levels and mutations in genes involved in bedaquiline resistance. These isolates displayed only 3 SNVs by pairwise comparison of their genomes, excluding a reinfection by a new strain or a mixed infection.

Of note, mutations in *atpE* or *Rv0678* were found only once and were not found at subsequent time-points. Despite continuous bedaquiline treatment, resistant strain S2 with the *atpE* mutation was not selected, and the patient was cured. A previous in vitro study suggested that, whereas *Rv0678* mutations were dynamic over time, *atpE* mutations were fixed once they appeared (8). This observation was not confirmed by our clinical case. One possible explanation for nonfixation of these mutations could be the associated fitness cost. However, an in vitro study did not show any fitness cost because of the I66M substitution (9). Because fitness also depends on the genetic background, the results of this in vitro study might not be transposable here. Regarding *Rv0678*, 2 mutations have been studied and did not have fitness impact (E138G and R94Q) (4). Additional in vivo and epidemiologic studies would help evaluate the fitness cost of such mutations. Another explanation for the variability of genotypic and

phenotypic bedaquiline susceptibility over time could be a spatial heterogeneity in the lesions as already described (10).

This case raises concerns about the ability of current phenotypic and genotypic methods to detect bedaquiline resistance. Further studies are needed before relying on these methods for therapeutic decisions. In the meantime, these data can help improve the World Health Organization database of drug resistance-related mutations (11). Overall, this case underlines the complexity of bedaquiline-resistance mechanisms and of the dynamics of mutation emergence and selection.

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We wish to honor the memory of our colleague, Wladimir Sougakoff, who passed away in January 2022.

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About the Author

Dr. Fournier Le Ray recently successfully defended a PhD thesis in microbiology. Her research was focused on the in vivo emergence of bedaquiline resistance.

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Emerging Novel Reassortant Influenza A(H5N6) Viruses in Poultry and Humans, China, 2021

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A novel highly pathogenic avian influenza A(H5N6) clade 2.3.4.4b virus was isolated from a poultry market in China that a person with a confirmed case had visited. Most genes of the avian and human H5N6 isolates were closely related. The virus also exhibited distinct antigenicity to the Re-11 vaccine strain.

Highly pathogenic avian influenza A(H5N1) virus emerged in China in 1996. H5 viruses have spread to Eurasia since 2003, Africa since 2005, and North America since 2014–2015. These viruses cause huge economic losses to the poultry industry and pose substantial threats to human health. By March 2022, a total of 75 confirmed cases of human infection with influenza A(H5N6) virus had been reported, including 48 cases in China since 2021 (<https://www.who.int/teams/global-influenza-programme/avian-influenza/monthly-risk-assessment-summary>).

On July 9, 2021, a human case of H5N6 infection was reported in Chongqing, China. One day later, we conducted an epidemiologic survey in the poultry market the patient had visited and collected swab samples from poultry. We identified the samples as H5N6 subtype by using H5- and N6-specific primers and probes. We propagated the virus in 10-day-old specific pathogen-free chicken embryos and designated the isolate as A/chicken/Chongqing/H1/2021(H5N6) (CK/CQ/H1). We sequenced the viral genome by using the Sanger method and deposited the sequences in GISAID (<https://www.gisaid.org>; accession nos. EPI1937512–9).

Phylogenetic analysis of the hemagglutinin (HA) genes showed that CK/CQ/H1 and A/Chongqing/