Metabolite Profiling of Curcuma zanthorrhiza Varieties Grown in Different Regions Using UHPLC-Q-Orbitrap-HRMS and Chemometrics Analysis

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Abstract: Curcuma zanthorrhiza, also known as java turmeric, is a plant that has long been used as a medicinal herb. The efficacy of C. zanthorrhiza is primarily determined by the bioactive composition, which is dependent on many variables, including where it is grown and the different varieties of java turmeric used. In this study, we determined the metabolite profile of C. zanthorrhiza 70% ethanol extract using UHPLC-Q-Orbitrap-HRMS coupled with chemometrics analysis to characterize the differences between C. zanthorrhiza varieties (namely Cursina-1, Cursina-2, and Cursina-3) grown in Bogor, Cianjur, and Sukabumi, West Java, Indonesia. An estimated total of 39 metabolites has been putatively identified. These metabolites were divided into amino acids, terpenoids, phenolics, diarylheptanoids, and other organic compounds groups. Chemometric results revealed significant differences in the geographical location metabolites profiles, which C. zanthorrhiza varieties had little effect. This study shows that UHPLC-Q-Orbitrap-HRMS-based metabolomics is efficient for profiling C. zanthorrhiza across various regions.

Keywords: Curcuma zanthorrhiza; Java turmeric; LC-MS/MS; metabolite profiling; multivariate analysis; Zingiberaceae.

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1. Introduction

Temulawak is the Indonesian name for Curcuma zanthorrhiza Roxb., a well-known rhizomatous Zingiberaceae herb native from Indonesia, widely distributed and cultivated in Southeast Asia Region [1]. Additionally, C. zanthorrhiza is used by the local food industry as an ingredient in jamu (Indonesian traditional herbal medicinal) [2]. Traditionally, C. zanthorrhiza is recommended to treat several diseases such as obesity, diabetes, liver disorders, stomach disease, lactation, constipation, rheumatism, and fever [3]. C. zanthorrhiza has a broad range of pharmacological effects, including antimitastatic [4], anticancer [1,5], antioxidant [6], antimicrobial [7,8], anti-inflammation [9], antiurolithiatic [10], nitric oxide inhibitor [3],
acetylcholinesterase inhibitor [11], and estrogenic properties [12]. In general, *C. zanthorrhiza* plants are composed primarily of curcuminoids (phenolic pigment) and xanthorrhizol (essential oil), the concentration of which varies between accessions from different geographical origins [1,13]. The curcuminoids have been reported to possess antibacterial, antioxidant [14], antiobesity [15], and antifungal activities [16]. Several pharmacological properties have been reported for xanthorrhizol, including anti-angiogenic [17], antimicrobial [18], antiinflammation, anti-osteoclastic [19], and anticancer activities [5].

The pharmacological properties of the medicinal plant are influenced by the quantity and composition of secondary metabolites found in the plant [20]. Because the composition of a plant’s metabolites is influenced by its origin or plant variety [21,22], variations in origin or plant variety may result in distinct metabolite phenotypes. Origin differences result from varying growing conditions, including various cultivation environments, soil types, and elevations. Therefore, a complete evaluation of *C. zanthorrhiza* metabolites requires evaluating various varieties and growth locations of *C. zanthorrhiza*.

Recently, several reports have been conducted to differentiate *C. zanthorrhiza* produced in different geographical regions or cultivars. Saputra et al. [23] investigated targeted compounds (xanthorrhizol and curcumin) in three *C. zanthorrhiza* varieties using Nuclear Magnetic Resonance (NMR). Xanthorrhizol as a targeted compound was also evaluated in 4 genotypes and one variety of *C. zanthorrhiza* using high-performance liquid chromatography (HPLC) coupled with dendrogram analysis which showed good grouping results [1]. The curcumin content and antioxidant activity showed no significant difference between *C. zanthorrhiza* samples from Purworejo and Semarang, Indonesia [24]. However, in contrast to this, our study showed significant variations in curcumin content and anticancer activity in *C. zanthorrhiza* samples from various locations [13]. Based on the results of several studies above, it is shown that the targeted compound can function as a cultivar or geographical indicator for discrimination of *C. zanthorrhiza* samples. However, metabolite profiling analysis in *C. zanthorrhiza* varieties grown in different locations has not been widely reported. LC-MS/MS-based metabolite fingerprinting is proving to be widely used in medicinal plant discrimination and authentication [25,26]. One widely used technology is ultrahigh performance liquid chromatography-mass spectrometry/mass spectrometry (UHPLC-Q-Orbitrap-MS/MS) for the metabolomics field. This tool has impressive sensitivity, selectivity, and resolution and can measure numerous metabolites well [27]. UHPLC-Q-Orbitrap-MS/MS-based metabolomics has been well applied to evaluate metabolites of *Prosopis strombulifera* [28], *Clausena lansium* [29], and *Andrographis paniculata* [30]. There is still much more to be done on how this system applies and how accurate it is to differentiate cultivars or the origin of *C. zanthorrhiza*.

Recently, no metabolomic studies have been conducted on the *C. zanthorrhiza* varieties or geographical origin, and in particular, no UHPLC-Q-Orbitrap-HRMS analyses have been performed on *C. zanthorrhiza*. The current study evaluated the metabolite compositions of three *C. zanthorrhiza* varieties (Cursina-1, Cursina-2, and Cursina-3) grown in Bogor, Sukabumi, and Cianjur of Indonesia using UHPLC-Q-Orbitrap-HRMS coupled with multivariate analysis. Here, we provide insight into metabolic profiling for discriminating the geographical origins from different *C. zanthorrhiza* varieties.
2. Materials and Methods

2.1. Plant materials.

Three *C. zanthorrhiza* varieties, namely Cursina-1 (C1), Cursina-2 (C2), and Cursina-3 (C3), were collected from Indonesian Spices and Medicinal Crops Research Institute, Bogor, Indonesia. Table 1 presents the *C. zanthorrhiza* varieties description used for this study. The study involved carrying out a field experiment at Tropical Biopharmaca Research Center and Pasir Sarongge of IPB University; and a field experiment at a local farmer’s field.

**Table 1.** A detailed description of the *C. zanthorrhiza* varieties used in this study.

<table>
<thead>
<tr>
<th>Characters</th>
<th>Cursina-1</th>
<th>Cursina-2</th>
<th>Cursina-3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Leaf form</td>
<td>Oblong elliptic</td>
<td>Oblong elliptic</td>
<td>Oblong elliptic</td>
</tr>
<tr>
<td>Leaf length (cm)</td>
<td>58 - 80</td>
<td>57 - 87</td>
<td>56 - 95</td>
</tr>
<tr>
<td>Leaf width (cm)</td>
<td>18 - 21</td>
<td>17 - 21</td>
<td>17 - 24</td>
</tr>
<tr>
<td>Number of tillers</td>
<td>3 - 6</td>
<td>3 - 6</td>
<td>3 - 6</td>
</tr>
<tr>
<td>Rhizome shape</td>
<td>Long conical</td>
<td>Oval</td>
<td>Conical</td>
</tr>
<tr>
<td>Curcuminoids (%)*</td>
<td>4.85</td>
<td>4.59</td>
<td>5.22</td>
</tr>
<tr>
<td>Essential oils (%)*</td>
<td>5.49</td>
<td>8.49</td>
<td>6.47</td>
</tr>
<tr>
<td>Xanthorrhizol (%)*</td>
<td>0.90</td>
<td>0.81</td>
<td>0.97</td>
</tr>
</tbody>
</table>

*% based on extract

2.2. Experimental locations.

Field experiments of this study were conducted in experimental farms of two agricultural research stations (Tropical Biopharmaca Research Center and Pasir Sarongge) of the IPB University and one at local farmer (Sukabumi), West Java, Indonesia. Tropical Biopharmaca Research Center Station is located in Bogor on latitude 6.55 S, longitude 106.72 E, altitude 141 m above sea level (m.a.s.l), pH soil 4.13–4.25, C-organic soil 1.33%, N soil 0.21%, rainfall 51–671 mm, and temperature 25.8 – 27.0 °C. Pasir Sarongge Station is located in Cianjur, situated at altitude 1083 m.a.s.l, rainfall 46 – 552 mm, pH soil 5.05-5.32, C-organic soil 4.01%, N soil 0.40%, and temperature 20.7 – 22.4 °C and has a latitude 6.77 S and longitude 107.05 E. The farmer local station is located in Sukabumi at latitude 6.87 S, longitude 106.80 E, altitude 493 m.a.s.l, rainfall 36 – 651 mm, pH soil 5.08-5.76, C-organic soil 1.96%, N soil 0.20%, and temperature 19.4 – 23.1 °C.

2.3. Experimental design, planting, and sample collection.

The study was carried out from September 2018 to June 2019 in three locations: Bogor, Cianjur, and Sukabumi (Figure 1), and performed in a completely randomized group design. The rhizome of *C. zanthorrhiza* variety (30 – 50 g) with aged nine-month after planting was used in this experiment. The experiment was repeated three times at each experimental site, with five plants in each replicate. Each variety was planted at 60 x 50 cm, with one rhizome per planting hill. Fertilization is applied once at the start of planting, with 1 kg manure per planting hill. During the growth period, maintenance is performed monthly by weeding and filling the soil. Finally, the rhizome was harvested at nine-month after planting. The rhizome samples were collected and analyzed in this study.

2.4. Sample preparation and extraction.

The method described by Septaningsih et al. [31] was adapted to extract the sample. Before extraction, the rhizome sample was cleaned, dried, and powdered of 80 mesh. The
powdered sample (5 g) was extracted using the maceration method in 70% ethanol (25 ml) for 24 h. Then, the sample mixture was separated using filter paper. Finally, the extracted sample was obtained using rotary evaporator R100 (Buchi, Flawil, Swiss) at 40 °C. The extract was used to analysis of profiling metabolites using UHPLC-Q-Orbitrap-HRMS.

Figure 1. Maps of three sites of the field experimental.

2.5. Metabolite analysis by UHPLC-Q-Orbitrap-HRMS.

Non-targeted metabolites analysis was performed using a modified version of the method described by Jin et al. [32]. Briefly, each sample extract was diluted with methanol using ultrasonic OVAN 60 Hz for 30 min. The mixture was filtered using PTFE 0.2 μm pore filter membrane (Ambala Cantt, India). The filtrate sample (2.5 μl) was injected into the UHPLC-Q-Orbitrap-MS/MS (Thermo Fisher, Waltham, USA).

The metabolite sample was separated using a vanquish flex UHPLC-Q-Orbitrap HRMS system equipped with column C18 (100 x 2.1 mm, 1.5 m). The mobile phases were (A) 0.1% formic acid in the water and (B) 0.1% formic acid in acetonitrile. The flow rate of the gradient elution system was 0.2 ml/min for 50 min. The gradient elution was as follows: 0 – 10 min, 20 – 35% B; 10 – 30 min, 35 – 55% B; 30 – 40 min, 55 – 95% B; 40 – 43 min, 95% B; 40 – 43.01 min, 95 – 20% B; and 43.01 – 50 min, 20% B. Positive and negative electrospray ionization (ESI+/ ESI-) mode was used for mass spectrometric analysis, with collision energies of 18, 35 and 53 eV. The following parameters were set on the instrument: MS full scan range, m/z 100 – 1200 Da; spray voltage, (-) 3.2 Kv and (+) 3.8 Kv; resolving power, 70,000 FWHM; capillary temperature, 320 °C; sheath and auxiliary gas, 15 and 3 ml/min; and MS full-scan type, full MS/ dd MS2.
2.6. Data analysis.

UHPLC-Q-Orbitrap HRMS raw data were processed and analyzed using Compound Discoverer 2.2 to identify metabolites detected in *C. zanthorrhiza* rhizome extract. The identification of suspected metabolites through selected spectrum stages, retention time alignment, detection of unknown compounds, unknown grouping compounds, composition prediction, mass list search, gap filling, area normalization, and marking of background compounds. Identification was carried out using a local database obtained from the literature on compounds of the genus *Curcuma*. Parameters set to predict compound composition are: minimum peak intensity: 6000000, adduct type: [M + H] + and [M – H] -, minimum elements counts: C, H and maximum element counts: C: 90, H: 190, N: 10, O: 30. Then, we determined the mass error value (5 ppm) for each identified compound. Compound Discoverer version 2.2 (Thermo Fisher, Waltham, MA, USA) was also used to analyze fragmentation patterns (MS and MS/MS).

Chemometric analyses, such as principal component analysis (PCA) and partial least square discriminant analysis (PLS-DA), were performed by using MetaboAnalyst 5.0 software (https://www.metaboanalyst.ca/).

3. Results and Discussion

3.1. Putative identification of metabolites using UHPLC-q-Orbitrap-HRMS.

In this research, untargeted metabolomics was employed to putatively identify the compounds present in 70% of ethanol extracts of *C. zanthorrhiza* rhizome with different varieties and locations of growth. Chromatogram samples from various sites had similar patterns but varying peak intensities, indicating that the metabolites were distributed at varying amounts (Figure 2). We putatively identified about 39 metabolites in all samples investigated based on the chromatograms, as reported in Table 2. The identified metabolite classes include amino acid (4 compounds), terpenoids (24 compounds), phenols (5 compounds), diarylheptanoids (5 compounds), and other organic compounds (1 compound).

![Figure 2](https://doi.org/10.33263/BRIAC131.026)

**Figure 2.** Total peak ion chromatograms in positive mode of *C. zanthorrhiza* varieties grown at different sites: (a) Cianjur, (b) Sukabumi, and (c) Bogor. 1 – 39, name metabolites, see in Table 2.

The Venn diagram in Figure 3 shows the 39 metabolites identified in the three cultivation sites studied. Among the metabolites, 28 were frequently discovered in the three
locations where *C. zanthorrhiza* cultivars were planted; the name of metabolites is presented in Table 2. Two metabolites, namely p-coumaric acid and agaruspirol, were detected in *C. zanthorrhiza* varieties cultivated in Bogor. Two metabolites in Sukabumi-cultivated *C. zanthorrhiza* varieties were coronarin E and gamma bicyclohomo farnesal. Two metabolites, zedoaraldehyde, and naringenin, were identified exclusively in *C. zanthorrhiza* varieties grown in Cianjur. The slices of the number of compounds identified in *C. zanthorrhiza* varieties grown in Bogor and Sukabumi were two compounds (terpinolene and safrole), Bogor and Cianjur were 1 compound (tryptophan), Sukabumi and Cianjur were two compounds (zedoarolide B and bisacurone).

![Figure 3](image.png)

**Figure 3.** Venn diagram of metabolites distribution of *C. zanthorrhiza* varieties at different cultivated sites (Bogor, Cianjur, and Sukabumi).

### 3.1.1. Amino acids.

Four amino acid groups were identified in the extract samples, i.e., leucine (1), valine (2), phenylalanine (3), and tryptophan (4) (Table 2) and were reported in a previous study [33]. According to prior research, leucine (1) and valine (2) produced just two fragments by successive H$_2$O + CO and NH$_3$ losses [34]. The fragmentation of leucine (1) and valine (2) were at *m/z* 86 and 69 for leucine (1), and 72 and 56 for valine (2). The fragmentation of phenylalanine (3) was by the loss of H$_2$O + CO at *m/z* 120 followed by releasing of NH$_3$ at *m/z* 103 [34]. Metabolite (4) at *m/z* 205 was identified as tryptophan (4) presented by fragments at *m/z* 188, 170, and 143.

### 3.1.2. Terpenoids.

Previous research has revealed terpenoid chemicals in the *C. zanthorrhiza* varieties, which are reported in this work [3]. About 24 terpenoid metabolites were identified in the extract samples of *C. zanthorrhiza* varieties (Table 2). Several hydroxyl groups are found in terpenoid monomer zedoarolide B (5), zedoalactone B (6), curcumanolactone C (7), bisacurone (8), zedoarol (9), camphor (12), 13-hydroxygermacrone (13), iso-velleral (15), coronarin E (17), curcumanolactone A (18), gamma-bicyclohomo farnesal (24), curcumalactone (25), agaruspirol (26) and spathulenol (27) that release H$_2$O molecules in the form [M + H-18]$^+$ [35,36]. The metabolite with *m/z* 261 identified as zedoaraldehyde (10) showed by fragments at *m/z* 204, 145, and 119. Compound (11) at *m/z* 137 [M+H]$^+$ was discovered as terpinolene and identified fragmentation by loss C$_3$H$_6$ [M+H-42]$^+$, CH$_2$ [M+H-42–14]$^+$, and followed by releasing CH$_3$ [M+H-42–14–15]$^+$.
Gweicurculactone (14) with [M+H]+ at m/z 299 was fragmented by releasing CO₂ molecule at [M+H-44]+, followed by loss CH₃ [M+H-44-14]+ and C₂H₅ [M+H-44-15-41]. Ar-turmerone (16) with [M+H]+ at m/z 217 and curzerenone (19) with [M+H]+ at m/z 231 were fragmented by releasing two CH₃ molecules at m/z 202 and 187, while curzerenone (19) at m/z 231 gave fragments at m/z 203 [M+H-28]+ and H₂O 185 [M+H-28-18]+. Curcumene (20) with [M+H]+ at m/z 203 was fragmented by releasing C₄H₈ at m/z 147 [M+H-56]+ and two C₂H₄ at m/z 191 and 91 [M+H-56-28-28]. Compound (21) at m/z 151 was found as m-thymol presented by fragments at m/z 108 and 66.

The marker compound of C. zanthorrhiza, xanthorrhizol (22) (m/z 219), was discovered by the fragments at m/z 201 [M+H-18]+ with releasing H₂O and m/z 69 [M+H-132]+ with loss C₁₀H₁₂. Several previous reports have identified this compound as a primary compound in C. zanthorrhiza rhizome [1,5,17]. Compound at m/z 315 was identified as p-cymene (23) showed by fragments at m/z 120, 92, and 78. The fragmentation of p-cymene started from the loss of CH₃ [M+H-15]+ and was followed by releasing C₂H₄ [M+H-15-16]+ and CH₂ [M+H-15-16-14]+ [37]. Element (28) was identified at m/z 223 and gave fragments at m/z 149, 121, and 81.

3.1.3. Phenols.

Five phenols groups were identified in the extract C. zanthorrhiza samples, i.e., naringenin (29), p-coumaric acid (30), (+)-rhododendrol (31), 4-hydroxybenzoic acid (32), and 2.5-dimethylphenol (33). Naringenin (29) was identified at m/z 273 and gave fragments at m/z 245, 151, and 119. P-Coumaric acid (30) was found at m/z 165 [M+H]+ and fragmented by releasing H₂ at m/z 163 [M+H-2]+ and followed by loss CO₂ at m/z 119 [M+H-44]+ [38]. Compound (31) at m/z 167 was identified as (+)-rhododendrol showed by fragments at 139, 84, and 69. Compound (32) at m/z 139 was identified as 4-hydroxybenzoic acid presented by fragments at 121, 93, and 65. The fragmentation of 4-hydroxybenzoic acid started from the loss of H₂O [M+H-18]+ and was followed by releasing CO [M+H-18-28]+ and CO [M+H-18-28-28]+ [39]. Compound (33) at m/z 123 was discovered as 2.5-dimethylphenol showed by fragments at 108 and 93.

3.1.4. Diarylheptanoids.

Diarylheptanoid compounds were identified in C. zanthorrhiza and were reported in prior work [33,40]. There were five diarylheptanoids compounds discovered in the C. zanthorrhiza samples studied (Table 2). Curcumin (38), demethoxycurcumin (36), and bisdemethoxycurcumin (34) belong to curcuminoid compound groups and are found in Curcuma sp. [41–43]. These compounds and dihydrocurcumin (37) were identified at fragments by releasing 1-aryl-3-hidroksi-1,3-butadiena (m/z 147 and 177) and followed by loss 3-arilkarboksi-prop-2-ena (m/z 145 and 175) [44]. Compound (35) at m/z 341 was identified as letestuianin A showed by fragments at m/z 255 and 240.

3.1.5. Other organic compounds.

Safrole (39), ether compound groups, was identified in C. zanthorrhiza varieties studied (Table 2). This compound (39) was identified at m/z 163 [M+H]+ and fragmented by releasing C₂H₂O₂ at m/z 105 [M+H-58]+ and followed by loss C₂H₃ at m/z 78 [M+H-27]+. Safrole compound was shown to have MS2 molecular ion peaks in fragment M-105 that presented by releasing C₂H₂O₂ [45].
3.2. Metabolomic profiles of C. zanthorrhiza varieties based on UHPLC-q-Orbitrap-HRMS.

The collected MS data of positive ion modes of C. zanthorrhiza varieties grown in Bogor, Cianjur, and Sukabumi were entered into MetaboAnalyst 5.0 for statistical analysis by the PCA PLS-DA modules. PCA is a non-supervised chemometric method for displaying generic clustering and patterns in multivariate data [46]. The score plot shows similarities and dissimilarities between samples and displays grouping and pattern forms in a two-dimensional space. As illustrated in Figure 4, PCA score plots of the metabolite profiles of three C. zanthorrhiza varieties revealed a more distinct separation between those cultivated in Bogor, Cianjur, and Sukabumi. In this case, PC1 and PC2 explain 65.3% of the overall variation, with PC1 accounting for 41.6% and PC2 accounting for 23.7%. These findings indicated that the geographical disparity was more significant than the disparity between C. zanthorrhiza varieties.

The metabolite profiles of three C. zanthorrhiza varieties were also subjected to a supervised partial least square discriminant analysis (PLS-DA). The PLS-DA is a supervised chemometric method that uses multiple linear regression for determining the highest covariance between the data set (X) and the class membership (Y) [46]. As shown PLS-DA score plot in Figure 5, the C. zanthorrhiza varieties grown in Bogor were more distinct than those cultivated in other locations, but Cianjur and Sukabumi were not. Bogor’s more acidic soil conditions have a low carbon-organic content, and are at a moderate elevation, enabling the chemicals to be created differently from the other two places. Similar investigations have shown that plant metabolite content is influenced by soil pH conditions, elevation, and organic carbon content in soil [47,48]. Component 1 accounted for 21.9% of the total variance, while component 2 accounted for 21.3% of the total variance. Figure 6 summarizes the significant metabolites (VIP > 1.0) detected by the PLS-DA module. The metabolites with a VIP greater than 1.0 could be considered potential markers for differentiating the samples, and a higher VIP score indicated greater discriminating power [49].

![Figure 4](https://biointerfaceresearch.com/)

**Figure 4.** Score plot of principal component analysis (PCA) from the metabolite profile of C. zanthorrhiza varieties grown in different regions.

A total of 15 metabolites from C. zanthorrhiza cultivars’ metabolite profiles demonstrated the ability to differentiate the samples grown in Bogor, Cianjur, and Sukabumi. As a result, those 15 metabolites could be used as potential markers in C. zanthorrhiza varieties to help differentiate them according to their geographical origin. Our findings suggest that C.
*zanthorrhiza* varieties cultivated in Bogor, Cianjur, and Sukabumi have distinct metabolite profiles. This can be ascribed to several factors, including genetics, soil environment, cultivation methods, and agroecological circumstances [50–52]. Future research is required to understand better the effect of soil and water conditions on the metabolites composition of *C. zanthorrhiza*.

![Scores Plot](image1)

**Figure 5.** Score plot of Partial least squares discriminant analysis (PLS-DA) from the metabolite profile of *C. zanthorrhiza* varieties grown in different regions.

![VIP Score Plot](image2)

**Figure 6.** The score of VIP of metabolites in partial least squares discriminant analysis (PLS-DA) from the metabolite profile of *C. zanthorrhiza* varieties grown in different regions.

### 4. Conclusions

A total of 39 metabolites were discovered in three different cultivars of *C. zanthorrhiza* cultivated in Bogor, Cianjur, and Sukabumi using UHPLC-q-Orbitrap-HRMS. These compounds consisted of 4 amino acids, 24 terpenoids, 5 phenols, and 1 other organic group. Using principal component analysis, the classification of *C. zanthorrhiza* cultivars metabolites cultivated in three different locations was successfully carried out. A total of 15 metabolites could potentially be used as markers for *C. zanthorrhiza* cultivars grown in Bogor, Cianjur, and Sukabumi.
Table 2. Metabolites detected in 70% ethanol rhizome extract of the *C. zanthorrhiza* varieties cultivated in Bogor, Cianjur, and Sukabumi using UHPLC-q-Orbitrap-HRMS in positive ionization mode.

<table>
<thead>
<tr>
<th>No.</th>
<th>Metabolite</th>
<th>Class chemical</th>
<th>RT (min)</th>
<th>MW (ppm)</th>
<th>Error (ppm)</th>
<th>MS fragment ion (m/z)</th>
<th>Bogor</th>
<th>Cianjur</th>
<th>Sukabumi</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Leucine</td>
<td>Amino acid</td>
<td>1,226</td>
<td>131</td>
<td>-0.31</td>
<td>132, 86, 69</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>2</td>
<td>Valine</td>
<td>Amino acid</td>
<td>1,229</td>
<td>117</td>
<td>0.23</td>
<td>118, 72, 56</td>
<td>✓</td>
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<td>✓</td>
</tr>
<tr>
<td>3</td>
<td>Phenylalanine</td>
<td>Amino acid</td>
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<td>165</td>
<td>-0.52</td>
<td>166, 120, 103</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>4</td>
<td>Tryptophan</td>
<td>Amino acid</td>
<td>1,292</td>
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<td>0.07</td>
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<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>5</td>
<td>Zedoarol B</td>
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<td>6</td>
<td>Zedoalactone B</td>
<td>Terpenoids</td>
<td>1,514</td>
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<td>281, 263, 245, 201, 186</td>
<td>✓</td>
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<td>7</td>
<td>Curcumolacetone C</td>
<td>Terpenoids</td>
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<tr>
<td>8</td>
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<td>253, 235, 217, 139</td>
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<tr>
<td>9</td>
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Name of *C. zanthorrhiza* varieties: C1 = Cursina 1; C2 = Cursina 2; and C3 = Cursina 3; MW, molecular weight; ppm, part per million; RT, retention time (min); ✓ = detected; * = not detected.
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Conflicts of Interest
The authors declare no conflict of interest.

References


