

Phytochemical and bioactivity alterations of *Curcuma* species harvested at different growth stages by NMR-based metabolomics

ABSTRACT

Curcuma species is a popular traditional folk medicine in India and Southeast Asia. This study aims to profile the metabolites in four *Curcuma* species, including *C. zedoaria*, *C. xanthorrhiza*, *C. aeruginosa* and *C. mangga* at three developmental stages (seven, eight and nine months old) using nuclear magnetic resonance (NMR)-based metabolomics. Principal component analysis (PCA) showed that there are metabolites changes due to the month of harvest in each of the four species. A large quantity of curcumin and demethoxycurcumin contributed to the separation of *C. xanthorrhiza*, whereas the diterpenoids, such as curcumanggoside, (E)-labda-8(17),12-diene-15,16-dial, calcaratarin A and zerumin B were responsible for the discrimination of *C. mangga*. Eight-month-old *C. xanthorrhiza* exhibited the highest nitric oxide (NO) inhibitory activity, while nine-month-old *C. mangga* exhibited the highest α -glucosidase inhibitory activity. The correlation among the bioactivities and phytochemical constituents was determined using partial least square (PLS) analysis. Curcumin, demethoxycurcumin, germacrone, zedoarol and xanthorrhizol were correlated with the NO inhibitory activity in *C. xanthorrhiza*, whereas curcumanggoside, labda-8(17),12-diene-15,16-dial and zerumin B were correlated with the α -glucosidase inhibitory activity in *C. mangga*. From the phytochemical markers and metabolic changes among growth stages of *C. xanthorrhiza* and *C. mangga*, the biosynthetic pathway was proposed to show the metabolites that might contribute to their health benefits.

Keyword: Food analysis; Food composition; Development stages; *Curcuma*; Multivariate data analysis; PCA; PLS; Nuclear magnetic resonance; Biosynthetic pathways