ABSTRAK

Penelitian ini mengkaji potensi laktogenik tanaman tirem (*Jacquemontia paniculata*), obat tradisional suku Tengger yang belum tereksplorasi basis ilmiahnya secara molekuler. Penelitian ini bertujuan mengidentifikasi profil metabolit ekstrak etanol 96% herba tirem serta memprediksi mekanisme molekuler aktivitas galaktatognya melalui pendekatan integratif *in silico*. Profiling senyawa dilakukan menggunakan *Liquid Chromatography–High Resolution Mass Spectrometry* (LC-HRMS), diikuti reduksi data via *Principal Component Analysis* (PCA). Penapisan kandidat bioaktif menggunakan kriteria *drug-likeness*, PASS Online, dan ProTox-II. Analisis interaksi molekuler dan visualisasi jalur biologis dievaluasi menggunakan *Network pharmacology* dan *Molecular docking* pada reseptor target ERα, ERβ, PGR, EGFR, dan JAK2. Hasil LC-HRMS dan PCA mengidentifikasi 28 senyawa dominan dari total 280 senyawa. Penapisan biologis menghasilkan 6 senyawa kandidat laktogenik utama, dengan *kaempferol* menunjukkan afinitas ikatan terkuat dan paling stabil, terutama pada *Progesterone Receptor* (PGR). Analisis *Network pharmacology* membuktikan ekstrak bekerja melalui mekanisme multitarget yang memodulasi *Estrogen Signaling pathway* dan *Prolactin Signaling pathway*. Penelitian ini memberikan kontribusi signifikan berupa validasi ilmiah pertama terhadap etnomedisin tanaman tirem, serta menyediakan landasan teoretis yang kuat bagi pengembangan produk galaktagog herbal berbasis *kaempferol* untuk mengatasi masalah hipogalaktia.

Kata Kunci: *Jacquemontia paniculata*, Galaktagog, *Network pharmacology*, *Molecular docking*, *Kaempferol*.

ABSTRACT

This study investigates the lactogenic potential of the tirem plant (*Jacquemontia paniculata*), a traditional medicine utilized by the Tengger tribal community whose molecular scientific basis remains unexplored. This research aims to identify the metabolite profile of the 96% ethanol extract of tirem leaves and predict its molecular mechanisms of galactagogue activity using an integrative *in silico* approach. Compound profiling was conducted using Liquid Chromatography–High Resolution Mass Spectrometry (LC-HRMS), followed by multivariate data reduction via Principal Component Analysis (PCA). Bioactive candidates were screened based on drug-likeness criteria, PASS Online, and ProTox-II. Molecular interactions and biological pathways were evaluated using *Network pharmacology* and *Molecular docking* simulations against ERα, ERβ, PGR, EGFR, and JAK2 target *receptor*s. LC-HRMS and PCA successfully identified 28 dominant compounds from a total of 280 detected metabolites. Biological screening yielded 6 primary lactogenic candidates, among which *kaempferol* exhibited the strongest and most stable *binding affinity*, particularly toward the Progesterone *Receptor* (PGR). *Network pharmacology* analysis demonstrated that the extract operates via a multi-target mechanism modulating the *Estrogen* and *Prolactin Signaling pathway*s. This study provides a significant contribution by offering the first scientific validation of tirem ethnomedicine and establishing a solid theoretical foundation for developing *kaempferol*-based herbal galactagogue products to manage postpartum hypogalactia.

Keywords: *Jacquemontia paniculata*, Galactagogue, *Network pharmacology*, *Molecular docking*, Kaempferol.