Profil Metabolit ^{1}H *NMR* Rimpang *Curcuma* dan *Zingiber* dari Tiga Lokasi Berbeda

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INTISARI

Rimpang Genus *Curcuma* L. dan *Zingiber* L. telah dikenal secara luas di Indonesia, terutama karena perannya sebagai bahan jamu. Rimpang *Curcuma* dicirikan oleh kandungan bioaktif curcuminnya, sementara genus *Zingiber* mempunyai sejarah panjang untuk pengobatan tradisional. Profil metabolit dipengaruhi salah satunya oleh lokasi atau tempat tumbuh. Penelitian ini bertujuan untuk membandingkan profil metabolit interspesies rimpang Genus *Curcuma* dan *Zingiber* dari tiga lokasi berbeda menggunakan ^{1}H NMR dan mengetahui senyawa yang berperan sebagai pembeda. Rimpang yang digunakan adalah *Curcuma mangga* Val., *Curcuma zedoaria* Roscoe, dan *Curcuma xanthorrhiza* Roxb (genus *Curcuma* L.) dan *Zingiber officinale* Roscoe, *Zingiber montanum* J.Konig dan *Zingiber zerumbet* L. yang dikoleksi dari Wonogiri, Karanganyar, dan Kulonprogo. Rimpang dikeringkan dengan oven pada suhu 40 °C dan diserbukkan dengan blender. Ekstraksi menggunakan methanol-d_4 yang mengandung 0,01% TMSP dan dilakukan ultrasonikasi selama 15 menit. Supernatan dipisahkan dan dilakukan sentrifugasi 10.000 rpm selama 10 menit. Supernatan dipindahkan ke tabung NMR dan dianalisa menggunakan JEOL 500 MHz NMR. Data yang diperoleh dianalisa dengan *software* Mnova 12 dan Simca 14.0. Hasil spektra menunjukkan sampel *C. zedoaria* dan *Z. montanum* memiliki pola spektra yang berbeda dari ketiga lokasi, sementara sampel lainnya mempunyai pola spektra yang sama. Berdasarkan pergeseran kimia yang muncul pada spektra, teridentifikasi senyawa β-glukosa, fruktosa, ATP, kolin (*C. mangga*), furanodienone (*C. zedoaria*), xanthorrhizol, sukrosa, asam fumarat, kolin (*C. xanthorrhiza*), [6]-paradol, [6]-gingerol (*Z. officinale*), neocassumunarin A, neocassumunarin B (*Z. montanum*) dan *Zerumbone* (*Z. zerumbet*). Hasil Uji *One-way* Anova senyawa marker potensial [6]-gingerol, zerumbone dan xanthorrhizol diperoleh hasil signifikan ($p<0,05$). Analisis multivariat model OPLS-DA sampel rimpang genus *Curcuma* dan *Zingiber* dari tiga lokasi berbeda mengalami pemisahan dengan baik. Nilai R^2Y (cum) dan Q^2Y (cum) model OPLS-DA lebih dari 0,5 yang menunjukkan model yang digunakan sudah baik. Hasil ini menunjukkan bahwa pendekatan metabolomik dengan ^{1}H NMR dapat digunakan untuk membedakan dan membandingkan profil metabolit rimpang genus *Curcuma* dan *Zingiber* dari tiga lokasi berbeda.

Kata kunci: ^{1}H NMR, *Curcuma*, Profil metabolit, *Zingiber*

^{1}H *NMR* Metabolite Profile from Rhizome of *Curcuma* and *Zingiber* from Three Different Location

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ABSTRACT

Rhizome of *Curcuma* and *Zingiber genera* has been widely known in Indonesia, mainly because it's role as jamu (herb) ingredient. Rhizome of *Curcuma* characterized by curcumin as the bioactive compound, while *Zingiber* genera already have long history in traditional medicine of Indonesia. Metabolite profile can be affected by the place where the plant was originated. The objectives of this research were to compare the metabolite profile of interspecific rhizome form *Curcuma* genera and *Zingiber* genera from three different location by using ^{1}H NMR and to identify the component that may act as distinguishing character.The sample were rhizomes from *Curcuma mangga* Val., *Curcuma zedoaria* Roscoe, and *Curcuma xanthorrhiza* Roxb (*Curcuma* L. genera), *Zingiber officinale* Roscoe, *Zingiber montanum* J.Konig and *Zingiber zerumbet* L. collected from Wonogiri, Karanganyar, and Kulonprogo. The rhizome was dried with oven within 40° C temperature and was mashed until become powder. Extraction process used methanol-d_4 containing 0.01% TMSP and then ultrasonication was conducted for 15 minutes. Supernatant was separated from the solution by 10.000 rpm centrifugation for 10 minutes. The supernatant was moved to NMR tube and then being analysed by using JEOL 500 MHz NMR. The obtained data then being analysed by using Mnova 12 software and Simca 14.0. The result spectra showed that *C. zedoaria* and *Z. montanum* have different spectra pattern depended on the location, while other samples have the same pattern. According to chemical shift that appeared on the spectra, these compound was identified from the rhizome: β-glucose, fruktose, ATP, cholin (*C. mangga*), furanodienone (*C. zedoaria*), xanthorrhizol, sucrose, fumaric acid, cholin (*C. xanthorrhiza*), [6]-paradol, [6]-gingerol (*Z. officinale*), neocassumunarin A, neocassumunarin B (*Z. montanum*) and zerumbone (*Z. zerumbet*). One-way test Anova of potential marker [6]-gingerol, zerumbone, and xanthorrhizol was resulted in significant conclusion ($p<0.05$). Multivariate analysis model OPLS-DA of rhizome sample of *Curcuma* and *Zingiber* genera from three different location was well separated. R^2Y and Q^2Y value of OPLS-DA model is more than 0.5 and shows that the current model being used is good. This result shows metabolomic approach with ^{1}H NMR can be used to differentiate and compare metabolite profile from rhizome of *Curcuma* and *Zingiber* genera from three different location.

Keyword: ^{1}H NMR, *Curcuma*, Metabolite profile, *Zingiber*