ABSTRAK

ULFIATUL FAUZAH, 2024, *NETWORK PHARMACOLOGY* RIMPANG KUNYIT *(Curcuma Longa* L.*)* SEBAGAI ANTIINFLAMASI PADA *ULSERATIVE COLITIS*, PROPOSAL SKRIPSI, PROGRAM STUDI S1 FARMASI, FAKULTAS FARMASI, UNIVERSITAS SETIA BUDI, SURAKARTA. Dibimbing oleh Dr. apt. Rina Herowati, M.Si. dan apt. Ismi Puspitasari, M.Farm.

Ulserative colitis merupakan penyakit *inflammatory bowel disease* yang kambuh dan hilang ditandai dengan terjadinya peradangan mukosa, dimulai dari distal dan dapat meluas ke segmen proksimal usus besar. Ciri khas gejala *ulserative colitis* meliputi peningkatan frekuensi buang air besar, keluarnya lendir, inkontinesia, dan diare berdarah. Rimpang kunyit diprediksi memiliki khasiat sebagai antiinflamasi pada *ulserative colitis*. Tujuan penelitian ini untuk melihat protein yang terlibat dalam patofisologi *ulserative colitis* mengetahui protein target yang diprediksi menjadi target kerja dari senyawa-senyawa rimpang kunyit sebagai antiinflamasi, dan untuk mengetahui profil *network pharmacology* kandungan senyawa kimia rimpang kunyit terhadap protein target *ulserative colitis*.

Penelitian ini menggunakan metode *network pharmacology*. Pengumpulan senyawa kimia rimpang kunyit menggunakan KNApSAcK, *Dr. Duke's Phytochemical Database,* dan jurnal-jurnal penelitian. Skrining zat aktif terhadap protein target didapatkan dari PubChem. Protein target kerja pada patofisiologi *ulserative colitis* diperoleh dari *KEGG Pathway*, dengan memvalidasi interaksi protein menggunakan *String*. Identifikasi protein dari senyawa bioaktif menggunakan *Swiss Target Prediction*, SEA, dan super-PRED. Validasi protein yang digunakan menggunakan UniPort. Visualisasi network pharmacology dari interaksi protein-protein dan interaksi senyawa protein menggunakan *Cytoscape*.

Visualisasi profil *network pharmacology* protein target yang terlibat dalam patofisiologi *ulserative colitis* dengan senyawa rimpang kunyit yaitu JAK2, JAK1, GATA3, STAT6, IL4R, IL4, IL13, IL12RG, IL10, IL2, IL5, TLR4, TLR5, TLR2, NOD2, MAF dan NFE2L2. Kandungan senyawa *curcumin, bisdemetoxycurcumin, asorbic acid, caffeic acid, limonene, quercetin, palmitic acid, beta caroten, octadecanoid acid, cinnamaldehyde, alpha pinene, cineole, demetoxycurcumin, ribitol, stigmasterol* dan *guaicol* pada rimpang kunyit dapat membentuk profil *network pharmacology* dengan protein target *ulserative colitis.*

Kata Kunci*: ulserative colitis*, kunyit, *network pharmacology, cytoscape*

ABSTRACT

ULFIATUL FAUZAH, 2024, NETWORK PHARMACOLOGY OF TURMERIC RHIZOME (Curcuma Longa L.) AS ANTIINFLAMMATORY IN ULCERATIVE COLITIS, THESIS PROPOSAL, S1 PHARMACY STUDY PROGRAM, FACULTY OF PHARMACY, SETIA BUDI UNIVERSITY, SURAKARTA. Supervised by Dr. apt. Rina Herowati, M.Si. and apt. Ismi Puspitasari, M.Farm.

Ulcerative colitis is a relapsing and remitting inflammatory bowel disease characterized by mucosal inflammation, starting from the distal and extending to the proximal segment of the colon. Characteristic symptoms of ulcerative colitis include increased frequency of bowel movements, mucous discharge, incontinence, and bloody diarrhea. Turmeric rhizome is predicted to have anti-inflammatory properties in ulcerative colitis. The purpose of this study was to look at the proteins involved in the pathophysology of ulcerative colitis to find out the target proteins that are predicted to be the target of action of turmeric rhizome compounds as anti-inflammatory, and to determine the network pharmacology profile of the content of turmeric rhizome chemical compounds against ulcerative colitis target proteins.

This study used the network pharmacology method. Collection of turmeric rhizome chemical compounds using KNApSAcK, Dr. Duke's Phytochemical Database, and research journals. Screening of active substances against target proteins was obtained from PubChem. Target proteins acting on ulcerative colitis pathophysiology were obtained from KEGG Pathway, by validating protein interactions using String. Protein identification of bioactive compounds using Swiss Target Prediction, SEA, and super-PRED. Validation of proteins used using UniPort. Visualization of network pharmacology of protein-protein interactions and protein-compound interactions using Cytoscape.

Visualization of network pharmacology profiles of target proteins involved in the pathophysiology of ulcerative colitis with turmeric rhizome compounds, namely JAK2, JAK1, GATA3, STAT6, IL4R, IL4, IL13, IL12RG, IL10, IL2, IL5, TLR4, TLR5, TLR2, NOD2, MAF and NFE2L2. The content of curcumin, bisdemetoxycurcumin, asorbic acid, caffeic acid, limonene, quercetin, palmitic acid, beta carotene, octadecanoid acid, cinnamaldehyde, alpha pinene, cineole, demetoxycurcumin, ribitol, stigmasterol and guaicol compounds in turmeric rhizomes can form a network pharmacology profile with ulcerative colitis target proteins.

Keywords: ulcerative colitis, turmeric, network pharmacology, cytoscape