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DOI: <https://doi.org/10.1128/AAC.00253-16>




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# *dfrA thyA* Double Deletion in *para*-Aminosalicylic Acid-Resistant *Mycobacterium tuberculosis* Beijing Strains

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*para*-Aminosalicylic acid (PAS) is a group 4 antituberculosis agent (1). It targets folate metabolism as shown in Fig. S1 in the supplemental material, which also summarizes the known mechanisms of resistance to this prodrug (2). Recently, we reported a multidrug-resistant (MDR) *Mycobacterium tuberculosis* Beijing strain harboring a deletion of both *dfrA* and *thyA* from Australia (Fig. 1A and Table S1) (3). Since then, we have found deletions affecting both genes in five further MDR Beijing strains (two isolated in Australia and three from Peru) and one extensively drug-resistant (XDR) Beijing strain from China. The Australian MDR strains were recovered from three patients with no apparent epidemiological links who were likely infected in their country of origin (Table S1). The three Peruvian isolates were closely related and consequently shared the same deletion, whereas the remaining strains were distantly related and had deletions that differed in size (Fig. 1A). Consequently, these five distinct deletions were acquired independently, which can be a signal for positive selection of resistance mechanisms. In line with this hypothesis, the strains from Australia and China were found to be PAS resistant when tested with the Bactec MGIT 960 system and on Löwenstein-Jensen medium, respectively (see Supplemental methods). Two out of the three Peruvian deletion mutants were also found to be PAS resistant on 7H10 medium at 8 µg/ml, whereas the two closely related ancestral wild-type strains were found to be susceptible (Fig. 1B). We were unable to retest the strains at 2 µg/ml, the critical concentration recommended by the Clinical and Laboratory Standards Institute and the World Health Organization, which would have clarified whether the result for the third deletion mutant as susceptible was an artifact (1, 4).

The observation that *dfrA* could be deleted was remarkable in light of our current understanding of folate metabolism in *M. tuberculosis*. Two studies suggested that *dfrA* is essential *in vitro* in the H37Rv laboratory strain (5, 6). More recently, it was shown that *dfrA* is conditionally essential and can be knocked out in H37Rv only if *Rv2671* is overexpressed *in trans*, presumably due to its greatly reduced dihydrofolate reductase activity compared to that of *DfrA* (7, 8). Our *in silico* analysis of the seven *dfrA thyA* double deletion mutants did not reveal any known *Rv2671* mutations (Table S1), such as the G-to-A upstream mutation at position –12 that results in its overexpression and consequently con-

fers PAS resistance (this mutation was incorrectly referred to as affecting position –11 in two of our prior studies [7, 9]). Assuming that no other pertinent differences that are specific to the Beijing genotype relative to H37Rv exist or that a yet-unknown acquired mutation elsewhere in the genome that resulted in the overexpression of *Rv2671* was present, we propose that this apparent contradiction can be reconciled if the essentiality of *dfrA* was dependent not only on the expression level of *Rv2671* but also on the presence of wild-type *thyA*. The fact that *thyA* was deleted in all seven *dfrA* mutants meant that only the second thymidylate synthase, encoded by the essential *thyX* gene, was active in these strains (Fig. S1). Contrary to *ThyA*, *ThyX* generates tetrahydrofolate rather than dihydrofolate upon catalysis and therefore does not require high dihydrofolate reductase activity to provide sufficient levels of tetrahydrofolate (2). This is in line with the fact that *dfrA* is not required in bacterial species that lack *thyA* (10). Consequently, *Rv2671* appeared to be sufficient to sustain growth, even without being overexpressed in these deletion mutants. It should therefore be possible to knock out *dfrA* in strains of *M. tuberculosis* with inactive *thyA*. Moreover, the adjacent locations of *thyA* and *dfrA* in the genome should make their simultaneous deletion possible (Fig. 1A).

Interestingly, all but one of the deletion mutants also convergently acquired mutations upstream of *thyX* compared to what was observed for the two closely related Peruvian control strains

Accepted manuscript posted online 28 March 2016

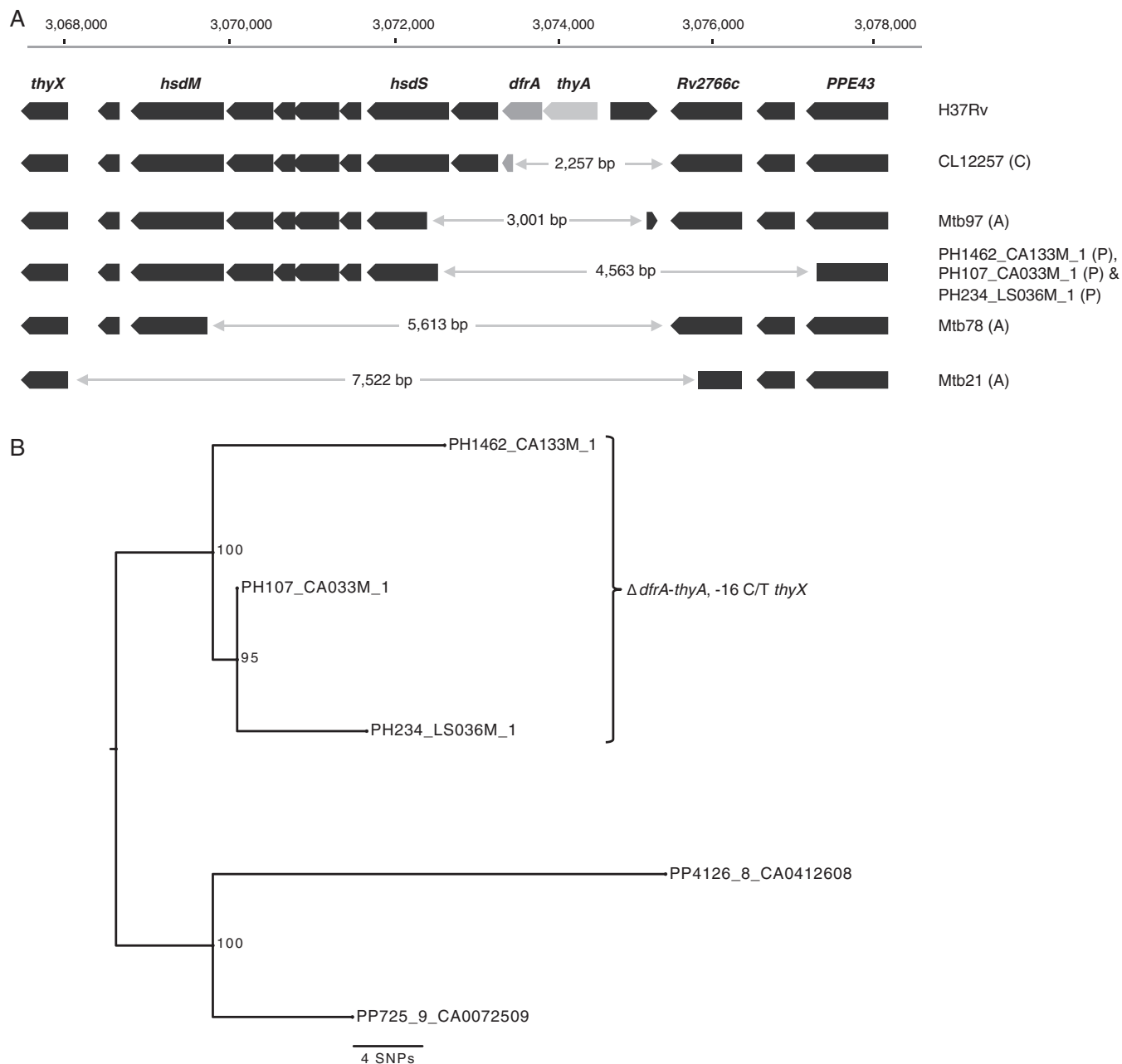
Citation Moradigaravand D, Grandjean L, Martinez E, Li H, Zheng J, Coronel J, Moore D, Török ME, Sintchenko V, Huang H, Javid B, Parkhill J, Peacock SJ, Köser CU. 2016. *dfrA thyA* double deletion in *para*-aminosalicylic acid-resistant *Mycobacterium tuberculosis* Beijing strains. Antimicrob Agents Chemother 60:3864–3867. doi:10.1128/AAC.00253-16.

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Supplemental material for this article may be found at <http://dx.doi.org/10.1128/AAC.00253-16>.

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**FIG 1** Analysis of *dfrA* and *thyA* deletion strains, all of which tested PAS resistant, with the exception of PH107\_CA033M\_1. (A) Diagram of deletions in seven clinical strains compared with the wild-type H37Rv laboratory strain. The scale at the top corresponds to the genome position in H37Rv. The letter in parentheses denotes the country of isolation (Australia [A], China [C], and Peru [P]). Mtb97 was reported previously (3). (B) Maximum likelihood tree based on whole-genome data of the three Peruvian deletion mutants, which also share a mutation upstream of *thyX* that is also present in Mtb97 and Mtb78 (Table S1), and two closely related wild-type strains, which were PAS susceptible.

(Fig. 1B and Table S1) (11). In fact, the cluster of three Peruvian strains and two of the unrelated Australian strains shared the same C-to-T upstream mutation at position -16 that has previously been found to be associated with resistance to several drugs and experimentally shown to result in the overexpression of *thyX* (12). It is therefore plausible that these changes compensated for the reduced expression levels and enzymatic activity of ThyX compared to those of ThyA (11, 13). Based on our data, however, it was not possible to deduce whether the *thyX* mutations were acquired

after the deletions of *thyA* and *dfrA* in each strain, as would be expected with compensatory mutations (11).

In summary, these data demonstrated that the folate metabolism and the genetic basis of PAS resistance are more complex than previously appreciated, which is relevant for the development of novel DfrA and ThyX inhibitors and potentially the use of trimethoprim-sulfamethoxazole to treat drug-resistant tuberculosis (Fig. S1) (14–25). Although deletions are often excluded from large-scale whole-genome studies, owing to the limited read

lengths of next-generation sequencers and the fact that algorithms are optimized for single-nucleotide polymorphism (SNP) calling, this study highlighted that deletions can no longer be ignored (3, 26).

## ACKNOWLEDGMENTS

We thank L. Camacho for helpful comments regarding this topic.

M. E. Török, J. Parkhill, S. J. Peacock, and C. U. Köser have collaborated with Illumina, Inc., on a number of scientific projects. M. E. Török and S. J. Peacock have received funding for travel and accommodation from Illumina, Inc. J. Parkhill has received funding for travel and accommodation from Pacific Biosciences, Inc., and Illumina, Inc. B. Javid is a Tsinghua-Janssen Scholar. C. U. Köser is a consultant for the Foundation for Innovative New Diagnostics and was a technical advisor for the Tuberculosis Guideline Development Group of the World Health Organization. The Bill & Melinda Gates Foundation and Janssen Pharmaceutica covered C. U. Köser's travel and accommodation to present at meetings. The European Society of Mycobacteriology awarded C. U. Köser the Gertrud Meissner Award, which is sponsored by Hain Lifescience. All other authors have no conflicts of interest to declare.

## FUNDING INFORMATION

This publication presents independent research supported by the Health Innovation Challenge Fund (HICF-T5-342 and WT098600), a parallel funding partnership between the United Kingdom Department of Health and the Wellcome Trust, and grant SRG2015-00006-FHS from the University of Macau. The views expressed in this publication are those of the authors and not necessarily those of the Department of Health, Public Health England, or the Wellcome Trust. M. E. Török is a Clinician Scientist Fellow funded by the Academy of Medical Sciences, the Health Foundation, and the NIHR Cambridge Biomedical Research Centre. E. Martinez was supported by the Australian National Health and Medical Research Council's Centre for Research Excellence in Tuberculosis. C. U. Köser is a Junior Research Fellow at Wolfson College, Cambridge, United Kingdom.

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