Identification of α-glucosidase inhibitory compounds from Curcuma mangga fractions

ABSTRACT

Curcuma mangga is a medicinal plant, and its rhizomes are often used to treat various conditions, such as fever, thorax pain, itching, stomachaches, skin diseases, gout, and asthma. Although C. mangga is commonly used, information on the relationship between its chemical constituents and the bioactivities of the rhizomes is still limited. The extraction solvents used have a strong effect on the metabolite profile and the bioactivity of the extract. A nuclear magnetic resonance (NMR)-based metabolomics approach was used to differentiate the metabolite profiles of hexane, chloroform, ethyl acetate, and methanol fractions of C. mangga rhizomes and to correlate the metabolites with α-glucosidase inhibitory activity. Primary and secondary metabolites were identified, including curcuminoids, carbohydrates, terpenoids, and amino acids. The ultra-performance liquid chromatography–tandem mass spectrometry (UPLC–MS/MS) analysis of the most active fraction (ethyl acetate) revealed the identification of additional metabolites, such as zerumin A, epigallocatechin, p-hydroxycinnamic, and copallic acids. A partial least square (PLS) biplot demonstrated that the existence of curcumin, demethoxycurcumin, curcumanggoside, calcaratarin A, labda-8(17),12-diene-15,16-dial, zerumin B, and difurocumenonol in the ethyl acetate fraction could be responsible for the α-glucosidase inhibitory activity.

Keyword: Curcuma mangga; Multivariate data analysis; Nuclear magnetic resonanceα-glucosidase inhibitory; Liquid chromatography mass spectrometry