Abstract

Type 2 Diabetes Mellitus (T2DM) is a major metabolic disorder characterized by persistent hyperglycemia and elevated postprandial blood glucose levels. Although synthetic α-glucosidase inhibitors such as acarbose are effective in controlling postprandial glucose elevation, their use may be associated with gastrointestinal side effects, highlighting the need to investigate alternative α-glucosidase inhibitors from natural sources. This study evaluated selected flavonoids identified from Indonesian *jamu* medicinal plants, namely *Gynura procumbens*, *Orthosiphon aristatus*, and *Moringa oleifera*, for their potential inhibitory activity against human intestinal maltase-glucoamylase (MGAM) using an in-silico approach. Molecular docking was performed using PyRx to evaluate the predicted binding affinity of the selected flavonoids toward MGAM, with acarbose included as the positive control. Protein–ligand interactions were subsequently examined using PyMOL and BIOVIA Discovery Studio Visualizer to characterize the predicted binding modes and interactions within the enzyme binding region. Molecular dynamics simulations using CABS-flex 3.0 were then performed on selected protein–ligand complexes to further evaluate their structural stability and flexibility. The docked compounds were assessed based on their predicted binding affinity, interactions with relevant residues within the MGAM binding region, and the dynamic behavior of the protein–ligand complexes. The findings provide computational insights into the potential of flavonoids derived from Indonesian *jamu* medicinal plants as candidates for further investigation as natural inhibitors of intestinal α-glucosidase activity.

Keywords: Type 2 diabetes mellitus, human intestinal maltase-glucoamylase, α-glucosidase, flavonoids, Indonesian *jamu* medicinal plants, molecular docking, molecular dynamics simulation