Abstract

Propolis, a natural resinous substance produced by bees, has long been recognized for its anti-inflammatory and wound-healing properties. This study was employed *in silico* methodologies to identify and evaluate bioactive compounds in propolis targeting key inflammatory markers (COX-2 and TNF-a) and wound-healing proteins (VEGF-a and MMP-9). A total of 34 compounds were screened using the PASS server for bioactivity prediction, followed by molecular docking using AutoDock Vina and Biovia Discovery Studio for their 2-D visualization to assess binding affinities. The ligands that had the best binding affinity were then analyzed for pharmacokinetics, drug-likeness, solubility, and toxicity via SwissADME and ToxTree. Molecular dynamics simulations were conducted to evaluate the stability of ligand-protein complexes. Results identified vanillic acid (COX-2), coniferyl benzoate (TNF-a), hexitol (VEGF-a), and B-amyrin (MMP9) as lead candidates with favorable binding affinities in which it had acceptable stability complex (RMSD < 1.5 Å). All selected ligands exhibited low predicted toxicity; and showed decent drug-likeness and pharmacokinetic properties with the exception of B-amyrin having poor solubility and having the most offences towards the drug-likeness principles. The study concludes that propolis contains promising bioactive compounds for therapeutic development in inflammation and wound healing, although further *in vitro* and *in vivo* validation is essential.

Keywords: Propolis, *in silico*, anti-inflammatory, wound healing, molecular docking