ABSTRACT

Tuberculosis (TB) is a disease caused by Mycobacterium tuberculosis. According to WHO 2020 data, Indonesia is one of the countries with a high number of TB sufferers, highlighting the importance of accessible TB treatment. Additionally, starting in 2021, the Department of Health of the Republic of Indonesia announced that Indonesia aims to be TB-free by 2030. TB is traditionally treated using Isoniazid, Rifampicin, Ethambutol, and Pyrazinamide. However, TB starts to develop resistance to the medications. Hibiscus rosa-sinensis is known to have antimicrobial effects. However, most of the research mainly focuses only on gram negative and positive bacteria. Thus, the objective of this study is to assess the antibacterial effect by targeting inha and katg protein of mycobacterium tuberculosis by using hibiscus rosa sinensis flower phytochemicals using in silico methods. In this study, the phytochemical compounds from the Hibiscus flower were docked into the InhA and katG proteins of *M. tuberculosis*. The result shows that tannin, rutin, and β -sitosterol had the lowest binding affinity toward the proteins. Based on the 2D visualization, all of the protein-ligand interactions form at least one hydrogen bond (important to inhibit the protein). Some limitations of this study are that the research is only based on *in-silico* data and one compound is too enormous to be visualized. In conclusion, Hibiscus rosa-sinensis phytochemicals potentially become antibacterial against InhA and katG proteins of *M. tuberculosis*. Nevertheless, further research to follow up on the data in this study is needed.

Keywords: M. tuberculosis, Hibiscus rosa-sinensis, TB, InhA, KatG, Rutin, β -sitosterol

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