ABSTRACT

Ahmad Faishal Farras Syuja, 24020221120018. Molecular Characterization, α-Amylase Inhibition Assay, and Molecular Docking of Gracilaria Macroalgae as an Antidiabetic Agent. Under the guidance of Hermin Pancasakti Kusumaningrum and Anto Budiharjo.

Diabetes mellitus is a chronic metabolic disease with a high prevalence in Indonesia. Treatment with synthetic α-amylase inhibitors such as acarbose is effective but associated with side effects, thus requiring alternatives from natural sources such as *Gracilaria sp.*. This study aimed to characterize the molecular identity of *Gracilaria sp.* using the 18S rRNA marker, evaluate its α-amylase inhibitory activity in vitro, and predict the interactions of active compounds through molecular docking. DNA isolation was carried out using the CTAB method and analyzed by PCR and sequencing. The results showed the highest homology with *Gracilaria gracilis*, with a sequence similarity of 94.48%. The α-amylase inhibition test using the DNS method showed that *Gracilaria sp.* extract had an IC50 value of 60.35 ppm, which was strong even though it was lower than the positive control acarbose (40.99 ppm). Molecular docking analysis of flavonoid compounds from the previous GC-MS report showed luteolin and rutin as the best ligands with a binding affinity value of -9.2 kcal/mol, which is better than acarbose (-7.2 kcal/mol). Based on the analysis of the five Lipinski rules, the luteolin ligand is suitable for development into an oral diabetes drug for humans. The results of this study indicate that Gracilaria sp. has the potential as a source of natural α-amylase inhibitors. The flavonoid compound luteolin is thought to play an important role as an antidiabetic candidate, thus supporting the use of this macroalgae in the development of herbal antidiabetic drugs.

Keywords: 18S rRNA, α-amylase, antidiabetic, *Gracilaria sp.*, IC50, molecular docking.