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IDM 2025 MPH Journal Club Review of:

Shi, T., Li, T., Li, J., Wang, J., Zhang, Z. (2018). Genetic diversity of drug resistant *Mycobacterium Tuberculosis* in local area of Southwest China: a retrospective study. *BMC Infectious Diseases*.

Overall comments:

Thank you for the opportunity to review this manuscript. This article is a retrospective study to analyze the genetic diversity of drug resistance in *Mycobacterium tuberculosis* primarily in Chongqing, located in southwest China, as well as in Sichuan Province located northwest of Chongqing. The samples came from two hospitals located in Chongqing. The authors wanted to determine drug resistance characteristics and genotypes in order to evaluate the transmission profile for drug resistant MTB (DRTB) in these two areas in China, as it has not been evaluated in this region of China.

Upon revision, this article should be accepted for publication.

Abstract:

The methods section mentions 538 DRTB, but in the paper they mention 503 DRTB isolates, which were also the cultures identified as *Mycobacterium tuberculosis* (MTB). The rest of the abstract was accurate, clear and succinct.

Introduction:

There is a brief intro on global MTB as well as the disease burden in China. The authors gave appropriate definitions to the different levels of drug resistance as well as a good explanation of the “gold standard” in genotyping and why they chose a different method. They also clearly stated their research aim to determine MTB characteristics in a specific region of China, which has not previously been evaluated. The authors mention this knowledge will lead to understanding MTB transmissions and spread of genotypes that will aid in control measures.

Would recommend adding a sentence about why the Beijing genotype is important to identify (or moving the first two sentences from the Discussion to the Introduction section).

Methods:

The methods have a nice layout with appropriate detail while being succinct. The statistical analysis section mentions an appropriate test and interpretation.

Would recommend in the Bacterial strains and culture condition section, the authors mention the type of samples tested (sputum, blood, biopsy, aspirate?). Additionally, as the study is stated to be retrospective, was there any concerns regarding sample integrity during storage, or maybe mentioning how the samples were stored prior to the research (for example, at -70C?).

Results:

The results are presented comprehensively, see recommendations for improving clarity. Additionally, the results cohere with the research aim and tables/figures.

Recommendations:

- Adding in a sentence stating something to the effect of “all further tests performed on the 503 *M. tb* culture positive samples.” This will add clarity to the remaining sections within the results.
- Make better use of referencing tables. For example, the demography sub-section mentioned Table 1 for geographic regions, but some demographics are presented in Table 4 which is

not mentioned here. Another example, under section MIRU-VNTR profiles and genotypes mentioned Figure 2 in the second paragraph without much interpretation, then at the end of the last paragraph mentions a dendrogram was generated, this would be a great place to reference Figure 2.

- Although, Figure 2 could be removed from the paper and just have Figure 3 as it is more readable.
- Combining Table 2 and Table 5 (also listed an error in one of the tables, say 2 strains in cluster 50 in Table 2, but 3 strains in the same cluster in Table 5).
- In section: Comparison between demographic characteristics and DRTB as well as in Table 4, would be nice to see the exact p-values and not just “P >0.05” or “P <0.05.”
- Formatting, which may be limited by the article: recommend moving Figures and Tables forward so as reading the paper, the audience does not have to flip through pages to find the referenced tables/figures

Discussion/Conclusion:

It seems as if someone else wrote the remainder of the paper. There are numerous grammar errors and some results that do not cohere with the Tables, this was not present in all the previous sections. For example, In the results section it lists from Table 3 four HGDI loci resulting in >0.6 as highly discriminating, then in the discussion section it lists seven as highly discriminating (pg.8). Additionally, in the discussion section the HGDI loci diversity lists a different range (0.29-0.67) than seen in the Table 3 (0.26-0.66).

There is a nice description of what the next study will focus on in the Discussion section and then in the conclusion section, it is mentioned vaguely. Would recommend mentioning future directions mainly in the conclusion section.

On Page 8: repeating almost word for word the explanation of “RD105 or spoligotyping,” as well there is switching between the two words thorough out this section. Recommend staying consistent with terms throughout the entire paper.