

## Documents

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**Gc-ms-and nmr-based metabolomics and molecular docking reveal the potential alpha-glucosidase inhibitors from psychotria malayana jack leaves**

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### Abstract

*Psychotria malayana* Jack leaf, known in Indonesia as “daun salung”, is traditionally used for the treatment of diabetes and other diseases. Despite its potential, the phytochemical study related to its anti-diabetic activity is still lacking. Thus, this study aimed to identify putative inhibitors of  $\alpha$ -glucosidase, a prominent enzyme contributing to diabetes type 2 in *P. malayana* leaf extract using gas chromatography-mass spectrometry (GC-MS)-and nuclear magnetic resonance (NMR)-based metabolomics, and to investigate the molecular interaction between those inhibitors and the enzyme through in silico approach. Twenty samples were extracted with different solvent ratios of methanol–water (0, 25, 50, 75, and 100% v/v). All extracts were tested on the alpha-glucosidase inhibition (AGI) assay and analyzed using GC-MS and NMR. Multivariate data analysis through a partial least square (PLS) and orthogonal partial square (OPLS) models were developed in order to correlate the metabolite profile and the bioactivity leading to the annotation of the putative bioactive compounds in the plant extracts. A total of ten putative bioactive compounds were identified and some of them reported in this plant for the first time, namely 1,3,5-benzenetriol (1); palmitic acid (2); cholesta-7,9(11)-diene-3-ol (3); 1-monopalmitin (4);  $\beta$ -tocopherol (5);  $\alpha$ -tocopherol (6); 24-epicampesterol (7); stigmast-5-ene (8); 4-hydroxyphenylpyruvic acid (10); and glutamine (11). For the evaluation of the potential binding modes between the inhibitors and protein, the in silico study via molecular docking was performed where the crystal structure of *Saccharomyces cerevisiae* isomaltase (PDB code: 3A4A) was used. Ten amino acid residues, namely ASP352, HIE351, GLN182, ARG442, ASH215, SER311, ARG213, GLH277, GLN279, and PRO312 established hydrogen bond in the docked complex, as well as hydrophobic interaction of other amino acid residues with the putative compounds. The  $\alpha$ -glucosidase inhibitors showed moderate to high binding affinities ( $-5.5$  to  $-9.4$  kcal/mol) towards the active site of the enzymatic protein, where compounds 3, 5, and 8 showed higher binding affinity compared to both quercetin and control ligand. © 2021 by the authors. Licensee MDPI, Basel, Switzerland.

### Author Keywords

GC-MS; Molecular docking; Multivariate data analysis; NMR; *P. malayana*;  $\alpha$ -glucosidase

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