

# Detection of Mutations in *katG* and *inhA* genes of *Mycobacterium tuberculosis* from Malaysia Clinical Isolates



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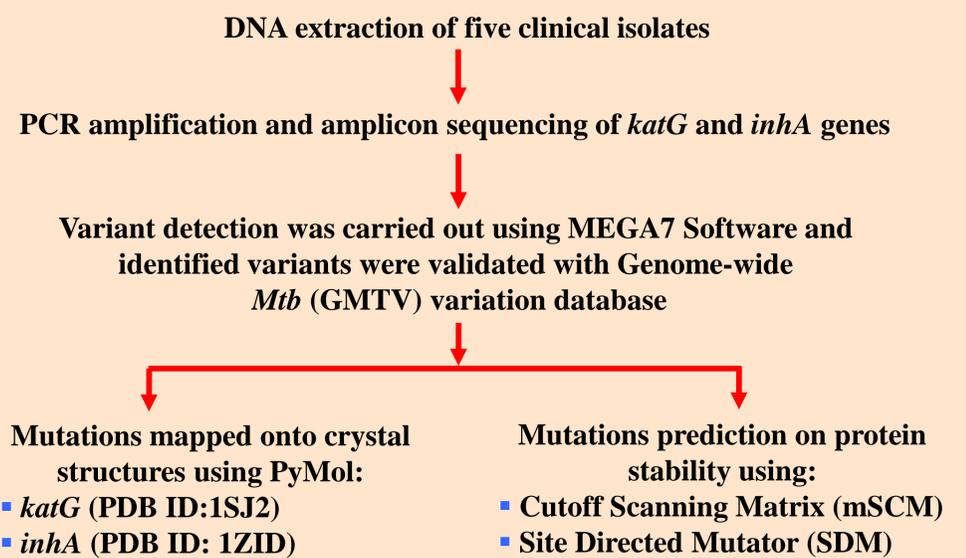
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## Introduction

- Tuberculosis (TB) is one of the infectious diseases leading to cause death worldwide [1].
- TB occurs due to spontaneous mutations in *Mycobacterium tuberculosis* (*M. tuberculosis*) genome [2].
- Majority of mutations are a main cause of drug resistant (DR) and thus understanding on the mechanism of resistance is important for improving the existing prescribed anti-TB drug [3].
- Therefore, the **objectives** of this study are to identify and predict the effect of mutations from five isoniazid resistant (INH-R) *M. tuberculosis* clinical isolates collected from TB patients.

## Materials and Methods



## Results and Discussions

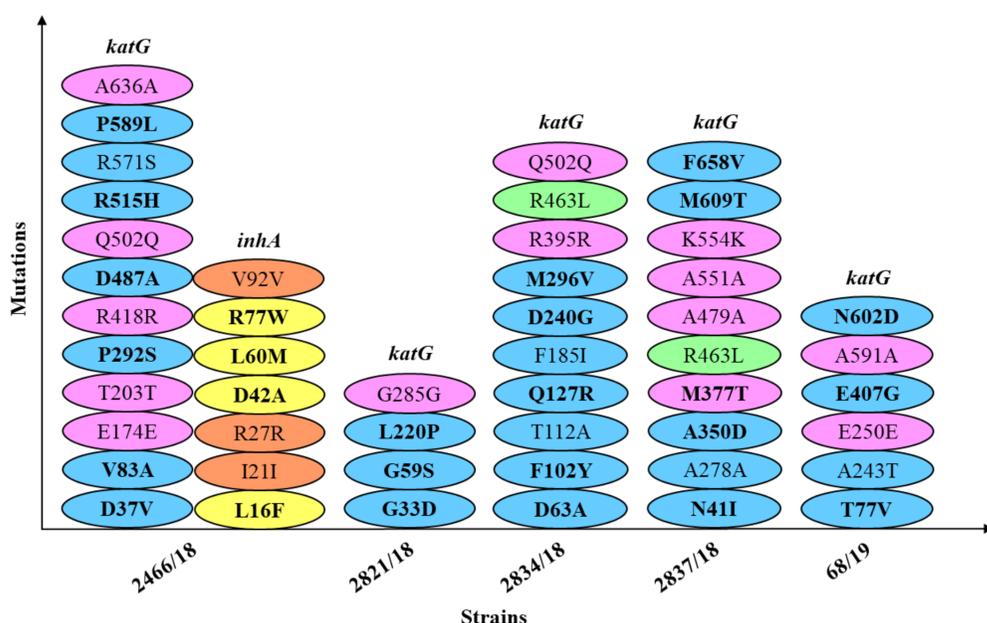


Figure 1: Mutations detected in *katG* and *inhA* genes from five strains.

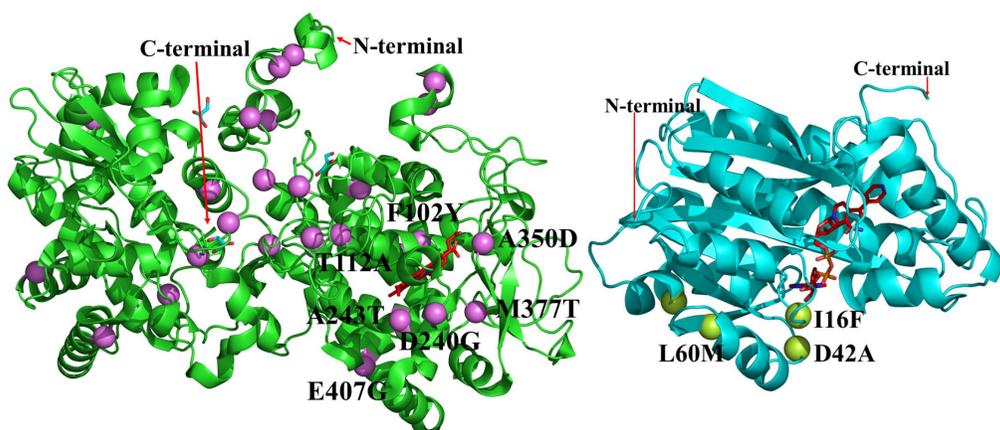


Figure 2: Distribution of missense mutations in *katG* (green colour) and *inhA* (cyan colour) protein structures. Labelled mutations are located in or near to the drug-binding pocket. The HEM and ZID ligands (red color) are located at binding pocket of *katG* and *inhA* protein structures.

- Figure 1 shows 40 and 7 loci of mutations were detected in *katG* and *inhA* genes, respectively.
- 27 missense (blue colour) and 13 silent (pink colour) mutations were identified in *katG* gene. 22 missense mutations were identified as novel (bold font).
- 4 novel missense (yellow colour and bold font) and 3 silent (orange colour) mutations were detected in *inhA* gene.
- Only 2466/18 strain contained mutations in both genes.
- Both strains (2834/18 and 2837/18) have mutation at loci R463L (green colour).

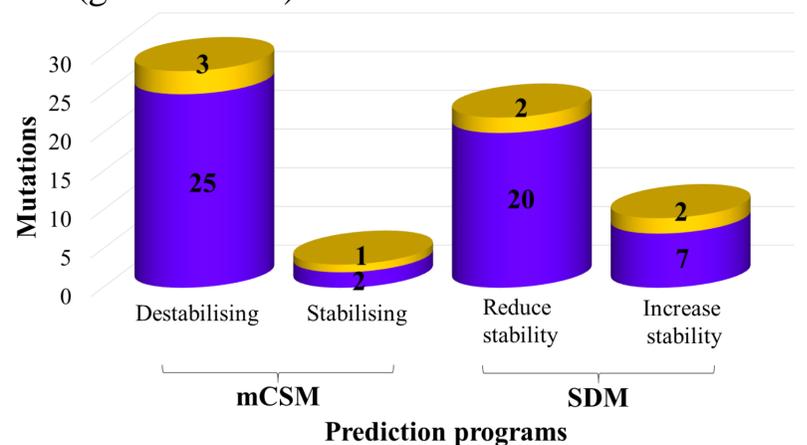


Figure 3: Prediction of protein stability in *katG* and *inhA* genes using mSCM and SDM programs.

- The mSCM and SDM programs predicted 28 and 22 missense mutations, respectively affected the stability of the *katG* and *inhA* protein.

## Conclusion

- Forty-seven loci of mutations identified in this study expanded the mutation spectrum of the *M. tuberculosis*.
- Most of the identified mutations are predicted to affect the stability of the protein.

## References

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