The Prediction Mechanism of M. cajuputi Extract from Lampung-Indonesia, as an Anti-Inflammatory Agent for COVID-19 by NFκβ Pathway

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Abstract : Coronavirus disease-19 (COVID-19) is still one of the health problems. It can be a severe condition that is caused by a cytokine storm. In a cytokine storm, several proinflammatory cytokines are released massively. It destroys epithelial cells, and subsequently, it can cause death. The anti-inflammatory agent can be used to decrease the number of severe Covid-19 conditions. Melaleuca cajuputi is a plant that has antiviral, antibiotic, antioxidant, and anti-inflammatory activities. This study was carried out to analyze the prediction mechanism of the M. cajuputi extract from Lampung, Indonesia, as an antiinflammatory agent for COVID-19. This study constructed a database of protein host target that was involved in the inflammation process of COVID-19 using data retrieval from GeneCards with the keyword "SARS-CoV2", "inflammation," "cytokine storm," and "acute respiratory distress syndrome." Subsequent protein-protein interaction was generated by using Cytoscape version 3.9.1. It can predict the significant target protein. Then the analysis of the Gene Ontology (GO) and KEGG pathways was conducted to generate the genes and components that play a role in COVID-19. The result of this study was 30 nodes representing significant proteins, namely NF-κβ, IL-6R, IL-2RA, IL-2, IFN2, C3, TRAF6, IFNAR1, and DOX58. From the KEGG pathway, we obtained the result that NF-κβ has a role in the production of proinflammatory cytokines, which play a role in the COVID-19 cytokine storm. It is an important factor for macrophage transcription; therefore, it will induce inflammatory gene expression that encodes proinflammatory cytokines such as IL-6, TNF- α , and IL-1 β . In conclusion, the blocking of NF-κβ is the prediction mechanism of the M. cajuputi extract as an anti-inflammation agent for COVID-19. **Keywords** : antiinflammation, COVID-19, cytokine storm, NF-κβ, M. cajuputi

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