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1 **Title:** Species identification of Indonesian agarwood using a DNA barcoding  
2 method

3

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13

## 1 **Abstract**

2 Agarwood is a type of resinous wood found in the trunks of *Aquilaria* and some other genera. It is  
3 widely used as an herbal medicine for sedation, detoxification, and treatment of stomachaches, as well  
4 as for incense sticks. However, the number of source plants is decreasing, and in 2005 they were added  
5 to Appendix II of the Convention on International Trade in Endangered Species of Wild Fauna and  
6 Flora (CITES). In order to identify source species of agarwood, we previously developed a DNA  
7 barcoding method using resin deposition sites. In this study, to identify additional agarwood source  
8 species, the barcoding method was applied to source plants and commercial agarwood samples  
9 collected from Sumbawa, Lombok, Sulawesi, and Kalimantan in Indonesia, a major agarwood  
10 producing country. In addition, the method was also applied to incense stick samples labeled as  
11 agarwood. As a result, several samples were identified as *Gyrinops*, which is not currently listed as an  
12 agarwood source plant in the Japanese standards for non-Pharmacopoeial crude drugs 2018 (Non-JPS  
13 2018). From the viewpoint of securing future resources, these findings suggest that *Gyrinops* species  
14 should therefore be added to the list of agarwood source species.

15

## 16 **Keywords**

17 *Aquilaria*, *Gyrinops*, agarwood, DNA barcoding, Indonesia, incense sticks

18

## 1 Introduction

2 Agarwood is a type of resinous wood found in the trunks of *Aquilaria* and some other genera. It is  
3 widely used as an herbal medicine for sedation, detoxification, and treatment of stomachaches, as  
4 well as for incense sticks. However, the numbers of source plants in their native environments are  
5 decreasing, and in 2005 they were added to Appendix II of the Convention on International Trade in  
6 Endangered Species of Wild Fauna and Flora (CITES) [1]. Artificial production of resin and  
7 agarwood using cultivated trees is therefore increasing; however, the resulting quality varies and  
8 authentication of agarwood cannot be done based on appearance or component information.  
9 Identification of agarwood source species is therefore important. In our previous study, we  
10 developed a DNA barcoding method for identification of source species using resin deposition sites  
11 of agarwood obtained from markets in Japan, Indonesia, Thailand, and Vietnam [2]. DNA sequences  
12 of the *trnL* (UAA)-*trnF* (GAA) and *matK* regions were subsequently obtained. However, the  
13 sequence data on GenBank does not cover all agarwood source species, and therefore, the origins of  
14 some samples could not be determined. According to the Japanese standards for non-Pharmacopoeial  
15 crude drugs 2018 (Non-JPS 2018), five species of *Aquilaria* have been designated as source species  
16 of agarwood [3]. However, in our previous study, *Gyrinops* species were also identified as sources of  
17 agarwood in the Japanese market [2]. Although *Gyrinops* species are not currently listed as source  
18 species of agarwood in the Non-JPS 2018, our findings suggest that they are used for medicinal

1 purposes in Japan. Moreover, due to decreasing resources, identification of additional source species  
2 on the market is important. In this study, the DNA barcoding method using *trnL-trnF* and *matK*  
3 DNA sequences was applied to leaves, fruit, and wood from agarwood source plants and commercial  
4 agarwood collected in Sumbawa, Lombok, Sulawesi, and Kalimantan in Indonesia, a major  
5 agarwood producing country (Fig. 1). In addition, the method was also carried out using incense  
6 sticks labeled as agarwood.

7

## 8 **Materials and methods**

### 9 **Plant materials and DNA extraction**

10 Three samples were collected from Sumbawa, 13 from Lombok, 13 from Sulawesi, and 7 from  
11 Kalimantan (Table 1). Three commercial agarwood samples were also purchased in Sumbawa (Table  
12 2), along with 8 incense stick samples (Table 3). Morphological images of the agarwood samples are  
13 shown in Fig. S1, and the incense sticks are shown in Fig. S2. The morphological characteristics of  
14 fruit collected from the Kalimantan samples are shown in Fig. 2. Voucher specimens were deposited  
15 in the Faculty of Mathematics and Natural Sciences, Mataram University, Indonesia, and the  
16 Experimental Station for Medicinal Plants at the Graduate School of Pharmaceutical Science, Kyoto  
17 University, Japan. Samples were crushed using ShakeMan (BioMedical Sciences, Japan) prior to DNA  
18 extraction using a DNeasy Plant Mini Kit (Qiagen, Germany) according to the manufacturer's protocol.

## 1 **Primer design and PCR amplification**

2 PCR amplification was performed as in our previous study [2]. The *trnL-trnF* region was amplified  
3 using the forward primer A1 and reverse primer A2, and the *matK* gene was amplified using the  
4 forward primer C1 and reverse primer C2 (Tables S1 and S2). The amplification enzyme was modified  
5 to KOD -Plus- Ver. 2 (Toyobo Co., Ltd., Japan).

## 6 **Amplification by nested PCR**

7 DNA samples from Lomb\_12, Lomb\_13, Sumb\_m1, Sumb\_m3, and IS\_1 through IS\_8 were also  
8 amplified using nested PCR as in our previous study [2]. To do so, forward primer B1 and reverse  
9 primer B2 were used for the *trnL-trnF* region, and forward primer D1 and reverse primer D2 were  
10 used for the *matK* gene (Tables S1 and S2). The amplification enzyme was modified to KOD -Plus-  
11 Ver. 2 (Toyobo Co., Ltd.).

## 12 **DNA sequencing and data analysis**

13 PCR amplification products were separated on 0.5% agarose/TAE gel, purified using PCR clean-up  
14 gel extraction (Macherey-Nagel, Germany) and sequenced on a 3730×1 DNA Analyzer using a BigDye  
15 Terminator V3.1 Cycle Sequencing Kit (Applied Biosystems, USA). Sequences were compared and  
16 aligned using DNASIS Pro version 2.09 (Hitachi Solutions Ltd., Japan).

17

## 18 **Results**

## 1 **Identification of source species based on DNA sequences of the *trnL-trnF* region**

2 Sequence information of the *trnL-trnF* region are shown in the Supplementary Material. The 47  
3 samples (source plant, commercial, and incense stick samples) were classified into seven groups  
4 according to DNA sequences of their *trnL-trnF* regions (Tables 4-6) then a similarity search was  
5 carried out using GenBank. No matching sequences were found for samples Kali\_1 through Kali\_5.  
6 Species identification of remaining samples was carried out based on GenBank sequence data for  
7 *Gyrinops versteegii* (LC467530) [2], *G. moluccana* (KT726325) [4], *Aquilaria microcarpa*  
8 (LC467528) [2], *A. malaccensis* (LC467525) [2], *A. khasiana* (AY216744), and *A. beccariana*  
9 (KT726319) [5].

## 10 **Genotype classification based on DNA sequences of the *matK* gene**

11 Sequence information of the *matK* gene is shown in the Supplementary Material. The 47 samples were  
12 subsequently classified into two genotypes according to DNA sequences of their *matK* genes (Tables  
13 7, 8). Thirty-four samples, Sumb\_1 through Sumb\_3, Lomb\_1 through Lomb\_13, Sula\_1, Sula\_2,  
14 Sula\_8 through Sula\_13, Sumb\_m1, Sumb\_m2, and IS\_1 through IS\_8, were classified as genotype  
15 A, and the remaining 13 samples, Sula\_3 through Sula\_7, Kali\_1 through Kali\_7, and Sumb\_m3, as  
16 genotype B (Table 8).

## 17 **Classification based on the *trnL-trnF* and *matK* regions**

18 Source species were subsequently determined by combining sequencing information of the *trnL-trnF*

1 region and the genotype classifications based on the *matK* gene as shown in Table 8.

2

### 3 **Discussion**

#### 4 **Identification of source species based on DNA sequences of the *trnL-trnF* region**

5 Boundary lines for species distribution known as the Wallace Line and Weber Line run through

6 Indonesia (Fig. 1). Shiou et al. (2018) carried out a comprehensive GenBank search to identify

7 agarwood plant species in Indonesia [4]. As a result, in line with the species boundaries, they

8 revealed that *Gyneros* species are mainly found in eastern Indonesia and *Aquilaria* species in the

9 western Indonesia.

10 In this study, of the samples collected on Sumbawa and Lombok, Sumb\_1 through Sumb\_3, Lomb\_1

11 through Lomb\_11, and Lomb\_13 were identified as belonging to *G. versteegii*, while Lomb\_12 was

12 identified to be *G. moluccana* according to a similarity search of the *trnL-trnF* region in GenBank

13 (Table 4). These results support previous studies whereby source plants collected from Lombok were

14 found to be morphologically identical to *G. versteegii* [4, 6]. Sequence information of the *trnL-trnF*

15 region of *G. moluccana* previously gave only one GenBank match (KT726325) [4], suggesting

16 inhabitation of the Maluku Islands in Indonesia (Fig. 1). However, in this study, identification of

17 sample Lomb\_12 as *G. moluccana* also suggests that this species inhabits Lombok. Analysis of

18 Kalimantan samples Kali\_1 through Kali\_5 revealed a single nucleotide polymorphism of A.



1 *microcarpa*, with (T) at 291 base pair (bp) rather than (G). The source species could therefore not be  
2 determined using sequence information of the *trnL-trnF* region alone (Table 4). However, since the  
3 fruit morphology of Kali\_5 was similar to that of *A. microcarpa*, it is believed to be very closely  
4 related. Meanwhile, although samples Kali\_6 and Kali7 were thought to be *A. beccariana* based on  
5 their sequence information, their fruit differed (Fig. 2), with the fruit form of Kali\_6 similar to that  
6 of *A. malaccensis*. Thus, because the *trnL-trnF* region is located on chloroplast DNA, which is likely  
7 to be conserved via maternal inheritance, Kali\_6 is thought to have been derived from hybridization  
8 between *A. malaccensis* and *A. beccariana*. To confirm this, establishment of a DNA barcoding  
9 method using nuclear gene of, for example, internal transcribed spacer (ITS) regions from agarwood  
10 source species is required in the future. The 13 samples collected on Sulawesi were classified into  
11 four groups according to DNA sequences of their *trnL-trnF* regions (Table 4). These results suggest  
12 that various agarwood source species inhabit Sulawesi. Sulawesi Island is located within the  
13 Wallacea region, which exists between the Wallace and Weber lines (Fig. 1). Agarwood plants from  
14 western and eastern Indonesia are therefore thought to inhabit this region, consistent with the DNA  
15 sequencing classification. Of the commercial agarwood samples collected from Sumbawa markets,  
16 sample Sumb\_m1 was identified as *A. microcarpa*, while Sumb\_m2 and Sumb\_m3 were thought to  
17 belong to *G. moluccana* and *A. malaccensis*, respectively (Table 5). Because the source species of  
18 these samples differed, production of commercial agarwood on Sumbawa is thought to use agarwood

1 collected locally as well as from other islands in Indonesia. Meanwhile, although the incense stick  
2 samples (IS\_1 through IS\_8) were purchased from different countries, all showed the same sequence  
3 pattern (Table 6), confirming that they were all made from agarwood.

#### 4 **Classification of genotypes based on DNA sequences of the *matK* gene**

5 Of the *matK* gene patterns shown in Table 7, *A. crassna*, *A. hirta*, and *A. subintegra*, which represent  
6 genotype A, are usually found in Vietnam and Thailand [5, 6], while *G. versteegii* and *G. caudate*,  
7 also representing genotype A, are usually found in eastern Indonesia and Papua New Guinea [4, 5,  
8 7]. Meanwhile, *A. malaccensis*, *A. beccariana*, and *A. microcarpa*, which represent genotype B, are  
9 usually found in western Indonesia and in Malaysia [4, 5], while *A. sinensis*, representing genotype  
10 C, is usually found in China [5]. DNA sequences of the *matK* gene obtained in this study were  
11 classified into two genotypes, A and B, with (C) at 358 bp indicating genotype A and (T) at 358 bp  
12 indicating genotype B. Samples collected from Sumbawa and Lombok (Sumb\_1 through Sumb\_3  
13 and Lomb\_1 through Lomb\_13) were genotype A, while those collected from Kalimantan (Kali\_1  
14 through Kali\_7) were genotype B. These results are consistent with the known habitat distribution  
15 [4–7]; however, of the samples collected on Sulawesi (Sula\_1 through Sula\_13), Sula\_1, Sula\_2, and  
16 Sula\_8 through Sula\_13 represented genotype A, while Sula\_3 through Sula\_7 were genotype B.  
17 Although Sulawesi, Sumbawa, and Lombok all fall similarly within Wallacea region, their history of  
18 continental migration may differ, resulting in differences in the distribution of agarwood source

1 plants (Fig. 1). Of the commercial agarwood samples collected from Sumbawa markets, Sumb\_m1  
2 and Sumb\_m2 represented genotype A, while Sumb\_m3 was genotype B, supporting the DNA  
3 sequencing results of the *trnL-trnF* region. Meanwhile, the incense stick samples (IS\_1 through  
4 IS\_8) were all genotype A, also consistent with sequencing patterns of the *trnL-trnF* region.

### 5 **Source species identification based on DNA sequences of the *trnL-trnF* region and** 6 ***matK* gene**

7 The source species of Lomb\_12, Sula\_8 through Sula\_13, and Sumb\_m2 could not be determined  
8 because sequence information of the *matK* gene in *A. khasiana* and *G. moluccana* does not exist in  
9 GenBank (Table 8). To do so, voucher specimens of *A. khasiana* and *G. moluccana* are therefore  
10 required.

11 Sumb\_m1 and IS\_1 through IS\_8 showed identical sequences in both regions, and were also  
12 identical to those of *A. microcarpa* in the *trnL-trnF* region; however, according to the *matK* gene,  
13 they were classified as genotype A. Due to these conflicting findings, the source species could not be  
14 determined (Table 8). Our previous report suggested similar difficulties in identifying all agarwood  
15 source plants using current genetic data in GenBank [2]. Furthermore, the *trnL-trnF* region alone,  
16 which is most frequently used, is thought to be insufficient for identification of agarwood species.

17

### 18 **Conclusions**

1 The results of this study revealed the distribution of agarwood source plants on four islands in  
2 Indonesia, supporting the previous study of Shiou et al. (2018), whereby *Gyrinops* species were  
3 found to inhabit mainly eastern Indonesia and *Aquilaria* species were found to inhabit mainly  
4 western Indonesia, separated by the Wallace boundary line [4]. However, because the agarwood  
5 plants collected from Sulawesi were classified into various species, the Wallace Line alone cannot be  
6 used to classify habitat distribution. In this study, DNA was also extracted from incense sticks labeled  
7 as agarwood, and their DNA barcoding regions were successfully amplified. These findings suggest  
8 that this method can therefore be applied not only to the resin-containing sites, which is considered  
9 difficult to extract DNA from, but also to processed products. However, because samples Kali\_6 and  
10 Kali\_7 had identical DNA sequences in both regions but differing fruit forms, establishment of a DNA  
11 barcoding method using nuclear genes such as the ITS region are also required in the future. In addition,  
12 based on the commercial agarwood samples from Sumbawa, it is thought that commercial production  
13 uses agarwood obtained both locally and from other islands in Indonesia. Agarwood products obtained  
14 from various source species are therefore thought to be distributed around the world. According to the  
15 Non-JPS 2018, five species of *Aquilaria*, *A. agallocha*, *A. crassna*, *A. malaccensis*, *A. sinensis*, and *A.*  
16 *filaria*, are currently designated as source species of agarwood [3]. However, our results suggest that  
17 agarwood produced from *A. microcarpa*, *A. beccariana*, and *Gyrinops* species also exist in the  
18 Japanese market. In addition, because all agarwood source species are classified in Appendix II of

1 CITES, it is recommended that certain species of *Gyrinops* also be added as source plants of herbal  
2 medicinal “Agarwood” under Non-JPS 2018, from the viewpoint of securing future resources.  
3 Moreover, sequence information lacking in GenBank should also be determined in the future using  
4 additional specimens.

5

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10 the Faculty of Mathematics and Natural Sciences, Mataram University, Indonesia, and the Graduate  
11 School of Pharmaceutical Sciences, Kyoto University, Japan.

12

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## 1 Tables

2 Table 1 Details of the agarwood samples collected from source species in Sumbawa, Lombok,

3 Sulawesi, and Kalimantan

Collection site	Sample no.	Part used	Collection date
Sumbawa	Sumb_1	Leaf	January, 2018
	Sumb_2	Fruit	January, 2018
	Sumb_3	Agarwood (branch)	January, 2018
Lombok	Lomb_1	Leaf	January, 2018
	Lomb_2	Leaf	January, 2018
	Lomb_3	Leaf	January, 2018
	Lomb_4	Leaf	January, 2018
	Lomb_5	Leaf	January, 2018
	Lomb_6	Leaf	January, 2018
	Lomb_7	Leaf	January, 2018
	Lomb_8	Leaf	January, 2018
	Lomb_9	Fruit	January, 2018
	Lomb_10	Fruit	January, 2018
	Lomb_11	Fruit	January, 2018
	Lomb_12	Agarwood (chunk)	January, 2018
	Lomb_13	Agarwood (branch)	January, 2018
Sulawesi	Sula_1	Leaf	July, 2018
	Sula_2	Leaf	July, 2018
	Sula_3	Leaf	July, 2018
	Sula_4	Leaf	July, 2018
	Sula_5	Leaf	July, 2018
	Sula_6	Leaf	July, 2018
	Sula_7	Leaf	July, 2018
	Sula_8	Leaf	July, 2018
	Sula_9	Leaf	July, 2018
	Sula_10	Leaf	July, 2018
	Sula_11	Leaf	July, 2018
	Sula_12	Leaf	July, 2018
	Sula_13	Leaf	July, 2018

Kalimantan	Kali_1	Leaf	November, 2018
	Kali_2	Leaf	November, 2018
	Kali_3	Leaf	November, 2018
	Kali_4	Leaf	November, 2018
	Kali_5	Fruit	November, 2018
	Kali_6	Fruit	November, 2018
	Kali_7	Fruit	November, 2018

1

2 Table 2 Details of the commercial agarwood samples collected from markets in Sumbawa

Market location	Sample no.	Sample type	Purchase date
Sumbawa	Sumb_m1	chip	January, 2018
	Sumb_m2	chunk	January, 2018
	Sumb_m3	small pieces	January, 2018

3

4 Table 3 Details of the incense stick samples bought from markets in China, Taiwan and Japan; one

5 sample of unknown origin was also included

Sample no.	Market location
IS_1	China
IS_2	China
IS_3	China
IS_4	China
IS_5	Taiwan
IS_6	Taiwan
IS_7	Japan
IS_8	Unknown

6

7 Table 4 SNPs in the *trnL-trnF* IGS region amplified from DNA extracted from the source species

8 samples



Sample no.	SNP								Species identification
	159	291	301	327	328	339	368	381	
Sumb_1	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Sumb_2	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Sumb_3	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Lomb_1	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Lomb_2	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Lomb_3	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Lomb_4	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Lomb_5	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Lomb_6	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Lomb_7	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Lomb_8	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Lomb_9	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Lomb_10	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Lomb_11	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Lomb_12	A	T	T	T	T	T	C	A	<i>G. moluccana</i>
Lomb_13	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Sula_1	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Sula_2	A	T	T	T	-	T	C	A	<i>G. versteegii</i>
Sula_3	A	T	T	-	-	G	C	A	<i>A. microcarpa</i>
Sula_4	C	T	T	T	-	G	C	A	<i>A. malaccensis</i>
Sula_5	A	T	T	-	-	G	C	A	<i>A. microcarpa</i>
Sula_6	A	T	T	-	-	G	C	A	<i>A. microcarpa</i>
Sula_7	A	T	T	-	-	G	C	A	<i>A. microcarpa</i>
Sula_8	A	T	T	-	-	T	C	A	<i>A. khasiana</i>
Sula_9	A	T	T	-	-	T	C	A	<i>A. khasiana</i>
Sula_10	A	T	T	-	-	T	C	A	<i>A. khasiana</i>
Sula_11	A	T	T	-	-	T	C	A	<i>A. khasiana</i>
Sula_12	A	T	T	-	-	T	C	A	<i>A. khasiana</i>
Sula_13	A	T	T	-	-	T	C	A	<i>A. khasiana</i>
Kali_1	A	G	T	-	-	G	C	A	Unknown
Kali_2	A	G	T	-	-	G	C	A	Unknown
Kali_3	A	G	T	-	-	G	C	A	Unknown
Kali_4	A	G	T	-	-	G	C	A	Unknown
Kali_5	A	G	T	-	-	G	C	A	Unknown

Kali_6	C	T	T	-	-	G	C	A	<i>A. beccariana</i>
Kali_7	C	T	T	-	-	G	C	A	<i>A. beccariana</i>

1 *SNP* single nucleotide polymorphism, *IGS* intergenic spacer

2

3 Table 5 SNPs in the *trnL-trnF* IGS region amplified from DNA extracted from commercial

4 agarwood samples

Sample no.	SNP								Species identification
	159	291	301	327	328	339	368	381	
Sumb_m1	A	T	T	-	-	G	C	A	<i>A. microcarpa</i>
Sumb_m2	A	T	T	T	T	T	C	A	<i>G. moluccana</i>
Sumb_m3	C	T	T	T	-	G	C	A	<i>A. malaccensis</i>

5 *SNP* single nucleotide polymorphism

6

7 Table 6 SNPs in the *trnL-trnF* IGS region amplified from DNA extracted from the incense stick

8 samples

Sample No.	SNPs								Species identification
	159	291	301	327	328	339	368	381	
IS_1	A	T	T	-	-	G	C	A	<i>A. microcarpa</i>
IS_2	A	T	T	-	-	G	C	A	<i>A. microcarpa</i>
IS_3	A	T	T	-	-	G	C	A	<i>A. microcarpa</i>
IS_4	A	T	T	-	-	G	C	A	<i>A. microcarpa</i>
IS_5	A	T	T	-	-	G	C	A	<i>A. microcarpa</i>
IS_6	A	T	T	-	-	G	C	A	<i>A. microcarpa</i>
IS_7	A	T	T	-	-	G	C	A	<i>A. microcarpa</i>
IS_8	A	T	T	-	-	G	C	A	<i>A. microcarpa</i>

9 *SNP* single nucleotide polymorphism, *IGS* intergenic spacer

10

1 Table 7 Genotype classification based on alignment of the *matK* gene

Genotype of the <i>matK</i> gene	SNPs						Classification of agarwood origin species based on each genotype
	156	265	294	358	371	406	
<b>A</b>	C	C	G	C	C	A	<i>A. crassna</i> , <i>A. hirta</i> , <i>A. subintegra</i> , <i>G. versteegii</i> , <i>G. caudata</i>
<b>B</b>	C	C	G	T	C	A	<i>A. malaccensis</i> , <i>A. beccariana</i> , <i>A. microcarpa</i>
<b>C</b>	A	T	C	C	A	C	<i>A. sinensis</i>

2 Classification of each species was based on GenBank sequence data: *A. crassna* (LC467499) [2], *A.*

3 *hirta* (KX424695), *A. subintegra* (KU244050) [6], *G. versteegii* (LC467513) [2], *G. caudata*

4 (MF443403) [9], *A. malaccensis* (LC467508) [2], *A. beccariana* (FJ572802), *A. microcarpa*

5 (LC467511) [2], and *A. sinensis* (LC467505) [2].

6

7 Table 8 Species identification based on sequences of the *trnL-trnF* and *matK* regions

Sample no.	Species identification based on		
	the <i>trnL-trnF</i> region	Genotyping of the <i>matK</i> gene	Species identification based on <b>both regions</b>
Sumb_1	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>
Sumb_2	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>
Sumb_3	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>
Lomb_1	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>
Lomb_2	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>
Lomb_3	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>
Lomb_4	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>
Lomb_5	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>
Lomb_6	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>
Lomb_7	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>
Lomb_8	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>
Lomb_9	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>
Lomb_10	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>
Lomb_11	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>

Lomb_12	<i>G. moluccana</i>	<b>A</b>	Unknown
Lomb_13	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>
Sula_1	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>
Sula_2	<i>G. versteegii</i>	<b>A</b>	<i>G. versteegii</i>
Sula_3	<i>A. microcarpa</i>	<b>B</b>	<i>A. microcarpa</i>
Sula_4	<i>A. malaccensis</i>	<b>B</b>	<i>A. malaccensis</i>
Sula_5	<i>A. microcarpa</i>	<b>B</b>	<i>A. microcarpa</i>
Sula_6	<i>A. microcarpa</i>	<b>B</b>	<i>A. microcarpa</i>
Sula_7	<i>A. microcarpa</i>	<b>B</b>	<i>A. microcarpa</i>
Sula_8	<i>A. khasiana</i>	<b>A</b>	Unknown
Sula_9	<i>A. khasiana</i>	<b>A</b>	Unknown
Sula_10	<i>A. khasiana</i>	<b>A</b>	Unknown
Sula_11	<i>A. khasiana</i>	<b>A</b>	Unknown
Sula_12	<i>A. khasiana</i>	<b>A</b>	Unknown
Sula_13	<i>A. khasiana</i>	<b>A</b>	Unknown
Kali_1	Unknown	<b>B</b>	Unknown
Kali_2	Unknown	<b>B</b>	Unknown
Kali_3	Unknown	<b>B</b>	Unknown
Kali_4	Unknown	<b>B</b>	Unknown
Kali_5	Unknown	<b>B</b>	Unknown
Kali_6	<i>A. beccariana</i>	<b>B</b>	<i>A. beccariana</i>
Kali_7	<i>A. beccariana</i>	<b>B</b>	<i>A. beccariana</i>
Sumb_m1	<i>A. microcarpa</i>	<b>A</b>	Unknown
Sumb_m2	<i>G. moluccana</i>	<b>A</b>	Unknown
Sumb_m3	<i>A. malaccensis</i>	<b>A</b>	<i>A. malaccensis</i>
IS1	<i>A. microcarpa</i>	<b>A</b>	Unknown
IS2	<i>A. microcarpa</i>	<b>A</b>	Unknown
IS3	<i>A. microcarpa</i>	<b>A</b>	Unknown
IS4	<i>A. microcarpa</i>	<b>A</b>	Unknown
IS5	<i>A. microcarpa</i>	<b>A</b>	Unknown
IS6	<i>A. microcarpa</i>	<b>A</b>	Unknown
IS7	<i>A. microcarpa</i>	<b>A</b>	Unknown
IS8	<i>A. microcarpa</i>	<b>A</b>	Unknown

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1

## 2 Figure legends

- 1 Fig. 1 Geographical separation of Indonesia based on the Wallace Line and Weber Line
- 2 Fig.2 Fruit forms of the Kalimantan samples used in this study

Fig. 1



Fig.2



Kali\_5



Kali\_6



Kali\_7