

INTISARI

Kolitis ulseratif (KU) merupakan salah satu dari *inflammatory bowel disease* (IBD) yang diakibatkan oleh adanya respon imun yang tidak normal. Seledri dan mengkudu diketahui dapat mengurangi inflamasi dan mengurangi kondisi keparahan KU, tetapi jalur persinyalan perbaikannya belum dijelaskan lebih lanjut. Penelitian ini bertujuan untuk menelusuri aktivitas senyawa pada seledri dan mengkudu dalam pengobatan KU dan memberikan gambaran mekanisme molekulernya berdasarkan analisis bioinformatika.

Penelitian ini dilakukan dengan *platform* Dr. Duke's Phytochemical and Ethnobotanical Databases, Gene-NCBI, GeneCards, STRING, SwissTargePrediction, STITCH dan DAVID. Gen yang berkorelasi dengan KU diiriskan dengan protein tertarget senyawa seledri dan mengkudu. Protein tersebut dianalisis interaksinya menggunakan STRING dan DAVID untuk menentukan jalur apa yang berperan dalam remisi KU. Selanjutnya, dilakukan *molecular docking* untuk mengetahui interaksi antara senyawa dengan protein target dibandingkan dengan ligan aslinya.

Hasil penelitian menunjukkan senyawa pada seledri dan mengkudu mampu mentarget berbagai gen yang berkorelasi dengan KU. Apigenin memiliki skor *docking* yang lebih kecil daripada skopoletin, tetapi keduanya masih belum bisa menyaingi *native ligand* COX-2, yaitu asam mefenamat. Senyawa pada seledri dan mengkudu terlibat dalam berbagai jalur persinyalan inflamasi, seperti PI3K-Akt *signaling pathway*, TNF *signaling pathway*, IL-17 *signaling pathway*, *chemokine signaling pathway*, Th17 *cell differentiation*, *inflammatory bowel disease* dan *colorectal cancer pathway*.

Kata kunci: seledri, mengkudu, kolitis ulseratif, bioinformatika

ABSTRACT

Ulcerative colitis (UC) is one of the inflammatory bowel diseases (IBD) which is caused by an abnormal immune response. Celery and noni are known to reduce inflammation and alleviate the severity of UC, but the signaling pathways of UC improvement have not been elucidated. This study aims to explore activity of compounds in celery and noni in treatment of UC and provide an overview of their molecular mechanisms based on bioinformatics analysis.

This study was conducted using Dr. Duke's Phytochemical and Ethnobotanical Databases, Gene-NCBI, GeneCards, STRING, SwissTargetPrediction, STITCH and DAVID platforms. Genes correlated with UC were sliced with targeted proteins of celery and noni compounds. The proteins interaction were analyzed using STRING and DAVID to determine what pathways play a role in UC remission. Furthermore, molecular docking was carried out to determine interaction between compound and target protein compared to original ligand.

The results showed that compounds in celery and noni were able to target various genes that correlated with UC. Apigenin has smaller docking score than scopoletin, but both still can not compete with the native ligand of COX-2, mefenamic acid. Compounds in celery and noni are involved in various inflammatory signaling pathways, such as PI3K-Akt signaling pathway, TNF signaling pathway, IL-17 signaling pathway, chemokine signaling pathway, Th17 cell differentiation, inflammatory bowel disease and colorectal cancer pathway.

Keywords: *celery, noni, ulcerative colitis, bioinformatics*