

**Comparative phylogeographic and population genetic analyses of
three tropical pioneer trees, *Macaranga winkleri*, *M. winkleriella*
and *M. tanarius* (Euphorbiaceae)**

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List of abbreviations

AFLP = Amplified Fragment Length Polymorphism

bp = base pair(s)

BP = before present

dbh = diameter at breast height

DIC = deviance information criterion

DNA = deoxyribonucleic acid

dNTP = deoxynucleoside triphosphate

e.g. = for example

et al. = et alia, and others

HT = haplotype

i.e. = id est, that

IAM = Infinite allele model

ITS = internal transcribed spacer

MCMC = Markov chain Monte Carlo

min = minute

msp. = morphospecies

Mya = million years ago

na = not applicable

PAA = polyacrylamide

PCoA = principal coordinate analysis

PCR = polymerase chain reaction

RFLP = restriction fragment length polymorphism

R_h = haplotypic richness

s = second

SMM = stepwise mutation model

spp. = species (plural)

SSLPs = simple sequence length polymorphisms

SSR(s) = simple sequence repeat(s)

STR(s) = short tandem repeat(s)

TE = Tris EDTA (Ethylenediaminetetraacetic acid)

vs. = versus

1 Introduction

1.1 General features of the genus *Macaranga* Thou. (Euphorbiaceae)

Macaranga is a genus of paleotropical trees, treelets and rarely lianas, which comprises 257 dioecious species. Many species are conspicuous large-leaved pioneers (Whitmore 2008). Habitats include forest understorey and completely open scrub vegetation, canopy openings in primary and secondary forests, early successional forest communities and logged forests (Slik 2001). *Macaranga* is distributed from West Africa eastwards to Fiji (Whitmore 1969). The genus' diversity centres are on the islands of Borneo and New Guinea, where almost half of the species occur (Whitmore 2008).

Macaranga species exhibit enormous morphological diversity. Stems can be glaucous or glabrous, hollow or solid, between 4 and 30 meters tall and from 8 to 65 cm in diameter at breast height (dbh). Leaves vary hugely in size and may be simple or lobed and are often peltate (see Figure 1-1). *Macaranga* shows differently shaped stipules from small and narrowly triangular, to large and ovate and sometimes recurved (see Figure 1-2) (Slik 2001). Staminate and pistillate inflorescences consist of numerous small and inconspicuous flowers. Main pollinators of *Macaranga* are thrips, followed by bugs and other insects (Moog 2002). Many *Macaranga* species flower episodically, few continuously (Davies & Ashton 1999, Moog 2002, Moog et al. 2002, Howlett & Davidson 2003). The often colourful arilli of the seeds indicate, that fruits are eaten by birds (Ridley 1930). Small mammals are supposed to aid with the dispersal of *Macaranga* fruit (Whitmore 1969), furthermore seeds are sometimes ballistically dispersed (Davies 2001).

Many *Macaranga* species live in association with ants from the genera *Crematogaster* and *Camponotus* (Fiala et al. 1989). Within the genus *Macaranga* different types of ant-plant mutualisms exist. The genus comprises the full range from species not ant-inhabited, but myrmecophilic, to occasionally colonised species, and to obligate ant-plants. Some species produce food bodies mostly under the stipules; others provide extrafloral nectaries for the ants (Fiala et al. 1999).

1.1.1 Systematic classification of the genus

Macaranga belongs to the flowering plant family Euphorbiaceae. In current molecular studies this family has been placed in the core eudicots in the order Malpighiales (Bremer et al. 2009). Within the Euphorbiaceae the genus *Macaranga* is placed in the tribe Acalypheae in the subfamily Acalyphoideae (Webster 1994, Wurdack et al. 2005).

The genus *Macaranga* appears as a monophyletic group (Blattner et al. 2001, Slik & Van Welzen 2001, Kulju et al. 2007). Kulju et al. (2007) show that *Mallotus* sensu stricto is a sister group of *Macaranga* and that *Macaranga* is embedded in *Mallotus* sensu stricto and *Cordemoya* sensu lato. According to Whitmore (2008) the genus *Macaranga* is organised in

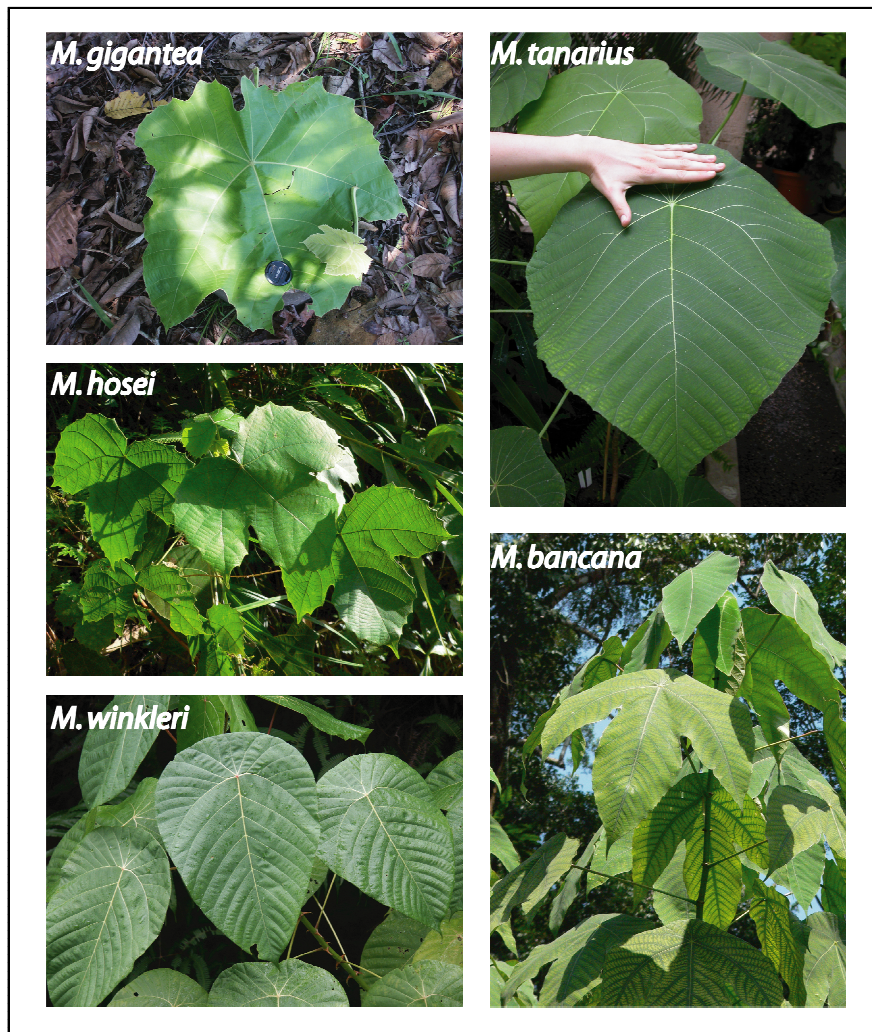


Figure 1-1. Peltate leaves of five species of *Macaranga*, clockwise from upper right; *M. tanarius*, (peltate not lobed, under surface glabrous to velvety hairy, gland-dotted), *M. bancana* (peltate, 3-lobed, seedlings not lobed), *M. winkleri* (peltate, not lobed, basal veins usually at a 90° or more angle with the midrib), *M. hosei* (deeply cordate to peltate, 3-lobed) and *M. gigantea* (shallowly to deeply 3-lobed, very large, up to 50 by 50 cm).

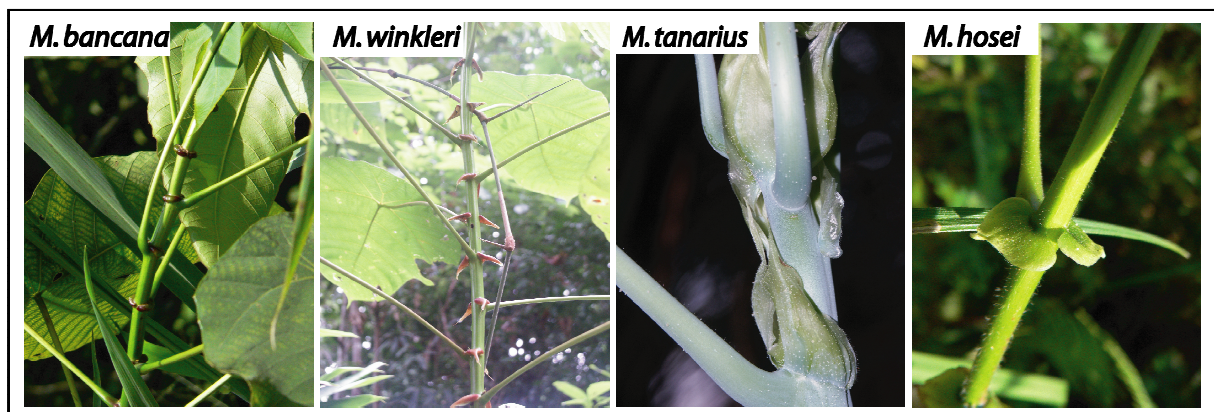


Figure 1-2. Stipules of four species of *Macaranga*, left to right; *M. bancana* (stipules recurved, completely surrounding the twigs, usually red), *M. winkleri* (erect stipules conspicuously longer than wide and red), *M. tanarius* (erect and persistent stipules, green to reddish) and *M. hosei* (stipules erect, persistent, surrounding the twigs, apex rounded).

four sections (*Pachystemon*, *Pruinosae*, *Winklerianae* and *Pseudorottlera*) and 14 informal species groups.

1.1.2 Ant-plant associations

Myrmecophytes, in the definition of Warburg (1892), are plants that form some sort of a steady and regular relationship with ants. He further classified the myrmecophytes into plants offering food (myrmecotrophic) or lodging (myrmecodomic) or both (myrmecoxenic).

In current usage, **myrmecophytes** are Warburg's myrmecodomic plus myrmecoxenic plants, that are permanently inhabited by specialised ant colonies, which protect their hosts against herbivores and climbers. For reviews see Davidson and Mckey (1993) and Heil and McKey (2003). Myrmecotrophic plants sensu Warburg are currently called **myrmecophiles** (Webber et al. 2007). They only attract ants from the vicinity by offering food. Especially in the case of plants with extrafloral nectaries, the visiting ants protect the plants (Bentley 1977, Koptur 1992).

As a term for the other half of the plant-ant association has been lacking, Quek et al. (2004) introduced the term 'phytoecy' to denote the obligate lifelong inhabitation of live plant cavities.

Myrmecophytes have evolved in diverse tropical plant lineages, such as *Acacia* and *Leonardoxa* (both Fabaceae). Extensive radiations occur, for example in the neotropical genera *Cecropia* (Cecropiaceae) and *Tococa* (Melastomataceae), both with approximately 40 myrmecophytic species (Davies 2001). The system of the pioneer species *Cecropia* associated with ant species of the genus *Azteca* is ecologically very similar to *Macaranga*. For a review of neotropical ant-plant associations see Oliveira and Freitas (2004). The only genera known from the oriental tropics showing a prominent radiation are *Macaranga* and *Neonauclea* (Rubiaceae) (Blattner et al. 2001, Razafimandimbison et al. 2005).

1.1.3 Myrmecophytism in *Macaranga*

In western Malesia there are 30 myrmecophytic *Macaranga* species, belonging to three sections. The most species-rich section is *Pachystemon* which includes about 25 species, 23 of which are myrmecophytes. Section *Pruinosae* consists of nine species (Whitmore 2008), five of them are myrmecophytic (Quek et al. 2004). Section *Winklerianae* comprises only two species, both are myrmecophytic (Whitmore 1975). On the ant side, at least eight distinct (morpho)species of *Crematogaster*, subgenus *Decacrema*, were found to colonise *Macaranga* myrmecophytes (Fiala et al. 1999, Feldhaar et al. 2010) one non-*Decacrema* ant and three species of *Camponotus* (Maschwitz et al. 1996).

Young *Macaranga* seedlings are first colonised when they are only about 10 cm tall. By then they have only one internode suitable for colonisation (Fiala 1996).

After their mating flight, ant queens search for an unoccupied plant. They recognise the host species by surface structure and volatiles (Jürgens et al. 2006). When an unoccupied plant is found, ant queens shed their wings, chew an entrance hole into an internode, seal it from inside and start laying eggs. When the workers emerge they reopen the entrance or chew new holes (Fiala et al. 1999).

In the genus *Macaranga* different types of ant-plant association occur. These will be explored in the next section.

1.1.4 Different types of ant-plant associations in the genus *Macaranga*

In the genus *Macaranga* food is offered to the ants by extrafloral nectaries, food bodies and honeydew: Extrafloral nectaries are nectar-secreting glands that are not involved in pollination and can play an important role in a plant's defense against herbivores (Heil et al. 2001a). In *Macaranga tanarius* they are located on the upper part of the leaf blade and on the leaf margins (Heil et al. 2000).

Food bodies are small epidermal and subepidermal structures with different shapes. They contain carbohydrates, lipids and proteins. Food body production in myrmecophytic species (see below) is usually concentrated on protected parts of the plant, such as recurved stipules, while in non-myrmecophytic plants food bodies are also offered on leaves and stems (Fiala & Maschwitz 1992). In myrmecophytic *Macaranga* species ants feed on honeydew excretions, produced by sap-sucking scale insects (Hemiptera, Coccoidea) (Ueda et al. 2008).

1. Myrmecophytic *Macaranga* species

The ants live mainly on food bodies and on honeydew produced by scale insects, while extrafloral nectaries do not play a role in most obligate myrmecophytes. The ants find shelter in the stem of *Macaranga*. In exchange for the provision of food and nesting sites (domatia) the ant-partners protect their plants against competition by climbers and damages by herbivores (Fiala et al. 1989) and also against fungal infection (Heil et al. 1999).

The degree of specificity of the colonisation is not absolute and varies between species on both sides (Fiala et al. 1999).

Two types of obligate myrmecophytes are distinguished:

a) obligate myrmecophytic *Macaranga* species (type1)

These plants offer nesting space for ants inside the internodes, which become hollow due to the degeneration of the pith. Myrmecophytes do not survive in the absence of the ant partner and specific ant partners have never been found nesting outside their plants, suggesting that both partners are highly dependent on each other (Heil et al. 2001b). *Macaranga winkleri* and *M. winkleriella* are obligate myrmecophytic species type 1.

b) obligate myrmecophytic species (type 2) previously called transitionals (Fiala 1996)

The stem interior of these species does not become hollow by itself. The ants have to excavate the rather soft pith, forming internal cavities. Often plants are only partly colonised and sometimes the plants are not inhabited at all. Species of this type occur mainly in section *Pruinosae* (e.g. *M. pearsonii*, *M. hosei* and *M. pruinosa*).

2. Myrmecophilic *Macaranga* species

These plants are not colonised by ants, but visited by a variety of different ant species (Fiala et al. 1994). The plant attracts the ants by offering food in the form of extrafloral nectaries and food bodies. Stems are never inhabited by ants in myrmecophilic plants. Common myrmecophilic species are *M. tanarius* and *M. gigantea* (Fiala 1996). *Macaranga tanarius*, for example, attracts a variety of different ant species by extrafloral nectaries and food bodies (Fiala et al. 1994) and is defended by the ants and other food-body-collecting and nectary-visiting insects against herbivores (Heil et al. 2001a).

3. Species with myrmecophytic and non-myrmecophytic plants

In *M. caladiifolia*, in contrast to other myrmecophytic *Macaranga* species, the colonising ants usually do not need to bite holes into the internodes, since they split open by themselves through growth processes of the plants. Colonising ants are facultative for the plant and are non-specific (Fiala 1996).

1.2 Objectives of the study

This study is part of a broader project together with the University Kassel and the University Würzburg that aimed to investigate speciation mechanisms in *Macaranga* ant-plants and their co-evolution with the corresponding ants. The island of Borneo was chosen as the main study region, since it is one of the genus' diversity hot spots (see Figure 1-3). Analyses of genetic differentiation for myrmecophytic and non-myrmecophytic *Macaranga* species from two myrmecophytic sections (*Pachystemon* and *Pruinosae*) were conducted at the University Kassel, in the working group 'Systematics and Morphology of Plants'. Genetic differentiation of the corresponding ants was analysed at the University Würzburg, working group 'Tropical ants and plants'.

Phylogenetic trees based on sequence analyses of the nuclear ribosomal DNA internal transcribed spacer (ITS) showed that myrmecophytes are mainly restricted to two clades, which correspond to sections *Pachystemon* and *Pruinosae* (Blattner et al. 2001, Davies 2001). Section *Pachystemon* comprises 23 myrmecophytic species and section *Pruinosae* five. High sequence similarity within these two sections was detected, more pronounced still in *Pachystemon*. This lack of genetic differentiation, which is in contrast to morphological and ecological differences, can indicate a rapid and relatively recent radiation of *Macaranga*

species of these sections (Weising et al. 2010). In contrast to this, section *Winklerianae* is comprised of only two species, both of which are myrmecophytic (see below). A possible mechanism that could have triggered radiations in sections *Pachystemon* and *Pruinosae* is the myrmecophytic trait, raising the question of why no signs of an ongoing radiation could be detected in section *Winklerianae* (Blattner et al. 2001). Since in myrmecophytic *Macaranga* both partners, the ants and the plants, do not mature without their specific symbionts, *Macaranga* seeds, germinating too far away from the next source of the specific ant partner cannot establish a new population. When populations become dissected due to geographical or climatic changes, this limited effective dispersal ability might lead to genetically isolated populations. Thus, the obligate association with ants could have triggered allopatric speciation. Assuming that this hypothesis of allopatric speciation is true, a reduced gene flow among populations of myrmecophytic species compared with those of non-myrmecophytic species would be expected. These reduced levels of gene flow would lead to a more pronounced population substructure. The detection of this substructure is expected to be measurable on a large geographical scale, in particular when geographic barriers, e.g. mountain ranges, separate populations. Chloroplasts are generally inherited maternally in angiosperms (Conde et al. 1979). As only seed-mediated gene flow is expected to be influenced by the proximity of the partner ant, a more pronounced difference between

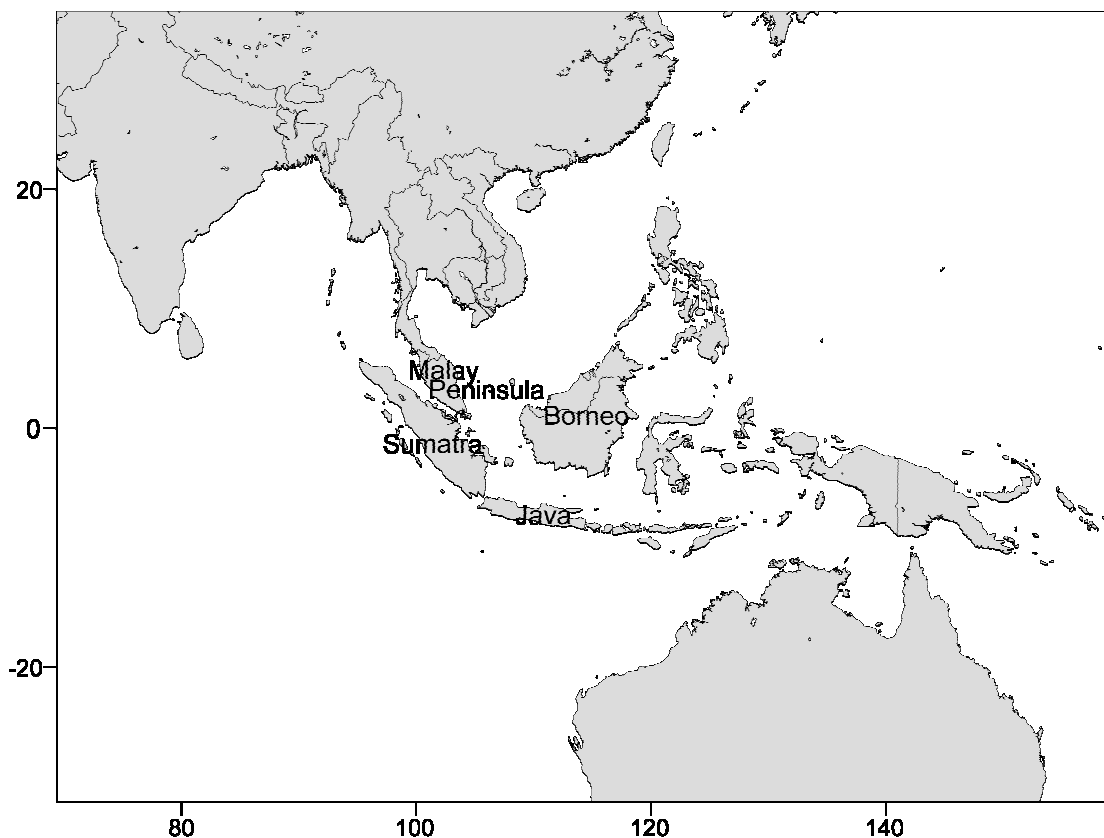


Figure 1-3. Geographical map, giving an overview of the study region.

myrmecophytes and non-myrmecophytes is expected in the chloroplast than in the biparentally inherited nuclear loci.

For section *Pruinosae*, which is comprised of non-myrmecophytic *Macaranga gigantea* and several myrmecophytes, a comparative analysis was conducted using both chloroplast sequences and nuclear microsatellites. For the non-myrmecophytic *M. gigantea* and the myrmecophytic *M. pearsonii* the analysis revealed not only comparative levels of genetic diversity in the microsatellite analysis, but also a similar number of chloroplast haplotypes (Guicking et al. 2011). Therefore, for these species the allopatric speciation hypothesis could not be supported. Also for analyses in section *Pachystemon* the allopatric hypothesis could not be supported (Guicking et al. in preparation).

A third section, *Winklerianae*, (Davies 2001) with ambiguous monophyly (Blattner et al. 2001, Bänfer et al. 2004, Kulju et al. 2007) comprises only two myrmecophytic species, *M. winkleri* and *M. winkleriella*. These two species are investigated in this study.

Macaranga winkleri is endemic to Borneo. It was sampled from various locations in Sarawak, Brunei and Sabah.

Assuming seed dispersal via birds, the ants are expected to surpass shorter dispersal distances, therefore dispersal via seed to new areas, where the ant is not present cannot lead to the establishment of the plant. Seed dispersal from one population to another population, where *M. winkleri*, and thus the colonising ant is present, however is possible. The dependence of the plant species on the ant species and the resulting limited effective dispersal ability might lead to genetically isolated populations when populations become dissected by geographic changes. Thus, a reduced seed-mediated gene flow would be expected, leading to a more pronounced population substructure in myrmecophytic *M. winkleri* than in non-myrmecophytic *M. tanarius* reflected in the chloroplast data (see below).

The main pollinators of *M. winkleri* are thrips from the tribe Tubulifera (*Neoheegeria* spec.) and Terebrantia (mainly genus *Thrips*) (Moog 2002). Assuming a restricted pollen-mediated gene flow due to short flight distances of these small pollinators for *M. winkleri*, a clear geographic differentiation is expected for the nuclear SSR data.

Macaranga winkleriella is endemic to a limestone area in northern Sarawak, a much smaller region than the distribution area of *M. winkleri*. For *M. winkleriella*, low genetic diversity in both the chloroplast and the nuclear DNA could be expected, since small populations are strongly affected by genetic drift and furthermore in fewer individuals also less new alleles originate. Higher genetic diversity could then indicate that *M. winkleriella* is a formerly more widespread species with a larger population size that shrank back to its current habitat. This is however, not very probable because the species is growing on limestone only and is thus restricted to this rare habitat in Borneo.

Alongside *M. winkleri* and *M. winkleriella* a third *Macaranga* species was included in this study, *M. tanarius*, belonging to the *Tanarius* group (Whitmore 2008). This species is a non-myrmecophytic species. It is myrmecophilic, i.e. it is not colonised by ants, but attracts them

by offering food. The ants protect the plant from herbivores. *Macaranga tanarius* is a highly abundant pioneer tree, found in disturbed to very disturbed vegetation and even in the outskirts of towns. In such a successful pioneer tree also good dispersal abilities are expected. Good seed dispersal abilities, which are not restricted by the necessity to co-disperse with an ant partner, or disperse to regions where the ant is already present, should be reflected by high levels of gene flow and low genetic differentiation among populations for the chloroplast data. Gene flow via pollen can be assessed by nuclear microsatellites, which are inherited biparentally. Due to the relatively large size of the pollinating flower bugs, elevated amounts of pollen-mediated gene flow is expected and, therefore, a low genetic differentiation between populations of *M. tanarius*.

For *M. tanarius* individuals from Borneo and Malay Peninsula a strong genetic differentiation is expected in both the chloroplast and microsatellite data, as the individuals are geographically separated, and thus evolving in vicariance.

For all species a young age and/or a recently undergone population bottleneck, would be reflected by generally low levels of genetic diversity and probably low geographic structuring in both the chloroplast and the SSR data. A high tempo of colonisation would be reflected by the occurrence of the same haplotypes or genetically highly similar haplotypes over a broad geographical range.

Previous studies have provided evidence that the biogeography of plants and animals on Borneo is influenced by the occurrence of a central mountain range, dividing Borneo into a southeastern and a northwestern part (Bänfer et al. 2006, Raes et al. 2009). To the north this range runs into the Crocker Range (see Figure 2-16). The Crocker Range is expected to act also as a geographic barrier to dispersal for *M. winkleri* and *M. tanarius*. Due to the assumed limited effective dispersal ability of myrmecophytic *M. winkleri* the barrier is expected to act stronger on this species than on non-myrmecophytic *M. tanarius*. Furthermore *M. tanarius* is found up to higher elevations than *M. winkleri* (2,100 vs. 1,800, respectively), facilitating the dispersal across the barrier.

While palynological and geological evidence indicates the confinement of the rainforest to a number of refugia during the last glacial maximum to the southwestern parts of Borneo, for Sabah a persisting rainforest is assumed (Gathorne-Hardy et al. 2002). Since populations in the southwest underwent genetic bottlenecks while in Sabah the rain forest persisted, a higher genetic diversity is expected for this region compared to Sarawak/Brunei for both *M. tanarius* and *M. winkleri*.

Hypotheses

The following hypotheses are developed based on expected seed and pollen dispersal abilities and the myrmecophytic vs. non-myrmecophytic trait of the species under study.

- 1) For *M. winkleri* a limited effective dispersal ability is expected due to the dependence on the ant species and, as a result, a pronounced population substructure, especially in the case of geographic barriers.
- 2) For *M. winkleri* restricted pollen-mediated gene flow is expected, due to assumed short flight distances of the pollinating thrips. Thus, a clear geographic differentiation is expected for the nuclear SSR data.
- 3) For *M. winkleriella*, low genetic diversity in both the chloroplast and the nuclear DNA is expected, since small populations are affected stronger by genetic drift and also less new alleles originate.
- 4) For *M. tanarius*, as a successful pioneer tree good seed dispersal abilities are expected. Good seed dispersal abilities, which are not restricted by the necessity to co-disperse with an ant partner, or disperse to regions where the ant is already present, should be reflected by high levels of gene flow and, thus, low genetic differentiation among populations.
- 5) For *M. tanarius*, elevated amounts of pollen-mediated gene flow are expected due to the relatively large size of the pollinating flower bugs and, therefore, a low genetic differentiation between populations, which should be reflected by the SSR data.
- 6) The population structure for myrmecophytic *M. winkleri* is expected to be more pronounced than for non-myrmecophytic *M. tanarius*.
- 7) The Crocker Range is expected to act as a geographic barrier to dispersal, acting stronger on myrmecophytic *M. winkleri* than on non-myrmecophytic *M. tanarius* due to the limited effective dispersal ability of *M. winkleri*.
- 8) For the *M. tanarius* individuals of Malay Peninsula and Borneo high levels of genetic differentiation are expected in both the chloroplast and SSR data, due to vicariant evolution.
- 9) Due to the long-term persisting rain forest in Sabah, a higher genetic diversity is expected for this region compared to Sarawak/Brunei for both *M. tanarius* and *M. winkleri* in the microsatellite and chloroplast data.

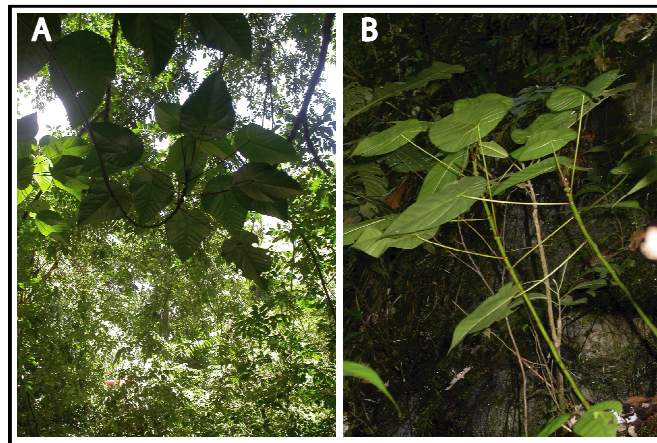


Figure 1-4. A) Peltate leaves of *M. winkleriella* B) stipules of *M. winkleriella* (photos: Brigitte Fiala).



Figure 1-5. A) *Macaranga winkleri* colonised by its specific ant and characteristic stipules B) Leaves of *M. winkleri* C) Staminate inflorescence of *M. winkleri* D) Typical habitat of *Macaranga* species E) *M. winkleri* tree with adult in picture for scale F) *M. winkleri* in a gap in primary forest G) Fruits of *M. winkleri* H) Uninhabited *M. winkleri* individual, showing herbivore damage and a climber at the stem.

1.3 The species under study

***Macaranga winkleri* Pax & K. Hoffm. (section *Winklerianae*)**

Macaranga winkleri is a tree measuring up to 15 m, with a dbh of 18 cm (Figure 1-5 E). The stem shows smooth and hooped bark, which is remaining green at maturity. Stipules are narrowly ovate with a long finely acuminate apex and 15-25 x 8-13 mm (Figure 1-5 A). The twigs are hollow and strongly angular when they are young. Leaves are peltate and ovate (Figure 1-5 B). The basal veins usually form an angle of 90 degrees or more with the midrib (Slik 2001). Staminate and pistillate inflorescences are branched (Figure 1-6 C). Male flowers are 1 mm long and female flowers are 1-3 mm long. Fruits of *M. winkleri* are bilocular and small (2-2.5 x 3-4 mm), the aril is fleshy and violet (Figure 1-6 G). Seeds have a diameter of 1.5 mm and are black (Whitmore 2008). *Macaranga winkleri* is an obligate myrmecophyte type 1. Thus, the plant cannot survive without its specific ant and vice versa. Figure 1-5 H shows an example of an uninhabited *M. winkleri* individual, which already shows evidence of damages by herbivores and a climber growing around the stem. The *Crematogaster* partner ant of *M. winkleri*, morphospecies (msp.) 8 (which does not belong to subgenus *Decacrema*) and its host are endemic to Borneo (Fiala et al. 1999). Both sides of this relationship seem to be extremely specific. *Macaranga winkleri* was never found colonised by another ant species and *Crematogaster* msp. 8 occurred only very rarely in saplings of other *Macaranga* species but never in larger plants.

Macaranga winkleri can be found at elevations of up to 1,800 m, in gaps in the primary (Figure 1-5 F) and secondary forests, including very disturbed forests after fire. It is often found along forest edges (Figure 1-5 D), the sides of roads and rivers and on land slides (Slik 2001).

***Macaranga winkleriella* Whitmore (section *Winklerianae*)**

Macaranga winkleriella is a tree or treelet that grows to ca. 4 m tall with a dbh of 7 cm. Leaves are as in *M. winkleri* peltate and ovate Figure 1-4 A. Stipules are broadly ovate and recurved and smaller than in *M. winkleri* (4-6 x 4-6 mm) Figure 1-4 B. Staminate and pistillate inflorescences are branched. Male flowers are 0.75 mm long and female flowers are 2 mm long. Fruits of *M. winkleriella* are also bilocular and slightly larger than the fruits of *M. winkleri* (3 x 4.5-5.5 mm), the colour of the fleshy aril is not verifiable. Seeds have a diameter of 2-2.5 mm (Whitmore 2008). *Macaranga winkleriella* is an early successional species found in disturbed sites in primary and secondary forests. It is found growing on limestone in a very narrow distribution range, namely Mulu in Sarawak (Whitmore 1974). *Macaranga winkleriella*, like *M. winkleri*, is an obligate myrmecophyte type 1 and colonised by *Crematogaster* msp. 8, a non-*Decacrema* species (Federle et al. 1997, Fiala et al. 1999, Federle et al. 2001).

***Macaranga tanarius* (L.) Müll.Arg. (*Tanarius* group)**

Macaranga tanarius is a shrub to small tree of up to 15 m tall with a dbh up to 20 cm (Figure 1-6 B). The stem is straight with smooth, hooped bark and red latex. Twigs are solid. Leaves are ovate and peltate (Figure 1-6 C). Stipules are erect, persistent and green to reddish (Slik 2001), (Figure 1-6 F). Staminate and pistillate inflorescences are variable (Figure 1-6 D). Both male and female flowers are subtended by bracts of the same range, not more than 5 mm, while the female bracts are longer than the male bracts (1 cm vs. less than 5 mm, respectively). Fruits are sticky and bilobed, up to 10 mm across by 6 mm tall with numerous long slender processes emanating from the upper half (Figure 1-6 E). Seeds are round and verrucous (Whitmore 2008). *Macaranga tanarius* is distributed from India and southern China to Australia and New Guinea. The species occurs in elevations up to 2,100 m, usually in very disturbed vegetation, often along roads (Figure 1-6 A) or streams. It is found on clay loam, sandy and sandstone soils (Slik 2001). *Macaranga tanarius* is a myrmecophilic species as mentioned above, visited by various ant species, unspecialised *Crematogaster* spp. being the most abundant (Fiala et al. 1994).

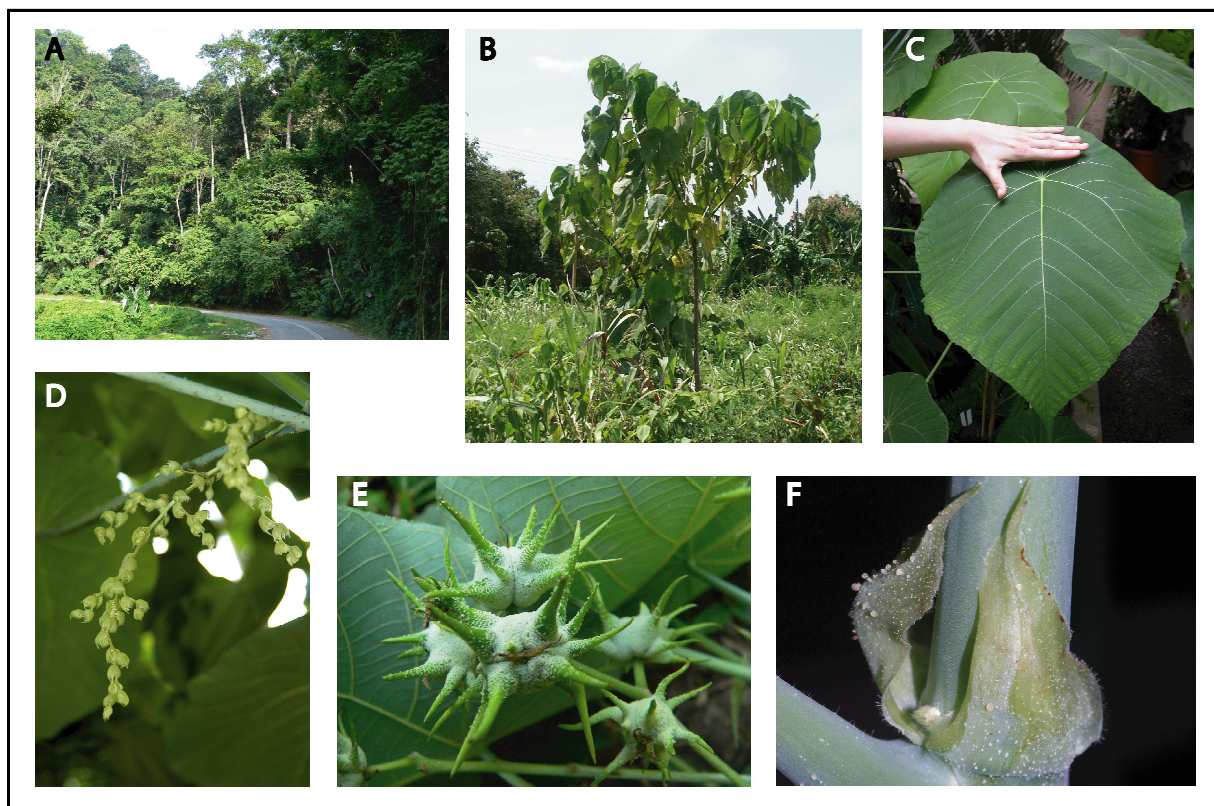


Figure 1-6. A) Typical habitat of *M. tanarius* B) *M. tanarius* tree habitus C) *M. tanarius* leaf with size comparison (photo: Nicolai Nürk) D) Staminate inflorescence of *M. tanarius* (photo: Birgit Schäfer) E) Fruits of *M. tanarius* (photo: Daniela Guicking) F) Stipules of *M. tanarius*.

1.4 Geological evolution of the Sunda Shelf

For the discussion of the biogeographical history of the species under study the more recent geological evolution of the Sunda Shelf has to be considered. The Malay Peninsula, Borneo, Java and Sumatra lie on the shallow continental Sunda Shelf. By the early Pliocene (~5 Mya) the Sunda Islands connection among the islands and Malay Peninsula had disappeared or had been reduced to narrow corridors. In the Pleistocene the Sunda landscape was again transformed when glacial cycles caused sea-level to drop repeatedly, exposing areas of the Sunda Shelf and creating land bridges. These land bridges reconnected formerly isolated regions of the shelf (Gorog et al. 2004). Voris (2000) showed in maps of the Pleistocene sea-level of Southeast Asia that during this epoch Borneo, Sumatra, Java and the Malay Peninsula were reconnected, when sea level was lowered between 40 m and the maximum lowering, which was 120 m below the present level. At 30 m below the present niveau, Malay Peninsula, Sumatra and Java would have been connected by land while Borneo would have been narrowly isolated. At the same time the dropping sea levels caused considerable fragmentation of the rainforest. Palynological and geological evidence indicate that at the last glacial maximum (~20,000 years BP) Malay Peninsula was covered by savannah, as were Java, parts of Sumatra and the southwestern part of Borneo, confining rainforest to a number of refugia (Gathorne-Hardy et al. 2002). The most recent glacial maximum began to recede at about 17,000 years BP and the current sea levels were reached about 6,000 years ago (Inger & Voris 2001). The latest land bridges which connected Borneo, Java, Sumatra and Malay Peninsula are described as recently as 9,500 years ago (Gorog et al. 2004).

1.5 Molecular markers

1.5.1 Microsatellites

Terms

Microsatellites, also known as simple sequence repeats (SSRs), short tandem repeats (STRs) or simple sequence length polymorphisms (SSLPs), are tandem repeats of sequence units generally less than 5 bp in length (Bruford & Wayne 1993). The microsatellites are usually less than 100 bp long (Lagercrantz et al. 1993). Main types of microsatellites consist of mono-, di-, tri- and tetra nucleotide motifs, but penta- and hexa-nucleotide repeats are also classified as microsatellites, repeats of longer motifs as minisatellites. Microsatellites are considered to be hypervariable in length (Tautz 1989), with variation resulting from differences in the number of repeat units. The variation in length is caused by errors in DNA replication when the DNA polymerase 'slips' while copying the repeated region, thus changing the number of repeats (Jarne & Lagoda 1996). Larger changes are supposed to be the result of unequal crossing over in the nucleus (Strand et al. 1993).

Occurrence in the genome

Microsatellites occur in all nuclear, chloroplast and mitochondrial genomes (Barkley et al. 2009). They are among the most variable types of DNA sequences in the genome. Among fully sequenced eukaryotic genomes, microsatellite density is highest in mammals. The bulk of simple repeats are embedded in non-coding DNA, either in intergenic sequence or in the introns, and thus assumed to evolve neutrally (Ellegren 2004). Assuming neutrality of microsatellites, extensive polymorphism can be explained by a high underlying rate of mutation.

Microsatellite motifs

Most chloroplast microsatellites (chloroplast SSR) are mononucleotide repeats whereas nuclear SSRs usually have dinucleotide repeats (Provan et al. 1999). Dinucleotide repeats are the most abundant repeats in vertebrates as well as in plants. In plant genomes GA/TC repeats are the most common (Lagercrantz et al. 1993). Contrasting distribution of microsatellite motifs in different genomes hint either to interspecific variation in the mechanisms of mutation, repair of specific motifs or to variation in the selective constraints associated with different SSR motifs or to differences in base frequencies in different genomes (Ellegren 2004).

Genesis and evolution of microsatellites

Short repetitive sequences are the starting point for a subsequent microsatellite expansion. The primary repeats can arise from normal base substitutions (e.g. A-G transition in GTATGT to GTGTGT). Additionally a high proportion of new two-repeat loci arise from insertion mutations that are duplications of adjacent sequence. Point mutations can break up perfect repeats and reduce the mutation rates of microsatellite loci. However, interruptions in microsatellites can also be a transitional stage in evolution and be removed by replication slippage or unequal crossing over (Ellegren 2004).

The rate and direction of microsatellite mutations

The mutation rate is affected by microsatellite length, increasing with the number of repeats. The precise correlation (linear, exponential) between the two factors is controversial. It is also possible that the flanking sequence affects the mutation rate. There is no uniform microsatellite mutation rate. Rates vary between loci, alleles and as a consequence perhaps among species (Ellegren 2004). Mutation rates of microsatellites range from 10^{-6} to 10^{-2} per generation and are thus significantly higher than base substitution rates (Schlötterer 2000).

Conflicting reports were made by different authors concerning the effect of length and base composition of the repeat unit on the mutation rate (Ellegren 2004). The existence of a threshold size necessary for a repeat sequence to undergo dynamic mutation was shown by Messier et al. (1996) and Rose and Falush (1998), while Pupko and Graur (1999) presented

contradictory evidence. They found that there is no critical number of repeats beyond which the observed frequencies of microsatellites exceed the frequencies expected in a random DNA sequence of the same size. Xu et al. (2000) showed the dependency of microsatellite mutations on the allele size. The rate of expansion mutations was shown to be constant, while the rate of contraction mutations increases exponentially with allele size.

Mutation models of microsatellites

Microsatellite variants are supposed to be generated in a stepwise manner by the addition or deletion of single repeat units (Valdes et al. 1993). Consequently, microsatellite variants with smaller differences in repeat length should be more closely related than those with larger differences in length. The stepwise mutation model (SMM) postulates that one mutation alters the repetitive part through addition or removal of one repeat of the repetitive unit.

A variety of models for the evolutionary dynamics of microsatellites, deriving from SMM have been presented incompatibilities with the SMM, for example the fact that SSR shows an upper size limit, have been solved by extensions to the model (Ellegren 2004).

The simplest and most general model is the Infinite allele model (IAM). In this model every mutational event creates a new allele, which is independent in size from the progenitor allele (Selkoe & Toonen 2006).

Microsatellites - the marker of choice

Microsatellite markers are single locus, co-dominant markers, generally with a high mutation rate. Polymorphic microsatellite markers are powerful tools for population genetic analysis. In species for which populations are small or have recently experienced a bottleneck, only loci with high mutation rates are likely to be informative (Hedrick 1999).

Furthermore microsatellite markers are used in paternity analysis, forensics and the inference of demographic processes. Due to their high mutation rate, they offer a means for studying the effect of environmental factors on genomic mutation rate (Ellegren 2004).

Once SSR loci have been characterised within a species, SSR polymorphism can be detected by PCR (polymerase chain reaction) using the flanking sequences of the microsatellite as primers. Due to high species specificity of microsatellite markers, cross-contamination by non-target organisms is much less probable than in PCR with universal primers (Selkoe & Toonen 2006). After PCR, the microsatellites can be genotyped by fragment size analysis using high resolution polyacrylamide (PAA) gels. This identification of alleles reduces time and cost compared with sequencing each allele in each individual.

Drawbacks of microsatellites markers

Despite the many advantages of microsatellite markers, they also have several challenges and pitfalls. One drawback is the fact that universal primers are usually not available. Markers

have to be developed for each species or species group. The high effort required for microsatellite marker development was described by Squirrel et al. (2003). Consistent amplification across all samples can only be assured by trial and error. Thus some loci will have to be discarded at the middle or end of genotyping all of the samples in a study due to amplification problems, too high or too low variability or the existence of an additional primer binding site in part of the samples. Another potential problem is the presence of null alleles. Null alleles, are alleles that do not amplify in the PCR due to mutations in the primer-binding site and, thus, are not detectable (Chapuis & Estoup 2007).

The advantage of highly variable markers carries the drawback of undetectable homoplasy by descent, i.e. alleles can have the same allele size and sequence but different genealogical history. Another type of homoplasy is size homoplasy, which occurs when alleles have the same fragment length but differences in base composition. This kind of homoplasy could be detected by sequencing the alleles, although typically this is not done since genotyping is size-based. Another subject to deal with, when using microsatellite markers, is the complex underlying mutational mechanism, which is still being discussed (see above).

1.5.2 Chloroplast DNA sequences

Generally chloroplast DNA is known to be slow in sequence evolution (Palmer 1987) and for a long time considered too conservative for intraspecific studies (Banks & Birky 1985).

Thus, in the past chloroplast DNA was limited to investigations among species, see references in Wagner (1992).

This perspective changed at the beginning of the 1990s (Soltis et al. 1992) after a number of studies found intraspecific and even intrapopulational chloroplast variation (Pleines et al. 2009) using chloroplast DNA. This intraspecific variation was shown to be high enough for population studies on gene flow, as reviewed by McCauley (1995).

In phylogeographic analyses mostly non-coding parts of the organelle genomes are used as markers (Pleines et al. 2009). Most non-coding parts of the plant genomes are free to vary without much restriction from selection, as such they may contain many polymorphic sites (Pleines et al. 2009). Two such non-coding parts, introns and spacers, are a rich and well-appreciated information source for evolutionary studies in plants (Borsch & Quandt 2009).

Chloroplast DNA, as an organelle DNA, has the advantage of uniparental inheritance, thus no recombination occurs.

In this study the following three markers were used:

***rpl16* intron**

The *rpl16* gene contains two exons separated by an intron varying in length from 1,000 – 1,500 bp in the species studied (Schnabel & Wendel 1998). *Rpl16* encodes ribosomal protein

L16 (Posno et al. 1986), and the intron has been used in several phylogeographic studies (King et al. 2009, Hedenas 2010).

***atpB-rbcL* intergenic spacer**

This region lies between the *atpB* gene and the *rbcL* gene. This marker has been used in many different phylogeographic analyses (Bänfer et al. 2006).

Ccmp5

This marker belongs to a set of consensus chloroplast microsatellite primers (ccmp1-ccmp10). This set of primers was developed with the general aim to amplify SSR regions in the chloroplast genome of dicotyledonous angiosperms (Weising & Gardner 1999).

These microsatellite loci were applied to a small set of *Macaranga* specimens by Vogel et al. (2003) and found to be informative.

1.6 Statistical methods

Haplotype analysis

To describe differentiation and the genetic diversity of populations, several diversity measures can be calculated and evaluated. In this study Nei's index of genetic diversity (H_e) estimated without bias (Nei 1973), the haplotypic richness (R_h) (Mousadik & Petit 1996) and the number and distribution of population-specific haplotypes, so called private haplotypes (Stehlik et al. 2002), were calculated. Furthermore the number of haplotypes per population and the effective number of haplotypes, which is the inverse probability that two randomly chosen haplotypes are identical, were evaluated. Moreover haplotype and nucleotide diversity were calculated.

Statistical parsimony network

Intraspecific gene evolution cannot always be represented by a bifurcating tree. Population genealogies are often multifurcated, where descendant genes coexist with persistent ancestors. Furthermore recombination events (in nuclear genes), hybridisation between lineages and homoplasmy generate reticulate relationships. Several network approaches have been developed to estimate intraspecific genealogies and to allow for reticulate relationships. Network approaches can incorporate population processes in the construction or refinement of haplotype relationships. Furthermore, networks have the ability to display the population information in more detail than strictly bifurcating trees. A variety of network methods have been reviewed in Posada and Crandall (2001). Of these network methods, the statistical parsimony network was chosen for this study. This method was chosen as within a species or closely related species single rather than multiple substitutions are assumed, favouring the

parsimony criterion. Network calculations were performed with the software TCS (Clement et al. 2000).

Principal coordinate analysis

A principal coordinate analysis (PCoA) is a means to get access to the genetic structure of data by exploring and visualizing similarities and dissimilarities. PCoA, a derived method of principal component analysis (PCA), is a procedure to simplify multivariate data with minimum loss of information (Cavalli-Sforza et al. 1996). PCoA starts with a pairwise distance matrix and assigns each item a location in a low-dimensional space, thus, reducing the dimensionality. The first axis accounts for as much of the variability in the data as possible, and each succeeding axis accounts for as much of the remaining variability as possible.

PCoA is a standard tool used to detect population structure within species based on genetic data (Schönswetter et al. 2003).

Analysis of molecular variance

Analysis of molecular variance (AMOVA) is a method of estimating population differentiation directly from molecular data and testing hypotheses about such differentiation. The statistics reflect the correlation of haplotypic diversity at different levels of hierarchical subdivisions. A variety of molecular marker data (e.g. RFLP, AFLP and SSR) and direct sequence data may be analysed using this method (Excoffier et al. 1992). GenAlEx was used to perform AMOVA.

Mantel test

The Mantel test (Mantel 1967) is a test of the correlation between two matrices. In this study one matrix contains the genetic distances between all possible pairs of individuals, while a second matrix contains the geographical distance between the individuals. The relationship between these two matrices cannot be assessed by only evaluating the correlation coefficient between the two sets of distances. Therefore a randomization or permutation test has been adopted. To assess significance of any apparent departure from a zero correlation, the rows and columns of one of the matrices are repeatedly subjected to permutation, with the correlation being recalculated after each permutation. The reason for this is that if the null hypothesis of there being no relation between the two matrices cannot be rejected, then permuting the rows and columns of the matrix should be equally likely to produce a smaller or a larger coefficient. The Mantel test is often applied to examine whether genetic differentiation among populations is related to geographical distances, (Excoffier et al. 1992, Hensen et al. 2010). In this study GenAlEx was used to perform the Mantel test.

Assignment analysis using Bayesian clustering approaches

Using Bayesian methods to analyse genetic data is a powerful tool to define boundaries between populations. Knowledge of such boundaries can be important, both for the understanding of population dynamics and for conservation planning (Rowe & Beebee 2007). Statistical inference is a method of extrapolation from a random sample set to a population. That is, it uses randomly sampled data from a population to make inferences about that population. Bayesian inference, a type of statistical inference based on Bayes' theorem, combines observational evidence with more traditional probabilities. In Bayesian inference an unconditional prior probability (degree of confidence) is determined before any data has been observed. When actual data is observed, this observation is used to refine the probability (called the posterior probability) to account for what was actually observed. The posterior probability is recalculated whenever additional observations are made, resulting in a probability that trends towards the real observations (Iverson 1984).

Two Bayesian clustering programs were used to perform an assignment analysis and detect the number of clusters: STRUCTURE (Pritchard et al. 2000) and INSTRUCT (Gao et al. 2007). STRUCTURE provides the posterior probability, and the log likelihood of the posterior probability is used in determining the optimal number of clusters. INSTRUCT gives the deviance information criterion (DIC) which is a generalization of the Bayesian information criterion. The DIC is based on the logarithm of the likelihood function, and is used in determining the optimal number of clusters for INSTRUCT.

2 Chloroplast analysis

2.1 Materials and Methods

2.1.1 Sampling and molecular methods

Sampling

The sampling area was the Malaysian part of Borneo and, in the case of *Macaranga tanarius*, the Malay Peninsula, Sumatra, Kalimantan, Java and Australia (see Figure 2-1). A total of 561 *Macaranga winkleri*, 353 *Macaranga tanarius*, and 13 *Macaranga winkleriella* were sampled. Furthermore one *M. diepenhorstii*, one *M. pruinosa* and two *M. gigantea* individuals were sampled to include them as outgroups in the analysis. For sampling locations, habitat, geographical coordinates and storage of herbarium samples see Appendix A. The plant material included in this study was mainly collected by myself, Dr. Brigitte Fiala, and Dr. Daniela Guicking. Single samples were also collected by Christina Fey-Wagner, Manfred Türke, Dr. Ute Moog (now Meyer), Dr. Ulrich Maschwitz, Dr. Heike Feldhaar and Dr. Ferry Slik. A part of a leaf was collected from each sampled tree and dried with silica gel containing a moisture indicator. The silica gel was exchanged each day until the leaves were completely dried, in order to avoid DNA degradation caused by leaf decomposition (Weising et al. 2005).

All samples were identified based on species descriptions in Davies (2001) and the key of Slik et al. (2000). Unclear samples were rechecked by Dr. Brigitte Fiala. Two unclear samples were furthermore identified via ITS-sequencing. Corresponding herbarium specimens are stored in the herbaria of the Universities of Kassel (KAS) and Würzburg (WB), Leiden (L) and the IPK Gatersleben (GAT) (see Appendix A).

DNA isolation

The silica dried leaves (each measuring between 1 and 2 cm²) were ground in a 2 ml tube together with two steel beads, using a FastPrep 120 homogenizer (Savant).

Total genomic DNA-isolation was carried out with the DNeasy Plant Kit (QIAGEN) according to the instructions of the manufacturer. One washing step was added to increase the quality of the DNA. Concentrations were estimated on 1% agarose gels stained with ethidium bromide. Samples showing difficulties in PCR amplification were subsequently purified via the QIAquick PCR purification Kit (QIAGEN) and resuspended in 50 µl 1x TE buffer.

Samples failing amplification were again isolated adding 0.01g PVP (Polyvinylpyrrolidone) per ml lysis buffer, to bind phenolic compounds. DNA stock solution was stored at –20 °C.

Table 2-1. The 13 different chloroplast regions tested for PCR amplification and the possibility of obtaining readable sequences and sequence variation for *M. winkleri*, *M. tanarius* and *M. winkleriella*. “/” is used to indicate where a test is not applicable. For *M. winkleriella* some PCR amplification were not tested if no sequence variation was detected in both the *M. winkleri* and *M. tanarius* samples.

Locus Name	<i>M. winkleri</i>			<i>M. tanarius</i>			<i>M. winkleriella</i>		
	PCR Amplification	Sequences	Detected Sequence Variation	PCR Amplification	Sequences	Detected Sequence Variation	PCR Amplification	Sequences	Detected Sequence Variation
1 ccmp1	Consistent	Not clearly readable	No	Consistent	Not clearly readable	No	Not tested	/	/
2 ccmp2	Consistent	Clearly readable only on Licor	Detectable only on Licor	Consistent	Clearly readable only on Licor	Detectable only on Licor	Not tested	/	/
3 ccmp3	Consistent	Not clearly readable	No	Consistent	Not clearly readable	No	Not tested	/	/
4 ccmp4	No	/	/	No	/	/	Not tested	/	/
5 ccmp5	Consistent	Clearly readable	Yes	Consistent	Clearly readable	Yes	Consistent	Clearly readable	No
6 ccmp6	Inconsistent	Not clearly readable	/	Inconsistent	Not clearly readable	/	Not tested	/	/
7 ccmp7	Inconsistent	Not clearly readable	No	Inconsistent	Not clearly readable	No	Not tested	/	/
8 ccmp10	Consistent	Not clearly readable	No	Consistent	Not clearly readable	No	Not tested	/	/
9 <i>atp B-rbc L</i>	Consistent	Clearly readable with re-designed sequencing primers	Yes	Consistent	Clearly readable with re-designed sequencing primers	Yes	Consistent	Clearly readable with re-designed sequencing primers	Yes
10 trnL-trnF	Consistent	Clearly Readable	No	Consistent	Clearly Readable	No	Not tested	/	/
11 <i>rpl16</i>	Consistent with re-designed amplification primer	Clearly readable with re-designed sequencing primers	Yes	Consistent	Clearly Readable	Yes	Consistent with re-designed amplification primer	Clearly readable with re-designed sequencing primers	Yes
12 trnD-trnT	No	/	/	No	/	/	No	/	/
13 trnS-trnF	No	/	/	No	/	/	No	/	/

1-8: Chloroplast microsatellites (Weising and Gardner 1999, Vogel et al. 2003)

9: Chloroplast microsatellites (Xu et al. 2000, Bänfer et al. 2006)

10: Chloroplast microsatellites (Taberlet et al. 1991, Jakob and Blattner 2006)

11-13: Chloroplast microsatellites (Shaw et al. 2005)

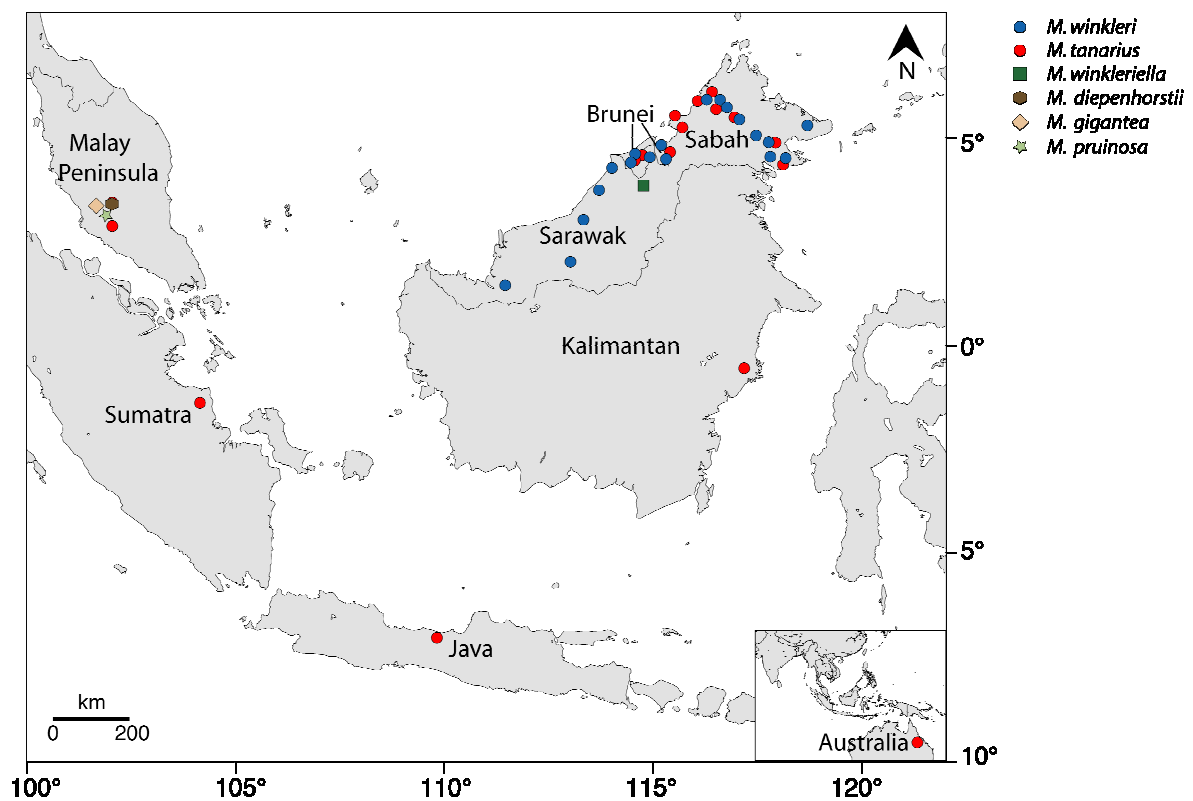


Figure 2-1. Map of the study area indicating the sampling regions for *M. winkleri*, *M. tanarius*, *M. winkleriella*, *M. gigantea*, *M. diepenhorstii* and *M. pruinosa*.

PCR amplification and sequencing of non-coding chloroplast regions

In the chloroplast sequence analysis a subset of the sampled individuals was used:

- i 87 samples of *M. winkleri* from 32 locations, using two to five individuals per location, except in five locations where only one individual was available (see Appendix D).
- ii 13 individuals of *M. winkleriella* and two individuals of *M. gigantea*, one individual each of *M. diepenhorstii* and *M. pruinosa* were included as an outgroup (see Appendix D), as they are found in close positions to *M. winkleri* and *M. winkleriella* in the *Macaranga* haplotype network (Bänfer et al. 2006).
- iii 100 samples of *M. tanarius* (see Appendix F) comprising 80 individuals from Borneo, 17 from the Malay Peninsula and one individual each from Sumatra, Java and Australia. The Bornean individuals included in the chloroplast analysis were from 24 different sampling locations. Between three and five individuals per location were included in the analysis, except for three locations in which only one individual was available. For one sampling site where the three included individuals showed genetic variation, a further five individuals were integrated in the analysis.

Thirteen different chloroplast regions were checked for the possibility of amplification and sequencing and sequence variation (see Table 2-1). All primer sequences, including those for the loci that were not used, are listed in Appendix G.

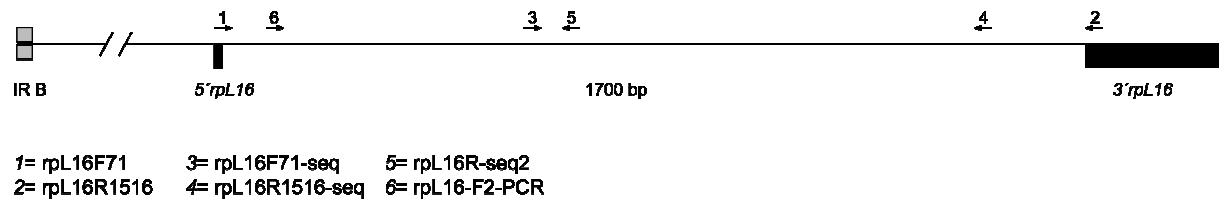


Figure 2-2. Scaled map of *rpL16* intron region based on Shaw et al. (2005). Proportions modified for *M. winkleri* individual 6462. IR B = inverted repeat B. Gene names in italics. Arrows show direction and relative position of the primer binding sites. Numbers refer to primer names in the text.

Table 2-2. Amplification and sequencing primers for the three loci used in this study.

Locus	Primer	Purpose ⁴	Direction	Primer sequence 5'-3'
<i>rpL16</i> ¹	<i>rpL16F71</i>	A&S	Forw	GCT ATG CTT AGT GTG TGA CTC GTT G
	<i>rpL16-F2- PCR*</i>	A	Forw	CTCATCGCTTTGCATTATCTGG
	<i>rpL16F71-seq*</i>	S	Forw	GATAGCGAAAGGAACCAGAAGAC
	<i>rpL16R1516-seq*</i>	S	Rev	ATACTAAATCATGGGATTTTTGAGATTT
	<i>rpL16R1516</i>	A&S	Rev	CCC TTC ATT CTT CCT CTA TGT TG
	<i>rpL16R-seq2*</i>	S	Rev	CGG GCG AAT ATT CAC TCT TT
<i>atpB-rbcL</i> ²	<i>atpB-rbcL-F</i>	A	Forw	GAAGTAGTAGGATTGATTCTC
	<i>atpB-rbcL-F-seq*</i>	S	Forw	TAG TAG GAT TGA TTC TCA
	<i>atpB-rbcL-F-seq-mitte*</i>	S	Forw	CTG CCA ATT TTC ACA TCT CGG
	<i>atpB-rbcL-R-seq*</i>	S	Rev	TGC TTT AGT CTC TGT TTG
	<i>atpB-rbcL-R</i>	A	Rev	CAACACTTGCTTTAGTCTCTG
<i>ccmp5</i> ³	<i>ccmp5F</i>	A&S	Forw	TGTTCCAATATCTTCTTGTCATTT
	<i>ccmp5R</i>	A	Rev	AGGTTCCATCGGAACAATTAT

1. Chloroplast markers (Shaw et al., 2005).

2. Chloroplast markers (Xu et al., 2000; Baenfer et al., 2006).

3. Chloroplast markers (Weising and Gardner, 1999, Vogel et al., 2003).

4. A - Amplification, S - Sequencing, A&S - both Amplification and Sequencing.

* self-designed.

Three non-coding chloroplast regions were chosen: *rpL16*, *atpB-rbcL* and *ccmp5*. For consistent amplification some of the primers had to be redesigned using sequences of closely related species from the EMBL database (see below). Amplification and sequencing primers for these loci can be found in Table 2-2.

rpL16 intron

In the following description primer codes used in brackets behind the primer name refer to Figure 2-2 and Table 2-2, where the positions and sequence of the primers are given.

To both amplify and sequence *rpL16* intron in *M. tanarius* PCR primers *rpL16F71* (1) and *rpL16R1516* (2) were used.

The *rpL16* region in *M. winkleri* and *M. winkleriella* is approximately 450-650bp longer than in *M. tanarius*, due to an AT-rich insertion. To get overlap in forward and reverse sequences, in addition to the forward and reverse PCR-primer (1, 2) another two sequencing primers were designed: *rpL16F71*-seq (3) and *rpL16R1516*-seq (4) on both sides of the AT-rich region (Figure 2-2).

In some *M. winkleri* individuals it was not possible to sequence with *rpL16F71* (1). To sequence these individuals another internal reverse sequencing primer was designed: *rpL16R-seq2* (5).

As amplification did not work for some *M. winkleri* and *M. winkleriella* individuals different combinations of primers were used to determine which primer contains mismatches. As *rpL16F71*-seq (3) and *rpL16R1516*-seq (4) and *rpL16F71*-seq (3) and *rpL16R1516* (2) amplified in these individuals, it was determined that the primer showing mismatches is *rpL16F71* (1). Another forward PCR primer, *rpL16-F2*-PCR (6), was used to replace the one showing mismatches. This primer was designed to bind in a conserved region, using published sequences of *Manihot esculenta*, *Carica papaya* and sequences of *M. winkleri* sequenced with *rpL16R-seq2* (5).

atpB-rbcL

As locus *atpB-rbcL* showed mostly unreadable sequences in the species under study, the following sequencing primers were designed using a reasonably readable *Macaranga* sequence: *atpB-rbcL-F*-seq; *atpB-rbcL-F*-seq-mitte; *atpB-rbcL-R*-seq (see Table 2-2). All sequencing primers worked. Sequences using sequencing primers *atpB-rbcL-F*-seq and *atpB-rbcL-F*-seq-mitte were overlapping and could be combined; subsequently *atpB-rbcL-R*-seq was not used.

ccmp5

This region is a microsatellite region, which was used for the detection of substructure in the *M. tanarius* parsimony network. For sequencing only the forward primer was used. It was found to be sufficient to get the variable mononucleotide repeat that was the most informative part.

PCR amplifications were performed using a Gene Amp 9700 PCR System (PE Biosystems) thermal cycler and the following profiles:

For *rpL16*:

Initial denaturation at 95 °C for 3 min, followed by 30 cycles of 95 °C for 50 s, 50 °C for 1 min, 68 °C for 1 min 20 s, 70 °C for 8 min, the ramp from annealing temperature to elongation temperature was set to 50%.

For *atpB-rbcL*:

Initial denaturation at 95 °C for 5 min, followed by 28 cycles of 95 °C for 48 s, 56 °C for 1 min, 72 °C for 2 min, 72 °C for 7 min.

For *ccmp5*:

Initial denaturation at 95 °C for 5 min, followed by 35 cycles of 95 °C for 1 min, 59 °C for 1 min, 65 °C for 5 min, 65 °C for 4 min.

For all three markers, PCR amplifications were performed in a volume of 20 µl, containing 2 to 10 ng of genomic template DNA, 1.13x buffer (containing 15 mM MgCl₂), 0.56 µM each of forward and reverse primer, 0.11 mM of dNTPs, and 0.23 units of Taq DNA polymerase (QIAGEN). To decrease the formation of primer dimers 0.11x bovine serum albumin (BSA) were added. To facilitate the amplification of GC-rich regions and to increase the specificity (Varadaraj & Skinner 1994) 3% dimethyl sulfoxide (DMSO) and 1.13x Q-solution were added.

In the beginning, the amplicons were purified using Nucleofast 96 PCR plates (Macherey-Nagel), however this purification method resulted in poor sequencing. Therefore, PCR products were subsequently purified by QIAquick PCR purification Kit (QIAGEN), following the manufacturers instructions, and resuspended in 28 µl warmed 1x TE buffer. Sequencing was performed either on a MegaBACE 1000 (Amersham Biosciences) or on an ABI 3730 XL (Applied Biosciences) capillary sequencer. Sequences will be submitted to EMBL GenBank to make them publicly available.

Sequence analysis and alignment

Sequences were manually edited and assembled into contig sequences using Sequencher 4.7 (Gene Codes Corporation). Sequence alignments were done manually in Se-Al v2.1 (Rambaut 2002). Three alignments were created:

- 1) An alignment for *M. tanarius*. *RpL16* and *atpB-rbcL* sequences were concatenated and combined into a single alignment.
- 2) An alignment for *M. winkleri* together with *M. winkleriella*, *M. gigantea*, *M. pruinosa*, and *M. diepenhorstii*, as these species were shown to be closely related to *M. winkleri* in Bänfer et al. (2006). Here *rpL16* and *atpB-rbcL* sequences were concatenated and combined in one alignment as well.
- 3) An alignment, consisting of the available database sequences of different *Macaranga* species, containing the intergenic spacer sequence *atpB-rbcL* together with the new *atpB-rbcL* sequences collected during this study (see Appendix H). This alignment is used in the phylogeographic analysis and to put the new sequences in a broader context.

The sequences of the microsatellite region *ccmp5* were aligned in a separate alignment to determine the substructure in the samples of alignments 1 and 2.

2.1.2 Data analyses

Statistical parsimony networks based on the chloroplast sequence analyses

The software TCS v1.21 (Clement et al. 2000) was used to perform the statistical parsimony network calculations. TCS is a program that estimates genealogical relationships of the sequences. TCS collapses identical sequences into haplotypes (HT). The frequencies of the haplotypes and an absolute distance matrix are calculated for all pairwise comparisons of haplotypes in the sample. The probability of parsimony is calculated for pairwise differences until the probability exceeds 0.95. The maximum number of mutational connections between pairs of sequences justified by the parsimony criterion is associated with the 95% probability. TCS generates a graphical output file containing the resulting network, where every step represents one mutational step.

In all three alignments the regions that are particularly prone to homoplasy were excluded. In *atpB-rbcL* sequences, the first and second poly-T/A-repeat were shortened to the same length, as was a poly-A/T-repeat in *rpL16*. Indels were coded as single mutational steps. In the *rpL16* alignment of *M. winkleri* together with *M. winkleriella*, *M. gigantea*, *M. pruinosa* and *M. diepenhorstii*, an AT-rich region in the sequence (between 450-650 bp) was excluded due to hypervariability and therefore unsafe alignment. Parsimony networks with 95% confidence limits were calculated in TCS for all three alignments. In the resulting networks the variation at the previously excluded microsatellite regions and the information of the *ccmp5* marker was used to include the genetic diversity within the haplotypes, i.e. to manually create subhaplotypes (Bänfer et al. 2006). The network was re-drawn from the TCS output using Adobe Illustrator CS 11.0.0.

Neighbor-joining analysis

A phenetic analysis of *M. winkleri* and *M. winkleriella* alignment of loci *atpB-rbcL* and *rpL16* with the neighbor-joining cluster algorithm using PAUP v4.0b10 (Swofford 2002) was conducted based on pairwise maximum likelihood distances. The HKY model (Hasegawa et al. 1985) of sequence evolution was then used to compare positions of the root within *M. winkleri*, between a network and a distance-based approach.

Principal coordinate analysis

A principal coordinate analysis (PCoA) was conducted to get access to the genetic structure of the data by exploring and visualizing similarities and dissimilarities. The polymorphic nucleotide positions (without the mononucleotide repeat regions) of the sequences of *M. winkleri* and *M. tanarius* (only the Bornean samples to compare similar geographic scales

in both species) were converted to numeric codes (A = 1, C = 2, G = 3, T = 4, gap = 5). A pairwise genetic distance matrix was calculated for all individuals from the polymorphic sites of the sequences, where two regions can be either identical (= 0) or different (= 1) using GenAlEx 6 (Peakall & Smouse 2006). These distances are then summed over all of the sites. For all *M. winkleri* and *M. tanarius* the PCoA was computed on these distance matrices using GenAlEx 6.

Assignment analysis with chloroplast sequences

Two different Bayesian assignment approaches were used to infer population structure of *M. winkleri* and *M. tanarius* using the programs STRUCTURE 2.3.3 (Pritchard et al. 2000) and INSTRUCT (Gao et al. 2007) on the Computational Biology Service Unit of Cornell University (<http://cbsuapps.tc.cornell.edu/index.aspx>). The matrices, with numerically coded polymorphic nucleotide positions (see Principal coordinate analysis), were used as input files.

STRUCTURE implements a model-based clustering method assuming Hardy-Weinberg equilibrium and linkage equilibrium within populations. In STRUCTURE a model is assumed in which there are K populations. Each K is characterized by a set of allele frequencies at each locus. The individuals in the samples are probabilistically assigned to K populations. Each individual can be assigned to one or several populations according to the individual's genotypes with corresponding frequencies. INSTRUCT is an alternative clustering program to STRUCTURE that does not assume Hardy-Weinberg equilibrium within populations. Results from both of these programs were compared.

STRUCTURE runs were performed with 1,000,000 iterations and a burn-in period of 250,000 iterations without any prior information on the population of origin of each sampled individual. STRUCTURE requires an additional admixture burn-in period, which was set to 125,000 iterations. Using this admixture burn-in as a starting point for the non-admixture model adds stability and is the suggested methodology in the current version of STRUCTURE. In the non-admixture model, individuals are assumed to be drawn purely from one of K populations, in the admixture model individuals are allowed to have mixed ancestry.

The non-admixture model was used, as we are dealing with plastid sequences, namely chloroplast data, and thus do not expect mixed ancestry. Ten independent simulations were performed in which the number of populations tested, ranged from K = 1 to K = 10.

INSTRUCT runs were performed with the same number of iterations, burn-in, and range of K without prior information also using the non-admixture model, only without the addition of the initial admixture burn-in period.

Determining the number of populations (K)

In STRUCTURE the implemented model choice criterion to detect the true K (or the optimal K) is an estimate of the posterior probability of the data for a given K, $\Pr(X|K)$ (Pritchard et al. 2000). This value is used to produce the log likelihood of the data at each step of the Markov chain Monte Carlo (MCMC), denoted $\ln\Pr(X|K)$. The mean and variance of these values are computed and half the variance is subtracted from the mean. This gives the model choice criterion which will be referred to as $L(K)$. The number of populations (i.e. the optimal K) is often identified using the maximal value of $L(K)$ returned by STRUCTURE (Falush et al. 2003). Therefore all $L(K)$ for $K = 1$ to $K = 10$ over all replicate runs of STRUCTURE were checked for the highest value for *M. winkleri* and *M. tanarius*. Furthermore Falush et al. (2003) proposed that the first value in the plateau phase of the mean $L(K)$ is often the best K. Therefore the average $L(K)$, $m(L(K))$ and the standard error of ten replicate runs of STRUCTURE were calculated and plotted for the non-admixture model for both species under study using Excel 2004 (Microsoft).

Another method to choose K is the calculation of Delta K (ΔK). This is a computational method to find the first K in the plateau phase, and thus less subjective. ΔK is calculated based on the second-order rate of change of likelihood to choose the optimal number of K (Evanno et al. 2005). ΔK is the mean of the absolute values of $L''(K)$ averaged over the ten replicate runs divided by the standard deviation of $L(K)$,

$$\Delta K = \frac{m|L''(K)|}{s[L(K)]},$$

where, $L'(K) \approx L(K) - L(K-1)$ and $|L''(K)| \approx |L'(K+1) - L'(K)|$.

INSTRUCT can infer the optimal number of subpopulations underlying a sample via the deviance information criteria (DIC) (Spiegelhalter et al. 2002). The DIC value is a direct indication of how well the model fits the data. The larger the value of the DIC, the less well the model fits the data. Therefore, the K, that produced the smallest DIC value was chosen (Gao et al. 2007). In addition, the DIC values were averaged over the replicate runs per K and plotted with referring standard deviation. As with the STRUCTURE results the plot was examined to find the first K in the plateau phase. For an objective determination a second order rate of change was calculated for DIC values similar to the ΔK of STRUCTURE, (denoted ΔK DIC).

For each K ($K = 1$ to $K = 10$) the replicate run with the best $L(K)$ in STRUCTURE and the smallest DIC value in INSTRUCT was chosen. For *M. winkleri* and *M. tanarius*, bar plots for the different numbers of clusters (K) were created in Excel, illustrating the assignment of each individual to the different clusters. This was done to visualize the results of the STRUCTURE and INSTRUCT runs for the non-admixture model. A visual inspection was performed for essentially empty clusters, i.e. clusters where individuals are assigned with very low frequency.

Analysis of molecular variance

Genetic structure was estimated through an analysis of molecular variance (AMOVA) (Excoffier et al. 1992) using GenAlEx 6. After 999 random permutations a check of the significance of the variance components was performed.

For both *M. winkleri* and *M. tanarius* two regions were assumed (region 1: Sabah; region 2: Sarawak/Brunei) as proposed by the PCoA for *M. winkleri*. Additionally, AMOVA was performed for *M. winkleri* for the individuals west and east of the Crocker Range and using three populations following the administrative borders, i.e. Sabah, Brunei and Sarawak, which also represent different geographical regions of Borneo.

Haplotype and nucleotide diversity analysis

Multiple intra-population metrics were calculated using Haplotype Analysis v 1.05 (Eliades & Eliades 2009) to compare the genetic structure between *M. winkleri*, *M. tanarius* and *M. winkleriella*, distinguishing Sabah from Sarawak/Brunei. The intra-population metrics that were calculated are listed below.

The **number of haplotypes per population**, to compare the amount of different haplotypes for Sabah and Sarawak/Brunei.

The **number of private haplotypes**, or the haplotypes that only occur in one region.

The **number of effective haplotypes** and the **haplotype diversity**. The effective number of haplotypes is the inverse probability that two randomly chosen haplotypes are identical.

The **haplotypic richness**, denoted R_h , is the number of haplotypes expected in each population for a rarefied sample size, i.e. the size of the smallest population of the dataset. The haplotypic richness rarefied for the sample size was also calculated for the mitochondrial sequence data of *M. winkleri*'s obligate ant partner *Crematogaster* msp. 8 (Braasch et al. 2008) also distinguishing Sabah from Sarawak/Brunei.

The **genetic diversity** (Nei 1973) presents the amount of genetic diversity within each population (region) ranging from 0 (= no variation) to 1.

Previous studies provided evidence that the biogeography of plants and animals on Borneo is strongly influenced by the occurrence of a central mountain range (Bänfer et al. 2006, Raes et al. 2009). Therefore, these calculations were also performed for individuals both west and east of the Crocker Range, the northern extension of the central mountain range, for *M. winkleri* and *M. tanarius*. For *M. tanarius* one calculation was performed with the information at the microsatellite loci and one without it.

Two additional intraspecific metrics were calculated using DnaSP v5.10.01 (Librado & Rozas 2009) for *M. winkleri*, *M. winkleriella* and *M. tanarius*.

The **haplotype diversity**, which summarizes information on the number and frequency of different variants at a locus regardless of their sequence relationships.

The **nucleotide diversity**, a weighted sequence divergence between individuals in a population, regardless of the number of different haplotypes.

DnaSP considers gaps in the alignment as missing data; therefore gaps were recoded as single mutation events. For *M. tanarius* the variation at the microsatellite loci was included. Again two calculations were performed, one calculation for all samples and the second was restricted to the individuals from Borneo for better comparability with *M. winkleri*. For *M. winkleri* the haplotypic and nucleotide diversity was also calculated separately for Sabah and for Sarawak/Brunei, as the haplotypic patterns for these two regions show clear differences.

Analysis of spatial-genetic correlation

A Mantel test was performed to look for the existence of a correlation between the geographic and genetic distances using GenAlEx 6. A pairwise individual-by-individual geographic distance using the coordinates of longitude and latitude and a pairwise genetic distance is calculated from the polymorphic regions of the sequences for all *M. winkleri* individuals and again for *M. winkleri* individuals west and east of the Crocker Range. For *M. tanarius* one correlation including only the Bornean individuals and another including all individuals was calculated. In all 9,999 random permutations were performed to check the null hypothesis, that there is no relation between the two matrices.

The results of the Mantel test are illustrated in a scatter plot combining histogram information to illustrate relative data density. The test results are aggregated into fixed sized bins along the geographical distance axis, using frequency analysis. The size of each data point is then relative to the size of each bin. In addition to relative sizes, different colours are used to indicate relevant subsets of the data points.

Regression analysis was performed on each set of Mantel test data. The resulting regression lines are shown directly on the corresponding scatter graph. The corresponding coefficient of determination (R^2) and the correlation coefficient (R) are presented for each set of matrices. The correlation coefficient ranges from -1 to 1, while -1 is the highest negative correlation possible, 1 the highest positive correlation and a value of 0 implies that there is no linear correlation between the variables.

2.2 Results of the chloroplast analysis

2.2.1 Sequence analysis and alignment

atpB-rbcL

Sequencing of the *atpB-rbcL* region in 100 *M. tanarius* individuals resulted in sequences with lengths from 799 to 801 bp. The *M. tanarius* alignment has a length of 801 bp. Four variable base positions each with two different bases occurred and additionally an indel of one nucleotide. Three variable microsatellite regions were detected.

Sequencing of the *atpB-rbcL* region in 87 *M. winkleri* individuals resulted in sequences with lengths from 788 to 792 bp. The *M. winkleri* alignment has a length of 801 bp. Two variable base positions each with two different bases occurred and additionally an indel of four nucleotides. Five variable microsatellite regions were detected. Inclusion of 13 *M. winkleriella*, one *M. diepenhorstii*, two *M. gigantea* and one *M. pruinosa* sequence leads to an alignment of 825 bp length. One additional indel of 24 bp and 16 additional variable base positions each with two different bases occurred.

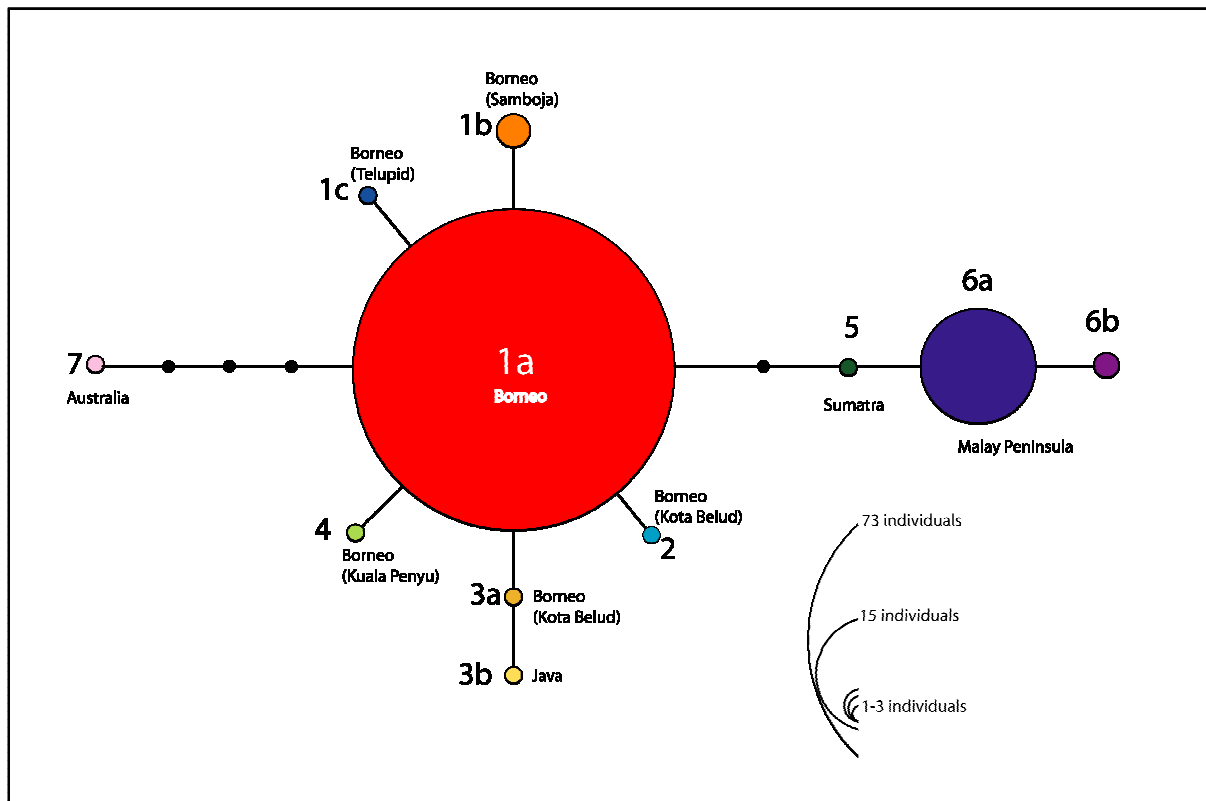


Figure 2-3. Chloroplast haplotype network, including subhaplotypes for *M. tanarius* calculated with TCS. The circle size is representative of the number of individuals in which the haplotype was found. Black dots represent missing intermediates.

rpL16

The length of the *M. tanarius* alignment in *rpL16* is 1,023 bp, the sequence lengths were between 1,020 and 1,023 bp. Five variable base positions each with two different bases occurred. One variable microsatellite region was detected.

Sequencing of the *rpL16* region in 87 *M. winkleri* individuals resulted in sequences with lengths of 1,281 to 1,475 bp. The *M. winkleri* alignment had a length of 1,595 bp. 22 variable base positions each with two different bases. Eight variable microsatellite regions were detected.

Inclusion of 13 *M. winkleriella*, one *M. diepenhorstii*, two *M. gigantea* and one *M. pruinosa* sequence lead to an alignment of 1,872 bp length. Six additional variable base positions each with two different bases occurred.

Ccmp5

The length of the *M. tanarius* alignment for *ccmp5* is 20 bp. Length of the sequences were between 17 and 20 bp, thus, four sequence variants could be found, each of which vary in the length of the T/A-repeat.

The alignment of *M. winkleri* together with 13 *M. winkleriella*, one *M. diepenhorstii*, two *M. gigantea* and one *M. pruinosa* sequences leads to an alignment of 20 bp. While all *M. winkleriella* individuals show identical sequences, for *M. winkleri* three of the four variants of the T/A-repeat that are found, in *M. winkleri* also occur in the other included *Macaranga* species.

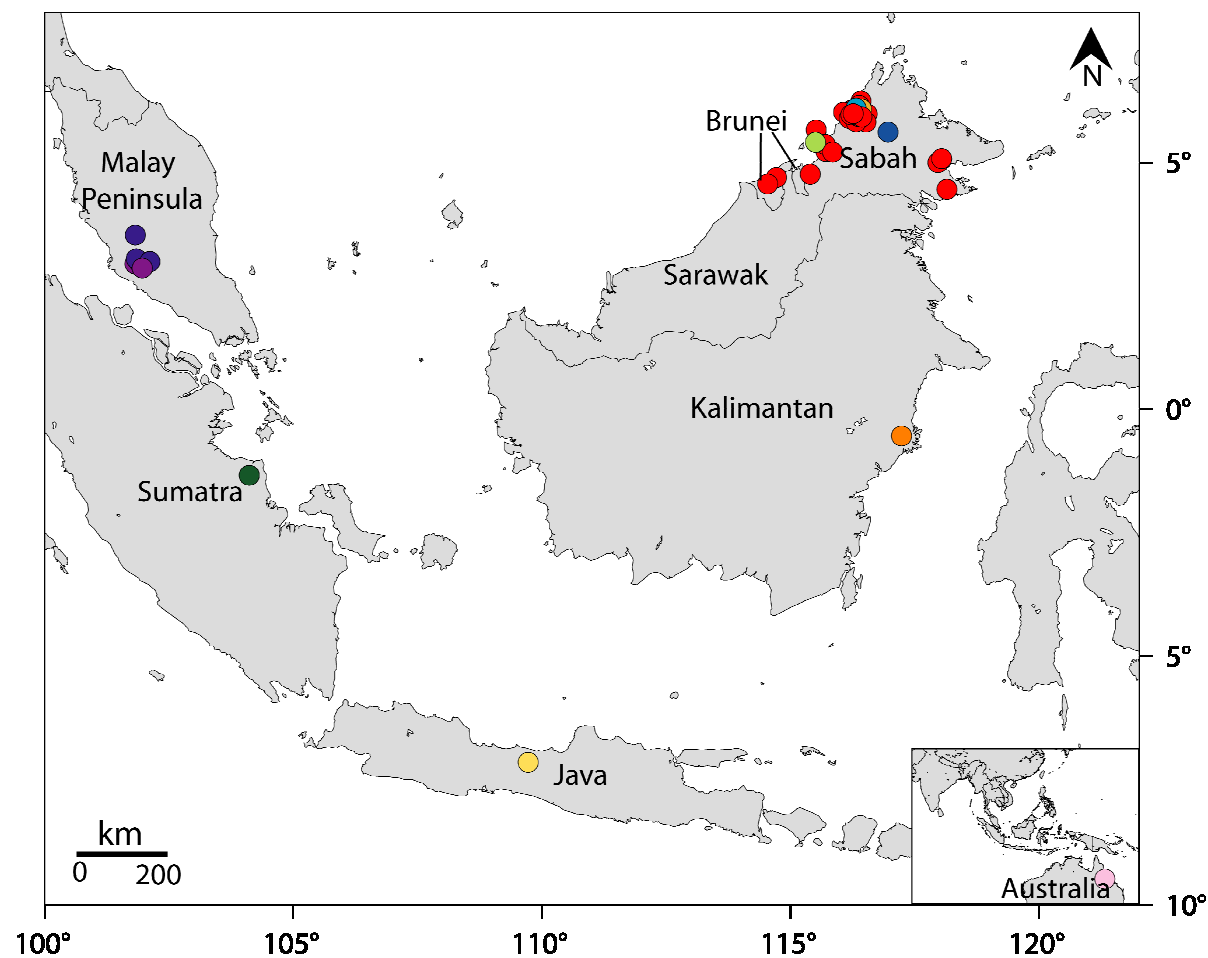
2.2.2 Statistical parsimony networks based on the chloroplast sequence analyses

Network of *Macaranga tanarius*

For the alignment of the 100 *M. tanarius* individuals (see Appendix F) TCS calculated a 95% parsimony connection limit of 18 steps resulting in a network of seven HTs. Inclusion of the previously excluded microsatellite regions resulted in subhaplotypes (sequence data see Table 2-3) for HT 1, 3 and 6 (Figure 2-3). Haplotypes 1a, 2, 3a and 4 are found in western Sabah and HT 5 - HT 7 exclusively occurred on Sumatra, Malay Peninsula or Australia. HT 1a comprises 73 individuals occurring in western and eastern Sabah and Sarawak/Brunei (Figure 2-4), but in central Sabah HT 1c occurs. HT 1b comprises three individuals from Samboja, Kalimantan. HT 2 and 3a are found in Kota Belud, Sabah. HT 3b occurs on Java. HT 6a comprises 15 individuals, HT 6b three individuals. Four HTs were not found in the analysed individuals and occur as missing intermediates, three missing intermediates are between HT 1a (Borneo) and HT 7 (Australia) and one between HT 1a (Borneo) and HT 5 (Sumatra).

Table 2-3. Sequence information of the variable microsatellite regions in *M. tanarius*.

Region in the sequence		Haplotypes showing the motif
<i>atpB-rbcL</i> 1st T-stretch:	TTTTTTTTTT	3b;4;5;6a;6b;7
	TTTTTTTTTT-	1a;1b;2;3a
<i>atpB-rbcL</i> 2nd T-stretch:	CTTTTTTTTTT	5;7
	CTTTTTTTTTT-	1a;2;3a;3b;4;6a;6b
<i>atpB-rbcL</i> 3rd T-stretch:	CTTTTTTTTT	1a;1b;2;3a;3b;4;7
	CTTTTTTTTT-	5;6a;6b
<i>rpL</i> A-stretch:	GAAAAAAAAAAAA	1a;2;3a;3b;4
	GAAAAAAAAAAAA-	1b; 7
	GAAAAAAAAAAAA--	6a; 6b
	GAAAAAAAAAAAA---	5
<i>ccmp5</i> T-stretch:	CTTTTTTTTTTTTTT	1a; 2; 3a; 3b; 4; 6 b
	CTTTTTTTTTTTTTT-	6a 1c
	CTTTTTTTTTTTTTT--	5
	CTTTTTTTTTTTTTT---	7

**Figure 2-4.** Geographical distribution of the chloroplast haplotypes of *M. tanarius*. The colour of each population circle corresponds to the HT colour of Figure 2-3.

Network of *Macaranga winkleri*, *M. winkleriella* and related *Macaranga* species

For the alignment of 104 individuals (see Appendix D) comprising 87 *M. winkleri* individuals, 13 *M. winkleriella* individuals, two individuals of *M. gigantea*, and one individual each of *M. diepenhorstii* and *M. pruinosa*, TCS calculated a 95% parsimony connection limit of 18 steps. The network includes 36 HTs, which were combined in HT groups for a clearer arrangement, when individuals from the same or similar area are one or two mutational steps apart. This resulted in 16 HT groups (Figure 2-5). Sequence information of the microsatellite regions is not included in the network and can be seen in Appendix E. In the total network 62 HTs were not found in the analysed individuals and occur as missing intermediates. Considering only the *M. winkleri* individuals 25 missing intermediates are detected. The most common HT group is number 1, comprising 17 individuals occurring in eastern and central Sabah (Figure 2-6).

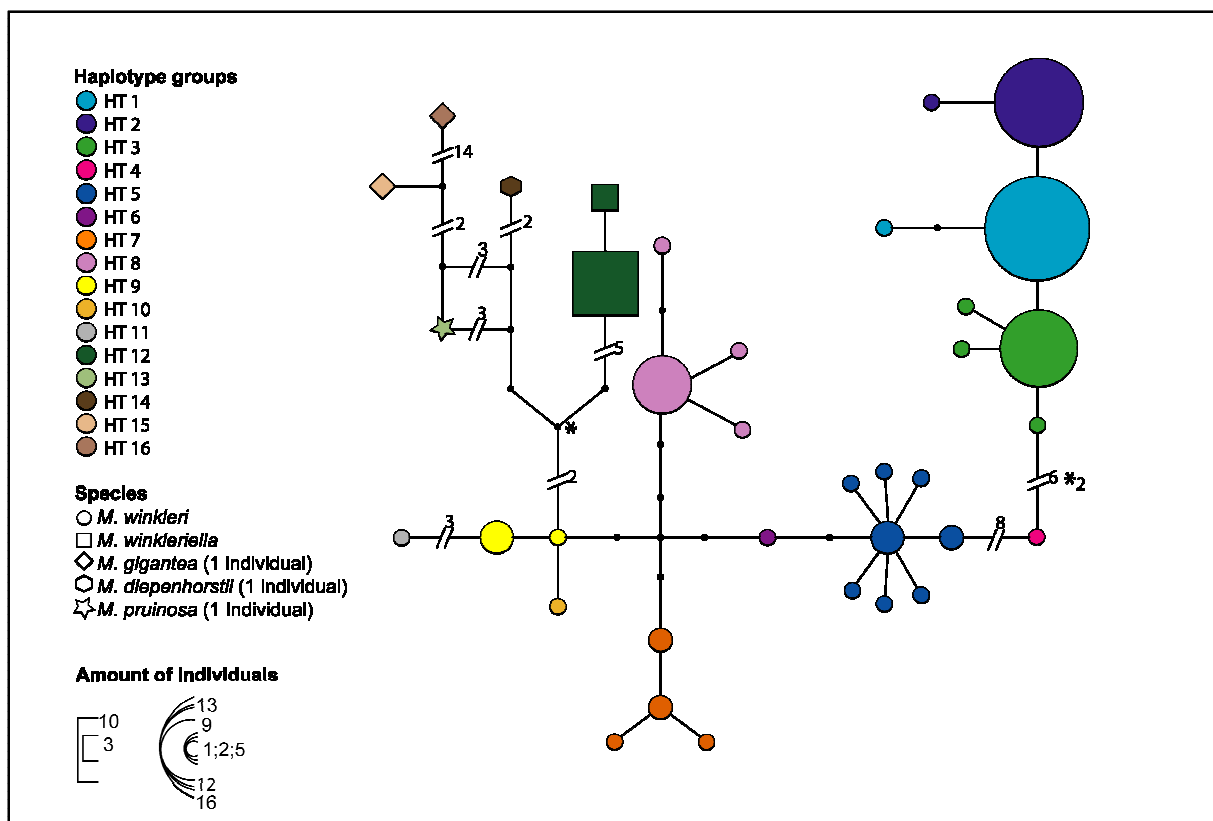


Figure 2-5. Chloroplast haplotype network of *M. winkleri* and *M. winkleriella* with closely related *Macaranga* individuals as outgroups. Shapes indicate the different species. The size of the circles and squares indicate the number of individuals in which the haplotype was found. Colours represent the haplotype groups. Black dots represent missing intermediates. Double slash with a number indicates the number of missing intermediates. * marks the root of the network for the ingroup. *2 marks the position of the root using the neighbor-joining cluster algorithm.

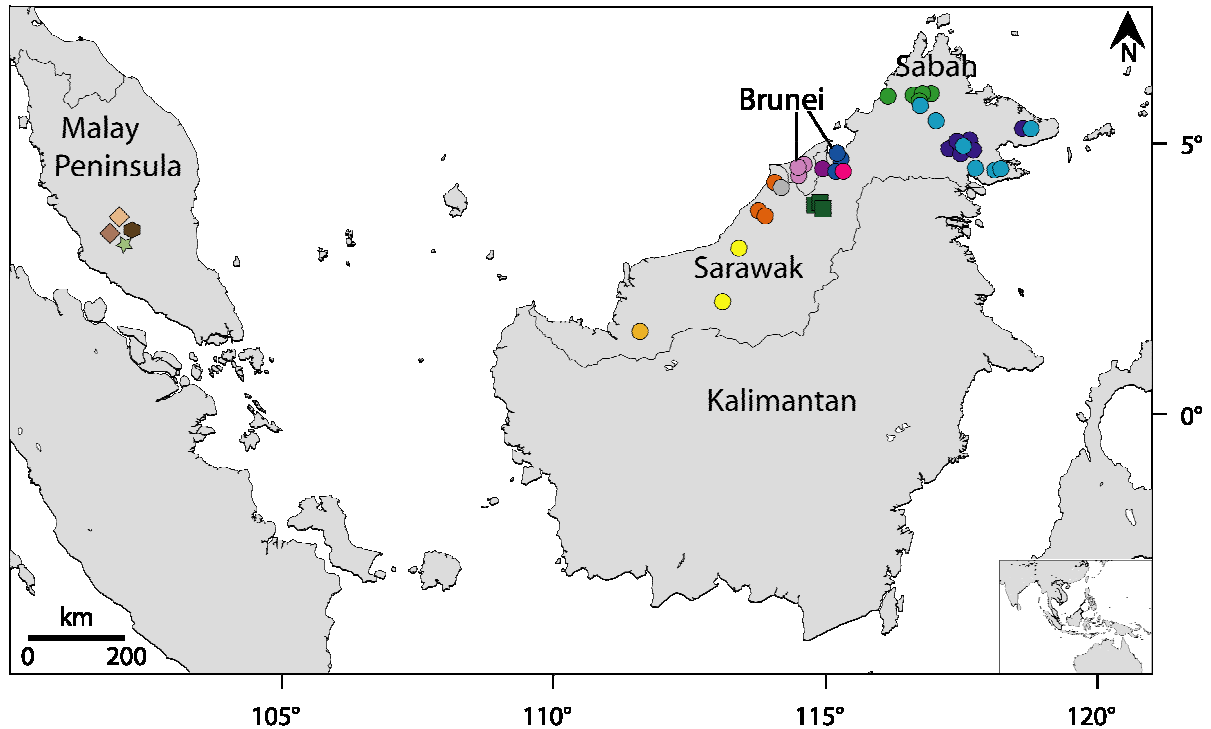


Figure 2-6. Geographical distribution of the chloroplast haplotypes of *M. winkleri*, *M. winkleriella* and related *Macaranga* individuals. The colour of each population circle corresponds to the HT colour of Figure 2-5.

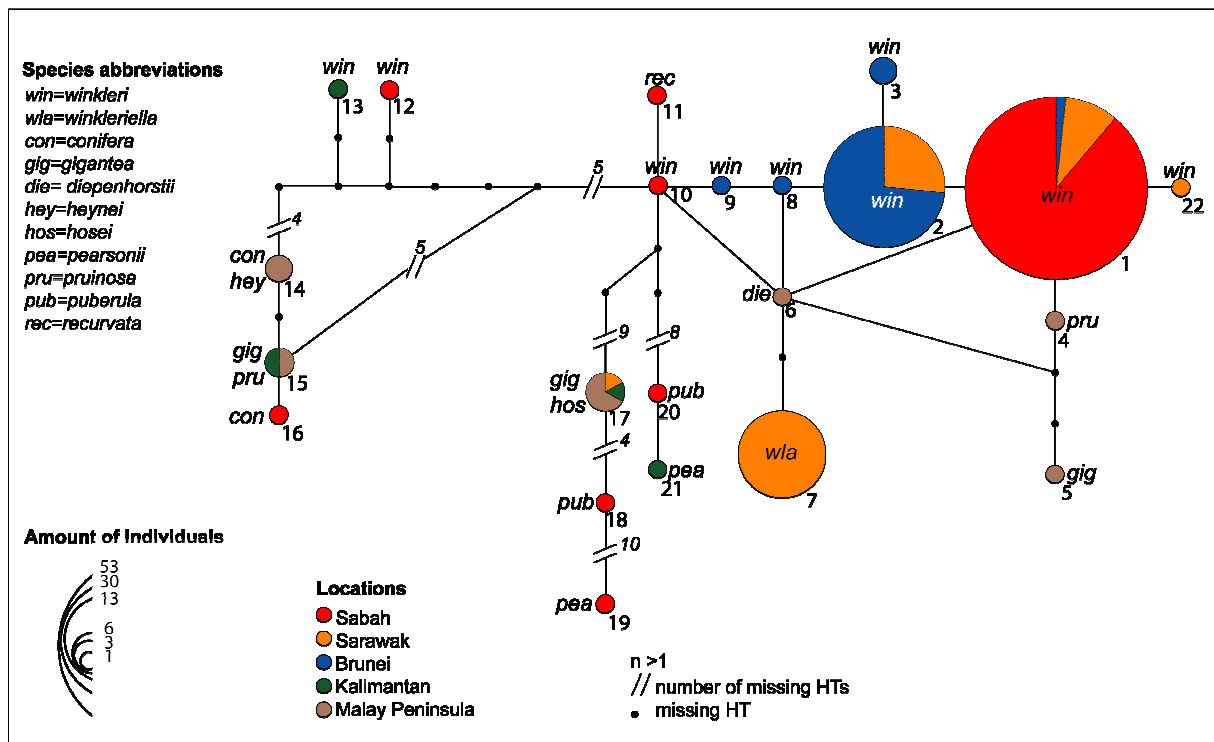


Figure 2-7. Statistical parsimony network of different *Macaranga* species based on the *atpB-rbcL* intergenic spacer. Black dots show missing intermediates. Numbers give the HT number. Circle size indicates the number of individuals in which the haplotype was found.

Within *M. winkleri* the highest number of mutational steps can be found between HT 2 and HT 11 (29 steps). Between *M. winkleri* and *M. winkleriella* there are at least nine mutational steps, between *M. winkleri* and *M. diepenhorstii* at least eight mutational steps, between *M. winkleri* and *M. pruinosa* at least eight steps, and between *M. winkleri* and *M. gigantea* at least 14 steps. The putative root of *M. winkleri* in the haplotype network is located between *M. winkleri*, *M. winkleriella* and the outgroup species. The putative root using the neighbor-joining cluster algorithm is located between individuals from Sabah and Sarawak/Brunei.

HT group 1 – HT group 3 are the groups found in Sabah, all the other HT groups occur in Sarawak/Brunei, or on the Malay Peninsula.

Network based on sequences of the *atpB-rbcL* intergenic spacer of different *Macaranga* species

TCS calculated a 95% parsimony connection limit of 12 steps using EMBL database sequence information of different *Macaranga* species on locus *atpB-rbcL* combined with *atpB-rbcL* sequences from this study. 123 individuals from 11 different *Macaranga* species from different regions were included (see Appendix H).

HT1 and HT2 comprise most of the *M. winkleri* individuals, 53 and 30 individuals, respectively (Figure 2-7). HT 7 comprises all *M. winkleriella* individuals. HTs 14, 15 and 16 are shared between different species. HT 6 has the most connections, being connected five times, resulting in three loops. These loops could not be resolved using assumptions from coalescence theory (Castelloe & Templeton 1994), as neither the microsatellite information nor the calculation of a neighbor-joining tree (data not shown) yields information that can be used to resolve these loops. The minimum number of mutational steps between *M. winkleri* and *M. pruinosa*, *M. winkleri* and *M. recurvata* and *M. winkleri* and *M. diepenhorstii* is one step.

2.2.3 Neighbor-joining analysis

The neighbor-joining tree shows a clear separation of Sabah and Sarawak/Brunei sequences in *M. winkleri*, except for one individual, 6875 from Brunei, which falls into the Sabah clade (Appendix A).

Table 2-4. Principal coordinate analysis (PCoA) of *Macaranga winkleri* and *M. tanarius*. Percentage of variation explained by the first three axes.

Species	Axis		
	1	2	3
<i>M. winkleri</i>	75.95%	9.69%	5.18%
Cumulative:	75.95%	85.63%	90.81%
<i>M. tanarius</i>	33.76%	33.76%	32.49%
Cumulative:	33.76%	67.51%	100.00%

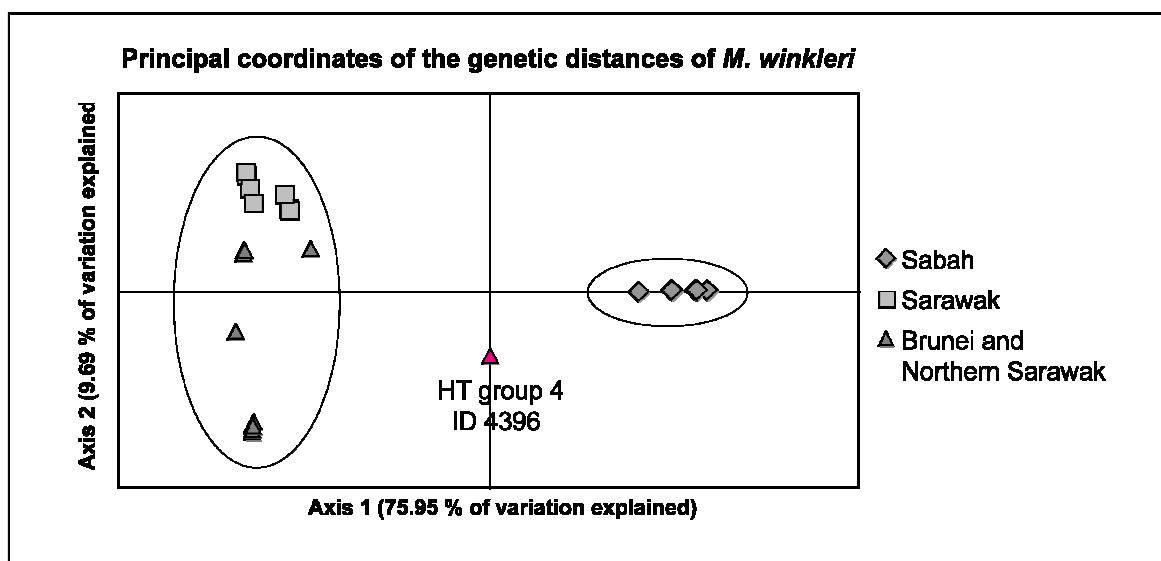


Figure 2-8. PCoA plot of the genetic distances of *M. winkleri*. Three clear groupings are differentiated, Sabah, Sarawak/Brunei and the intermediate HT group 4 (made up of the single individual 4396).

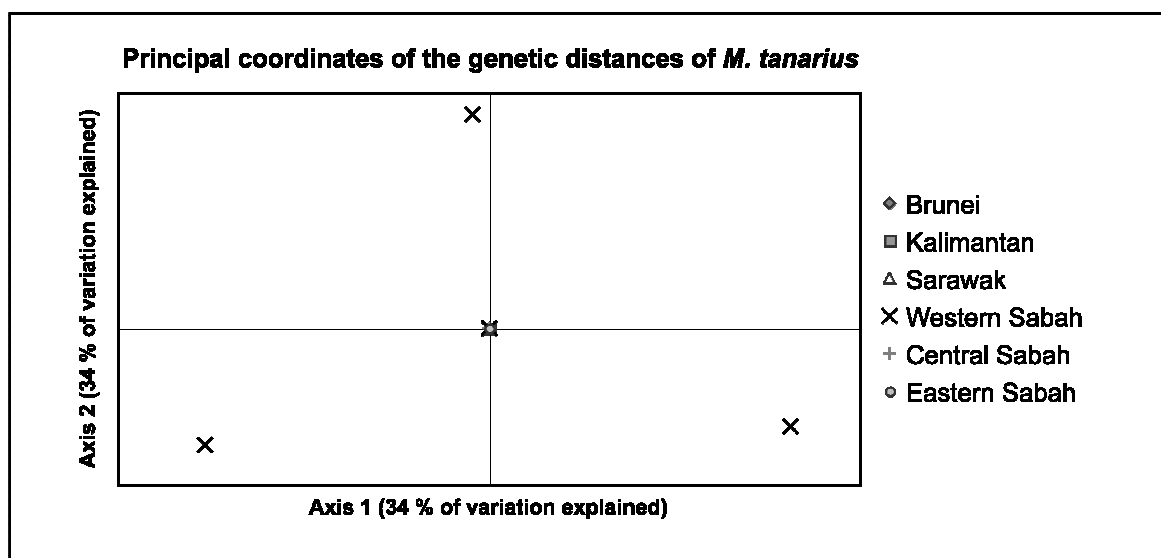


Figure 2-9. PCoA plot of the genetic distances of Bornean *M. tanarius* from Brunei, Kalimantan, Sarawak, western Sabah, central Sabah and eastern Sabah. All but three individuals, have the same position in the projection.

2.2.4 Principal coordinate analysis

Macaranga winkleri

In the PCoA of *M. winkleri* the first two axes account for roughly 86% of the variance (Table 2-4). The first axis explains most of the variance (75.95% variance) and the PCoA plot (Figure 2-8) clearly visualizes the existence of two groups: The individuals of Sabah form one group, the individuals of Sarawak/Brunei the other group. The individual that is in between represents HT4 in Figure 2-5 and Figure 2-6.

Macaranga tanarius

In the PCoA for *M. tanarius*, all but three individuals from western Sabah have the same position in the projection (Figure 2-9).

2.2.5 Assignment analysis in *M. winkleri* and *M. tanarius* assuming the non-admixture model

The highest L(K) in *M. winkleri* is detected for K = 6 and in *M. tanarius* the highest L(K) occurs for K = 7 (Table 2-5). The plot of m(L(K)) as a function of K (K = 1 to K = 10) is shown in Figure 2-10A for *M. winkleri* and in Figure 2-11A for *M. tanarius*.

The first K value in the plateau phase, is K = 2 in *M. winkleri* and K = 1 in *M. tanarius* (Figure 2-10A & Figure 2-11A). The calculation of ΔK was used, and the highest value for ΔK is detected for K = 2 in both species (Figure 2-10B & Figure 2-11B).

The smallest DIC value for *M. winkleri* is found for K = 9 and for *M. tanarius* it is detected for K = 2 (Table 2-5). The first K in the plateau phase of the plots of the DIC values averaged over the ten replicate runs of INSTRUCT using the non-admixture model gives K = 2 for

Table 2-5. *Macaranga winkleri* and *M. tanarius*. Best K values determined with different methods assuming the non-admixture model using STRUCTURE and INSTRUCT.

	STRUCTURE			INSTRUCT		
	K with highest log probability of all replicate runs	First K in the plateau phase of the plot of the Mean-Log-Likelihood	K with the highest value for ΔK	K showing the smallest DIC value	First K in the plateau phase of the DIC values	K with the highest value for ΔK DIC
<i>M. winkleri</i>	K=6	K=2	K=2	K=9	K=2	K=2
<i>M. tanarius</i>	K=7	K=1	K=2	K=2	N/D	K=2

N/D - Not Discernable

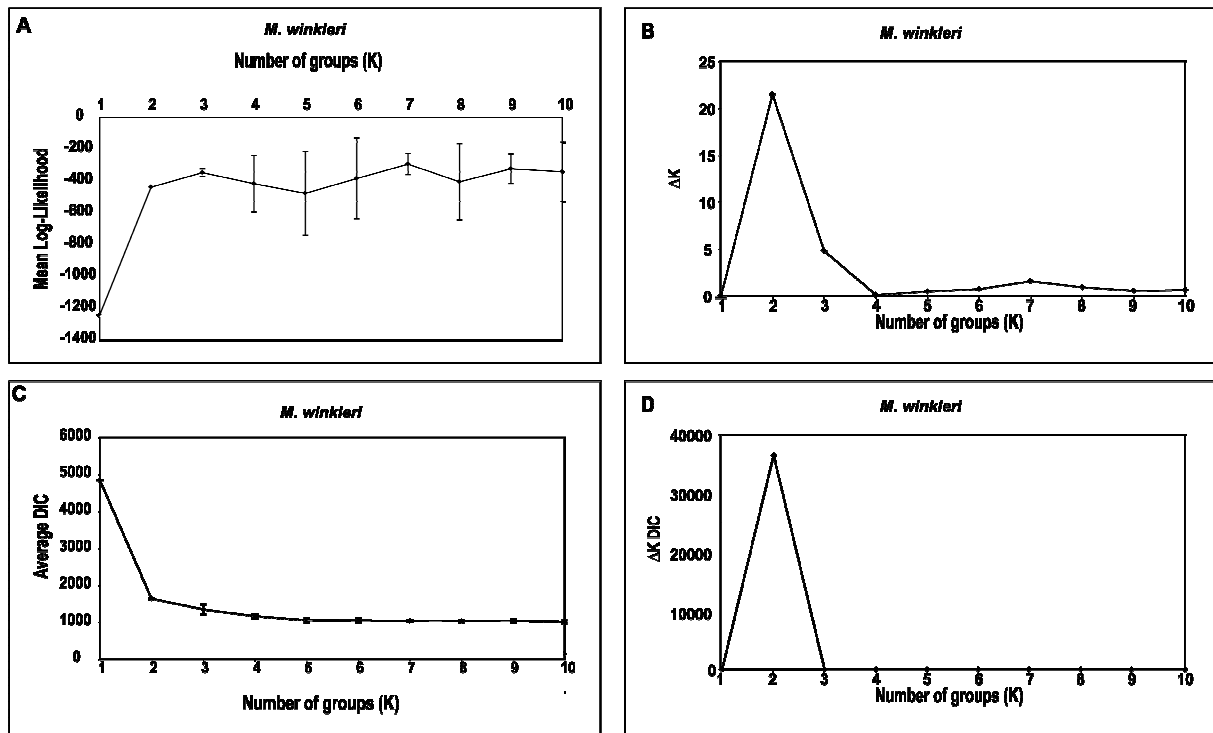


Figure 2-10. Plots for the determination of the optimal K value in *M. winkleri* for all individuals using the non-admixture model.

A) The log probability $L(K)$ averaged over the ten replicate runs $m(L(K))$ of STRUCTURE. Vertical bars indicate standard deviations.

B) To assess the number of groups (K) supported by the analysis with STRUCTURE, the second order rate of change in the log-likelihood (ΔK) was calculated.

C) The DIC values averaged over the ten replicate runs of INSTRUMENT. Standard deviations are indicated by the use of vertical bars. For nearly all number of groups (K) the magnitude of the standard deviations are too small to be seen at this scale.

D) To assess the number of groups (K) supported by the analysis with INSTRUMENT, the second order rate of change in the DIC was calculated (ΔK DIC).

M. winkleri and is not discernable for *M. tanarius* (Figure 2-10C & Figure 2-11C). The objective calculation of ΔK DIC indicates an optimal K of 2 for both *M. winkleri* and *M. tanarius* (Figure 2-10D & Figure 2-11D).

Bar plots of the studied *M. winkleri* individuals were created to visualize the STRUCTURE and INSTRUMENT results for the non-admixture model (see Figure 2-12) of the runs with the highest $L(K)$ in STRUCTURE and the lowest DIC in INSTRUMENT each for $K = 2$ to $K = 10$, with the same order of the individuals (see Appendix I).

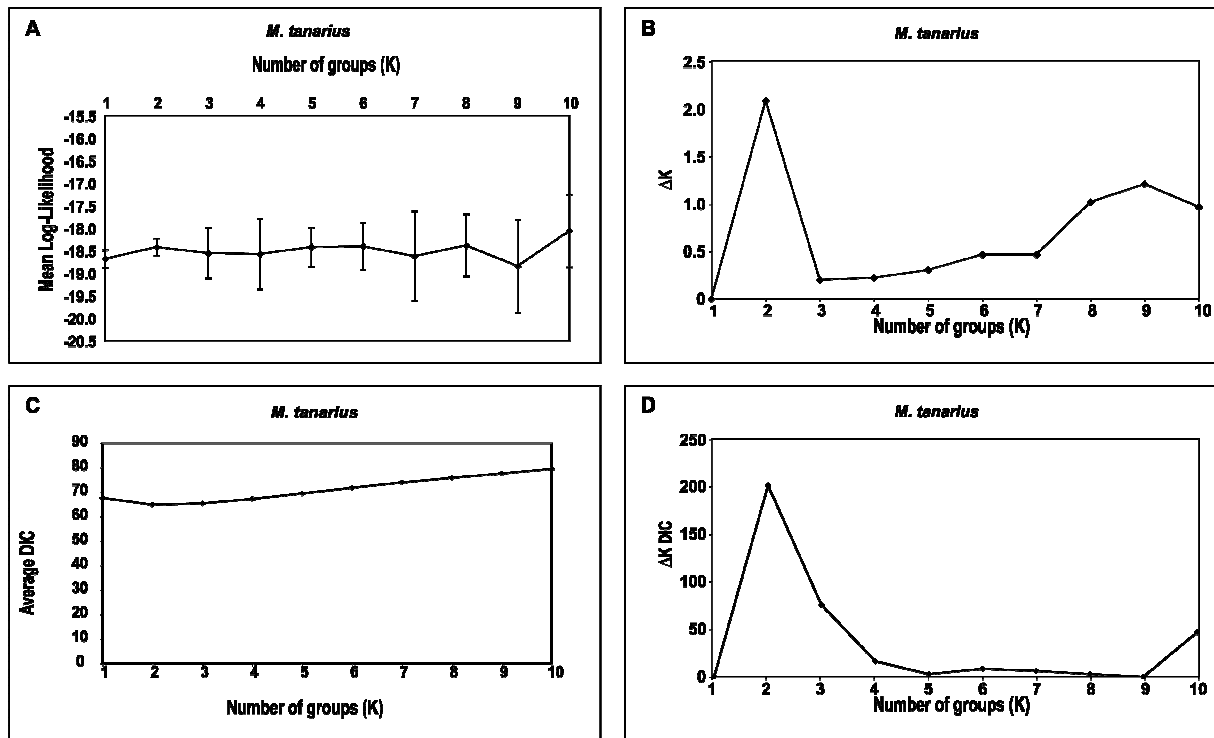


Figure 2-11. Plots for the determination of the optimal K value in *M. tanarius* for all individuals using the non-admixture model.

A) The log probability $L(K)$ averaged over the ten replicate runs $m(L(K))$ of STRUCTURE. Vertical bars indicate standard deviations.

B) To assess the number of groups (K) supported by the analysis with STRUCTURE, the second order rate of change in the log-likelihood (ΔK) was calculated.

C) The DIC values averaged over the ten replicate runs of INSTRUMENT. Standard deviations are indicated by the use of vertical bars. In nearly all number of groups the magnitude of the standard deviations are too small to be seen at this scale.

D) To assess the number of groups (K) supported by the analysis with INSTRUMENT, the second order rate of change in the DIC was calculated (ΔK DIC).

For *M. tanarius* the bar plots for INSTRUMENT K = 2, because it shows the smallest DIC value and for STRUCTURE K = 7, because it shows the highest $L(K)$, are illustrated in Figure 2-13.

Comparing the STRUCTURE and INSTRUMENT bar plots for the non-admixture model in *M. winkleri* in each K, using the best run per K it can be seen that:

-K = 2 Two clear clusters are created, one for Sabah, the other one for Sarawak/Brunei. STRUCTURE and INSTRUMENT give mostly the same result, but individual 4396 (HT4) is assigned with high frequency to Sabah by STRUCTURE and to cluster Sarawak/Brunei by INSTRUMENT.

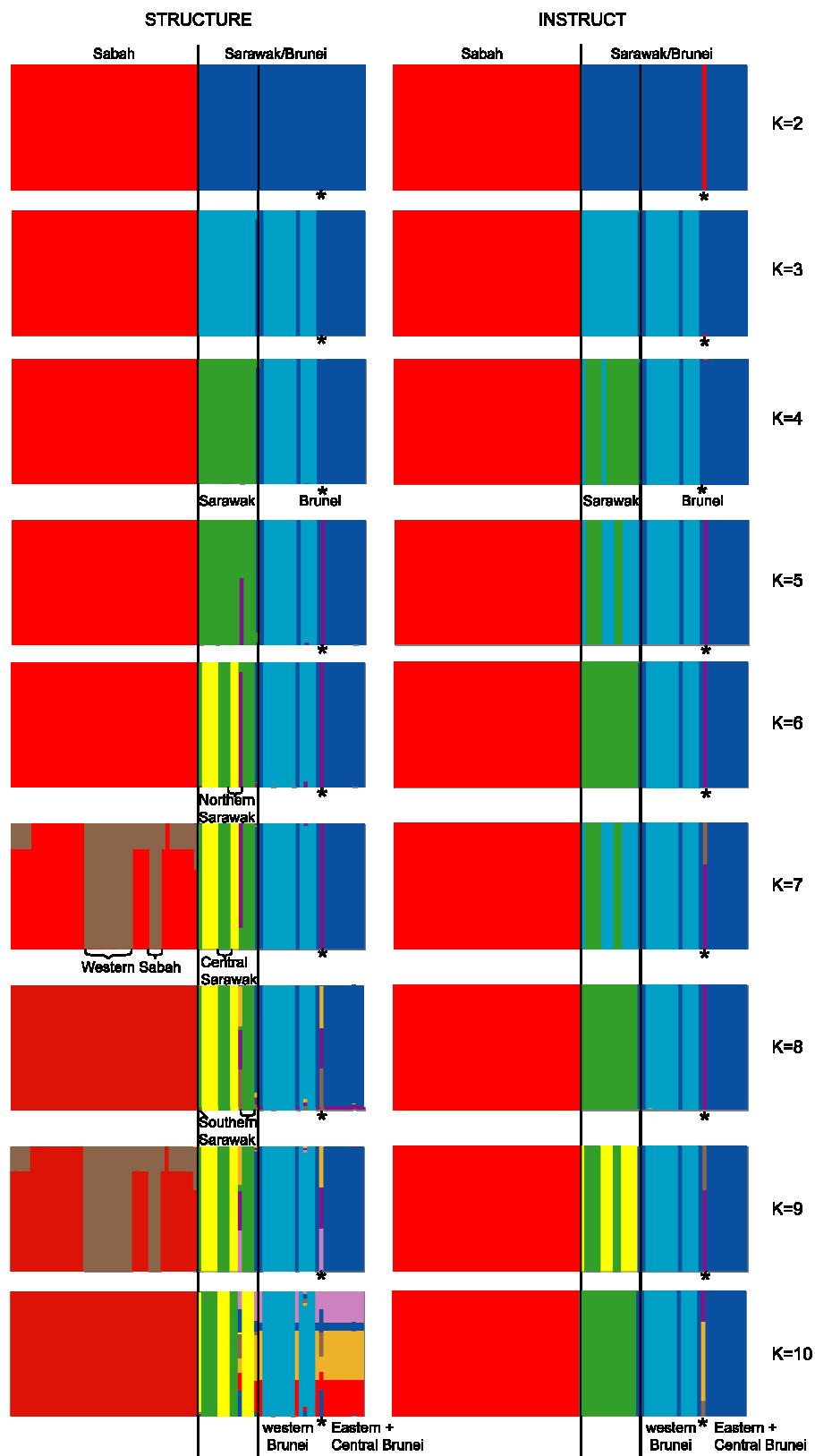


Figure 2-12. *Macaranga winkleri*. The graph represents the bar plot of the run with the highest likelihood of STRUCTURE for a number of populations (K), and the run of INSTRUCT that showed the lowest deviance information criterion (DIC), assuming the non-admixture model. Individuals are in the same order in all bar plots (Appendix I). The * indicates individual 4396 (HT4) from Brunei.

-K = 3 STRUCTURE and INSTRUCT give very similar results, just slightly differing in frequency for some individuals.

-K = 4 INSTRUCT in contrast to STRUCTURE is further subdividing the samples from Sarawak.

-K = 5 both INSTRUCT and STRUCTURE put individual 4396 (HT4) from Brunei in a separate cluster.

-K = 6 STRUCTURE is subdividing the Sarawak population, INSTRUCT is detecting only five populations as it is not detecting the Sarawak subpopulations which it was creating in K = 5.

-K = 7 STRUCTURE further subdivides the Sabah cluster. INSTRUCT gives nearly the same results as for K = 5, only individual 4396 (HT4) is assigned with roughly 30% to a sixth cluster.

-K = 8 STRUCTURE does not subdivide the Sabah cluster and assigns most individuals to five different clusters, individual 4396 (HT4) and individual 6566 from Northern Sarawak (Lambir) are assigned approximately equally to each of three remaining clusters. For INSTRUCT the same five populations are detected as for K = 6 (INSTRUCT).

-K = 9 STRUCTURE gives mostly the same results as for K = 8 only that the subdivision of the Sabah cluster which was shown in K = 7, and lost in K = 8 is again detected. INSTRUCT gives a very similar result to K = 7, detecting mainly five populations. Individual 4396 (HT4) is assigned with roughly 60% to a sixth cluster and with 40% to a seventh cluster, that is to say that two clusters are completely empty.

-K = 10 assigns individuals with high percentage to four clusters. Many individuals of Brunei are assigned with equal probability to another four clusters. Individual 4396 (HT4) and individual 6566 from Northern Sarawak (Lambir) are assigned to the latter plus another one. So in total nine clusters are created by STRUCTURE. INSTRUCT puts the individuals in mostly four clusters. Individual 4396 (HT4) is put into another three clusters, so in total seven clusters are created.

Both STRUCTURE and INSTRUCT put each of the 80 Bornean *M. tanarius* individuals with approximately the same frequency into the number of assumed clusters (Figure 2-13). This is indicative of a group with little or no genetic differentiation, that is, only one major cluster.

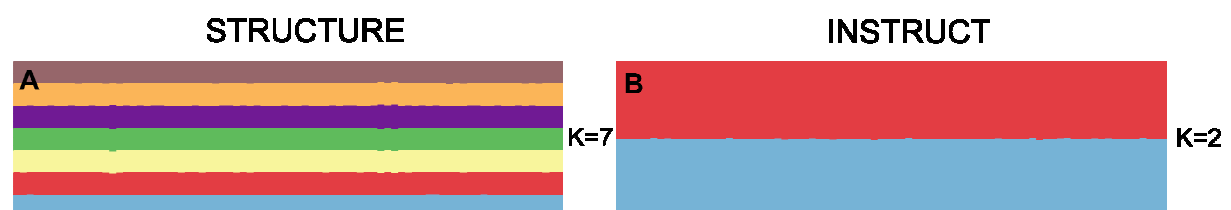


Figure 2-13. *Macaranga tanarius*. Assuming no admixture. Exemplarily chosen bar plots of K for: A) the highest L(K) and B) the smallest DIC value.

Table 2-6. Intra-population genetic diversity values for *M. winkleri*, *M. tanarius* and *M. winkleriella*, distinguishing Sabah from Sarawak/Brunei rarefied for a sample size of 11.

Species	Population	N ¹	A ²	P ³	N_e ⁴	R_h ⁵	H_e ⁶
<i>M. winkleri</i>	Sabah	46	8.0	8.0	3.69	3.16	0.74
	Sarawak/Brunei	41	22.0	22.0	10.57	7.28	0.93
	Mean:	43	15.0	15.0	7.13	5.21	0.84
<i>M. tanarius</i>	Sabah	66	4.0	3.0	1.10	0.50	0.09
	Sarawak/Brunei	11	1.0	0.0	1.00	0.00	0.00
	Mean:	39	2.5	1.5	1.05	0.25	0.04
<i>M. tanarius</i> *	Sabah	66	5.0	4.0	1.13	0.67	0.12
	Sarawak/Brunei	11	1.0	0.0	1.00	0.00	0.00
	Mean:	39	3.0	2.0	1.07	0.33	0.06
<i>M. winkleriella</i>	Mulu (Sarawak)	13	3.0	3.0	1.86	2.00	0.50

¹ Sample size in each population.

² Number of haplotypes detected in each population.

³ Number of private haplotypes, (= haplotypes that occur only in one region).

⁴ Effective number of haplotypes (inverse probability that 2 randomly chosen haplotypes are identical).

⁵ Haplotypic richness (= number of haplotypes expected in each population for a rarefied sample size, here, i.e. the size of the smallest population of the dataset).

⁶ Genetic diversity (Nei's index of genetic diversity (H_e) estimated without bias (Nei, 1973) ranging from zero (no diversity) to one, presents the amount of the diversity within each population.

* Indicates that microsatellite information was included.

Table 2-7. Intra-population genetic diversity values for *M. winkleri* and *M. tanarius* distinguishing samples west and east of the Crocker Range (the haplotypic richness was rarefied for a sample size of 28).

Species	Population	N ¹	A ²	P ³	N_e ⁴	R_h ⁵	H_e ⁶
<i>M. winkleri</i>	West of Crocker Range	44	23.0	22.0	11.52	15.75	0.93
	East of Crocker Range	43	8.0	7.0	3.62	5.26	0.74
	Mean:	44	15.5	14.5	7.57	10.50	0.84
<i>M. tanarius</i> *	West of Crocker Range	49	4.0	3.0	1.13	1.71	0.12
	East of Crocker Range (Sabah)	28	2.0	1.0	1.07	1.00	0.07
	Mean:	39	3.0	2.0	1.10	1.36	0.10

* Indicates that microsatellite information was included.

2.2.6 Analysis of molecular variance

Discerning the regions Sabah and Sarawak/Brunei for the *M. winkleri* samples, 81% of the variation are detected among these two regions in *M. winkleri* and 19% within these regions, ($P = 0.001$). When the same two regions in *M. tanarius* are discerned, no significant result can be obtained, but all the haplotypic variation is found in western Sabah.

For *M. winkleri* individuals west and east of the Crocker Range the percentage of molecular variation detected among the populations was 75% and 25% within the populations ($P = 0.001$). Discerning three populations of *M. winkleri* along the administrative borders, i.e. Sabah, Sarawak and Brunei, 83% of the variation was detected among the populations and 17% within the populations ($P = 0.001$).

2.2.7 Haplotype and nucleotide diversity analysis

To better analyse the intra-population diversity, several genetic diversity metrics were calculated using Haplotype analysis v1.05. These metrics are summarized in Table 2-6 and Table 2-7 and are further described in this section.

For *M. winkleri* 22 haplotypes are detected for the Sarawak/Brunei population and eight haplotypes for the Sabah population. All of the haplotypes for *M. winkleri* are private haplotypes (22 for Sarawak/Brunei and eight for Sabah). For *M. tanarius* one haplotype was found in Sarawak/Brunei, while four haplotypes are detected in Sabah, three of which are private.

For *M. winkleri* the effective number of haplotypes is 10.57 for Sarawak/Brunei. This is roughly three times the effective number of haplotypes for Sabah, 3.69. Conversely, the effective number of haplotypes for *M. tanarius* is similar in both Sarawak/Brunei, 1.00, and Sabah, 1.10.

The mean value of the haplotypic richness (R_h), rarefied for a sample size of 11, is 5.21 in *M. winkleri*, while for *M. tanarius* it is 0.25 (Table 2-6). The unbiased genetic diversity index (Nei 1973) presents the amount of genetic diversity within each population ranging from 0 (= no variation) to 1. Total genetic diversity for *M. winkleri* (0.80) is 16 times the value of *M. tanarius* (0.05).

In order to distinguish regional haplotypic richness individual calculations were performed for both Sabah and Sarawak/Brunei for *M. winkleri* these are 3.16 and 7.28, respectively. The same regional calculation was performed for the *Crematogaster msp.* 8 sequence data (Braasch 2008). The haplotypic richness was 3.18 in Sabah and 9.04 in Sarawak/Brunei. Considering genetic diversity west and east of the Crocker Range (Table 2-7), the rarefied haplotypic richness for *M. winkleri* is approximately two and a half times west compared to east of the mountain range, while in *M. tanarius* the values are in a similar range west and east of the Crocker Range.

Table 2-8. Intraspecific values for haplotype and nucleotide diversity for all *M. winkleri*, *M. tanarius* and *M. winkleriella* samples. These values were also calculated for *M. tanarius* with only Borneo, for *M. winkleri* with only Sabah and for *M. winkleri* with only Sarawak/Brunei.

Species	Samples	Hd	π [%]	Category of Hd #	Category of π #	Interpretation #
<i>M. winkleri</i>	all individuals	0.914 (± 0.015)	0.520 (± 0.022)	High Hd	High π	1
<i>M. tanarius</i>	all individuals*	0.449 (± 0.058)	0.065 (± 0.010)	Low Hd	Low π	2
<i>M. winkleriella</i>	all individuals	0.385 (± 0.132)	0.021 (± 0.007)	Low Hd	Low π	2
<i>M. tanarius</i>	only Borneo*	0.167 (± 0.056)	0.010 (± 0.003)	Low Hd	Low π	2
<i>M. tanarius</i>	only Borneo	0.074 (± 0.040)	0.004 (± 0.002)	Low Hd	Low π	2
<i>M. winkleri</i>	only Sabah	0.745 (± 0.031)	0.063 (± 0.007)	High Hd	Low π	3
<i>M. winkleri</i>	Sarawak / Brunei	0.928 (± 0.026)	0.358 (± 0.018)	High Hd	Low π	3

Categories and implications (#) after Lowe et al. (2004): Haplotype and nucleotide diversity is low if < 0.5 and high if > 0.5 .

Behind the values in brackets the standard deviation is shown.

Asterisk indicates that microsatellite information was included. Numbers in column "Interpretation" are deciphered below the table.

Hd = haplotype diversity

π = nucleotide diversity

1. Large stable population with long evolutionary history. Secondary contact between differentiated lineages.
2. Recent population bottleneck. Founder effect with single or few organelle lineages.
3. Bottleneck followed by rapid population growth and mutation accumulation.

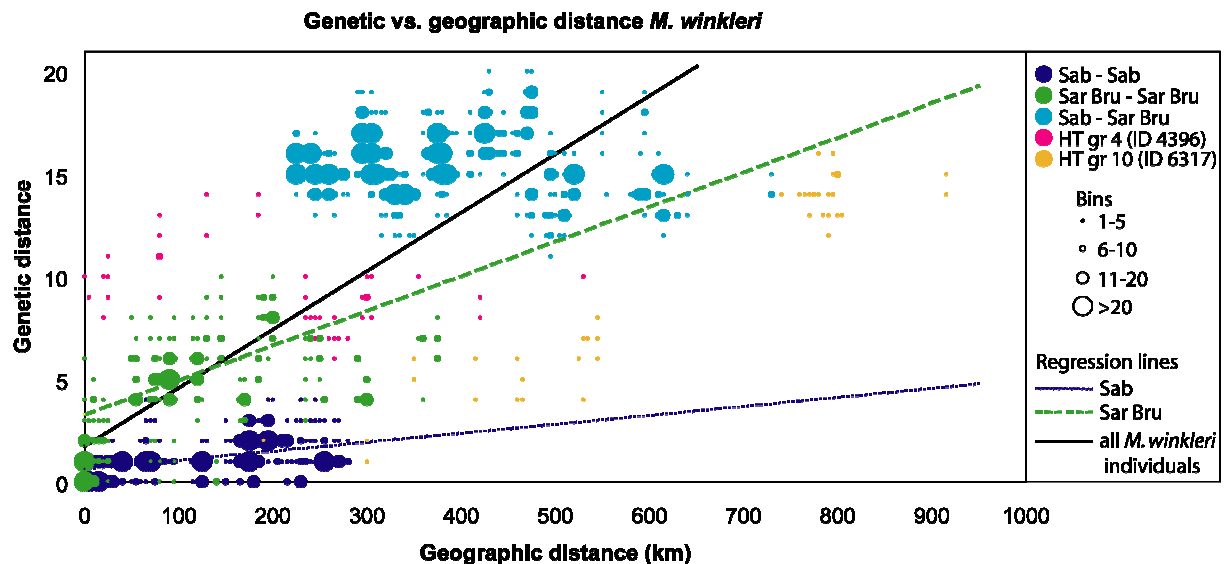


Figure 2-14. Plot of genetic vs. geographic distance. Each dot represents one individual of *M. winkleri*. The lines are results of regression analyses. This figure illustrates a combination of a histogram and a scatter plot. Each point in the scatter plot represents one bin of size five along the geographical distance axis and the size of each point is determined by the number of pairwise comparisons in the corresponding bin as specified in the legend.

Abbreviations in the legend as follows: Sab = Sabah, Sar = Sarawak, Bru = Brunei, HT gr = Haplotype group, w = west, e = east.

Haplotype diversity (Hd) and nucleotide diversity (π) were calculated in DnaSP for *M. winkleri*, *M. winkleriella*, and *M. tanarius*. In both measurements, *M. winkleri* has the largest genetic diversity and *M. winkleriella* the smallest (Table 2-8).

When considering only the samples from Borneo, to which *M. winkleri* is endemic, Hd is five times higher in *M. winkleri* than in *M. tanarius* (including the microsatellite information), while π is 50 times higher.

The haplotype and nucleotide diversity is categorized as either low or high, which then allows for the assigned interpretation of the population history, according to Lowe (2004,p. 173). Both categorizations as well as the corresponding interpretation are shown in Table 2-8.

2.2.8 Analysis of spatial genetic correlation

The Mantel test for all samples of *M. winkleri* (Figure 2-14) shows a positive correlation. The coefficient of determination is $R^2 = 0.540$ and the correlation coefficient is $R = 0.735$ between geographic and genetic distance. The probability that there is no relation between the matrices using 9,999 random permutations is $P < 0.001$. Considering only the *M. winkleri* individuals west of the Crocker Range, the correlation between geographic and genetic distance is positive ($R^2 = 0.346$; $R = 0.588$; $P < 0.001$). *Macaranga winkleri* individuals east of the Crocker Range also show a positive correlation between geographic and genetic distance ($R^2 = 0.163$; $R = 0.404$, $P < 0.001$).

The Mantel test for the Bornean individuals of *M. tanarius* shows no significant correlation ($P = 0.272$). When the *M. tanarius* individuals from Malay Peninsula, Java, Sumatra and Australia are included, the Mantel coefficient of determination is $R^2 = 0,782$ ($R = 0.884$) and the probability is $P < 0.001$ (Figure 2-15).

The use of relative sizes (based on frequency analysis) in the scatter plot helps to better understand the calculated regression lines. The larger sized points represent a weighting in the regression analysis of multiple data couples having with the same relationship between geographic and genetic distance.

When visualized in this way, these weighting clusters clearly illustrate the nature of the slope of the regression line. Otherwise, what are clearly statistical outliers would appear equally weighted with higher density data, and it would not be clear visually why these appear to be ignored by the regression analysis.

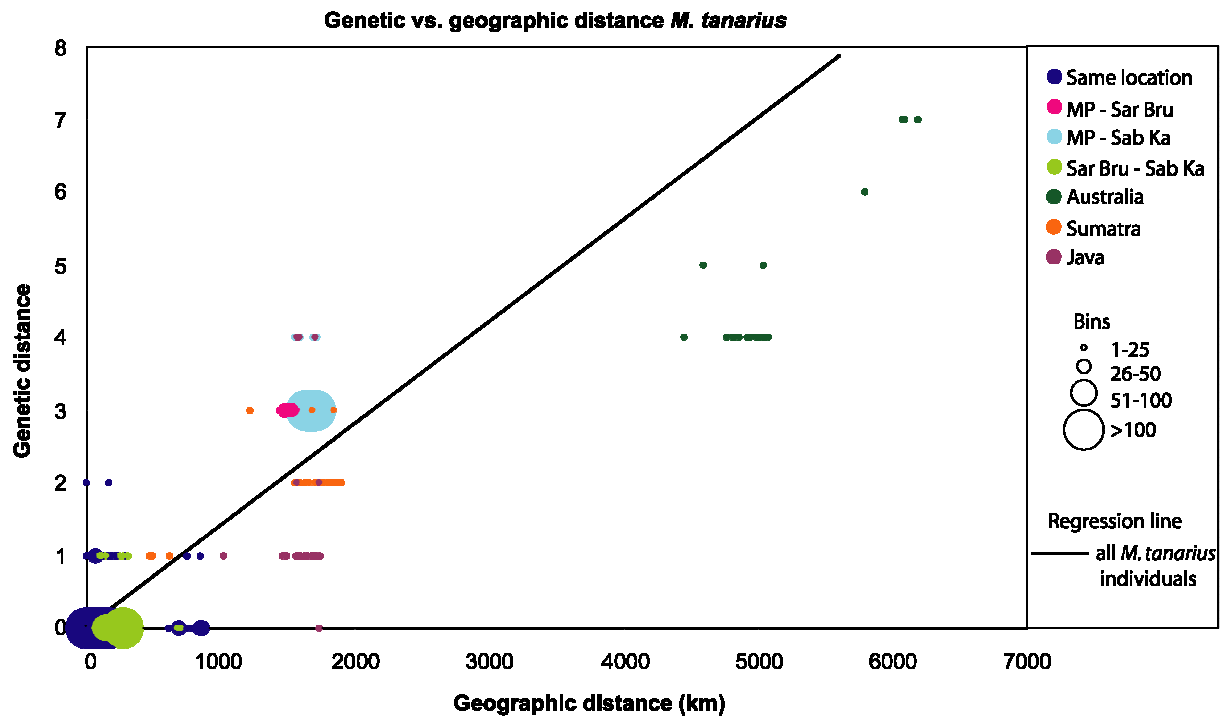


Figure 2-15. Plot of genetic vs. geographic distance for *Macaranga tanarius*. Each dot represents one individual of *M. tanarius*. Individuals from Sumatra, Java, Malay Peninsula and Australia are included. The line is the regression line. This figure is a combination of a histogram and a scatter plot to better illustrate the large number of comparisons with the same relationship between geographic and genetic distance. Each point in the scatter plot represents one bin of size ten along the geographical distance axis and the size of each point is determined by the number of pairwise comparisons in the corresponding bin as specified in the legend.

Abbreviations in the legend as follows: MP = Malay Peninsula, Sab = Sabah, Ka = Kalimantan, Sar = Sarawak, Bru = Brunei.

2.3 Discussion of the chloroplast data

The aim of the study is to test the hypotheses of a limited effective seed dispersal ability of *M. winkleri* due to the dependence on the ant, and good seed dispersal abilities of *M. tanarius*, which does not depend on an ant partner. Therefore a more pronounced population structure is expected for myrmecophytic *M. winkleri* than for non-myrmecophytic *M. tanarius*. Geographic barriers are expected to act stronger on the myrmecophytic species, due to its limited dispersal ability. For *M. winkleriella*, sister species of *M. winkleri*, low levels of genetic diversity are expected, due to its restricted occurrence. In order to evaluate the validity of the hypotheses phylogeographic analyses, analyses of genetic diversity and of spatial genetic correlation were conducted based on DNA sequences of three chloroplast regions.

2.3.1 Phylogeography of *Macaranga winkleri*

Macaranga winkleri is a myrmecophytic pioneer species. Both *M. winkleri* and its obligate partner ant, *Crematogaster* msp. 8, are endemic to Borneo. Chloroplast DNA gives valuable information concerning gene flow by seeds (Demesure et al. 1996). Therefore the distribution of the chloroplast haplotypes reflects the gene flow via seed dispersal for *M. winkleri*. Birds and small mammals are described as presumable primary dispersal agents in the genus *Macaranga* (Bänfer et al. 2006, Weising et al. 2010). As the species has small seeds with a violet aril, bird dispersal can be expected. This may result in long-distance dispersals, although these would be rare events, as the seed passage through the intestinal tract of birds is quite fast. Seeds remain in a bird for only few hours or at most a few days (Cruden 1966).

To test the hypothesis of a limited effective dispersal ability due to the dependence on the ant partner, (hypothesis 1, chapter 1.2) in *M. winkleri*, the geographic distribution of the chloroplast haplotypes (Figure 2-6) was analysed. It shows that identical haplotypes occur in the same geographical region. This is in accordance with the hypothesis and can indicate that long distance dispersal of seeds rarely happens. Additionally, it may reflect that long-distance dispersal of the seeds to new areas, where neither the ants nor the plants are present, cannot lead to the establishment of the plant as the colonising ant is missing. This can be explained either by limited dispersal abilities or by philopatric behaviour of the ants (Feldhaar et al. 2010). The authors showed that ant queens rarely disperse over more than a few kilometres.

Genetic differentiation of *M. winkleri* for Sarawak/Brunei vs. Sabah and west vs. east of the Crocker Range

The chloroplast haplotype network of *M. winkleri* (Figure 2-5) shows two groups with a clear split between individuals from Sarawak/Brunei and Sabah. HT group 4 (one individual) from eastern Brunei is found between the two groups, 6 mutational steps away from Sabah and 8 steps from Brunei. In *M. winkleri* no haplotypes are shared between Sabah and

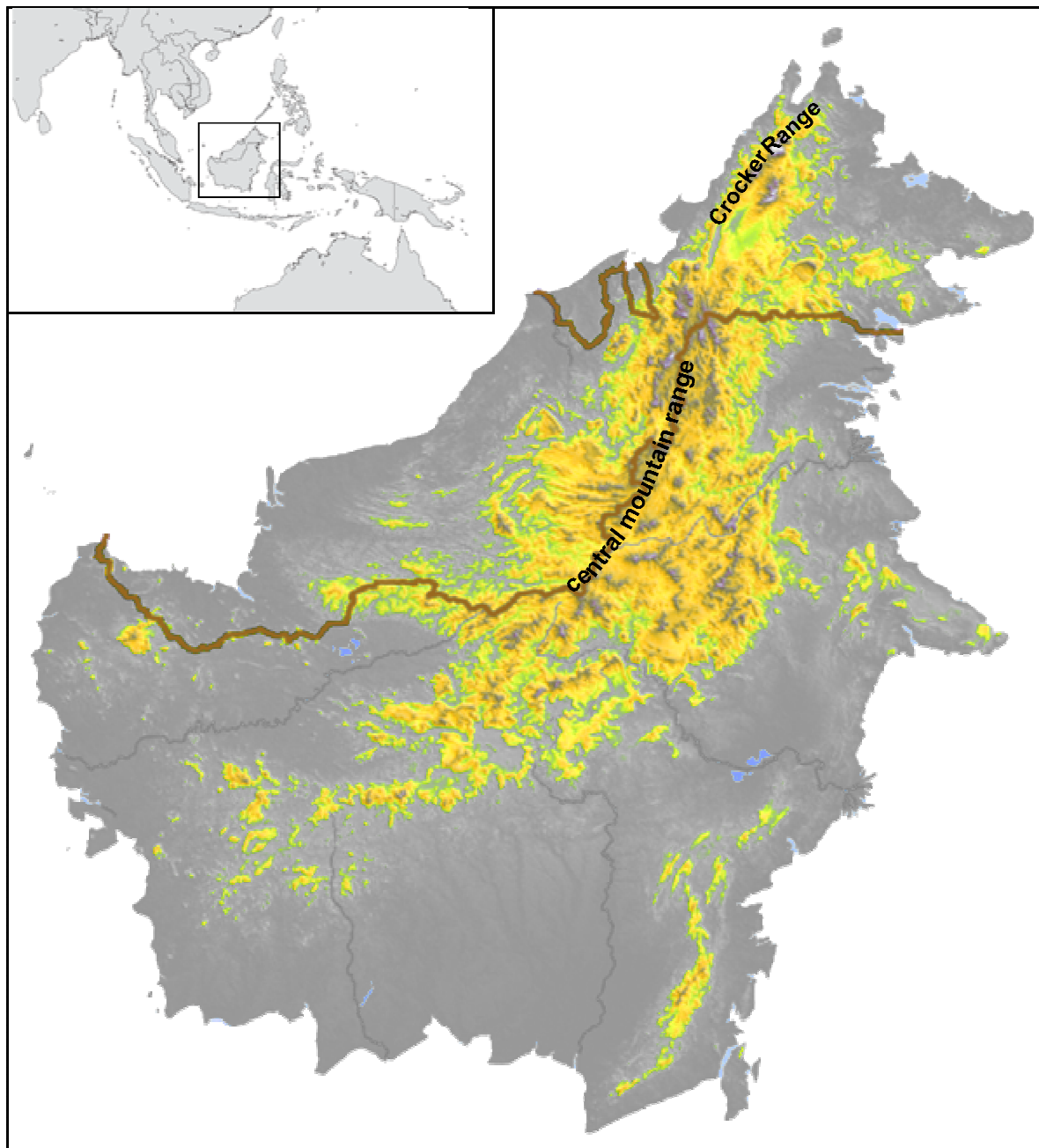


Figure 2-16. Topographical map of the island of Borneo, indicating the central mountain range that separates the island and the Crocker Range to the north, dividing Sabah into a western and eastern part. Map modified after Wikipedia.org.

Sarawak/Brunei, i.e. all haplotypes detected in Sabah are private for this region and all haplotypes detected in Sarawak/Brunei are private for that region. Also the PCoA clearly illustrates this split (Figure 2-8), by showing Sarawak/Brunei and Sabah as two distinct groups. The intermediate position of HT group 4 in the chloroplast network is also obvious in the results of the PCoA, as it is detected between the two groups. The high differentiation between the two groups is reflected by the results of the AMOVA, in which 81% of the differentiation in *M. winkleri* is detected between the individuals of Sabah and those of

Sarawak/Brunei, while within these groups only 19% of differentiation was detected. Accordingly, the results of the assignment analysis using both STRUCTURE and INSTRUCT clearly indicate these two groups, Sarawak/Brunei and Sabah. The intermediate state of HT group 4 becomes again obvious as this individual is assigned to Sarawak/Brunei by STRUCTURE and to Sabah by INSTRUCT for $K = 2$.

Within the regions, the geographic distribution of the haplotypes (Figure 2-6) suggests isolation by distance effects, as identical haplotypes are found almost exclusively in the same geographic regions. Furthermore a Mantel test was performed to check for spatial genetic correlation for individuals of Sarawak/Brunei vs. Sabah. It resulted in both significant and positive correlations, ($R = 0.588$, $R = 0.404$, respectively). Cohen (1988) categorized the power of the correlation coefficient R as follows: “none” (0.0 to 0.09), “small” (0.1 to 0.3), “medium” (0.3 to 0.5) and “large” (0.5 to 1.0). Following this categorization, the correlation of geographic and genetic distance in *M. winkleri* in Sarawak/Brunei is large, while it is medium for Sabah. Thus, for both groups a clear effect of isolation by distance can be detected, with the genetic decline by distance being higher in Sarawak/Brunei than in Sabah. Furthermore the Mantel test indicates isolation between these two groups, as shown by the regression line for all *M. winkleri* individuals (Figure 2-14), which has the largest relationship between geographic and genetic distances (i.e. the highest slope). This means that for the same geographic distance, two individuals from different groups will have a larger expected genetic distance than two individuals from the same groups.

Taken together, each of these analyses for *M. winkleri* indicates a strong genetic differentiation between the groups. In this context the results can further indicate that *M. winkleri* has been evolving separately in both regions for a long time, and that intermediate states have become extinct.

As already discussed the biogeography of plants and animals on Borneo is strongly influenced by a range, which runs to the Crocker Range in the north (Figure 2-16). The central mountain range forms a dispersal barrier for the lowland flora and fauna (Cannon & Manos 2003, Slik et al. 2003, Moyle et al. 2005, Bänfer et al. 2006, Raes et al. 2009). Therefore, it was also analysed whether the Crocker Range is a geographic barrier for *M. winkleri* dividing the individuals in those west and east of the mountain range. Division of the samples of *M. winkleri* into individuals west and east of the Crocker Range results in 22 private haplotypes out of 23 haplotypes in total for the samples west and seven private haplotypes out of eight haplotypes for the samples east of the mountain range. Thus, the separation indicated for the groups Sarawak/Brunei vs. Sabah is more pronounced than for the groups on either side of the mountain range. This is in accordance with the results of the AMOVA. The level of molecular variance among individuals from Sarawak/Brunei vs. Sabah is slightly higher than for the *M. winkleri* individuals west and east of the Crocker Range (81% and 75%, respectively), not indicating the mountain range as a primary barrier to dispersal.

Taken together, the genetic differentiation detected for the groups Sarawak/Brunei vs. Sabah is stronger than for individuals west and east of the Crocker Range, suggesting this to be an

older genetic separation of *M. winkleri*. The Crocker Range, thus, could not be shown to be a strong barrier to dispersal, as hypothesised (hypothesis 7, chapter 1.2).

The split within *M. winkleri* between Sarawak/Brunei and Sabah may be due to fragmentation into two (or more) separate refugia during arid periods of the Pliocene. When better conditions resumed, the subpopulations again expanded, but have not yet been in genetic exchange, as indicated by the fact that the haplotypes are private for these two regions. This can be explained by a low effective speed of colonisation via seed. *M. winkleri* does not occur in the southwestern part of Sabah (personal communication by Brigitte Fiala, and personal observation), probably due to anthropogenic deforestation during the last century. Therefore, gene flow among *M. winkleri* from the subpopulations Sarawak/Brunei and Sabah is probably limited. Between Sabah and Sarawak/Brunei there is a high number of missing intermediate haplotypes, which could reflect haplotypes that became extinct due to anthropogenic deforestation. However, it seems improbable that this large number of missing intermediates is only a reflection of the relatively recent deforestation. Since no intermediate haplotypes were detected, even in proximity of the deforested area, an older separation of the two groups is suggested. The identical chloroplast haplotype detected in *M. winkleri* on both sides of the mountain range can be explained by a refugium in Sabah, located in or near the Crocker Range and the species spreading out to both sides of the range.

However, due to the low abundance of *M. winkleri* in Sabah west of the Crocker Range, only three samples from this region were included in the analyses. This low number is limiting the informative value of the comparison of the genetic differentiation between the groups Sabah vs. Sarawak/Brunei and individuals west and east of the Crocker Range.

Two colonisation scenarios for *Macaranga winkleri*

The chloroplast haplotype network of *M. winkleri* and *M. winkleriella* allows for two different putative biogeographic histories of the species:

(i) The putative root of the chloroplast haplotype network (indicated by the * in Figure 2-5), suggests this position to be the ancestral one in *M. winkleri*. However, the position of the root is not certain. In statistical parsimony network analyses, the reliability of the method drops with genetic distances and especially with missing intermediates (Woolley et al. 2008). Between *M. winkleri*, *M. winkleriella* and the outgroup, a high number of mutational steps in the form of missing intermediates were detected, decreasing the reliability. Assuming that interior positions in the network represent ancestral haplotypes while tip positions represent derived haplotypes (Castelloe & Templeton 1994) and considering the putative root of the network, the ancestral haplotypes are detected in Sarawak/Brunei, while the more derived ones are detected in Sabah. The spatial distribution of the chloroplast haplotypes together with their positions in the haplotype network suggest a stepwise colonisation of Borneo from the southwest to the northeast, more detailed from southern and central Sarawak to northeastern Sarawak, then to Brunei, from there to western Sabah, then to Central Sabah and from there to

eastern Sabah. Congruently, Bänfer et al. (2006) inferred a migration for the *kingii* group of *Macaranga* from northeastern Sarawak to eastern Sabah.

The haplotypes are geographically confined, with one exception, HT group 11 (northeastern Sarawak), which is genetically closest to HT group 9 (central Sarawak). This can be explained by long distance dispersal from central Sarawak. In Sabah the haplotype and nucleotide diversity is lower than in Sarawak/Brunei. This is in accordance with the fact that the haplotypes in Sabah are the more derived and younger ones, and populations did not have as much time as in Sarawak/Brunei to accumulate genetic differences. This is further shown in the haplotypic richness, when calculated for Sabah it is only 3.16, while it is approximately two and a half times larger (7.28) in Sarawak/Brunei.

This contradicts the hypothesis of a higher genetic diversity for Sabah compared to Sarawak/Brunei due to the persisting rain forest in Sabah (hypothesis 9, chapter 1.2). A possible explanation could be that the species, which occurs in gaps in primary forest, did not have many suitable habitats (as no gaps or open areas were created during drier phases), and thus had a small population size in Sabah.

(ii) Another putative position of the root of the chloroplast haplotype network (indicated by the *2 in (Figure 2-5) was inferred using the neighbor-joining cluster algorithm. In this case the root is located between individuals from Sabah and Sarawak/Brunei. This location of the root can indicate an early fragmentation of individuals from Sabah and Sarawak/Brunei. In this scenario the chloroplast haplotype network suggests the existence of one (or two) refugia for *M. winkleri* located in Sabah and four refugia in Sarawak/Brunei. The retreat of *M. winkleri* into refugia was probably caused by the fragmentation of the rainforest during arid periods in the Pliocene (Morley 2000, Inger & Voris 2001, Quek et al. 2007). When preferable conditions resumed, the species began spreading out anew from their refugia. The small number of haplotype groups and the close genetic relatedness of the latter in Sabah suggest that only a small number of individuals, and thus a small number of chloroplast haplotypes survived in one or two refugia. However, according to Gathorne-Hardy et al. (2002), Sabah was persistently covered with rain forest. For *M. winkleri* in Sarawak/Brunei the chloroplast haplotype network shows more differentiation, but each haplotype group was detected on a smaller scale than for Sabah. The chloroplast haplotype network suggests the existence of four refugia in Sarawak/Brunei for *M. winkleri*: one in central/southern Sarawak (HT group 9 and 10), one in northeastern Sarawak (HT group 7), one in western Brunei (HT group 8) and one in eastern Brunei (HT group 5). In Sarawak/Brunei a high number of missing intermediate steps were detected. Missing intermediates can either be haplotypes that were not sampled, or haplotypes that went extinct. Between HT groups 5, 7 and 8 the sampling is geographically dense, thus, it is more probable that the species went through a genetic bottleneck and these chloroplast haplotypes became extinct. The high haplotype diversity of *M. winkleri* (0.928) together with the low nucleotide diversity (0.358%), as categorized by Lowe et al. (2004), in Sarawak/Brunei reflects a rapid population growth, with mutation accumulation after the genetic bottleneck. The haplotype groups detected in central

and southern Sarawak (HT group 9 and 10) are separated from the haplotype groups northeast of it by huge deforested areas with plantations, where the species does not occur any more. This may explain the missing intermediates in the chloroplast haplotype network between these groups.

In Sabah only one missing intermediate was detected, indicating a dense sampling and a continuous presence of the species in this region. The value for the haplotype diversity in Sabah (0.745) is smaller than in Sarawak/Brunei, but still clearly categorized as high. In combination with the low nucleotide diversity (0.063%), a genetic bottleneck can be assumed to have also occurred in Sabah, according to Lowe et al. (2004).

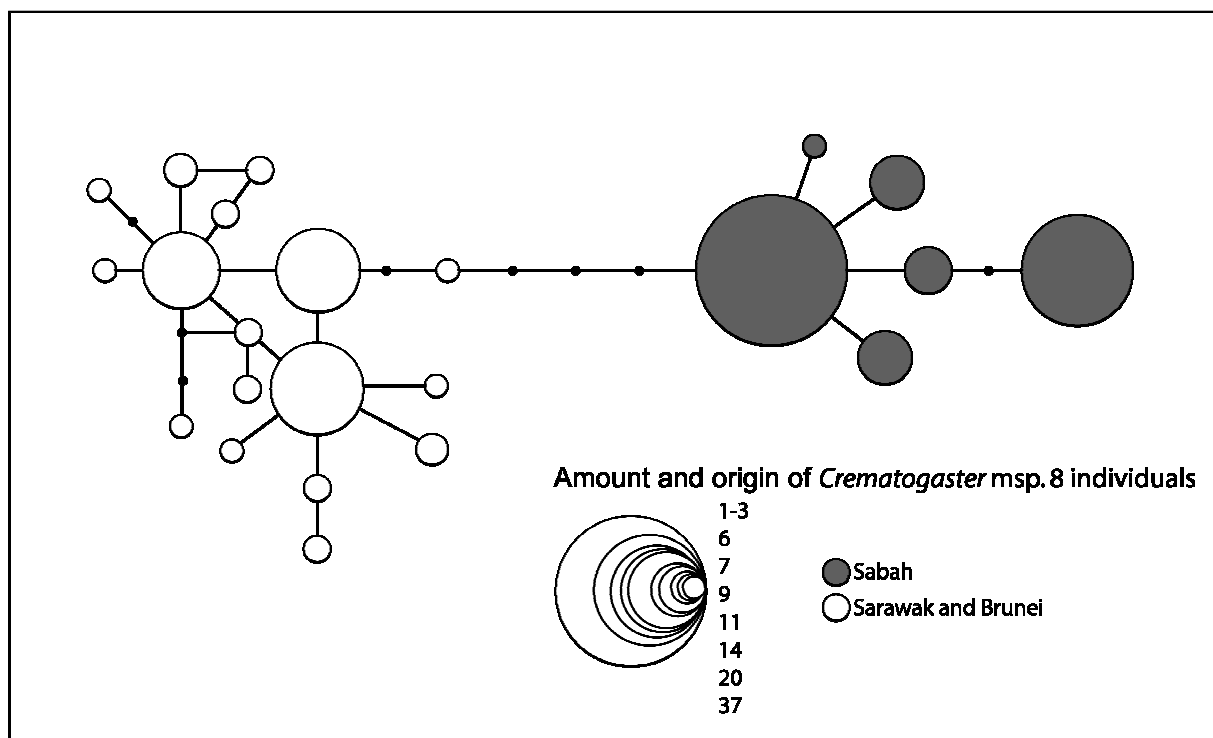


Figure 2-17. *Crematogaster* msp. 8 haplotype network calculated with TCS of 135 sequences of mitochondrial DNA redrawn and modified after Braasch (2008). The circle size is representative of the number of individuals in which the haplotype was found. Black dots present missing intermediates.

Macaranga winkleri and its specific ant

In Sabah for *M. winkleri* only three haplotype groups (comprising eight haplotypes in 46 samples) were detected, while in Sarawak/Brunei eight haplotype groups (comprising 22 haplotypes in 41 samples) were detected. Similarly, the number of haplotypes detected in *Crematogaster* msp. 8 (Figure 2-17), based on data of Braasch (2008), is much smaller in Sabah (6 haplotypes in 78 samples) than in Sarawak/Brunei (17 haplotypes in 58 samples). For a better comparability, taking the different sample sizes into account, the rarefied haplotypic richness was calculated for *M. winkleri* and its specific ant. The haplotype richness of *M. winkleri* in Sarawak/Brunei is 7.28 and for *Crematogaster* msp. 8 in the same region is

9.04. In Sabah the haplotype richness of *M. winkleri* is 3.16 and for *Crematogaster* msp. 8 it is 3.18. In both the plant and the ant, the same relationship exists between regions with the haplotype richness in Sarawak/Brunei roughly two and a half times the richness found in Sabah. This is an indication that both the *M. winkleri* and *Crematogaster* msp. 8 populations are younger in Sabah than in Sarawak/Brunei. This was contradictory to the expectations of a higher genetic diversity for this region, due to the persisting forest in Sabah during the Pleistocene (Gathorne-Hardy et al. 2002).

Braasch (2008) found that the population of *Crematogaster* msp. 8 showed a clear split between Sabah and Sarawak/Brunei (Figure 2-17). This is in conjunction with its host plant. The smallest mutational distance detected between the *Crematogaster* msp. 8 individuals of Sabah and those of Sarawak/Brunei, is four steps. These four steps correspond to three missing intermediate haplotypes. Accordingly, in *M. winkleri* 5 missing intermediate steps were detected between Sabah and the intermediate HT group 4, and 7 missing intermediate haplotypes between the intermediate group and Sarawak/Brunei. Just as with *M. winkleri*, *Crematogaster* msp. 8 has no haplotypes shared between these regions (Braasch 2008). This can indicate for the ant, as with the plant, that intermediate states have become extinct and that the ant has been evolving separately in both regions for a long time. A strong differentiation between Sabah and Sarawak/Brunei was also detected for *Crematogaster* ants by Feldhaar et al. (2010).

Considering the chloroplast haplotype network of *M. winkleri* it is difficult to decide which colonisation scenario of the species (see page 52) is the more probable. In *M. winkleri* the scenarios were created according to assumptions of two putative positions of the root. For the mitochondrial haplotype network of *Crematogaster* msp. 8 no root was presented, thus, this network does not provide further hints to which scenario is the more probable.

Although *Crematogaster* msp. 8 is highly dependent on *M. winkleri*, the level of genetic structure was less pronounced than in other less host-specific *Crematogaster* ants from the subgenus *Decacrema* (Braasch 2008). This hints towards a better dispersal ability of *Crematogaster* msp. 8, compared with the other ant species. This can be explained by the bigger body size of msp. 8 ant queens in comparison to the ants from subgenus *Decacrema* (Feldhaar et al. 2010), providing better mobility. A positive correlation between body size and flight distances of other insects, was shown by Shirai (1995).

To sum up, Figure 2-5 illustrates the genealogical relationship of the chloroplast haplotypes of myrmecophytic *M. winkleri*, indicating two possible colonisation scenarios for the species under study: (i) suggests a stepwise colonisation of Borneo from the southwest to the northeast and (ii) suggests the spread of the species from one or two refugia in Sabah and four refugia in Sarawak/Brunei. Possibly the retreat of the species into refugia was caused by fragmentation of the rainforest during arid periods of the Pliocene. Both scenarios seem equally probable.

Within both regions west and east of the mountain range isolation by distance was detected, indicating limited seed dispersal distances. This limited dispersal is more evident between

regions west and east of the Crocker Range as shown by the Mantel test. This can indicate that the mountain range acts as a geographic barrier to dispersal.

The results for *M. winkleri* and its specific ant are congruent in showing (i) the split between Sabah and Sarawak/Brunei and (ii) the higher haplotypic richness for Sarawak/Brunei than for Sabah.

2.3.2 Phylogeography of *Macaranga winkleriella*

This species is found growing on limestone in a very narrow distribution range, namely Gunung Mulu National Park in Sarawak (Whitmore 1974). *Macaranga winkleriella* is probably an obligate myrmecophyte type 1 and colonised by msp. 8 of *non-Decacrema Crematogaster* (Fiala et al. 1999).

A low genetic diversity for *M. winkleriella* was hypothesised, (hypothesis 3, chapter 1.3), as small populations are affected more strongly by genetic drift and the chances for new alleles to originate are lower among fewer individuals. The hypothesis is supported by the results, as one haplotype group (two haplotypes), comprising the thirteen *M. winkleriella* individuals, was detected. This is in accordance with studies of Brett and Randall (1995), who showed a small number of haplotypes for a locally endemic species, *Deschampsia mackenzieana* (Poaceae).

The haplotypes of *M. winkleriella* are nine and ten mutational steps away from its sister species *M. winkleri*, specifically *M. winkleri*'s HT group 9 from central Sarawak. The mutational distance for this interspecific relationship is not large, considering that for *M. winkleri* 29 mutational steps were detected on the intraspecific level, which might indicate that they resulted from a more recent split.

To sum up, the individuals of the narrowly endemic *M. winkleriella* included in this analysis comprise a small number of haplotypes (2). They are nine and ten mutational steps away from their sister species *M. winkleri*. A low genetic diversity is also expected for this rare and endemic species.

2.3.3 Phylogeography of *Macaranga tanarius*

Macaranga tanarius is a non-myrmecophytic pioneer tree. It is the most widespread of all species in the genus, ranging from India to China and south through Thailand and throughout Malesia to New South Wales, Australia, and the Solomon islands.

In the chloroplast haplotype network of 100 individuals of *M. tanarius* (Figure 2-3), from Borneo, Malay Peninsula, Sumatra, Java and Australia, only seven haplotypes excluding and 11 haplotypes including the SSR loci were detected. This low number of haplotypes is also reflected by the haplotype diversity of all *M. tanarius* individuals of 0.449, even when the microsatellite information was included. However, it should be noted that this value is on the

border of the high category according to Lowe et al. (2004). The inclusion of the variation in the faster evolving microsatellite regions did yield small levels of genetic subdivision. HT 1 (occurring exclusively in samples from Borneo) was divided into three subhaplotypes and HT 3 (one sample from the west coast of Sabah and one sample from Java) as well as HT 6 (17 samples from Malay Peninsula) into two subhaplotypes each.

Western Sabah is harbouring the highest number of haplotypes per area (HT 1a, 2, 3a, and 4), but the nucleotide diversity is low, as HT 2, 3a and 4 are only one mutational step away from the most widespread HT 1a. This can indicate a rapid population growth from a small founder population, assuming that there has been sufficient time for the recovery of haplotype variation, but too little time to accumulate larger sequence variation (Lowe et al. 2004). This elevated haplotype diversity may have been uncovered in western Sabah due to the more intensive sampling within this region.

For *M. tanarius* a very low genetic differentiation within Borneo was detected. This is shown by the PCoA results (Figure 2-9), where all but three individuals from western Sabah are projected onto the same point (microsatellites excluded). Furthermore the results of STRUCTURE and INSTRUCT (Figure 2-13) reflect this low genetic differentiation, as neither program detects any population structure in the analysed individuals. The low genetic differentiation and the lack of genetic substructure within the samples from Borneo (Figure 2-3 & Figure 2-4) can be indicative for a young age and a rapid extension of the distribution range of the species. Alternatively, the species could have recently undergone a population bottleneck followed by a fast colonisation. This is in accordance with the fact that this species is a non-myrmecophytic species and, thus, independent of the presence of a colonising ant species. This independence facilitates successful dispersal to new areas. Furthermore the sticky and small seeds of *M. tanarius* may stick easily to the fur of mammals and also to feathers, feet and beaks of birds and can thus be efficiently dispersed.

The nucleotide diversity is low (0.010%) for all Bornean *M. tanarius*. One possible reason for low haplotype and nucleotide diversity in Bornean *M. tanarius* could be a lack of variation in the organelle markers used. However, the three chloroplast markers that were used proved to be highly variable in *M. winkleri*. The *ccmp 5* marker was also variable in other *Macaranga* species analysed (Vogel et al. 2003). Therefore the markers should reflect the true situation of low haplotype and nucleotide diversity in this species.

In the chloroplast haplotype network of *M. tanarius* four missing haplotypes were inferred. Missing haplotypes can indicate an extinct or ancestral haplotype, or a haplotype, that was not sampled. Only one missing haplotype was detected between the most common haplotype found on Borneo and the Sumatran haplotype. Three missing haplotypes were detected between Borneo and Australia, which is not surprising as no additional samples of the geographic region in between were included. The haplotypes of the neighbouring islands, Java and Sumatra, are both two mutational steps away from HT 1a. The largest mutational distance that was detected in the chloroplast haplotype network of 100 *M. tanarius* individuals, is only eight steps and was detected between individuals from Malay Peninsula and an Australian

individual (~5,000 km distance). The mutational distance from the main Bornean HT 1a to the Australian haplotype is only 4 mutational steps over a distance of ~3,500 km. Between Borneo and Malay Peninsula 3 and 4 mutational steps were detected on a geographic distance of ~1,600 km.

Genetic differentiation of *M. tanarius* individuals from Borneo and Malay Peninsula

From Borneo to the Malay Peninsula, *M. tanarius* exhibits 3 and 4 mutational steps, indicating a high genetic differentiation compared with the other geographic distances in the chloroplast haplotype network (see above). This is in accordance with the hypothesised high genetic differentiation between individuals from Malay Peninsula and Borneo (hypothesis 8, chapter 1.2) and fits with the findings of Bänfer et al. (2006), who detected a clear separation for the *Macaranga* section *Pachystemon* between Malay Peninsula, Sabah and Sarawak/Brunei. Also Feldhaar et al. (2010) detected genetic differentiation among populations of Malay Peninsula and Borneo for *Crematogaster* ants. The strong genetic differentiation between Borneo and Malay Peninsula can be explained by vicariant evolution between the island and the mainland, which may correlate with the Pliocene fragmentation of the Sunda block (Gorog et al. 2004).

The Crocker Range - a geographic barrier for *Macaranga tanarius* ?

To test the hypothesis of the Crocker Range acting as a geographic barrier (hypothesis 7, chapter 1.2) for *M. tanarius*, the haplotypic richness (rarefied for the sample size) for individuals west and east of the mountain range was calculated. In *M. tanarius* the haplotypic richness is higher west than east of the mountain range (1.7 and 1.0, respectively), but still in a similar range suggesting that the species has occurred for a similar amount of time on either side of the range. West of the range, three private haplotypes were detected, and one east of the range. Taking into account the generally low haplotype diversity in this species, this indicates a certain amount of genetic differentiation. However, the haplotypes detected west and east of the range are genetically highly similar (the one private haplotypes east of the range is only different in one fast evolving microsatellite region from the most common haplotype), and no indications for long-term independent evolution were detected. This contradicts the hypothesis of the Crocker Range as a long-term barrier to gene flow. In contrast to this result, Guicking et al. (2011) detected in *M. gigantea* indications for long-term independent evolution.

Possible colonisation route for *Macaranga tanarius*

Assuming that interior positions in the network represent ancestral haplotypes, while tip positions represent derived haplotypes, the indicated origin of the chloroplast haplotypes for the analysed data set of *M. tanarius* is in Borneo.

The chloroplast haplotype network can indicate a colonisation route of the species from northern Borneo to Sumatra and from there to Malay Peninsula, while Java was also colonised from Borneo. These patterns can be explained by migration across land connections. During Pleistocene cold cycles land bridges existed (Morley 2000, Cannon et al. 2009, Woodruff 2010), as the glacial cycles caused sea levels to drop repeatedly (see geological history of the Sunda Shelf in the Introduction). However, it cannot be determined whether the inclusion of further samples, either from the regions of the distribution area that are not included or from the regions presented with only one sample, would change the network arrangement. For example, tip positions may become inner positions, changing the assumed origin of the chloroplast haplotypes, and thus the colonisation routes of *M. tanarius*.

Pioneer tree habit of *Macaranga tanarius*

Pioneer species have unique life histories and population structures. They are often characterized as showing early and frequent flowering and the production of small and easily dispersed seeds (Swaine & Whitmore 1988).

This is in accordance with *M. tanarius*, which flowered for the first time after only three years in the greenhouse (personal observation). In Whitmore (2008), *M. tanarius* is said to be flowering frequently throughout the year and producing small fruits. In addition, the nature of the *M. tanarius* seeds lends itself to efficient long-distance seed dispersal by birds and small mammals.

The seed germination of tropical rainforest pioneer trees such as *M. tanarius* is triggered by an increase in red light or the strongly fluctuating temperature of soil exposed to full sunlight for part of the day (Swaine & Whitmore 1988). Thus, both triggers are provided by gap creation. Also for seedling establishment and growth, pioneer trees require full sunlight (Swaine & Whitmore 1988). That is why pioneer trees are found in openings in the forest or in other open areas. As a consequence of logging, road building and other human activities, pioneer trees have become more abundant in many tropical landscapes (Guicking et al. 2011).

Two contrasting models have been set up to explain the genetic structure of pioneer species. Wright (1940) postulated a strong population substructure due to the usually small number of individuals which colonise new areas, while Slatkin (1985) postulated reduced differentiation among populations due to elevated rates of gene flow by frequent local extinction and recolonisation. The low level of genetic structuring of *M. tanarius* is consistent with previous studies on tropical pioneer trees (Alvarez-Buylla & Garay 1994, Muloko-Ntoutoume et al. 2000, Cavers et al. 2005) thus favouring Slatkin's hypothesis and the good seed dispersal abilities hypothesised in this study (hypothesis 4, chapter 1.2). Cavers et al. (2005) for example detected only two chloroplast haplotypes in 101 individuals in the tropical pioneer tree *Vochysia ferruginea* (Vochysiaceae) in Costa Rica in a range of ~350 km.

To sum up, Figure 2-3 illustrates the genealogical relationship of the chloroplast haplotypes of non-mymecophytic *M. tanarius*, indicating a young age of the species and a rapid spread of

the distribution range or a recently undergone population bottleneck followed by a rapid colonisation. The geographic distribution of the haplotypes (Figure 2-4) shows the generally low nucleotide diversity, and thus genetic similarity between the *M. tanarius* individuals in the sampled distribution range. The reduced differentiation among populations can indicate elevated rates of gene flow by frequent local extinction and recolonisation. This is in accordance with the independence of the species from colonising ant species.

The colonisation route, indicated by the haplotype network, is from northern Borneo to Sumatra continuing to Malay Peninsula, while Java was also colonised from Borneo. This route may reflect the existence of land bridges between Borneo, Java and Sumatra during Pleistocene cold cycles.

2.3.4 Comparison of *Macaranga winkleri* and *Macaranga tanarius*

Comparison of the data of myrmecophytic *M. winkleri* with non-myrmecophytic *M. tanarius* reveals clear differences in the population structure. *Macaranga tanarius* shows a much lower differentiation in the chloroplast markers than *M. winkleri*. The number of effective haplotypes for *M. winkleri* is greater than that for *M. tanarius* (7.13 vs. 1.05). Furthermore the mean genetic diversity, which is measured on a scale from 0 to 1, is much greater for *M. winkleri*, which approaches the maximum measure with 0.84, compared to *M. tanarius*, which is at the extreme opposite end of the scale with 0.04. This diversity is more emphasized by the rarefied haplotypic richness, with a high 13.73 for *M. winkleri* vs. a low 0.24 for *M. tanarius*.

While *M. winkleri* shows effects of isolation by distance, these cannot be detected on the same geographic scale (Borneo) for *M. tanarius*. Thus, in total, while *M. tanarius* shows a low genetic differentiation and a lack of genetic substructure, the data of *M. winkleri* looks clearly different, showing a much higher genetic diversity and in accordance with the expectations (hypothesis 6, chapter 1.2), a much more pronounced population structure.

The differences in genetic diversity between *M. winkleri* and *M. tanarius* can indicate

(i) a younger age of *M. tanarius*, compared to *M. winkleri*. However, it is not possible to compare the ages of these species, using available phylogenies of the genus (Blattner et al. 2001, Davies 2001, Slik & Van Welzen 2001, Kulju et al. 2007).

(ii) differences in dispersal abilities of *M. winkleri* and *M. tanarius*. These can be due to different dispersal distances and seed production. The distances of dispersal can vary because of different dispersal agents. Unfortunately studies on the dispersal agents of the species under study are not available, only general information on the genus' dispersal vectors (birds and small mammals), making a precise comparison between the study species difficult. However, the seeds of *M. tanarius* are sticky, which can alleviate long distance dispersal.

(iii) differences caused by the ant-association of *M. winkleri*. Although high levels of gene flow in section *Winklerianae* are expected, as no signs for radiation were detected, the plant

can only establish if the colonising ant species is present. In contrast, the establishment of *M. tanarius* is independent of a specific ant species, allowing for successful establishment of the plant in new areas. Thus, in *M. tanarius* gene flow is elevated compared to the myrmecophytic *M. winkleri*, leading to reduced differentiation among populations and fast colonisation. The requirement of the presence of the partner organism in *M. winkleri* for successful establishment, can explain the geographic structure of the chloroplast haplotypes, as the plants have to establish within flight distance of the *Crematogaster* msp. 8 ants. However, Guicking et al. (in preparation) could not attribute the population structure of myrmecophytic *M. hypoleuca* and *M. beccariana* from section *Pachystemon* to their association with ants, even though the relationship is highly specific. Using three chloroplast microsatellite markers the detected population structure was no more pronounced than in other *Macaranga* species. In addition, Guicking et al. (2011) detected a similar number of chloroplast haplotypes and similar levels of genetic diversity for both non-myrmecophytic *M. gigantea* and myrmecophytic *M. pearsonii* (both section *Pruinosae*). Weising et al. (2010) showed the extent of population differentiation within myrmecophytic vs. non-myrmecophytic species to be in a similar range and concluded that the hypothesis of enhanced allopatric speciation cannot be sustained for the analysed species. In accordance with this, the haplotype diversity detected for myrmecophytic *M. winkleri* is similar to those for non-myrmecophytic *M. gigantea* and myrmecophytic *M. pearsonii* (0.914, 0.915 and 0.894, respectively) (Guicking et al. 2011). However, a direct comparison of the values for *M. winkleri* with the values of the other two species might be misleading, as different chloroplast markers were used and the mutation rate may vary.

Comparing another non-myrmecophytic and ecologically similar species, *M. gigantea*, with *M. tanarius*, for the Bornean samples, the values for haplotype diversity are much smaller (0.915 vs. 0.449, respectively). This suggests that the observed genetic structure and diversity should not be exclusively attributed to the non-myrmecophytic trait of *M. tanarius*, but other factors such as the probably young age of the species should be considered.

Weising et al. (2010) rejected the hypothesis of enhanced allopatric speciation and proposed instead to consider the colonisation by ants as a key innovation that opened a new adaptive zone for both partners, making new habitats available. While the ants that entered the mutualistic association were able to circumvent competition with arboreal ants for nesting space and foraging grounds, the plants that recruited ants could grow more successfully in disturbed or open forest areas, because their partners protect them from competing plants. Therefore, myrmecophytes have a clear advantage in pioneer habitats over plants which are not inhabited by ants. Consequently, *Macaranga* plants could have diversified in their pioneer tree habitats and the ants could have driven the differentiation of the plants by changes in their morphology and behaviour. In turn, changes in plant traits relevant for the mutualistic relationship (e.g. nesting space, food resources) could have driven the differentiation of the ant partners. In section *Winklerianae*, where only one ant species occurs as mutualistic partner, the specific ant apparently did not drive the differentiation of the plant.

(iv) differences in the habitats the species grow in. *Macaranga winkleri* is a pioneer tree that occurs in open areas and on edges of primary and secondary forest, but is not likely to cross completely deforested areas, while *M. tanarius* is likely to also cross areas of completely disturbed vegetation. This can lead to a stronger effect of the fragmentation of the landscape on *M. winkleri* than on *M. tanarius*. In the last decades the tropical rain forest has been used extensively, and thus the tropical landscape has been fragmented. Fragmentation is likely to lead to reduced gene flow among populations, causing stronger genetic differentiation. Additionally, the effects of genetic drift act more strongly on smaller populations and may cause some genetic variants to disappear completely, thereby reducing genetic variation within the population. The regional genetic patterns in *M. winkleri* could thus be explained by species fragmentation, while populations of *M. tanarius* are still connected via gene flow and those of *M. winkleri* are isolated by deforested areas.

However, it is hard to imagine that the anthropogenic fragmentation of the forest, which has existed for only a few tree generations, has already had such a strong influence on the population structure. For such a significant population differentiation to occur, it may require more time from the interruption of the gene flow caused by this isolation (Weising et al. 2010).

(v) differences in the population history. *M. tanarius* could have undergone a population bottleneck, resulting in low levels of genetic diversity.

To sum up, *M. tanarius* shows a much smaller genetic differentiation than *M. winkleri*. These differences in genetic diversity can indicate (i) a younger age of the population expansion of *M. tanarius* than for *M. winkleri*, (ii) a better dispersal ability of *M. tanarius*, (iii) facilitated dispersal by independence of the ant, in contrast to *M. winkleri*, and (iv) the ability of *M. tanarius* to cross very disturbed vegetation in contrast to *M. winkleri*.

Generally, the population structure of the myrmecophytic species *M. hypoleuca* and *M. beccariana* from section *Pachystemon* cannot be attributed to their association with ants. Comparing the non-myrmecophytic *M. gigantea* and the myrmecophytic *M. pearsonii* from section *Pruinosae* with *M. winkleri* shows very similar values for the haplotype diversity, leading to the conclusion that the hypothesis of enhanced allopatric speciation cannot be sustained for the analysed species. Instead the colonisation by ants can be considered as a key innovation that opened a new adaptive zone, allowing for adaptive radiation and the diversification of the genus in sections *Pachystemon* and *Pruinosae*, but not in *Winklerianae*.

The comparison of the non-myrmecophytic species *M. tanarius* and *M. gigantea* shows great differences in the genetic diversity suggesting that the differences between *M. tanarius* and *M. winkleri* are not only attributed to the non-myrmecophytic vs. myrmecophytic trait, but also putatively to the age of the species, population history or dispersal abilities.

3 Microsatellite analysis

3.1 Materials and Methods

3.1.1 Development of microsatellite markers and transfer of markers within the genus

Nuclear microsatellite markers for *M. tanarius* and *M. winkleri* were created to augment population genetic analyses of these species. Advantages of microsatellite markers are their codominance, hypervariability and reproducibility (Sharma et al. 2007).

In total three rounds of microsatellite development procedures were performed. In the first round (using *M. winkleri* DNA isolated from a silica dried leaf) the enrichment did not work out. In the second round (again using *M. winkleri* DNA isolated from a silica dried leaf), the enrichment procedure was successful using a lower hybridisation temperature for the biotinylated oligonucleotides (see below). However, the 18 designed primer pairs did not yield consistent PCR amplification products. The third round of microsatellite development was successful using DNA isolated from a fresh leaf from both *M. tanarius* and *M. hypoleuca*. The marker development was done in conjunction with the University of Kassel, which had the fresh leaf of *M. hypoleuca* available from their green house. No fresh sample was available for *M. winkleri* as this species cannot be grown in a greenhouse (Brigitte Fiala, personal communication).

The microsatellite enrichment procedures followed a modified protocol of Fischer and Bachmann (1998), as described in detail in Baier et al. (2009), and is summarized as follows:

Using two different equimolar pools of biotinylated oligonucleotides for hybridisation, two microsatellite-enriched genomic libraries were established. The first pool was made up of (GT)₁₂, (CAA)₈ and (CAG)₈, while the second pool contained (GA)₁₂, with hybridisations performed at 76 °C and 68 °C, respectively. The microsatellite-enriched DNA fragments were then ligated into pGEM-T Easy Vector System I (Promega) and used to transform *E. coli* DH10B competent cells (Invitrogen). The screening of colonies was performed using X-Gal (5-Bromo-4-chloro-3-indolyl-beta-D-galactopyranoside) and IPTG (Isopropyl-β-D-thiogalactopyranoside), first for the positive (white) colonies which were subsequently screened for microsatellite motifs. Positive clones were identified by colony PCR with vector-specific primers and subsequent Southern hybridisation with ³²P end-labelled oligonucleotides that carried the microsatellite motifs used for enrichment. PCR products showing strong hybridisation signals were re-amplified and sent to a commercial sequencing facility (GATC Biotech). From the four libraries (two pools for each of the two species), 120 positive clones were sequenced, of which 108 yielded readable sequences. Of these 108 sequences,

Table 3-1. Newly developed primer pairs and corresponding test results for PCR amplification and polymorphism for *M. winkleri*, *M. tanarius* and *M. winkleriella* plus other 6 *Macaranga* species.

publication	Locus	PCR product						Variation / Multiple peaks											
		<i>tanarius</i>	<i>winkleri</i>	<i>winkleriella</i>	<i>motleyana</i>	<i>depressa</i>	<i>indistincta</i>	<i>pearsonii</i>	<i>gigantea</i>	<i>hypoleuca</i>	<i>tanarius</i>	<i>winkleri</i>	<i>winkleriella</i>	<i>motleyana</i>	<i>depressa</i>	<i>indistincta</i>	<i>pearsonii</i>	<i>gigantea</i>	<i>hypoleuca</i>
Baier et al. 2009	MactaG12	No	No	No	N/T	N/T	N/T	N/T	No	-	-	-	-	-	-	-	-	-	-
Baier et al. 2009	MactaG01	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes/No	Yes	Yes	Yes/No	Yes/No	Yes/No	Yes/No	No/No	Yes/No	-
Baier et al. 2009	MactaG09	Yes	No	No	Yes	Yes	Yes	Yes	No	Yes/No	-	-	-	-	-	-	-	-	-
Baier et al. 2009	MactaG04	No	No	No	N/T	N/T	N/T	N/T	No	-	-	-	-	-	-	-	-	-	-
Baier et al. 2009	MactaG07	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes/No	Yes/No	Yes/No	Yes/No	Yes/No	Yes/Yes	Yes/No	Yes/No	Yes/Yes	Yes/No
Baier et al. 2009	MactaG11	No	No	No	N/T	N/T	N/T	N/T	No	-	-	-	-	-	-	-	-	-	-
Baier et al. 2009	MactaG08	No	No	No	N/T	N/T	N/T	N/T	No	-	-	-	-	-	-	-	-	-	-
Baier et al. 2009	MactaE09	No	No	No	N/T	N/T	N/T	N/T	No	-	-	-	-	-	-	-	-	-	-
Baier et al. 2009	MactaF10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes/Yes*	Yes/Yes	Yes/No	Yes/No	Yes/Yes	Yes/Yes	Yes/Yes	No/Yes	No/Yes	-
Baier et al. 2009	MactaF02	No	No	No	N/T	N/T	N/T	N/T	No	-	-	-	-	-	-	-	-	-	-
Baier et al. 2009	MactaE01	Yes	No	No	N/T	N/T	N/T	N/T	No	No/No	-	-	-	-	No/No	-	-	-	-
Baier et al. 2009	MactaE06	No	No	No	N/T	N/T	N/T	N/T	No	-	-	-	-	-	-	-	-	-	-
Baier et al. 2009	MactaF09	No	No	No	N/T	N/T	N/T	N/T	No	-	-	-	-	-	-	-	-	-	-
Baier et al. 2009	MactaF03	Yes	No	Yes	No	No	No	No	No	Yes/No	-	-	-	-	-	-	-	-	-
Baier et al. 2009	MactaF12	No	No	No	N/T	N/T	N/T	N/T	No	-	-	-	-	-	-	-	-	-	-
Baier et al. 2009	MachyA06	No	Yes	N/T	N/T	N/T	N/T	N/T	No	-	-	-	-	-	-	-	-	-	Yes/No
Baier et al. 2009	MachyA07	No	No	No	N/T	N/T	N/T	N/T	Yes	-	-	-	-	-	-	-	-	-	Yes/No
Baier et al. 2009	MachyB07	No	No	N/T	N/T	N/T	N/T	N/T	Yes	-	-	-	-	-	-	-	-	-	Yes/No
Baier et al. 2009	MachyB10	Yes	Yes	Yes	N/T	N/T	N/T	N/T	Yes	Yes/No	Yes/No	Yes/No	Yes/No	Yes/No	Yes/No	Yes/No	Yes/No	Yes/No	Yes/No
Baier et al. 2009	MachyG07	Yes	Yes	No	N/T	N/T	N/T	N/T	Yes	Yes	-	-	-	-	-	-	-	-	Yes/No
Baier et al. 2009	MachyH11	Yes	Yes	Yes	N/T	N/T	N/T	N/T	Yes	Yes	Yes	Yes	-	-	-	-	-	-	Yes/No
Baier et al. 2009	MachyB04	Yes	Yes	N/T	N/T	N/T	N/T	N/T	Yes	No/Yes	No/No	-	-	-	-	-	-	-	No/No
Baier et al. 2009	MachyB11	Yes	No	N/T	N/T	N/T	N/T	N/T	Yes	Yes/Yes	-	-	-	-	-	-	-	-	No/No
Guicking et al. 2006	Macin8h	Yes	Yes	Yes	N/T	N/T	N/T	N/T	N/T	Yes/No	Yes/No	Yes/No	Yes/No	-	-	-	-	-	-
Guicking et al. 2006	Macin8n	Yes	Yes	Yes	N/T	N/T	N/T	N/T	N/T	Yes/No	Yes/No	Yes/No	Yes/No	-	-	-	-	-	-
Guicking et al. 2006	Macpe6h	Yes	Yes	Yes	N/T	N/T	N/T	N/T	N/T	Yes/No	Yes/No	Yes/No	Yes/No	-	-	-	-	-	-
Guicking et al. 2006	Macpe6j	Yes	Yes	Yes	N/T	N/T	N/T	N/T	N/T	Yes/No	Yes/No	Yes/No	Yes/No	-	-	-	-	-	-
pers comm. Guicking	Macin11j	No	Yes	Yes	N/T	N/T	N/T	N/T	N/T	-	Yes/Yes*	Yes/No	Yes/No	-	-	-	-	-	-
pers comm. Guicking	Macin8f	Yes	Yes	Yes	N/T	N/T	N/T	N/T	N/T	Yes/No	Yes/No	Yes/No	Yes/No	-	-	-	-	-	-

N/T - Not tested.

Macta = species of origin *M. tanarius*Machy = species of origin *M. hypoleuca*Macin = species of origin *M. indistincta*Macpe = species of origin *M. pearsonii*

* Multiple peaks occurred in part of the samples.

all but one contained a microsatellite. Primer pairs for 15 loci each of *M. tanarius* and *M. hypoleuca* were designed for use in these genetic analyses. Initial design of the primer pairs was performed using Primer3 software (Rozen & Skaletsky 2000), with final adjustments and verification performed manually.

3.1.2 Test of the newly developed primer pairs and test for cross-amplification within the genus *Macaranga*

A test of cross-PCR-amplification was performed for *M. winkleri*, *M. tanarius* and *M. winkleriella* using the following markers: Macin8h, Macin8n (originating from *M. indistincta*), Macpe6h, Macpe6j (originating from *M. pearsonii*) (Guicking et al. 2006). Locus Macin8f, Macin11j (originating from *M. indistincta*) (Daniela Guicking, personal communication). All but one marker (Macin11j, which did not amplify in *M. tanarius*) cross-amplified in the three species under study, (Table 3-1). All markers were showing polymorphism in the genotyping analysis and were, thus, included in the further analyses. Macin11j for *M. winkleri* was excluded at a later state, when the samples began to show multiple peaks (Table 3-1).

Newly designed primer pairs (Baier et al. 2009) were tested for amplification in the species under study, plus other *Macaranga* species for analyses at the University of Kassel (*M. motleyana*, *M. depressa*, *M. indistincta*, *M. pearsonii* and *M. gigantea*). After the PCR, 5 µl of the putative PCR product were checked in a 1.2% agarose gel.

All primer pairs that amplified successfully were further tested for usability as markers in terms of variability and absence of multiple peaks (Table 3-1) including ten individuals per species and primer pair determining the fragment size on a MegaBACE 1000 automatic DNA sequencer (Amersham Biosciences).

Fourteen primer combinations were successfully amplified in *M. winkleri*: MactaG01, MactaG07, MachyA03, MachyA06, MachyB04, MachyB10, MachyG07, MachyH11, Macpe6h, Macpe6j, Macin8f, Macin8h, Macin8n and Macin11j (Table 3-1). Primer combinations showing multiple peaks or lacking variation during genotyping analysis were excluded from further analysis. Eleven primer combinations were subsequently used for the genotyping analysis. Marker Macin11j was later excluded as it was resulting in multiple fragments in the latter analysed part of the samples. Ultimately the following ten microsatellite markers were included in the SSR analysis for *M. winkleri*: MactaG01, MactaG07, MachyB10, MachyG07, MachyH11, Macin8f, Macin8h, Macin8n, Macpe6h and Macpe6j. 561 individuals of *M. winkleri* (see Appendix A) were analysed for these markers.

Table 3-2. The microsatellite markers for *M. winkleri*, *M. tanarius* and *M. winkleriella*, their primer sequences, fluorescent label, repeat motif, size of the original clone, the genbank accession number, annealing temperature and PCR program used.

Publication	Locus	Primer sequences (5'-3') and fluorescent label	Repeat motifs	Original clone (bp)	GenBank Accession Number	PCR product				Annealing temperature (PCR program)	
						<i>M. tanarius</i>	<i>M. winkleri</i>	<i>M. winkleriella</i>	Variation/ Multiple Peaks		
Baier et al. 2009	MactaG01	F:Hex-5'-TCTAAGAAACTAGAGAC-3' R:5'-AATCTCTCCCTTCAATC-3'	(AG) ₃₂	147	FM244656	Yes	Yes	Yes	Yes/No	Yes	51°C (1)
Baier et al. 2009	MactaG09	F:Hex-5'-CGAACCTGTAATCGATCTG-3' R:5'-GCCCTTGTCTTCCAAAAGCC-3'	(GA) ₂₃	199	FM244660	Yes	No	No	Yes/No	-	53°C (1)
Baier et al. 2009	MactaG07	F:Tamra-5'-GGGATTTGACAGGCAAGG-3' R:5'-GGACGATATTGATAATGTGGAC-3'	(GA) ₃₂	279	FM244659	Yes	Yes	Yes	Yes/No	Yes/No	59°C (1)
Baier et al. 2009	MactaF10	F:Fam-5'-AGTGGAGGTTGTTAGTGAG-3' R:5'-CCCTTCCAAAAGTCTTGTAGATG-3'	(GT) ₂₆	204	FM244657	Yes	Yes	Yes	Yes/Yes*	Yes/Yes	57°C (1)
Baier et al. 2009	MactaF03	F:Hex-5'-ACAAGTGAAGATGGAGA-3' R:5'-AAGAAACATCAAAATCACCA-3'	(TG) ₂₉	169	FM244658	Yes	No	Yes	Yes/No	-	57°C (1)
Baier et al. 2009	MachyA06	F:Hex-5'-CCACTGACATCCAGGTCACA-3' R:5'-AGCTCCAAAAGTGGTTCCG-3'	(GA) ₂₅	152	FM244662	No	Yes	N/T	-	No/No	53°C (1)
Baier et al. 2009	MachyA07	F:5'-TGGGTTGGAGCTTCAATTC-3' R:5'-CCAAATGCTAATGAAAATAATAACC-3'	(GA) ₂₄	173	FM244663	No	No	No	-	-	-
Baier et al. 2009	MachyB07	F:5'-GCAACGAACATCCTCCAGAT-3' R:5'-TGTTTCGGCTTCTGACTACCAA-3'	(GA) ₃₀	241	FM244661	No	No	N/T	-	-	-
Baier et al. 2009	MachyB10	R:5'-TCTCAGTTTAGTTTTGGACTC-3'	(GA) ₂₁	107	FM244653	Yes	Yes	Yes	Yes/No	Yes/No	53°C (1)
Baier et al. 2009	MachyG07	F:Fam-5'-TCTTCACTTCAATATTAGTATGTGC-3' R:5'-GTCTCGCTACCGTGTCTCG-3'	(GT) ₂₃	219	FM244655	Yes	Yes	No	Yes	Yes	53°C (1)
Baier et al. 2009	MachyH11	F:Fam-5'-TCCACAAGTTAACGAGCAACC-3' R:5'-TGGTTTCGATTGGCTTTGAT-3'	(GCA) ₁₀ (N) ₂₇ (GCA) ₁₁	235	FM244654	Yes	Yes	Yes	Yes	Yes	53°C (1)
Guicking et al. 2006	Macin8h	F:Tamra-5'-ACAGACTCAAGCGGTCAAGG-3' R:5'-GGCTACCATCTCTTCGTTGC-3'	(CAG) ₉ N ₉ (CAG) ₈	182	DQ168588	Yes	Yes	Yes	Yes/No	Yes/No	52°C (2)
Guicking et al. 2006	Macin8n	F:Fam-5'-AAGCTCAACCACCTCAGCAT-3' R:5'-ATCTCTCCGCTGTTGTTGCT-3'	(CAG) ₅ (CAA) ₂ (CAG) ₁₀ (CAA) ₂ N ₆ (CAG) ₃ (CAACAG) ₂ (CAA) ₂ CAG (CAA) ₂	221	DQ168589	Yes	Yes	Yes	Yes/No	Yes/No	52°C (2)
Guicking et al. 2006	Macpe6h	F:5'-AGCAGTAGCAGCCACTTCAA-3' R:Tamra-5'-ATCCCAAGTCCCAATCATCA-3'	(GCA) ₅ ACA(GCA) ₃	160	DQ168590	Yes	Yes	Yes	Yes/No	Yes/No	52°C (2)
Guicking et al. 2006	Macpe6j	F:Fam-5'-CCTCAAGTGGGCTTTTGGGA-3' R:5'-GCCCTGTTCTCTGTTCTG-3'	(GCT) ₁₃ N ₆₀ (AAAAAG) ₅	242	DQ168591	Yes	Yes	Yes	Yes/No	Yes/No	52°C (2)
pers comm. Guicking	Macin11j	F:5'-ACCCCAAGGTGTGATGAAT-3' R:Fam-5'-TGATGTAGCCCTCCAGG-3'	(TG)	-	-	No	Yes	Yes	-	Yes/Yes*	54°C (3)
pers comm. Guicking	Macin8f	F:5'-AAGATGAGCCCAAGAGCA-3' R:5'-AGGAGTATCGCTGTTGACG-3'	(ACC)(CAG)(CAA)	-	-	Yes	Yes	Yes	Yes/No	Yes/No	54°C (3)

N/T - Not Tested.

Fourteen primer combinations successfully amplified in *M. tanarius*: MactaG01, MactaG07, MactaG09, MachyB10, MachyG07, MachyH11, Macin8f, Macin8h, Macin8n, Macpe6h and Macpe6j, MachyA03, MachyB04, MachyB11 (Table 3-1). After exclusion of the primer combinations showing multiple peaks or lacking length variation, in the end 11 markers were included in the SSR analysis for *M. tanarius*: MactaG01, MactaG07, MactaG09, MachyB10, MachyG07, MachyH11, Macin8f, Macin8h, Macin8n, Macpe6h and Macpe6j. 353 individuals of *M. tanarius* (see Appendix A) were analysed for these markers.

In *M. winkleriella* 14 primer combinations were successfully amplified: MactaF03, MactaG01, MactaG07, MachyA03, MachyA06, MachyB04, MachyB10, MachyH11, Macin8f, Macin8h, Macin8n, Macin11j, Macpe6h and Macpe6j (Table 3-1). Of these ten microsatellite markers were included in the SSR analysis for *M. winkleriella*. These markers correspond to those included for *M. winkleri* with one exception, MactaF03 was used instead of MachyG07 (Table 3-1). 12 individuals of *M. winkleriella* were analysed for these markers (see Appendix A).

The markers for *M. winkleri*, *M. tanarius* and *M. winkleriella*, their primer sequences and fluorescent label, repeat motif, size of the original clone and the genebank accession number are summarized in Table 3-2.

PCR amplifications were performed with two different types of programs, using different annealing temperatures for the different markers. The annealing temperatures can be found in Table 3-2, together with the specific PCR program, either 1, 2 or 3 (given in brackets after each temperature) as described below:

- (1) Initial denaturation at 95 °C for 5 min, followed by 33 cycles of 95 °C for 30 s, the annealing temperature for 30 s, 70 °C for 40 s, 70 °C for 8 min.
- (2) Initial denaturation at 95 °C for 5 min, followed by 35 cycles of 95 °C for 45 s, the annealing temperature for 60 s, 68 °C for 1 min, 70 °C for 8 min.
- (3) Initial denaturation at 95 °C for 5 min, followed by 35 cycles of 95 °C for 30 s, the annealing temperature for 30 s, 72 °C for 2 min, 72 °C for 7 min.

Amplifications were performed in a volume of 10 µl, containing 1 to 5 ng of genomic template DNA, 1x buffer (containing 15 mM MgCl₂), 10 pmol each of forward and reverse primer, 0.2 mM of each dNTP, and 0.5 U of Taq DNA polymerase (QIAGEN). To decrease the formation of primer dimers 5µg bovine serum albumin (BSA) were added. To facilitate the amplification of GC-rich regions and to increase the specificity (Varadaraj & Skinner 1994) 3% dimethyl sulfoxide (DMSO) was added.

Microsatellite genotyping analysis

PCR was performed for the genotyping analysis using one primer per pair containing a fluorescent labelled dye, (FAM, HEX or TAMRA) for both genotyping systems, as described below.

For the genotyping analysis on the ABI Prism 377 automated sequencer (ABI) (from Applied Biosystems) a loading buffer mix (containing 180 μ l of formamid, 70 μ l of loading buffer ABI and 50 μ l of a genotyping size standard, as specified below) was prepared. 1.2 μ l of the PCR amplification product (in different dilutions depending on the strength of the PCR product and the colour of the label) was mixed with 0.5 μ l of the loading buffer mix and heat-denatured at 96 °C for 2 min. Fragment lengths of the fluorescently labelled PCR products were determined with an internal standard (GeneScan 500 ROX; Applied Biosystems) on a 6% polyacrylamide gel on the ABI.

For the genotyping analysis on the MegaBACE 1000 automatic DNA sequencer (Amersham Biosciences), a loading buffer mix (700 μ l of loading buffer MegaBACE and 20 μ l of the size standard) was prepared. 3 μ l of PCR amplification products were mixed with 7 μ l of the loading buffer mix and heat-denatured at 96 °C for 2 min. The genotyping size standard was the MegaBACETM ET 400-R Size Standard (Amersham Biosciences). Different dilutions depending on the marker specific strength of the PCR product and the colour of the fluorescent label were used. A general approximation for the dilutions according to the colours was as follows: FAM: 1:60, HEX: 1:20, TAMRA: 1:40. Fluorescent labels used can be found in Table 3-2, with the respective primer sequences.

For time and cost-efficiency between two and four markers were run in one MegaBACE run, as three differently coloured fluorescent dyes are available, and dyes of the same colours can be run in one run if the fragments sufficiently vary in length. Two reference samples were placed in each genotyping plate to reference fragment lengths over all genotyping runs, as well as to be able to reference between the two different genotyping systems (ABI and MegaBACE).

For the data obtained from the ABI system automatic lane tracking was performed and refined by hand in GeneScan 3.1 (Applied Biosystems). The lanes were then extracted and the data imported into Genotyper 2.5 (Applied Biosystems), where the fragments were manually scored. Data obtained from the MegaBACE was analysed using Fragment Profiler 1.2 (Amersham Bioscience).

3.1.3 Assignment analysis using the SSR data

Two different Bayesian assignment approaches were applied to infer population structure of *M. winkleri* and *M. tanarius* using the programs STRUCTURE and INSTRUCT. The same parameters as in the chloroplast assignment analysis were used, but the input matrices contain the fragment sizes of the alleles in this analysis. For all calculations the admixture model was assumed, which allows for mixed ancestry of each individual, as we are dealing with nuclear data, and thus expect mixed ancestry, i.e. biparental ancestry. For *M. tanarius* one calculation was done using only the individuals from Borneo and another containing all individuals. In this analysis, the number of populations tested ranged from $K = 1$ to $K = 20$, as the value for $L(K)$ had not yet reached a plateau after $K = 10$. The still increasing $L(K)$ indicates that to

only analyse until $K = 10$, as in the chloroplast analysis, would not have been sufficient. Ten replicate runs, per population K , were performed.

Determining the number of populations (K)

The determination of the optimal K was performed in the same manner as in the chloroplast analysis (see page 29). The maximal value of $L(K)$ as taken over all replicate runs, the first value in the plateau phase of the mean $L(K)$, and the calculation of Delta K (ΔK) were used to determine the optimal K in the STRUCTURE analysis. Similarly, the determination of the optimal K for the INSTRUCT analysis was to choose the smallest DIC value of all replicate runs, the first K in the plateau and the second order rate of change in the averaged DIC value (ΔK DIC).

Bar plots for *M. winkleri* and *M. tanarius* were created using the optimal K s (except where plots show no additional information), illustrating the assignment of each individual to K clusters.

3.1.4 Principal coordinate analysis

Principal Coordinate Analyses (PCoAs) were conducted to better resolve the similarities and dissimilarities of the genetic structure within the microsatellite data. Pairwise genetic distance matrices, where two alleles can be either identical ($= 0$) or different ($= 1$), were calculated for (i) all 561 *M. winkleri* individuals, (ii) all 353 *M. tanarius* individuals and (iii) for only the Bornean *M. tanarius* individuals (305) using GenAlEx 6 (Peakall & Smouse 2006). For each of these three data sets, the distances were summed over the loci and PCoAs were computed on these summed distances using GenAlEx 6.

3.1.5 Analysis of genetic diversity and differentiation

To compare the genetic diversity between the species under study, the rarefied allelic richness was calculated using ADZE-1.0 (Szpiech et al. 2008). This measure allows for comparison of the nuclear allelic diversity, without the bias that is introduced by uneven sample sizes. The rarefied allelic richness and the mean rarefied allelic richness (i.e. averaging over the used SSR loci) were calculated. For the entire microsatellite data set of each of *M. winkleri*, *M. tanarius* and *M. winkleriella* the rarefaction number was set to $g = 24$ (the smallest sample size). The rarefied allelic richness was also calculated for several subsets of both *M. winkleri* and *M. tanarius*, rarefied for different values based on the desired comparison. This calculation was performed rarefied for both $g = 6$ and $g = 70$ for individuals west and east of the Crocker Range, and just for $g = 6$ for individuals from Sarawak/Brunei vs. individuals from Sabah.

To estimate amounts of gene flow and genetic differentiation between subpopulations of *M. winkleri* and *M. tanarius* several measures of population differentiation were calculated. The pairwise population Nei's genetic distance (Nei 1972) and Wright's inbreeding

coefficient, F_{ST} (Wright 1922), were computed using GenAlEx. In addition to these, Nei's coefficient of gene differentiation, G_{ST} , was also considered. However, more recent work has shown that the G_{ST} calculation can result in low values for highly variable markers, even when no alleles are shared between subpopulations (Hedrick 2005). As microsatellite markers are highly polymorphic, in place of the G_{ST} , Hedrick's standardized G_{ST} , G'_{ST} , was calculated manually using the values of the average subpopulation Hardy-Weinberg heterozygosity and the total population heterozygosity from GenAlEx and formula 4b from Hedrick (2005).

The differentiation values were calculated for *M. winkleri* and *M. tanarius* between the populations west and east of the Crocker Range and Sarawak/Brunei and Sabah. For *M. tanarius* alone, these measures were additionally calculated between populations of Borneo and Malay Peninsula to provide a baseline comparison with the other regional subsets.

To compare amounts of gene flow across similar geographic scales between *M. tanarius* and *M. winkleri*, G'_{ST} was calculated between three sets of regions. These regions are: a) Northern Sarawak and Brunei (plus southwestern Sabah for *M. tanarius*), b) northwestern Sabah and c) eastern Sabah (see Figure 3-11).

The following are the genetic diversity and differentiation metrics that are used in this work:

The **allelic richness** estimates the expected number of distinct alleles that will be observed in a population rarefied for the sample size (i.e. a subsample of size g , randomly drawn from the population) (Hurlbert 1971, Petit et al. 1998).

The **pairwise population Nei genetic distance** (Nei 1972) is a measure for the genetic differentiation. This genetic distance is specified on a log scale, and is a measure of the normalized identity (I) of genes between two populations with respect to all loci.

The **pairwise population F_{ST} value** represents the degree of population genetic differentiation. If the F_{ST} is small, it means that the allele frequencies within each population are similar; if it is large, it means that the allele frequencies are different (Holsinger & Weir 2009). The values range from 0 to 1, where a value of 0 implies complete panmixis and a value of 1 complete separation between the populations.

The **standardized G_{ST}** (Nei 1973), G'_{ST} , (Hedrick 2005), also represents the degree of population genetic differentiation. While G_{ST} measures the amount of variation between subpopulations, relative to the total population variation, for G'_{ST} , the magnitude is the proportion of the maximum differentiation possible for the level of subpopulation homozygosity observed. This allows for better comparison between loci with different levels of genetic variation.

For *M. winkleri* and its sister species *M. winkleriella*, nine common SSR markers were used in the microsatellite analysis (see page 65). For these common markers the shared alleles between *M. winkleri* and *M. winkleriella* are determined and discussed.

3.2 Results of the microsatellite analysis

3.2.1 Assignment analyses using the SSR data

Assignment analysis in *Macaranga winkleri* assuming the admixture model

Screening through all log probabilities in *M. winkleri* ($K = 1$ to $K = 20$) for all replicate runs of STRUCTURE assuming the admixture model leads to the highest log probability for $K = 16$ (Table 3-3). The first K value in the plateau phase of the plot of the averaged log probability of data $L(K)$, which is supposed to be the optimal, is $K = 3$ for *M. winkleri* (Figure 3-1A). Also the less subjective determination of K , via the calculation of ΔK , results in $K = 3$ (Figure 3-1B). The smallest DIC value for *M. winkleri* is found for $K = 11$ (Table 3-3). Plotting the averaged DIC values the first K in the plateau phase is $K = 3$ (Figure 3-1C). Also the plot of ΔK DIC shows a peak for $K = 3$ (Figure 3-1D). Table 3-3 summarizes the optimal K values for *M. winkleri* assuming admixture using the programs STRUCTURE and INSTRUCT.

Assignment analysis in *Macaranga tanarius* assuming the admixture model

Screening through all log probabilities in *M. tanarius* ($K = 1$ to $K = 15$) in all replicate runs of STRUCTURE assuming the admixture model leads to the highest log probability for $K = 11$ in both the analyses with all individuals and the one with only the Bornean *M. tanarius* individuals (Table 3-3).

The first K value in the plateau phase of the plot of the averaged log probability of data $L(K)$ as a function of K ($K = 1$ to $K = 15$), which is supposed to be the optimal, is $K = 5$ for Bornean *M. tanarius* (Figure 3-2A) and $K = 6$ for all *M. tanarius* (Figure 3-3A).

Table 3-3. *Macaranga winkleri* and *M. tanarius*. Optimal K values for the microsatellite data sets of both STRUCTURE and INSTRUCT assuming the admixture model, determined with different methods.

	STRUCTURE			INSTRUCT		
	K with highest log probability of all replicate runs	First K in the plateau phase of the Mean-Log-Likelihood plot of the	K with the highest value for ΔK	K showing the smallest DIC value	First K in the plateau phase of the DIC values	K with the highest value for ΔK DIC
<i>M. winkleri</i>	K=16	K=3	K=3	K=11	K=3	K=3
<i>M. tanarius</i> ¹	K=11	K=5	K=5	K=10	K=6/K=7	K=3
<i>M. tanarius</i> ²	K=11	K=6	K=2	K=11	K=7	K=2

¹ Only Bornean individuals.

² All individuals.

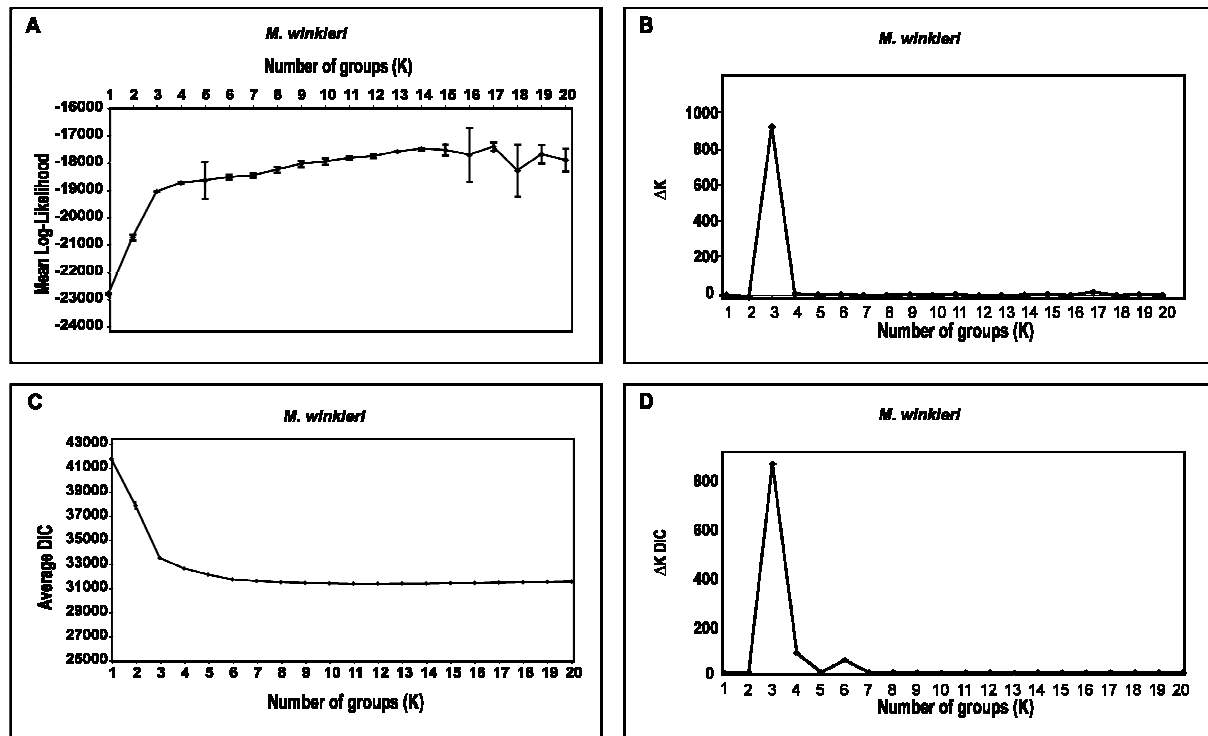


Figure 3-1. Plots for the determination of the optimal K value in *M. winkleri* for all individuals using the admixture model.

A) The log probability $L(K)$ averaged over the ten replicate runs $m(L(K))$ of STRUCTURE. Vertical bars indicate standard deviations.

B) To assess the number of groups (K) supported by the analysis with STRUCTURE, the second order rate of change in the log-likelihood (ΔK) was calculated (Evanno et al. 2005).

C) The DIC values averaged over the ten replicate runs of INSTRUCT. Standard deviations are indicated by the use of vertical bars. In nearly all number of groups (K) the magnitude of the standard deviations are too small to be seen at this scale.

D) To assess the number of groups (K) supported by the analysis with INSTRUCT, the second order rate of change in the DIC was calculated (ΔK DIC).

The highest value for ΔK is $K = 5$ for the Bornean individuals (Figure 3-2B) and $K = 2$ for all individuals (Figure 3-3B). The smallest DIC value for Bornean *M. tanarius* is found for $K = 10$, for all *M. tanarius* individuals it is $K = 11$ (Table 3-3). Plotting the averaged DIC values for Bornean *M. tanarius* the first K in the plateau phase is either $K = 6$ or $K = 7$ (Figure 3-2C) as the low gradient results in both $K = 6$ and $K = 7$ being equally considered as the first K in the plateau phase. For all *M. tanarius* individuals the first value in the plateau phase of the averaged DIC value is $K = 7$ (Figure 3-3C).

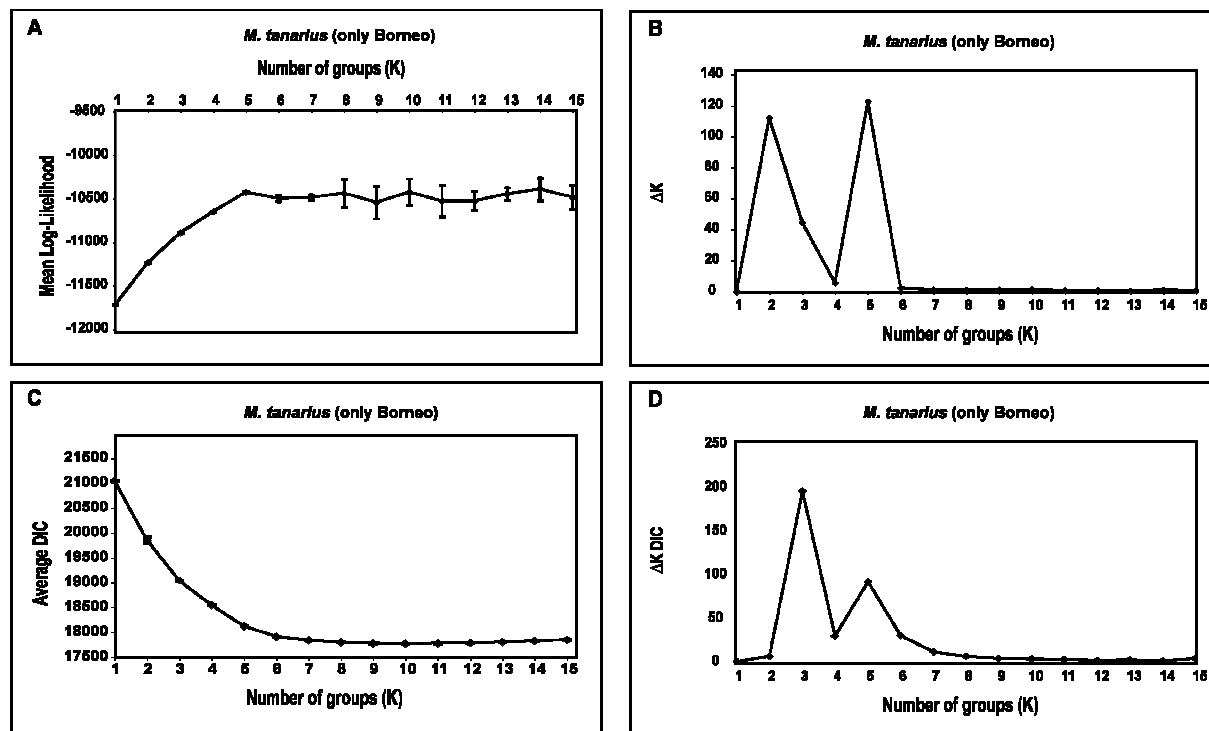


Figure 3-2. Plots for the determination of the optimal K value in Bornean *M. tanarius*, using the admixture model.

A) The log probability $L(K)$ averaged over the ten replicate runs $m(L(K))$ of STRUCTURE. Vertical bars indicate standard deviations.

B) To assess the number of groups (K) supported by the analysis with STRUCTURE, the second order rate of change in the log-likelihood (ΔK) was calculated.

C) The DIC values averaged over the ten replicate runs of INSTRUMENT. Standard deviations are indicated by the use of vertical bars. In nearly all number of groups (K) the magnitude of the standard deviations are too small to be seen at this scale.

D) To assess the number of groups (K) supported by the analysis with INSTRUMENT, the second order rate of change in the DIC was calculated (ΔK DIC).

The plot of ΔK DIC shows the highest peak for $K = 3$ for Bornean *M. tanarius* (Figure 3-2D) and $K = 2$ for all *M. tanarius* (Figure 3-3D).

Table 3-3 gives an overview of the optimal K values for *M. tanarius* assuming admixture with the programs STRUCTURE and INSTRUMENT.

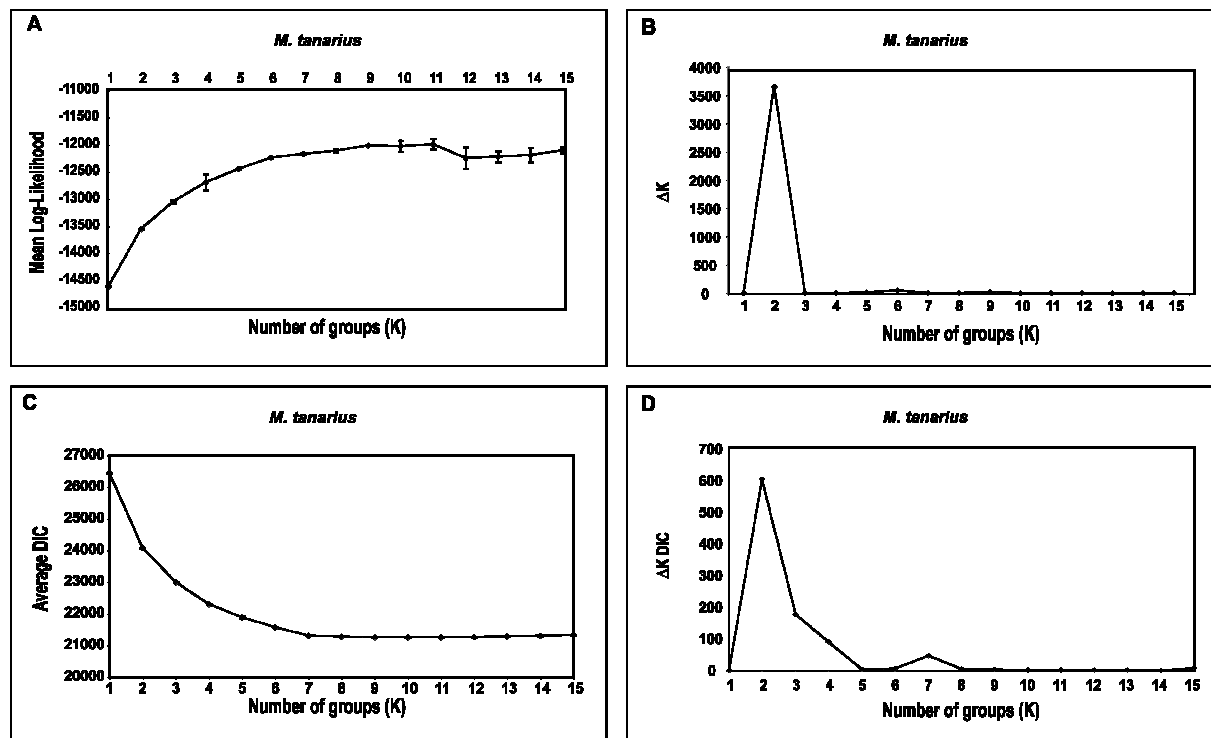


Figure 3-3. Plots for the determination of the optimal K value in *M. tanarius* for all individuals using the admixture model.

A) The log probability $L(K)$ averaged over the ten replicate runs $m(L(K))$ of STRUCTURE. Vertical bars indicate standard deviations.

B) To assess the number of groups (K) supported by the analysis with STRUCTURE, the second order rate of change in the log-likelihood (ΔK) was calculated.

C) The DIC values averaged over the ten replicate runs of INSTRUCT. Standard deviations are indicated by the use of vertical bars. In nearly all number of groups (K) the magnitude of the standard deviations are too small to be seen at this scale.

D) To assess the number of groups (K) supported by the analysis with INSTRUCT, the second order rate of change in the DIC was calculated (ΔK DIC).

3.2.2 Bar plots illustrating the assignment analyses of the SSR data

Bar plots of *M. winkleri* assuming the admixture model

For STRUCTURE the populations yielding the highest log probability ($K = 16$) and the start of the plateau phase ($K = 3$, see Mean-Log-Likelihood plot, Figure 3-1A) are shown in bar plots (Figure 3-4A & B). While for INSTRUCT the populations that are shown are for the start of the plateau phase ($K = 3$, see DIC plot, Figure 3-1 C) and for the smallest DIC ($K = 11$) (Figure 3-4 C & D).

The bar plots for both STRUCTURE and INSTRUCT (Figure 3-4), reveal that generally the *M. winkleri* individuals from Sarawak/Brunei belong to the same cluster independent of the number of populations (K) used. While individuals from Sarawak/Brunei tend to a single cluster, those from Sabah tend to two clusters for $K = 3$ and $K = 11$ (graphs B, C and D).

For both STRUCTURE and INSTRUCT with $K = 3$ (B and C) the same clustering of individuals emerges, represented by the corresponding colours, blue, red and yellow. The specific percentages with which each individual belongs to a cluster is given in Appendix J for $K = 3$ (STRUCTURE) and for all best K s in Table 1 in the digital appendix. The blue cluster consists entirely of individuals from Sarawak/Brunei, while the individuals from Sabah are split into the red and yellow clusters. The individuals making up the yellow cluster originate primarily from the west grid of Danum Valley (see Appendix B and the accompanying description).

For the assignment of STRUCTURE with $K = 16$ (A), the major division separating Sarawak/Brunei and Sabah remain. However, 17 individuals originating from Brunei (~ 30%) are assigned to an additional cluster each with more than 50%, dividing Sarawak/Brunei partly into their separate respective regions. The group indicated as K.K.-Ranau-Poring is divided into two major clusters comprising individuals from Poring and the rest. In the Danum Valley group for $K = 16$ an additional bigger cluster obtained is the orange one, comprising mostly individuals from the West 10 part of the west grid. In the remainder of Sabah several small clusters can be detected as well as individuals of mixed assignment.

The bar plot D, INSTRUCT with $K = 11$, does not give additional information beyond what is already shown in the $K = 3$ plots of STRUCTURE (B) or INSTRUCT (C). This plot clearly indicates the same three clusters as in $K = 3$ (B and C) only with the red cluster now shown as one cluster with consistently mixed assignment to 11 groups for all individuals.

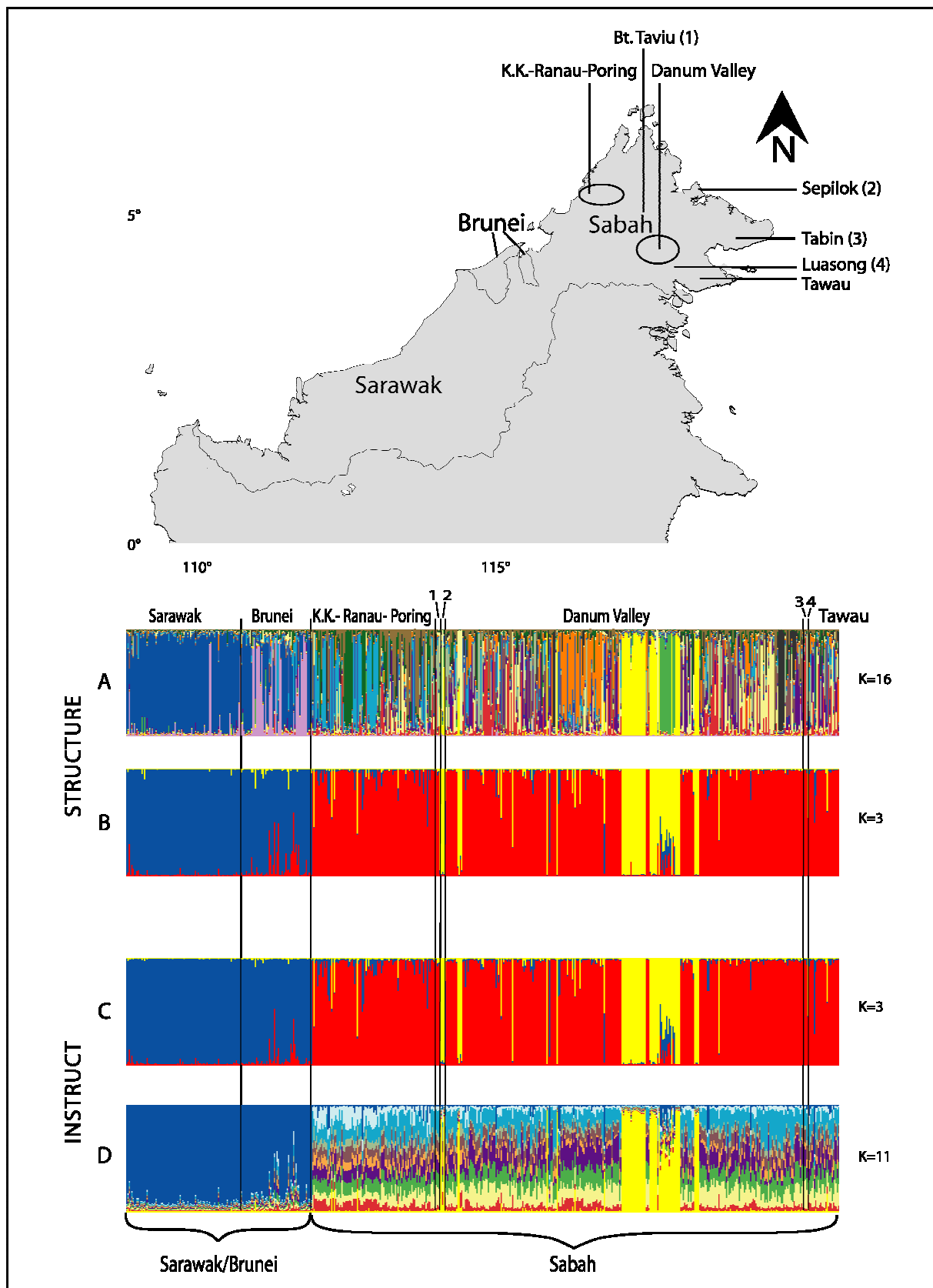


Figure 3-4. A series of bar plots of the assignment analysis and corresponding geographic distribution of *M. winkleri* individuals, using both STRUCTURE (A-B) and INSTRUCT (C-D). Each graph illustrates the clustering of microsatellite data assuming the admixture model. In each graph, the individuals are presented in the same order (see Appendix J). The map illustrates the regions from

A more detailed dissection of the geographic distribution of individuals in the Danum Valley of Sabah and along the major arteries in and out of the valley (including the road to Malua and Lahad Datu) is shown in Appendix B. The bar plot consists of the Danum Valley section of the INSTRUCT analysis with population $K = 3$ (Figure 3-4C). The individuals from this region that cluster in yellow tend to be from the west grid, mostly from region W0 to W07. A second set of individuals in yellow are also found along the road to Malua and one individual between the field centre and Lahad Datu.

Bar plots of *M. tanarius* assuming the admixture model

Bar plots for *M. tanarius* were created to visualize the STRUCTURE and INSTRUCT results for the microsatellite data applying the admixture model showing the optimal K values. These plots illustrate the assignment of each individual to the assumed number of clusters (K). A bar plot of the assignment analysis and corresponding geographic distribution of the *M. tanarius* individuals (Figure 3-5) generally show that individuals of one region tend to cluster (depending on the number of populations, K , used) in the assignment analysis. Each individual is assigned one value for each cluster (between 0 and 1) representing the degree that the individual belongs in each cluster. A value of 1 indicates that the individual belongs exclusively to one cluster, while a value of 0 indicates that the individual shares no commonality with the corresponding cluster. Any other non-zero value is an indication of the mixed ancestry of the individuals.

A more detailed analysis of *M. tanarius* (Figure 3-5) is illustrated for the optimal clustering, $K = 6$, showing the geographic origins of identifiable clusters. The percentage with which each individual belongs to a cluster (see Appendix K) is represented by the corresponding colour, blue, orange, yellow, green, red and brown. All individuals from the Malay Peninsula were found to cluster together, in the blue cluster, with an average of 94.8%, with only one individual belonging to this cluster with a percentage less than 80% (individual 6090 with 62.4%). The orange cluster includes all individuals from Sarawak/Brunei (identified as region 1 in the figure) and individuals from southern Sabah in the surroundings of Tenom (region 3).

which the *M. winkleri* individuals were sampled. Each cluster in the bar plot is related visually to its geographic origin(s), in detail by numbers and regions (above A), and in broader geographic terms (below D). The four graphs represent the preferred value (this is the highest value for STRUCTURE runs, and the lowest for INSTRUCT) found over ten replicates for:

- A) the highest log probability of all replicate runs of STRUCTURE, $K = 16$,
- B) the first K in the plateau phase of the plot of the Mean-Log-Likelihood of STRUCTURE, $K = 3$,
- C) the first K in the plateau phase of the plot of the DIC values of INSTRUCT, $K = 3$, and
- D) the K with the smallest DIC value of INSTRUCT, $K = 11$.

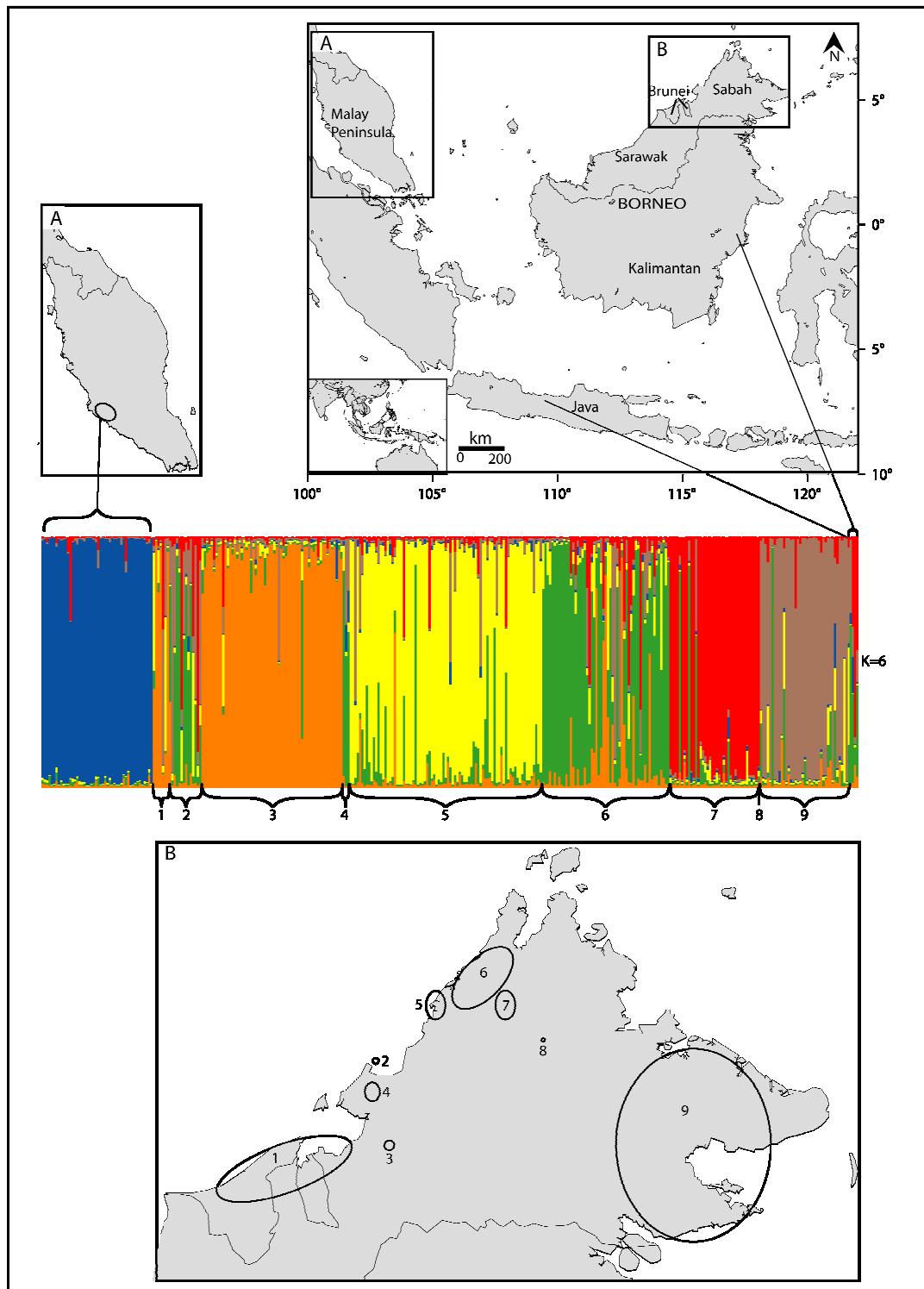


Figure 3-5. A bar plot of the assignment analysis and corresponding geographic distribution of *M. tanarius* individuals. The centre graph illustrates the clustering of microsatellite data assuming the admixture model, and the first K in the plateau phase of the plot of the mean-log-likelihood, $K = 6$, from STRUCTURE (Appendix K, Figure 3-6C). The main map (upper, right hand side) illustrates the regions from which the *M. tanarius* individuals were sampled. The Malay Peninsula and Sabah with northern Sarawak and Brunei are shown, respectively, in greater detail in boxes A (upper, left) and B (lower, centre). Each cluster in the bar plot is related visually to its geographic origin(s), by lines to the upper maps, and numbers in the lower map.

The yellow cluster is comprised of individuals from the western coastal region around Kota Kinabalu and the island Pulau Gaya (region 5). The green cluster is more diverse than the other clusters, mainly consisting of individuals from around the region between Kota Kinabalu and Kota Belud and between Kota Kinabalu and Ranau (region 6), but also including individuals from further south along the coast around Beaufort (region 4) and the island Pulau Tiga (region 2). Furthermore individuals from region 5, which fall mainly in the yellow cluster, show individuals that are assigned with percentages between 0.05 and 87.7 (average 8.6) to the green cluster. Geographically the yellow cluster is located near to the main green cluster (6) and between the northern (6) and southern (2 & 4) green clusters.

The red cluster is also from western Sabah, more inland around Poring and Ranau (region 7). The individuals from this cluster closely border the green cluster to the west, and this is shown again by the high percentage of the green cluster in several individuals. The brown cluster consists of all samples in central and eastern Sabah (regions 8 and 9, respectively). Although these regions are more geographically distant we still see high percentages from both the green and yellow clusters.

With $K = 6$ the individuals from East Kalimantan did not tend to join a single cluster, as did individuals from other regions, with substantial percentages in the green, red, brown, orange and blue clusters, however all of them have the highest percentage in the red cluster (between 36.1% and 80.1%). This may be a mathematical artefact, due to the small number of individuals, however even with much larger numbers of clusters (see Figure 3-6B & D each with $K = 11$), these individuals tend to join multiple clusters with a significant percentage (see Table 2 in the digital appendix).

The *M. tanarius* individual from Java mainly belongs to the green cluster (64.0%), with 29.2% to the brown, and with small percentages in the other four clusters.

Comparing the bar plots for all optimal K values from STRUCTURE and INSTRUCT (Table 3-3) for the assignment analysis of all *M. tanarius* individuals assuming the admixture model shows clearly the separation of the Malaysian individuals (blue cluster) from all the other individuals for all K values (Figure 3-6A-E).

In general the graphs B-E (Figure 3-6) show the same clustering for the *M. tanarius* individuals, as indicated by the long vertical lines and small letters (a-f) below graph C.

Shorter vertical lines indicate the substructure that was detected within some of the main clusters. Cluster d shows a further subdivision (indicated by the *) in the population structure for $K = 11$ (STRUCTURE) in graph B, separating individuals from the Island Pulau Gaya and the individuals from Kota Kinabalu's surrounding. Cluster c3 shows substructure detected by both STRUCTURE and INSTRUCT for $K = 11$ as well as for $K = 7$ (INSTRUCT), separating the individuals which originate from the region between Kota Kinabalu and Kota Belud, close to Kota Kinabalu (*1), from the other individuals of cluster c3. Cluster f shows substructure for the STRUCTURE results in $K = 11$, separating individuals of Danum (*2) from those of Tabin and Tawau (*3).

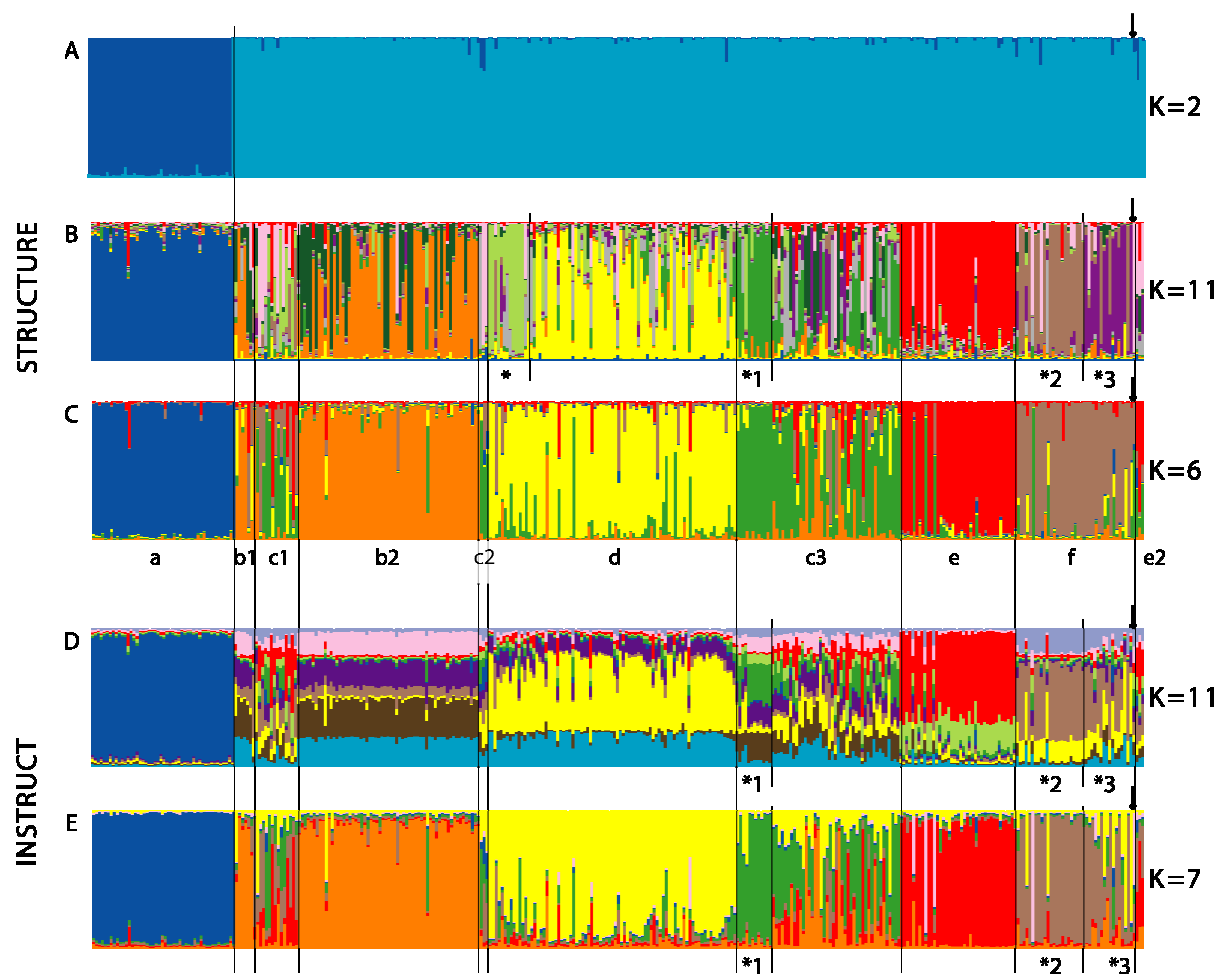


Figure 3-6. Series of bar plots of the assignment analysis of all *M. tanarius* individuals using both STRUCTURE (A-C) and INSTRUCT (D-E). Each graph illustrates the clustering of microsatellite data assuming the admixture model. In each graph, the Individuals are presented in the same order (Appendix K). The five graphs represent the preferred value (this is the highest value for STRUCTURE runs, and the lowest for INSTRUCT) found over ten replicates for:

- A) the optimal ΔK of STRUCTURE; $K = 2$,
- B) the highest likelihood of STRUCTURE; $K = 11$,
- C) the first K in the plateau phase of the plot of the mean-log-likelihood of STRUCTURE; $K = 6$,
- D) the smallest DIC value in INSTRUCT; $K = 11$, and
- E) the first K in the plateau phase of the DIC values of INSTRUCT; $K = 7$.

The vertical lines indicate the common population clusters detected for different values of K ($K = 6, 7$ and 11) for both STRUCTURE and INSTRUCT. These clusters are labelled by the single lower case letters under plot C (letters a-f). Individuals belonging to the same cluster (for example the green cluster c) that are separated in the bar plot have an additional index term (e.g. c1, c2 & c3). The arrow marks the singleton individual from Java. Further substructure is demarcated by short vertical lines within the corresponding plot.

Basically INSTRUCT gives a very similar assignment result for $K = 7$ (graph E), as STRUCTURE for $K = 6$ (graph C), only the green individuals in the red cluster (e) and the green individual from the brown cluster (f) are assigned to one additional cluster, the pink one.

In the barplot for $K = 11$ (graph D) individuals were in principle assigned to the clusters a-f, (only additionally distinguishing (*1) for cluster c3), but INSTRUCT assigns genetically similar individuals not to mainly one cluster, but with highly similar percentages for each individual to each of the several different clusters. In cluster b1 and b2 for example individuals are assigned to all the 11 different clusters created for this barplot with different percentages, but all individuals were assigned with a highly similar percentage to each cluster.

The STRUCTURE barplot for $K = 11$ (B) basically structures the analysed individuals into clusters a-f, but providing more information on the population substructure (indicated by the asterisks below the graph) than the other barplots. Furthermore individuals from clusters c1 and c2 (regions 4 and 2 in Figure 3-5) were distinguished from individuals of cluster c3 (region 6).

Figure 3-7 illustrates a comparison of the STRUCTURE barplot for $K = 11$ between all *M. tanarius* individuals and the subset of *M. tanarius* individuals from Borneo alone. This figure illustrates the key difference in features between these two classes of *M. tanarius* individuals, one additional cluster for the individuals of Malay Peninsula. Although the remaining individuals are grouped into one more cluster for the Bornean individuals, no additional features emerge.

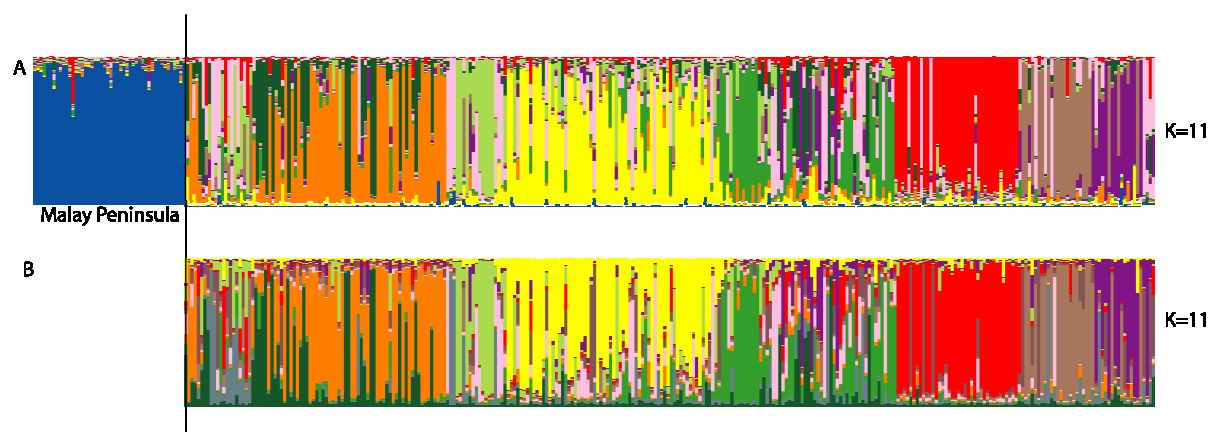


Figure 3-7. Bar plots of the assignment analysis for *M. tanarius* assuming the admixture model, with the highest likelihood of STRUCTURE; $K = 11$, for:

- A) all *M. tanarius* individuals, and
- B) only Bornean *M. tanarius* individuals.

3.2.3 Principal coordinate analysis

Macaranga winkleri

In the PCoA of *M. winkleri* the first two axes account for roughly 60% of the variance (Table 3-4). The first axis is the most descriptive, explaining 35.20% of the variance. This is clearly visualized in the PCoA plot (Figure 3-8), with the existence of two main groups dividing the individuals of Sabah from the individuals of Sarawak/Brunei. The individual presented in pink is the individual that is found between the two groups in the PCoA of the chloroplast data (Figure 2-8). Here this individual clusters with those from Sarawak/Brunei, but not in the main body of Sarawak/Brunei individuals, instead it lies with the outliers in the direction of the Sabah group. Within the group of Sabah individuals, seven individuals lie west of the

Table 3-4. *Macaranga winkleri* and *M. tanarius*. Principal coordinate analysis (PCoA). Percentage of variation explained by the first three axes.

Species	Axis		
	1	2	3
<i>M. winkleri</i>	35.20%	26.47%	11.87%
Cumulative:	35.20%	61.67%	73.54%
<i>M. tanarius</i> ¹	34.79%	17.56%	13.92%
Cumulative:	34.79%	52.34%	66.27%
<i>M. tanarius</i> ²	25.32%	18.14%	17.32%
Cumulative:	25.32%	43.46%	60.78%

1. All individuals.

2. Only Bornean individuals.

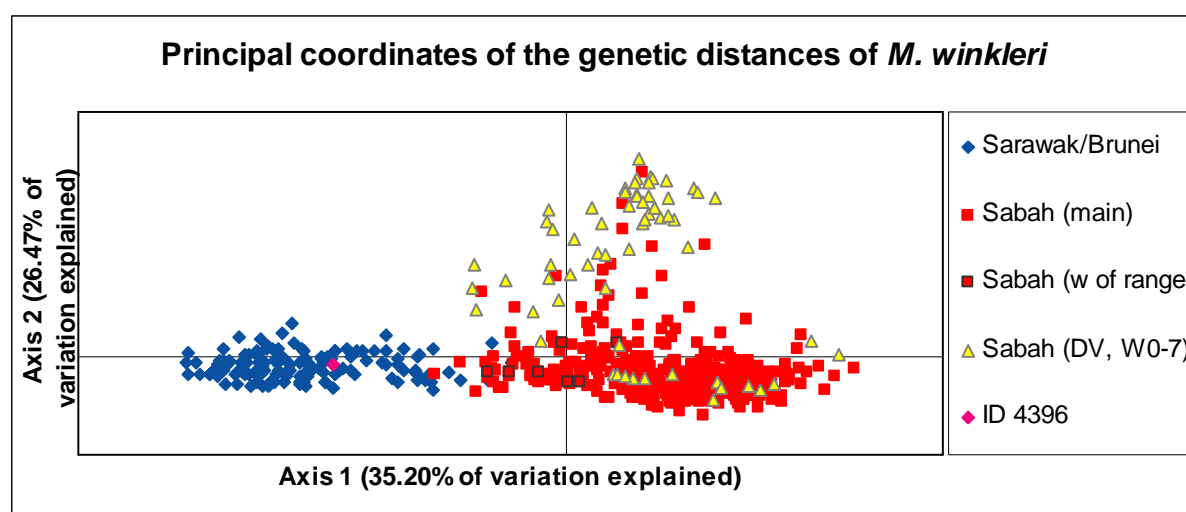


Figure 3-8. Plot of the first and second axes of the PCoA analysis of the genetic distances of *M. winkleri*. Two main divisions along the primary axis divide individuals from Sarawak/Brunei (blue) and individuals from Sabah (red and yellow). The secondary axis primarily divides the individuals from Sabah into those from the Danum Valley, west grid 0-7 (DV, W0-7 shown in yellow), from the main body (in red). Individual 4396 (HT group 4 in the chloroplast analysis) is indicated in pink.

Crocker Range, these are indicated with a solid outline. As with the chloroplast transition individual (pink) these Sabah individuals west of the Crocker Range are not clustered within the main body. Instead these individuals tend towards the periphery of the main body of Sabah individuals. The second axis incorporates a further 26.47% of the variance, clearly illustrating the split of individuals in Sabah into two subgroups. Geographically the second axis splits those individuals along the west grid (0-7) of the Danum Valley from the main group of individuals from Sabah.

Macaranga tanarius

Individuals from Borneo, Java and the Malay Peninsula were analysed in the PCoA of *M. tanarius*. The first two axes account for roughly 50% of the variance (Table 3-4), with the first axis accounting for 34.79% the variance. The PCoA plot of the first two axes (Figure 3-9) shows two main groupings, the individuals from Borneo and the individuals from the Malay Peninsula. The individual from Java clusters with the Bornean individuals, but not with the main body.

A closer analysis of the *M. tanarius* individuals from Borneo was also performed. The first two axes of the PCoA for Bornean *M. tanarius* account for less than 50% of the variance (Table 3-4). At first the plot of the primary and secondary axes (Figure 3-10A) appears to yield little additional information. However, when grouped into geographic regions (corresponding to those in Figure 3-5B) all but one group tends to cluster within the first two axes. The lone holdout (NW Sabah 5) is made up of individuals from Kota Kinabalu and the island Pulau Gaya. These individuals are better differentiated along the third axis (three dimensional plot not shown) found by PCoA, which accounts for 17.32% of the variance,

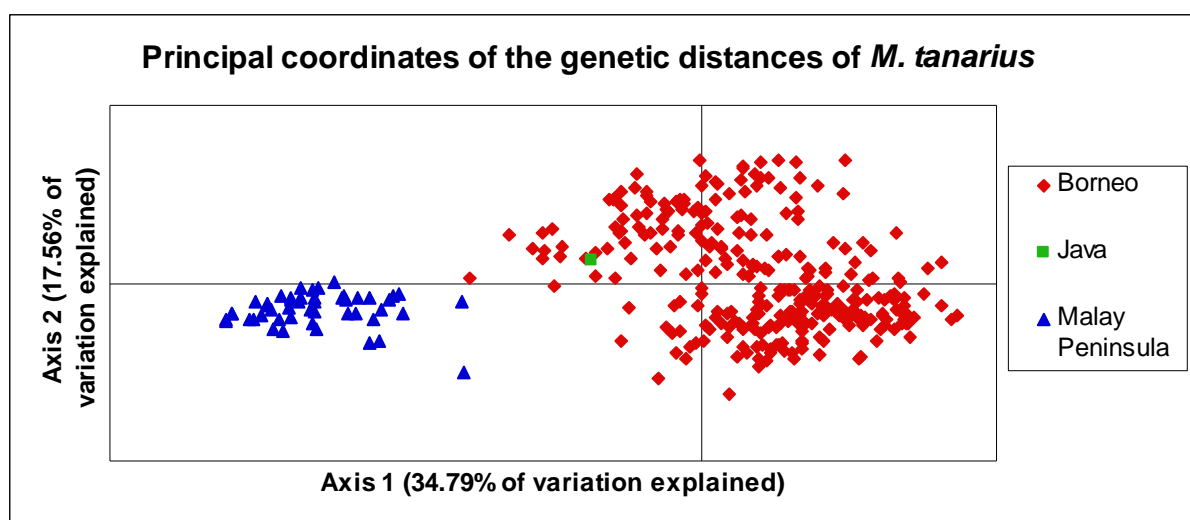


Figure 3-9. Plot of the first and second axes of the PCoA analysis of the genetic distances of *M. tanarius* from Borneo, Java and the Malay Peninsula. The individuals from Borneo are clearly separated from the individuals of the Malay Peninsula. The individual from Java clusters with the Bornean individuals.

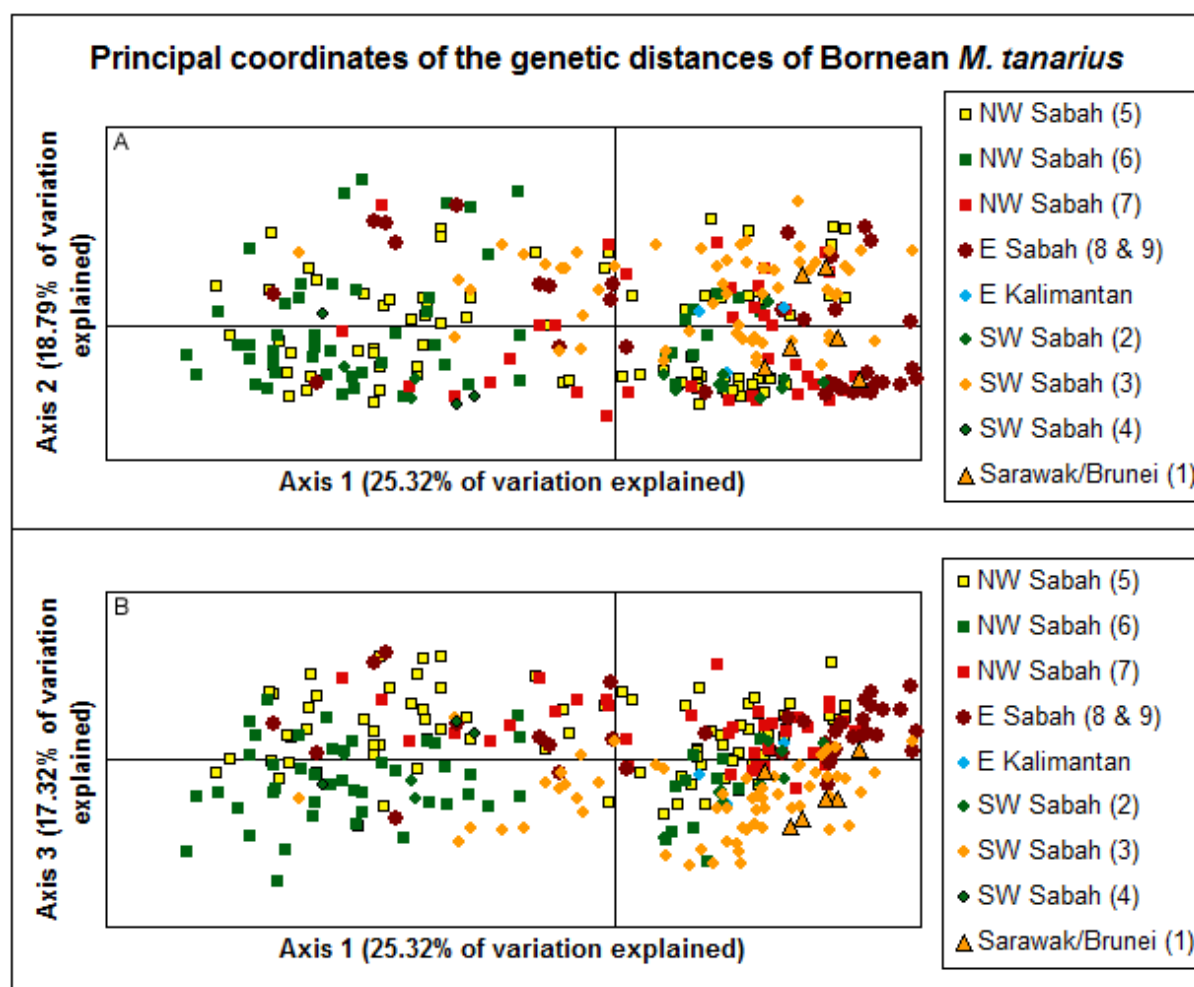


Figure 3-10. A) Plot of the first and second axes of the PCoA analysis. B) Plot of the first and third axis of the genetic distances of *M. tanarius* from Borneo. Abbreviations used: NW = Northwest, E = East, SW = Southwest. Numbers in the legend correspond to the numbers of the geographical regions in B.

Table 3-5. Mean allelic richness for all *M. winkleri*, *M. tanarius* and *M. winkleriella* individuals, and the Bornean *M. tanarius* individuals rarefied for a *g* of 24.

species	group	rarefied for (g)	mean allelic richness	standard error	number of loci
<i>M. winkleri</i>	all	24	8.85	1.27	10
<i>M. tanarius</i>	all	24	7.11	1.57	12
<i>M. tanarius</i>	Borneo	24	7.16	1.58	12
<i>M. winkleriella</i>	all	24	4	0.63	10

Table 3-6. Determination of shared alleles of *M. winkleriella* compared with *M. winkleri* for the nine common SSR markers.

	MactaG01	MactaG07	MachyB10	MachyH11	Macin8f	Macin8n	Macin8h	Macpe6h	Macpe6j
Shared:	6 alleles	3 alleles	4 alleles	3 alleles	2 alleles	3 alleles	3 alleles	1 allele	4 alleles
Unique:	-	-	-	-	-	-	1 allele	-	-

nearly the same as the second axis with 18.14%. Together the first three axes describe over 60% of the variance in the Bornean individuals of *M. tanarius*. While limited to visualizing the multidimensional results of the PCoA, a second view of this data (Figure 3-10B) showing the plot of the first and third axes helps to illustrate the differentiation of different geographical regions.

3.2.4 Genetic diversity and differentiation

To better analyse the genetic diversity, the allelic richness was calculated for each of the ten loci analysed for *M. winkleri* and *M. winkleriella* and the 12 loci analysed for *M. tanarius* using ADZE-1.0.

The mean allelic richness (averaged over the ten loci) with sample size rarefied for $g = 24$ is 8.85 in *M. winkleri*, which is more than twice the value of *M. winkleriella* (4.00). The mean allelic richness of *M. tanarius* is 7.11 for all individuals and 7.16 for the Bornean individuals, and thus smaller than for *M. winkleri* (Table 3-5). For the nine common markers between *M. winkleri* and *M. winkleriella* it was determined that all but one of the alleles found in *M. winkleriella* is shared with *M. winkleri* (Table 3-6).

For *M. winkleri* the mean allelic richness west and east of the Crocker Range (Table 3-7) is rarefied for $g = 70$, and is ~1.5 times larger east than west of the range (14.74 and 9.88, respectively). For *M. tanarius* the mean allelic richness (Table 3-7) west and east of the Crocker Range, rarefied for the same g is of a similar magnitude on either side (10.25 and 11.21, respectively). Comparing *M. tanarius* individuals from Borneo and Malay Peninsula, they are also in a similar range with the individuals from Borneo having a richness of 11.58 and those from Malay Peninsula 9.38. Although both comparative groups of *M. tanarius* have a similar mean allelic richness, the Borneo/Malay Peninsula groups exhibit a larger difference than those on either side of the Crocker Range.

The mean allelic richness (Table 3-8) was again computed, this time rarefied for $g = 6$, for both *M. winkleri* and *M. tanarius*. This rarefaction was necessary in order to compare the division by the Crocker Range with the division between Sabah and Sarawak/Brunei. Both calculations show a similar trend consistent for both *Macaranga* species, that the division between Sarawak/Brunei and Sabah is slightly more pronounced than the division east and west of the mountain range.

To quantify differences among the population west and east of the mountain range Nei's genetic distance, Wright's inbreeding coefficient (F_{ST}) and Hedrick's standardized G_{ST} , were calculated (Table 3-9). The genetic differentiation between the *M. winkleri* population west and east of the mountain range is more than seven times larger than in *M. tanarius* using Nei's genetic distance (0.377 vs. 0.050) and more than five times larger for both F_{ST} (0.093 vs. 0.017) and G'_{ST} (0.398 vs. 0.067). In both cases the value for G'_{ST} more closely approximated Nei's genetic distance than Wright's inbreeding coefficient.

Table 3-7. Mean allelic richness for *M. winkleri* and *M. tanarius* rarefied for $g = 70$. Comparison of *M. winkleri* west and east of the Crocker Range and between Sarawak/Brunei and Sabah. Comparison of *M. tanarius* west and east of the Crocker Range and between Borneo and Malay Peninsula.

species	group	rarefied for (g)	mean allelic richness	standard error	number of loci
<i>M. winkleri</i>	west of Crocker Range	70	9.88	1.74	10
<i>M. winkleri</i>	east of Crocker Range	70	14.74	2.15	10
<i>M. winkleri</i>	Sarawak/Brunei	70	8.87	1.68	10
<i>M. winkleri</i>	Sabah	70	14.41	2.19	10
<i>M. tanarius</i>	west of Crocker Range	70	10.25	2.48	12
<i>M. tanarius</i>	east of Crocker Range	70	11.21	2.76	12
<i>M. tanarius</i>	Borneo	70	11.58	2.85	12
<i>M. tanarius</i>	Malay Peninsula	70	9.38	1.94	12

Table 3-8. Mean allelic richness for *M. winkleri* and *M. tanarius* rarefied for $g = 6$. Comparison west and east of the Crocker Range and Sarawak/Brunei vs. Sabah division.

species	group	rarefied for (g)	mean allelic richness	standard error	number of loci
<i>M. winkleri</i>	west of Crocker Range	6	3.00	0.44	10
<i>M. winkleri</i>	east of Crocker Range	6	3.75	0.35	10
<i>M. winkleri</i>	Sarawak/Brunei	6	2.87	0.44	10
<i>M. winkleri</i>	Sabah	6	3.72	0.36	10
<i>M. tanarius</i>	west of Crocker Range	6	3.14	0.43	12
<i>M. tanarius</i>	east of Crocker Range	6	3.10	0.43	12
<i>M. tanarius</i>	Sarawak/Brunei	6	2.38	0.31	12
<i>M. tanarius</i>	Sabah	6	3.18	0.44	12

Table 3-9. Population differentiation for *M. tanarius* and *M. winkleri* individuals from Borneo west vs. east of the Crocker Range and Sarawak/Brunei vs. Sabah.

Species	populations	Nei genetic distance	pairwise population F_{ST}	pairwise population G'_{ST}
<i>M. winkleri</i>	west vs. east of Crocker Range	0.377	0.093	0.398
<i>M. tanarius</i>	west vs. east of Crocker Range	0.050	0.017	0.067
<i>M. winkleri</i>	Sarawak/Brunei vs. Sabah	0.395	0.099	0.414
<i>M. tanarius</i>	Sarawak/Brunei vs. Sabah	0.150	0.068	0.204
<i>M. tanarius</i>	Malay Peninsula vs. Borneo	0.505	0.114	0.467

These genetic differentiation values were then calculated for both the *M. winkleri* and *M. tanarius* populations divided between Sarawak/Brunei and Sabah (Table 3-9). The genetic differentiation between the *M. winkleri* population between Sarawak/Brunei and Sabah is more than twice that in *M. tanarius* using Nei's genetic distance (0.395 vs. 0.150) and G'_{ST} (0.414 vs. 0.204), and nearly one and a half times larger for F_{ST} (0.099 vs. 0.068). For both *Macaranga* species each of these genetic differentiation measurements was larger for this division than for the west/east division caused by the mountain range. This is most pronounced in the case of *M. tanarius*, with differentiation values three times higher for the division between Sarawak/Brunei and Sabah, while for *M. winkleri* the increase in these values was smaller, but consistent.

The same quantification was performed for the *M. tanarius* populations on Borneo and Malay Peninsula (Table 3-9). Nei's genetic distance is 0.505, the F_{ST} is 0.114 and the G'_{ST} is 0.467. Quantified in each of these ways, the genetic differentiation is much larger than for the *M. tanarius* populations west and east of the mountain range and between Sarawak/Brunei and Sabah.

When considering the geographic regions where both *M. winkleri* and *M. tanarius* were found, there emerge three distinct regions. These three regions are described as: a) Northern Sarawak and Brunei (plus southwestern Sabah for *M. tanarius*), b) northwestern Sabah and c) eastern Sabah. Between these three main sampling regions of Borneo, the inter-regional calculations of the G'_{ST} values for *M. winkleri* vary considerably from those of *M. tanarius* (Figure 3-11). For *M. winkleri* the highest differentiation is detected between population a and c (0.437) and is in a similar range for populations a and b (0.373). The G'_{ST} value is smaller for the populations between b and c (0.092). For *M. tanarius* the value for G'_{ST} is the same for a-c and b-c (0.114) and for a-b it is slightly smaller (0.087).

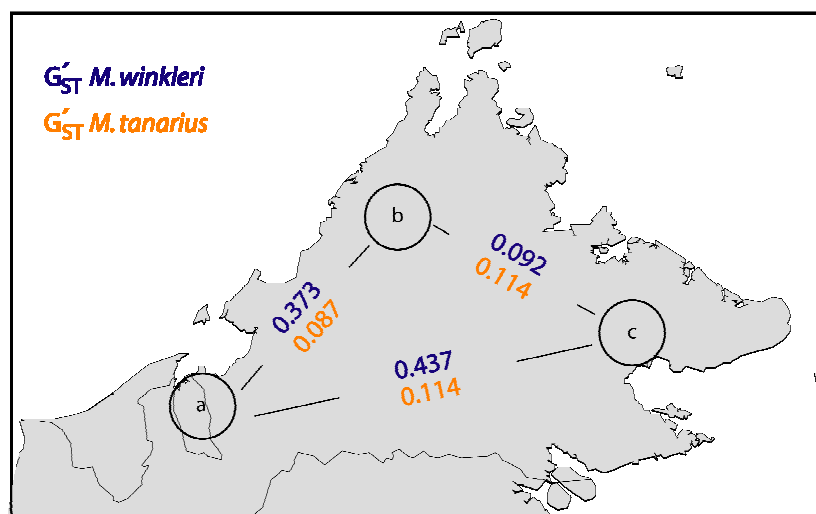


Figure 3-11. G'_{ST} values for *M. winkleri* (shown in blue) and *M. tanarius* (shown in orange) between three populations: a) Northern Sarawak and Brunei (plus southwestern Sabah for *M. tanarius*), b) northwestern Sabah and c) eastern Sabah. The circles indicate the approximate centres of these three sampled regions for both species.

3.3 Discussion of the microsatellite data

In this part of the study nuclear microsatellite markers, which are co-dominant markers generally with a high mutation rate (Sharma et al. 2007), were used. Because of their high variability they can be used as powerful tools for population genetic analysis. The nuclear genome is inherited biparentally (Petit et al. 2005), and thus in contrast to chloroplast data, also reflects pollen-mediated gene flow.

While the main focus in the chloroplast data set of this study is on phylogeographic analyses, which aim to reveal historical processes that formed the extant distribution of genetic variation, here population genetic approaches are used, which interpret differences in allele distribution under the assumption of recent gene flow.

3.3.1 Population genetic structure of *M. winkleri*

Macaranga winkleri is a myrmecophytic pioneer species. It occurs together with its obligate partner ant *Crematogaster* morphospecies (msp.) 8, only in Borneo.

To test the hypothesis of restricted pollen-mediated gene flow in *M. winkleri*, (hypothesis 2 chapter 1.2) assignment analyses were performed using two different programs STRUCTURE and INSTRUCT. Different ways of determining the optimal K lead to the same result. The calculation of ΔK for STRUCTURE (Figure 3-1B) resulted in $K = 3$, as did the more subjective detection of the first K in the plateau phase of the log probability (Figure 3-1A). In accordance with this, the plot of the average DIC values (Figure 3-1C) for INSTRUCT leads to $K = 3$ as an optimal number of clusters, as does the ΔK calculation of the averaged DIC values (Figure 3-1D). These unanimous results for the optimal number of clusters indicate a clear structure of the *M. winkleri* data. The clear geographic differentiation of the nuclear data indicates a geographic restriction of gene flow via pollen, which is in accordance with the hypothesis.

Geographically these three groups of *M. winkleri* are clearly differentiated between the two major regions Sarawak/Brunei and Sabah with a further differentiation within Sabah, indicating a third group (yellow cluster), which is located in the west grid of Danum Valley (Figure 3-4A, B & C and Appendix B). The cluster comprises individuals from west grid 0-7 and individuals sampled at the road to Malua. This genetically distinct cluster can be explained by dispersal events, introducing this combination of genotypes to this region followed by the establishment of a population.

Another optimality criterion (the smallest DIC value) for INSTRUCT is met at $K = 11$. However, this number of clusters continues to illustrate the true clustering ($K = 3$), by classifying the main group from Sabah in such a way as to assign each individual roughly evenly to each of the remaining groups (Figure 3-4D). Thus, the same three groups are indicated again. This shows the importance of a careful choice when determining the optimal

number of clusters. Here, using only the number of K , assessed by the smallest DIC value results in a number of clusters, much higher than the real optimal number of clusters, which becomes obvious by visual inspection of the bar plot.

For STRUCTURE a further optimality criterion (the highest log probability of all replicate runs) is met at $K = 16$. In contrast to the INSTRUCT ad-hoc determination of K , for this analysis, the assignment algorithm works to identify as many subgroups as possible, making it better suited to identifying substructure from smaller geographical regions (Figure 3-4A).

In the assignment analyses it becomes evident that a comparison and careful evaluation of the differently obtained optimal K values and visual inspection of the bar plots is necessary, to access the true population structure. Only using the ad-hoc determination for INSTRUCT results in a K much higher than the true K . However, visual inspection of the bar plot reveals the optimal K . The ad-hoc determination of the number of clusters for STRUCTURE provides information on subpopulations of *M. winkleri*, showing that different numbers of clusters can provide information on different hierarchical levels of structure in the data. In contrast, INSTRUCT when given an excess number of groups ($K \gg$ optimal K), continues to illustrate the true clustering, which makes it more suitable to identifying the upper hierarchical structure, which is represented by $K = 3$ in the *M. winkleri* data set. $K = 3$ was also detected for the calculation of ΔK (STRUCTURE). This is in accordance with Evanno et al. (2005), who found, that calculating ΔK (STRUCTURE) detected accurately the uppermost hierarchical levels of structure for a test scenario. Taking the different approaches for the determination of the best K s together, $K = 3$ as the optimal number of clusters for the *M. winkleri* data set is indicated.

Further analysis using PCoA emphasizes these three genetic geographic groupings of *M. winkleri* (Figure 3-8). Within the first two axes over 60% of the genetic variation are already accounted for. A plot of the primary and secondary axes shows a clear division between the Sarawak/Brunei and Sabah individuals along the primary axis. Along the secondary axis the division between the main body of the Sabah individuals and those individuals from the west grid of the Danum Valley, building the third group, becomes apparent.

Genetic differentiation in *Macaranga winkleri* between Sarawak/Brunei vs. Sabah and individuals west vs. east of the Crocker Range

There are seven *M. winkleri* individuals from Sabah that are west of the Crocker Range. These individuals could be logically grouped, either with the individuals from Sarawak/Brunei to form a group of all individuals west of the Crocker Range (Figure 2-16), or together with the rest of the individuals from Sabah. To determine the groupings with the higher genetic differentiation, and thus lower amounts of pollen-mediated gene flow, three differentiation measures, Nei's genetic distance, the pairwise population F_{ST} and the G'_{ST} , were calculated for each of these groupings.

All analyses performed show a clear genetic differentiation between individuals of *M. winkleri* in Sarawak/Brunei and those of Sabah.

The results of the assignment analysis using both STRUCTURE and INSTRUCT (Figure 3-4) support the existence of the two main clusters, Sarawak/Brunei and Sabah. For the optimal $K = 3$ all individuals from Sarawak/Brunei were assigned to one cluster, and the individuals from Sabah into two clusters. The individual (ID 4396) that was found between the two groups in the chloroplast analysis is assigned to Sarawak/Brunei by both STRUCTURE and INSTRUCT, based on the nuclear SSR data, in accordance with its geographical origin. The differentiation between the groups Sarawak/Brunei and Sabah persists from $K = 2$ up to $K = 16$ (not all plots shown). The persistence of the assignment of membership to the two groups is indicative of the high level of genetic differentiation between these two groups.

In addition the PCoA plot illustrates the split between the two groups along the primary axis (Figure 3-8). The *M. winkleri* individual, ID 4396, is located on the primary axis within the Sarawak/Brunei cluster in the nuclear SSR analysis. However, it is located on the peripheral arm towards the Sabah cluster.

To test the hypothesis of a higher genetic diversity in Sabah compared to Sarawak/Brunei due to long-term persisting rain forests, (hypothesis 9, chapter 1.2), the rarefied mean allelic richness, a measure of genetic diversity, which considers differences in sample sizes was calculated. The value shows a difference between individuals from Sarawak/Brunei and those from Sabah (Table 3-7 & Table 3-8) rarefied for $g = 70$ as well as $g = 6$. *Macaranga winkleri* individuals from Sabah show a higher mean allelic richness than those from Sarawak/Brunei. This is in accordance with the hypothesised higher genetic diversity for Sabah. Castric and Bernatchez (2003) proposed that populations located at the expanding edge of a species' range typically show a low allelic richness. As *M. winkleri* does not occur in the southern parts of Sarawak (Lucy Chong, Sarawak Forest Department, personal communication), this might be the expanding edge of the range and explain the lower allelic richness of the Sarawak/Brunei population compared with the Sabah population.

The differentiation of the *M. winkleri* individuals west and east of the Crocker Range is not as pronounced as for the Sarawak/Brunei and Sabah groupings.

The results of the assignment analysis using both STRUCTURE and INSTRUCT (Figure 3-4) are to assign the *M. winkleri* individuals from Sabah west of the range (IDs 6403-6409) with a high percentage (89.0 - 96.7%) to the Sabah cluster for $K = 3$ (see Appendix J). Accordingly for $K = 11$ these individuals were assigned only with very low percentage to the Sarawak/Brunei cluster (1.6 - 3.7%) while assigned to Sabah clusters with higher percentages (from 14.1 to 21.0%). Correspondingly for $K = 16$ they were assigned with even smaller percentages to Sarawak/Brunei (0.6 - 1.9%) (Table 1 in the digital appendix) and instead strongly grouped in Sabah subgroups (from 38.9 to 90.9%). Both assignment analyses agree that these individuals are more closely related to individuals from Sabah east of the Crocker Range than to individuals from Sarawak/Brunei.

The higher genetic differentiation for *M. winkleri* individuals from Sarawak/Brunei and Sabah compared to those from different sides of the mountain range do not suggest the Crocker Range as a barrier to current gene flow. This can indicate Sarawak/Brunei vs. Sabah as an older split within the species than the split by the Crocker Range. This split within *M. winkleri* between Sarawak/Brunei and Sabah can be explained, as with the chloroplast data (see page 49), by the retreat of the species into two (or more) separate refugia during arid periods of the Pliocene. When better conditions resumed, the subpopulations again expanded, but have not yet been in genetic exchange.

Also the PCoA plot illustrates a clear split between *M. winkleri* individuals from Sarawak/Brunei and Sabah. However, the relationship between the individuals from Sabah west of the Crocker Range to those from Sarawak/Brunei is a close one. These individuals west of the mountain range tend to the periphery of the main Sabah cluster, along the axial arm in the direction of the Sarawak/Brunei cluster (Figure 3-8). While still clearly in the Sabah group, this may indicate that these western Sabah individuals are not as distantly related to the Sarawak/Brunei individuals as the assignment analyses would indicate.

The mean allelic richness west and east of the Crocker Range rarefied for $g = 70$ (9.88 and 14.74, respectively) and for $g = 6$ (3.00 and 3.75, respectively) provide another indicator that the *M. winkleri* individuals from Sabah west of the Crocker Range are more closely related to the Sabah subpopulation. When compared with the mean allelic richness for Sarawak/Brunei vs. Sabah, the allelic diversity of the Sarawak/Brunei individuals (8.87 rarefied for $g = 70$ and 2.87 rarefied for $g = 6$) was less than that for those individuals west of the Crocker Range. For the Sabah individuals the mean allelic richness (14.41 and 3.72, respectively) was approximately the same as for those individuals east of the Crocker Range. Although both means for Sabah were slightly below the respective means east of the mountain range, they were well within the tolerance of the standard error. At first it may seem contradictory that the allelic diversity for Sabah did not show any significant increase. One explanation evident in the PCoA plot is that the individuals from Sabah west of the Crocker Range group with other outliers of Sabah east of the range. It is possible that alleles that were distinct when these individuals were excluded from Sabah are no longer distinct, when including these individuals.

The genetic differentiation metrics for the groups Sarawak/Brunei and Sabah vs. the group west and east of the Crocker Range for *M. winkleri* show very similar values. For Nei's genetic distance, the pairwise population F_{ST} and the G'_{ST} values are consistently slightly bigger for the groups Sarawak/Brunei vs. Sabah than for west and east of the Crocker Range. This indicates a higher differentiation for individuals from Sarawak/Brunei vs. Sabah than for individuals west and east of the range. However, only seven *M. winkleri* individuals (IDs 6403-6409) originate within Sabah and west of the mountain range, the small number possibly biasing these results.

3.3.2 Population genetic structure of *Macaranga tanarius*

Macaranga tanarius is a non-mycorrhizal pioneer tree. It is found in mildly to very disturbed vegetation. Assignment analyses for *M. tanarius* were performed using both STRUCTURE and INSTRUCT. The determination of the best K for STRUCTURE results in $K = 5$ for Bornean *M. tanarius* both for the first K in the plateau phase (Figure 3-2A) and the calculation of ΔK (Figure 3-2B). Calculation of ΔK DIC (INSTRUCT) results in $K = 3$ for Bornean *M. tanarius*.

When considering all *M. tanarius* individuals, which includes the individuals from Malay Peninsula, the assignment analysis typically builds one extra cluster – specifically for those individuals from Malay Peninsula, indicating that these are highly differentiated from the Bornean individuals. This is in accordance with the expectation of a high genetic differentiation between these two groups, caused by vicariant evolution (hypothesis 8, chapter 1.2).

This extra cluster is detected in the optimal K values found using the plateau phase for both STRUCTURE and INSTRUCT as well as with the smallest DIC for INSTRUCT (Table 3-3). Interestingly, this is not the case with the highest log probability, where the optimal K for both the Bornean and all individuals of *M. tanarius* is 11. In this case the analysis for all individuals still maintains one cluster for Malay Peninsula, but redistributes the remaining individuals among 10 rather than 11 clusters (Figure 3-7). This indicates a possible superfluous cluster in this optimality identifier for the Bornean individuals. Again, this shows that a careful check of the optimal number of clusters detected is always necessary.

In the situation of the calculation of ΔK and ΔK DIC values, the optimal K for all *M. tanarius* individuals is found to be $K = 2$, and thus smaller than for only the Bornean individuals ($K = 5$). Similarly for the INSTRUCT analysis the optimal K for all *M. tanarius* individuals is found to be $K = 2$ and for the Bornean individuals $K = 3$. This lower number of optimal clusters can be explained by the fact that the calculation of ΔK detects the uppermost hierarchical level of structure in a data set (Evanno et al. 2005). Thus, a high genetic differentiation between individuals from Borneo and Malay Peninsula is indicated.

An interesting side note when examining the second order rate of change, ΔK and ΔK DIC (Figure 3-2B & D), for the Bornean individuals is a double peak. In both cases the highest peak is reported, but they are not consistent between STRUCTURE and INSTRUCT ($K = 5$ and $K = 3$, respectively). In both cases when the rate of change is combined with the plots of the curves they are based on (Figure 3-2A & C), it becomes apparent that the true optimal occurs at the higher K value ($K = 5$). This is consistent between the analyses, and is in accordance with the result $K = 6$ for all *M. tanarius*, as the individuals from Malay Peninsula are always grouped into a single cluster. In this case combining different approaches for the determination of the optimal K value helps to find the optimal number of clusters in the data.

The different approaches to detect the optimal K, combined with visual inspection of the bar plots, consistently results in five groupings among the Bornean *M. tanarius* individuals as

identified in Figure 3-6 (labelled b-f). This clear small-scale geographic structure, is contradicting the expectations of elevated amounts of pollen-mediated gene flow in the species (hypothesis 5 chapter 1.2), which would result in mixed clusters for the regions.

Further analysis using PCoA confirms the clear genetic geographic differentiation between *M. tanarius* individuals from Borneo and the Malay Peninsula. This differentiation is illustrated along the primary axis which already accounts for nearly 35% of variation (Figure 3-9 & Table 3-4). A further PCoA of the first two axes of only the Bornean individuals (Figure 3-10) already shows groupings previously described by the geographical clusters identified in the assignment analysis (Figure 3-5, K = 6). The larger number of subgroups makes it difficult to visualize the groupings, but the first two axes already account for ~43% of the variation.

The rarefied mean allelic richness for *M. tanarius* shows a difference between individuals from Sarawak/Brunei and those from Sabah (Table 3-7). As with *M. winkleri*, individuals of *M. tanarius* from Sabah show a higher mean allelic richness than those from Sarawak/Brunei indicating the expanding edge of *M. tanarius* to be in Sarawak/Brunei.

Genetic differentiation in *M. tanarius* between individuals west and east of the Crocker Range, Sarawak/Brunei vs. Sabah, and Borneo vs. Malay Peninsula

There are 154 *M. tanarius* individuals from Sabah that were collected west of the Crocker Range. As with *M. winkleri*, these individuals could be grouped with either the individuals from Sarawak/Brunei to form a group of all individuals west of the Crocker Range, or together with the rest of the individuals from Sabah. To determine the grouping with the highest differentiation, the differentiation measures were calculated for each of these groupings.

The results of the assignment analysis using both STRUCTURE and INSTRUCT show that individuals of *M. tanarius* from Sarawak/Brunei and southwestern Sabah consistently cluster together from K = 2 to K = 11 (Figure 3-5 & Figure 3-6, not all plots shown). No indications for a split between individuals from these two regions are given by the assignment analyses. However, as *M. tanarius* only occurs in northern Sarawak, the number of samples from Sarawak/Brunei is limited to six. The PCoA plot does not suggest a split between these groupings either (Figure 3-10). Unlike for *M. winkleri*, the PCoA plot of the first two axes of the Bornean *M. tanarius* does not show a clear differentiation between Sarawak/Brunei and Sabah (Figure 3-10A). In this plot the individuals from Sarawak/Brunei cluster together (towards the far right along the primary axis), but the individuals from Sabah, both west and east, are spread out along both sides of this axis.

The results of the assignment analysis using both STRUCTURE and INSTRUCT (Figure 3-5) do not indicate the Crocker Range as a barrier to current gene flow, as individuals from geographic regions 1, west of the range, and from region 3, east of the range cluster together.

Furthermore the PCoA plot does not suggest high levels of differentiation between individuals west and east of the range, but instead shows groupings consistent with the bar plot analysis.

Nei's genetic distance, the pairwise population F_{ST} and the G'_{ST} for *M. tanarius* are consistently higher for the Sarawak/Brunei and Sabah grouping than for the grouping west and east of the Crocker Range. This indicates a higher genetic differentiation for Sarawak/Brunei, and thus lower levels of gene flow between these groupings. Further it does not indicate the Crocker Range in its current position as a barrier to gene flow. In order to determine a baseline for the measures of differentiation, the three differentiation values were also calculated between the *M. tanarius* individuals from Malay Peninsula and Borneo (as *M. winkleri* is endemic only to Borneo). This comparison was chosen as it represents two geographically distinct populations which should yield the maximum expected differentiation. This way an upper bound for each of these measures is provided allowing for a relative comparison of their magnitudes. All differentiation metrics for *M. tanarius* between Malay Peninsula and Borneo are consistently higher than for the two other comparisons (Sarawak/Brunei vs. Sabah and west vs. east of the Crocker Range). This is in accordance with the PCoA plot, which clearly shows the high differentiation between *M. tanarius* individuals from Malay Peninsula and Borneo along the first axis. This high genetic differentiation between individuals from Malay Peninsula and Borneo is in accordance with the hypothesis of vicariant evolution (hypothesis 8, chapter 1.2). Comparing Nei's genetic distance for *M. tanarius* between Malay Peninsula and Borneo, with the values for individuals west and east of the Crocker Range, shows a roughly 10 times higher value for Malay Peninsula vs. Borneo than for individuals west and east of the Crocker Range and a roughly 3.5 times higher value than for individuals from Sarawak/Brunei vs. Sabah. For the G'_{ST} value, proportions between the different groupings are highly similar to proportions of Nei's genetic distance. For the F_{ST} values, the proportions are slightly changed, yet show the highest value for Malay Peninsula vs. Borneo, the second highest for Sarawak/Brunei vs. Sabah and the lowest value for west vs. east of the Crocker Range.

3.3.3 Comparison of *M. winkleri*, *M. winkleriella* and *M. tanarius*

Assignment analyses were performed on *M. winkleri* and *M. tanarius* using STRUCTURE and INSTRUCT. For *M. winkleri* the true number of clusters (K) was found to be three. For *M. tanarius* the true number of clusters (K) was found to be six for all individuals and five for just the Bornean individuals. This result for *M. tanarius* is consistent as the sixth cluster for all individuals is comprised entirely of individuals from the Malay Peninsula.

The larger K value in *M. tanarius* could mean that there is more differentiation than in *M. winkleri*. However, without additional knowledge regarding the clusters, it is not possible to directly compare the number of optimal clusters from different analyses. For example an alternative scenario is that it could be a measure of the magnitude of differentiation among the allele data. In this scenario the number of clusters alone are not sufficient to determine higher genetic differentiation, but are relative to the magnitude of the peak differentiation. This

scenario is corroborated by the strong local geographic correlation found among the *M. tanarius* clusters, as opposed to the large scale geographic correlation found among the *M. winkleri* clusters. An analogous situation is the comparison of *M. tanarius* for $K = 2$ vs. $K = 6$ (Figure 3-6). At $K = 2$ the clustering is very strong between Malay Peninsula and Borneo and gives no indication of further local differentiation, but does not preclude further differentiation, as seen with $K = 6$. Further evidence that not only supports the second scenario, but points to *M. winkleri* actually having a higher differentiation is the highest log probability (for STRUCTURE) and the smallest DIC value (for INSTRUCT). These values are a determination by each program of the optimal number of clusters supported by the raw data. For STRUCTURE *M. winkleri* is determined to have 16 clusters, as opposed to 11 for Bornean (and all) *M. tanarius*. These values are closer for INSTRUCT, which finds a maximum of 11 possible clusters for *M. winkleri* and 10 for Bornean *M. tanarius* (11 for all).

PCoA plots of the nuclear SSR data for *M. winkleri* and Bornean *M. tanarius*, considered over similar geographic scales, show a much more pronounced population structure in *M. winkleri* than in *M. tanarius*. While *M. winkleri* shows three clear clusters, for *M. tanarius* the clustering is less obvious. This is also reflected by the fact that for *M. winkleri* the first two axes explain ~62% of the variation and for *M. tanarius* only ~43%.

The genetic diversity, assessed by the calculation of the mean allelic richness, rarefied for the same sample size, $g = 24$, is ~1.2 times larger for *M. winkleri* than for Bornean *M. tanarius* (8.85 vs. 7.16). This can indicate differences in the population history of the species e.g. *M. tanarius* could have gone through a genetic bottleneck or local extinction and lost some of its allelic diversity. The lower mean allelic richness can also indicate that *M. winkleri* is older than *M. tanarius*, the latter having had less time for the accumulation of different alleles.

However, comparisons of genetic diversity between different organisms is always difficult, since differences in the mutation rate between closely related species can be detected even for the same DNA regions (Fieldhouse et al. 1997).

Macaranga winkleriella, which is sister species of *M. winkleri*, is endemic to a small area of Northern Sarawak. The species shows a mean allelic richness that is not even half the value of *M. winkleri*. This is in accordance with the hypothesised low levels of genetic diversity for *M. winkleriella* (hypothesis 3, chapter 1.2). It can be explained by the very restricted distribution area, which leads to a small effective population size. Due to fewer individuals, less new alleles originate. Furthermore the change in the frequency of an allele in a smaller population due to random sampling (i.e. genetic drift) is higher. Due to the effect of this elevated genetic drift the probability that more alleles are lost from the population is increased, and the resulting allelic richness is lower. This is in accordance with the studies of Brett et al. (1995) and Hamrick and Godt (1996), who showed that endemic and narrowly distributed species tended to have lower genetic diversity than species with more extensive geographic ranges. For *M. winkleriella* the mean allelic richness detected was low. According to Groombridge et al. (2009) lower genetic diversity can be due to either a recent population crash or a consequence of an evolutionary history of sustained isolation and small effective

population size. When comparing the alleles of *M. winkleriella* and *M. winkleri* for the nine common SSR markers, it was found that all but one allele, found in *M. winkleriella*, is shared with *M. winkleri* (Table 3-6). The fact that these two species share all but one allele can indicate genetic similarity, and thus maybe a recent separation of *M. winkleriella* from *M. winkleri*. However, as in microsatellite genotyping analyses only the fragments sizes are assessed, the possibility of size homoplasy, i.e. that fragments show the same size but not the same sequence, is given. But over short evolutionary scales homoplasy seems of little concern (Jarne & Lagoda 1996) and furthermore this seems unlikely, when analysing nine loci. The assumption of a recent split of *M. winkleriella* from *M. winkleri* can be supported by the low genetic diversity detected for this species.

A comparison of the amount of genetic differentiation, using Hedrick's standardized G'_{ST} between three geographic regions where both *M. winkleri* and *M. tanarius* were found was performed to compare the amounts of gene flow between the species under study. The three geographic regions are: a) Northern Sarawak and Brunei (plus southwestern Sabah for *M. tanarius*), b) northwestern Sabah and c) eastern Sabah. Between these three regions, the inter-regional calculations of the G'_{ST} values for *M. tanarius* vary considerably from those of *M. winkleri* (Figure 3-11). For *M. tanarius* the value for G'_{ST} is the same for a-c and b-c (0.114) and for a-b it is slightly smaller (0.087). This indicates similar amounts of gene flow between all three populations of *M. tanarius*. The detected values are small, indicating low levels of genetic differentiation and, thus, moderate to high levels of gene flow between the three analysed populations.

The case is completely different for *M. winkleri*. Between populations b-c the genetic differentiation for myrmecophytic *M. winkleri* is in a similar range (0.092) as for non-myrmecophytic *M. tanarius*. In contrast to that, the genetic differentiation between population a-c and a-b is much higher (0.437 and 0.373, respectively).

These results are in accordance with the results of the PCoA for *M. winkleri*, which illustrate a pronounced genetic differentiation between the individuals from Sarawak/Brunei (identified here as group a) and the individuals from Sabah (groups b and c) along the primary axis.

The lower genetic differentiation for *M. tanarius* compared to *M. winkleri* indicates a better connectivity of the *M. tanarius* populations via gene flow. This enhanced gene flow between the populations prevents genetic differentiation between them. An explanation for the higher amounts of gene flow in *M. tanarius* than in *M. winkleri* can be the difference in pollinators. While *M. tanarius*' main pollinators are flower bugs, *M. winkleri* is mainly pollinated by thrips. Flower bugs have a larger body size than thrips. As insects with larger body sizes were shown to fly longer distances (Shirai 1995), the flower bugs are supposed to cover larger distances than the thrips pollinating *M. winkleri*. As gene flow limits genetic structure (Duminil et al. 2009), higher levels of pollen-mediated gene flow connect the populations for *M. tanarius*, thus limiting the genetic population differentiation.

To sum up, the genetic differentiation metrics indicate a higher differentiation between the population west and east of the Crocker Range as well as for regions Sarawak/Brunei and

Sabah for the myrmecophytic species *M. winkleri* than for the non-myrmecophytic species *M. tanarius*. This indicates higher levels of gene flow between populations of *M. tanarius* via pollen in the non-myrmecophytic species, which can be explained by better flying ability of its pollinators. In addition a younger age of *M. tanarius* may explain the lower level of genetic differentiation.

4 Combined discussion of the microsatellite and chloroplast analyses

Macaranga winkleri

For myrmecophytic *M. winkleri*, all analyses performed using both the chloroplast and the microsatellite data set show a clear genetic differentiation between individuals from Sarawak/Brunei and individuals from Sabah. This genetic differentiation is more pronounced than the differentiation by the Crocker Range, as individuals from Sabah, west of the range, are clearly more similar genetically to the other individuals from Sabah. Contrary to the expectations (hypothesis 7, chapter 1.2), this does not indicate that this mountain range acts as a primary barrier to either seed or pollen flow, instead it indicates that Sarawak/Brunei vs. Sabah represent an older split within the species.

The chloroplast data shows a pronounced population structure on the regional scale, as reflected by the geographical distribution of the haplotypes (Figure 2-6). This is in accordance with the expected limited dispersal ability for seeds of *M. winkleri* (hypothesis 1, chapter 1.2). Also the population structure inferred by the microsatellite data shows a clear geographic structure, but on a larger geographic scale. In the microsatellite data, the low genetic differentiation within the groups Sarawak/Brunei and Sabah indicates high levels of gene flow within these groups (but not among them). Therefore, the larger distances surpassed by pollen-mediated gene flow, connecting populations can counter-balance low distances detected for the seed flow. Weising et al. (2010) developed a scenario to explain long dispersal distances for thrips, whereby the thrips are passively distributed by the wind.

Macaranga winkleriella

The typical expectations of small populations are that they are more strongly affected by genetic drift (Honnay & Jacquemyn 2007) and also have a smaller number of new alleles originating due to fewer individuals. In accordance with these expectations, *M. winkleriella* had low levels of genetic diversity in both the chloroplast and the nuclear data. The chloroplast haplotype analysis of 13 individuals, using an alignment of *atpB-rbcL* and *rpL16* (2,650 bp) resulted in only two haplotypes. Also the genetic diversity in the microsatellite data, assessed by the mean allelic richness (rarefied for the sample size), is less than half the richness calculated for *M. winkleri*. However, this value may be higher than expected when taking into account the very restricted distribution area of *M. winkleriella*.

In the chloroplast analysis no haplotypes are shared between the sister species *M. winkleri* and *M. winkleriella*. The haplotypes of both species are nine and ten mutational steps apart. This mutational distance is not large, considering that for *M. winkleri* 29 mutational steps were detected on the intraspecific level and can indicate a recent split of *M. winkleri* and *M. winkleriella* into distinct species. The microsatellite data might indicate an even more recent split, as all but one allele of *M. winkleriella*, for the nine common SSR markers, occur also in *M. winkleri* and the nuclear microsatellites are assumed to evolve faster than the

chloroplast DNA (Wolfe et al. 1987). This can indicate that *M. winkleri* populations and the population with the ancestral chloroplast type of *M. winkleriella* were still connected via pollen-based gene flow, while no longer connected via seed-based gene flow.

Macaranga tanarius

As in *M. winkleri*, all analyses performed with the SSR data in non-myrmecophytic *M. tanarius* show a higher genetic differentiation between individuals from Sarawak/Brunei vs. Sabah than for individuals west and east of the Crocker Range. This contradicts the expectations of the mountain range as a major geographic barrier to dispersal (hypothesis 7, chapter 1.2).

The low genetic diversity for the chloroplast data of *M. tanarius*, suggesting a young age of the species, is in contrast to the higher genetic diversity detected for the nuclear SSR data. The higher genetic diversity in the microsatellite data set, compared with the chloroplast data, can reflect the generally higher mutation rate of the nuclear SSR loci compared with the chloroplast loci. This may be due to the sequence motifs and the biparental inheritance of the nuclear genome, which in contrast to the chloroplast, allows for recombination to occur.

The low genetic differentiation within the chloroplast data of *M. tanarius*, reflected by the geographical distribution of the chloroplast haplotypes, is due to low levels of genetic diversity, which is itself a reflection of the young age of the species. In contrast, the low genetic differentiation between the populations in the SSR data is indicative of high levels of pollen-mediated gene flow, as hypothesised (hypothesis 5, chapter 1.2), which in turn prevents high levels of genetic differentiation between the populations.

For *M. tanarius* both the microsatellite and the chloroplast data show relatively high levels of genetic differentiation between individuals from Borneo and Malay Peninsula, as expected due to vicariant evolution (hypothesis 8, chapter 1.2). The level of genetic differentiation is higher in the microsatellite data than in the chloroplast data. This can be explained by a higher mutation rate of the nuclear SSR loci, compared with the chloroplast, and thus a faster accumulation of genetic differences over time.

Comparison of *Macaranga winkleri* and *Macaranga tanarius*

As hypothesised (hypothesis 6, chapter 1.2), the population structure was found to be more pronounced in *M. winkleri* than in *M. tanarius* for both the chloroplast and the microsatellite data. This is consistent with all performed analyses of the chloroplast data. The analyses performed with the SSR data, clearly reveal generally lower levels of genetic differentiation between the populations of *M. tanarius* than of *M. winkleri*, indicating higher levels of pollen-mediated gene flow for *M. tanarius*. For the assignment analyses, a more careful interpretation of the results is necessary, as for *M. winkleri* the optimal number of clusters in a similar geographic range is smaller ($K = 3$) than for *M. tanarius* ($K = 5$), which if considered alone might seem inconsistent. However, when viewed together with the results from the

other analyses it becomes apparent that the higher number of clusters for *M. tanarius* is probably indicating a lower genetic peak differentiation in the data and therefore, a larger number of smaller differences are being distinguished. In other words, for *M. winkleri* a small number of major genetic differentiations (i.e. clusters) are found, whereas for *M. tanarius*, a larger number of minor differentiations are found.

The mean allelic richness is higher within Sabah than within Sarawak/Brunei, for both *M. winkleri* and *M. tanarius*. This is in accordance with the expectations of higher genetic diversity in a long-term persisting rain forest in Sabah compared with Sarawak/Brunei (hypothesis 9, chapter 1.2). In accordance with this, the haplotypic richness for *M. tanarius* is also higher in Sabah than in Sarawak/Brunei. For the chloroplast data of *M. winkleri* the ratio is reversed, being higher in Sarawak/Brunei. A possible explanation can be a stronger influence of genetic drift of the haploid chloroplast genome than on the diploid nuclear genome, due to the smaller effective population size (Ennos 1994).

5 Conclusions

In the genus *Macaranga* roughly 30 species are myrmecophytes. They offer food and nesting space for the ant partners in their hollow stems. In return, the ants protect the plants from herbivores and lianas.

The project, which this dissertation was part of, aimed at the analysis of co-evolutionary and speciation processes in the genus *Macaranga* (Euphorbiaceae) and on the investigation of how the ant could have promoted speciation in the *Macaranga* host plants. Myrmecophytic *Macaranga* species occur in three sections: *Pachystemon*, *Pruinosae* and *Winklerianae*. The number of myrmecophytes in the sections varies strongly. While *Pachystemon* comprises 23 myrmecophytic species (out of 25) and *Pruinosae* five (out of eight), *Winklerianae* comprises only two species, which are both myrmecophytes. To investigate reasons for differences in species richness of ant-plants, analyses of population genetic parameters for sections *Pachystemon* and *Pruinosae* were conducted in parallel projects.

In this dissertation, population structure and dispersal abilities of the species of section *Winklerianae*, were investigated. The two species are *Macaranga winkleri* and *M. winkleriella*, both of which occur together with the same ant species. Furthermore, a non-myrmecophytic species, *M. tanarius*, was included for a comparison with the myrmecophytic *Winklerianae* species.

In contrast to non-myrmecophytic species, myrmecophytic species can be expected to show limited effective colonisation, as they can only disperse to areas where the ant partner is already present or within flight distance of the colonising ant. For *M. winkleri* a limited ability of seed dispersal, due to the dependence on the ant partner could be shown by the geographical distribution of the chloroplast haplotypes. The chloroplast data show a pronounced population structure on the regional scale (Figure 2-6).

The population structure inferred by the data of the biparentally inherited nuclear microsatellites also reveals a clear geographic structure for *M. winkleri*, but on a larger geographic scale (Figure 3-4). This indicates that pollen-based gene flow reaches further than gene flow mediated by seeds (see page 99). In *M. tanarius* high levels of gene flow are indicated by low G'_{ST} suggesting that the pollinating flower bugs of *M. tanarius* connect populations via gene flow even better than the thrips of *M. winkleri*.

The stronger population structure for the chloroplast compared to the SSR data can partly be attributed to the smaller effective population size of the haploid chloroplast genome. However, it is also indicative of a more efficient pollen dispersal in *M. winkleri* than was previously anticipated due to expected restricted flying abilities of the thrips, which are the main pollinators. In *M. tanarius* low levels of genetic diversity were detected for the chloroplast analyses. The phylogeographic analysis suggests either a young age and a rapid colonisation or a relatively recent population bottleneck followed by a fast colonisation for this species.

In the narrow endemic species *M. winkleriella* low levels of genetic diversity were detected by both chloroplast sequences and nuclear microsatellite markers. This can be explained by the very restricted distribution area, leading to a small effective population size and genetic drift acting more strongly on the smaller population. In the chloroplast haplotype network *M. winkleriella* is clearly separated (by 9 and 10 mutational steps) from its sister species *M. winkleri* (Figure 2-5). In contrast to this, in the microsatellite analysis all but one of the alleles found in *M. winkleriella* is shared with *M. winkleri* (Table 3-6), indicating genetic similarity and thus may be a recent separation of *M. winkleriella* from *M. winkleri*. It can be concluded that *M. winkleri* populations and the population with the ancestral chloroplast type of *M. winkleriella* were connected much longer via pollen-based gene flow, while no longer connected via seed-based gene flow.

For myrmecophytic *M. winkleri*, all analyses performed with the chloroplast and the microsatellite data show a clear genetic differentiation between individuals from Sarawak/Brunei and those from Sabah. This genetic differentiation is more pronounced than the differentiation of populations west and east of the Crocker Range. This indicates that Sarawak/Brunei vs. Sabah represent an older split within this species.

This split can be explained by the species being in refugia, in both Sarawak/Brunei and Sabah when the rainforest became fragmented during arid periods of the Pliocene, and then when better conditions resumed, spreading out from there. The fact that the haplotypes are private for the regions Sarawak/Brunei and Sabah would then indicate that the two (or more) subpopulations from both regions have not been in genetic exchange after spreading out of the refugia. This can be explained by a low effective speed of seed dispersal. Nowadays *Macaranga winkleri* does not occur close to the southwestern coast of Sabah, because in this region no more forest exists. Therefore, gene flow among *M. winkleri* from the subpopulations Sarawak/Brunei and Sabah is probably limited.

A high number of missing intermediates between haplotypes from Sabah and Sarawak/Brunei were detected. These missing haplotypes could be reflecting haplotypes that became extinct due to anthropogenic deforestation. However, it seems improbable that the large number of missing intermediates in the chloroplast network of *M. winkleri* between regions Sarawak/Brunei and Sabah is only reflecting the recent anthropogenic deforestation during the last century. In this case some intermediate haplotypes would still be expected to occur in the proximity of the deforested area. Since no intermediate haplotypes were detected an older separation of the two groups is suggested.

The identical chloroplast haplotype detected in *M. winkleri* on both sides of the mountain range can be explained by a refugium in Sabah, located in or near the Crocker Range and spreading out of the species from the refugium to both sides of the Crocker Range. This is in accordance with the population structure of *M. winkleri* reflected by the nuclear microsatellite markers.

The fact that section *Winklerianae* comprises only two species, thus lacking a pronounced radiation of myrmecophytes, can generally be explained by a higher connectivity by gene

flow. These elevated amounts of gene flow have so far prevented the separation of subpopulations, and thus allopatric speciation. However, a clear split within *M. winkleri* for subpopulations from Sarawak/Brunei and Sabah was shown, indicating allopatric separation and possibly a beginning of allopatric speciation.

An explanation for the higher connectivity by gene flow compared with the other sections could be less restricted effective seed dispersal due to a more mobile ant-partner. The specific ant partner of *M. winkleri*, *Crematogaster* msp. 8, is highly dependent on its host. Nevertheless, the genetic structure was shown to be less pronounced than in other less host-specific *Crematogaster* ants from the subgenus *Decacrema* (Braasch 2008). This implies a better dispersal ability of *Crematogaster* msp. 8 compared with the other ant species. An explanation for the longer flight distances can be the larger body size of these ant queens in comparison to the ants from subgenus *Decacrema* (Feldhaar et al. 2010), providing better mobility. In addition, good genetic exchange among populations may also be maintained by elevated amounts of pollen-mediated gene flow, shown in this work.

In a next step my data will be combined and compared with population genetic parameters of the parallel projects analysing the obligate myrmecophytes of the more radiated sections *Pachystemon* and *Pruinosae*. To do this, the same population genetic differentiation measures, preferably standardized for the maximum variability of the markers utilised, using the nuclear microsatellite data for all *Macaranga* species analysed in the frame of the project will be calculated. This way a direct comparison of the amounts of pollen flow among populations will be possible. Also for the chloroplast analyses, the population differentiation will be compared, allowing for conclusions of differences in the population structure and seed dispersal abilities of the myrmecophytes from the more species rich sections with section *Winklerianae*.

Abstract

The genus *Macaranga* Thou. (Euphorbiaceae) comprises about 260 dioecious species that are distributed in the tropics from West Africa through Southeast Asia to some remote Pacific islands. Some of the most important pioneer trees of lowland dipterocarp forests of the Malay Archipelago belong to this genus. An interesting characteristic of *Macaranga* is its various associations with ants. Roughly 30 species are ant-plants (myrmecophytes), providing food and nesting space for the ants in their hollow stems. The ants protect their hosts from herbivores and climbers.

The population structure and dispersal abilities of the two myrmecophytic species of section *Winklerianae*, *M. winkleri* and *M. winkleriella* were investigated. *Macaranga winkleri* is endemic to Borneo, while *M. winkleriella* occurs only in a small limestone area in northern Sarawak (Borneo). Both species are obligate myrmecophytes, which means that both partners, the ant and the plant, cannot survive without each other. Myrmecophytic species can be expected to show limited effective seed dispersal, as, in contrast to non-myrmecophytic species, they can only disperse to areas where the ant partner is already present or within flight distance of the colonising ant. To compare the population structure and dispersal abilities of myrmecophytes and non-myrmecophytes the non-myrmecophytic species, *M. tanarius* (Tanarius group), distributed from India and southern China to Australia and New Guinea, was included in this study.

A chloroplast sequence analysis was conducted using three non-coding chloroplast markers, *atpB-rbcL*, *rpL16* and *ccmp5* to reconstruct the phylogeographic history and differences in seed dispersal abilities of the species under study. Additionally, population genetic analyses for the three species were conducted based on nuclear microsatellite markers. For this purpose up to 11 microsatellite markers per species were developed.

Macaranga winkleri shows a pronounced population structure on the regional scale for the chloroplast data, reflecting limited seed dispersal abilities. Also the data of the biparentally inherited nuclear microsatellites reveal a clear population structure, but on a larger geographic scale, which can indicate that pollen-based gene flow reaches further than seed-mediated gene flow.

In the locally restricted species, *M. winkleriella*, only small amounts of genetic diversity were detected by both marker systems used.

In *M. tanarius* low levels of genetic diversity were detected for the chloroplast analyses. The phylogeographic analysis for this species suggests either a young age and a rapid colonisation or a relatively recent population bottleneck followed by fast colonisation. Lower levels of genetic differentiation among populations for the nuclear microsatellites, than in *M. winkleri*, can indicate higher amounts of pollen-mediated gene flow.

In contrast to other myrmecophytic sections of *Macaranga*, section *Winklerianae* comprises only two species, thus lacking a pronounced radiation of myrmecophytes. This lack of

radiation can be explained by a better genetic connectivity of populations of *M. winkleri* compared with species in the more radiated sections, so far preventing processes of allopatric speciation.

Zusammenfassung

Die Gattung *Macaranga* Thou. (Euphorbiaceae) umfasst ungefähr 260 diözische Arten, die von Afrika über Südostasien bis zu abgelegenen Inseln im Pazifik vorkommen. Einige der wichtigsten Pionierbäume des typischen Dipterokarpenwaldes des Tieflands des Malayischen Archipels gehören zu dieser Gattung. Eine Besonderheit von *Macaranga* ist die vielfältige Vergesellschaftung mit Ameisen. Ungefähr 30 Arten sind Ameisenpflanzen (Myrmecophyten), die Futter und Nistraum für die Ameisen im hohlen Stamm bieten und im Gegenzug Schutz gegen Herbivore und Bewuchs mit Lianen von den Ameisen erhalten.

Die Populationsstruktur und Ausbreitungsfähigkeiten der beiden Arten der Sektion *Winklerianae*, *Macaranga winkleri* und *M. winkleriella*, wurden untersucht.

Macaranga winkleriella ist in ihrer Verbreitung auf ein Kalksteingebiet im nördlichen Sarawak (Borneo) beschränkt, während *M. winkleri* endemisch für Borneo ist. Beide Arten sind obligate Myrmecophyten, das heißt beide Partner, die Pflanze und die Ameise, können nicht alleine überleben. Für Myrmecophyten wird eine begrenzte effektive Ausbreitung über Samen erwartet, da sie sich im Gegensatz zu Nichtmyrmecophyten nur in Gebiete ausbreiten können, wo die spezifische Ameise bereits ist oder sich in Flugdistanz befindet. Um die Populationsstruktur von myrmecophytischen und nicht-myrmecophytischen Arten zu vergleichen, wurde die von Indien und Südchina bis nach Australien und Neuguinea verbreitete *M. tanarius* (*Tanarius* group) ebenfalls analysiert.

Drei nichtkodierende Chloroplastenregionen, *atpB-rbcL*, *rpL16* und *ccmp5*, wurden sequenziert, um die Populationsstruktur der drei *Macaranga* Arten zu untersuchen. Um populationsgenetische Analysen durchführen zu können, wurden zwischen 10 und 11 nukleare Mikrosatellitenmarker pro Art entwickelt und eine Genotypisierung durchgeführt.

Die eingeschränkte Ausbreitungsfähigkeit über Samen von *M. winkleri* zeigt sich in der starken geographischen Struktur der Chloroplasten Haplotypen. Auch die biparental vererbten nuklearen Mikrosatelliten zeigen eine deutliche Populationsstruktur, aber auf einer großen geographischen Skala, was zeigt, dass der Genfluss über Pollen weiter reicht als der über Samen.

Für *M. winkleriella*, die lokal begrenzt vorkommt, wurde sowohl in den Chloroplasten- als auch den Mikrosatellitenmarkern nur geringe genetische Diversität detektiert.

Macaranga tanarius zeigt geringe genetische Diversität in den Chloroplastenmarkern. Die phylogeographische Analyse für diese Art lässt entweder auf ein geringes Alter und eine schnelle Ausbreitung schließen, oder einen durchlaufenen „genetischen Flaschenhals“, ebenfalls gefolgt von schneller Ausbreitung. Die in der Mikrosatellitenanalyse festgestellte geringere genetische Differenzierung zwischen den Populationen spiegelt höheren Genfluss über Pollen wider.

Im Gegensatz zu den anderen myrmecophytischen *Macaranga* Sektionen, besteht die Sektion *Winklerianae* nur aus zwei Arten. Die geringe Zahl an Arten in der Sektion lässt sich dadurch erklären, dass die Populationen von *M. winkleri*, verglichen mit den Populationen der Arten in den anderen Sektionen, im besseren genetischen Austausch stehen und dadurch allopatrische Artbildung bisher verhindert wurde.

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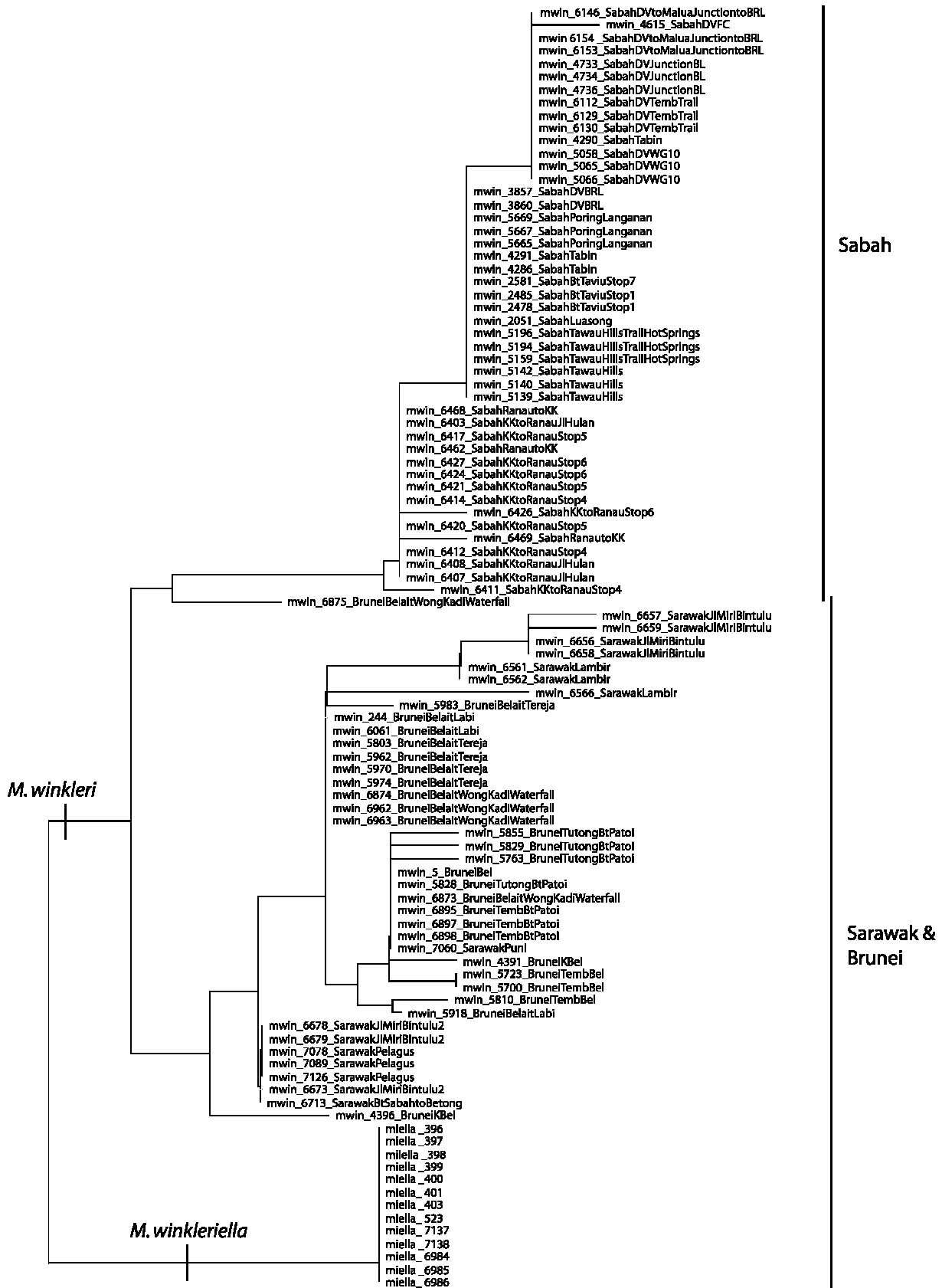
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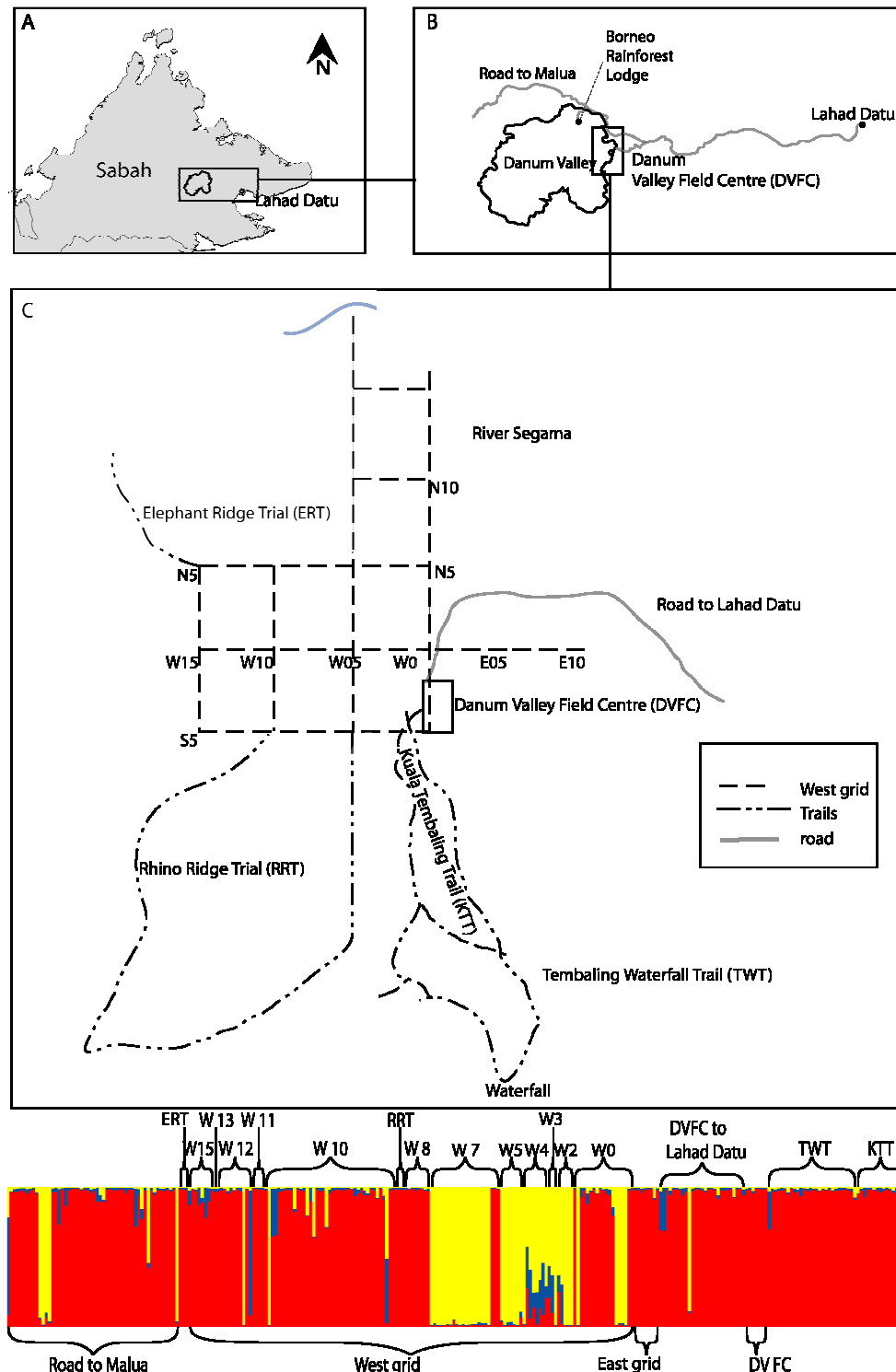
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Neighbor-joining tree of *M. winkleri* and *M. winkleriella*



Appendix B A bar plot of the assignment analysis and corresponding geographic distribution of *M. winkleri* individuals (Appendix J) highlighting the small scale population structure of the species in the Danum Valley of Sabah (Figure 3-4C). The graph along the bottom illustrates the clustering of microsatellite data assuming the admixture model, and the first K in the plateau phase of the plot of DIC values, from INSTRUCT, $K = 3$. The map of Sabah (A) shows the relative position of the Danum Valley (B). The majority of the *M. winkleri* individuals were sampled from the specific region of the valley as detailed in (C). Each cluster in the bar plot is related to its geographic origin(s), in detail by grid position (specified above the bar plot) and more generally below the graph. Abbreviations used with the bar plot are expanded in (C).



Appendix C Plant material used in this study. ID, field number, habitat/ecology, collection date collector and herbarium number are given. Latitude and longitude was whenever possible determined with a GPS, otherwise using fallingrain.com.

Plant ID Number	Species	Field number	Latitude	Longitude	Location	Habitat / Ecology	Collection Date (dd.mm.yy)	Collector	Herbarium (Number)
448	<i>M. tarantus</i>	01-034	4.450	101.370	Malaysia, Peninsula, Pahang, Cameron Highlands, Tanah Rata		15.02.01	UMoog	Leiden
2734	<i>M. tarantus</i>	DG05-10	3.239	101.633	Malaysia, Peninsula, Selangor, FRIM, forest road	roadside	22.07.05	DGuicking	KAS
2743	<i>M. tarantus</i>	DG05-19	3.238	101.633	Malaysia, Peninsula, Selangor, FRIM, forest road	roadside	22.07.05	DGuicking	
45	<i>M. tarantus</i>	M6	3.148	101.711	Malaysia, Peninsula, Selangor, Kuala Lumpur		04.09.98	UMaschwitz	
2682	<i>M. tarantus</i>	M73	3.320	101.750	Malaysia, Peninsula, Selangor, Gombak Valley		04.09.98	UMaschwitz	
6083	<i>M. tarantus</i>	CB-06-16	3.340	101.820	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	roadside	08.08.06	CBAier	
6084	<i>M. tarantus</i>	CB-06-17	3.340	101.820	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	roadside	08.08.06	CBAier	
6085	<i>M. tarantus</i>	CB-06-18	3.340	101.820	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	roadside	08.08.06	CBAier	
6086	<i>M. tarantus</i>	CB-06-19	3.340	101.820	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	roadside	08.08.06	CBAier	
6087	<i>M. tarantus</i>	CB-06-20	3.340	101.820	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	roadside	08.08.06	CBAier	
6088	<i>M. tarantus</i>	CB-06-21	3.340	101.820	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	roadside	08.08.06	CBAier	
6089	<i>M. tarantus</i>	CB-06-22	3.340	101.820	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	roadside	08.08.06	CBAier	
6090	<i>M. tarantus</i>	CB-06-23	3.340	101.820	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	roadside	08.08.06	CBAier	
6092	<i>M. tarantus</i>	CB-06-25	3.340	101.820	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	roadside	08.08.06	CBAier	
6093	<i>M. tarantus</i>	CB-06-26	3.340	101.820	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	roadside	08.08.06	CBAier	GAT-6397
6094	<i>M. tarantus</i>	CB-06-27	3.340	101.820	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	roadside	08.08.06	CBAier	GAT-6393
6095	<i>M. tarantus</i>	CB-06-28	3.330	101.770	Malaysia, Peninsula, Selangor, old Genting road, 43 km to K.L.	roadside	08.08.06	CBAier	
6096	<i>M. tarantus</i>	CB-06-29	3.330	101.770	Malaysia, Peninsula, Selangor, old Genting road, 43 km to K.L.	roadside	08.08.06	CBAier	
6097	<i>M. tarantus</i>	CB-06-30	3.330	101.760	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	roadside	08.08.06	CBAier	
6098	<i>M. tarantus</i>	CB-06-31	3.330	101.760	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	roadside	08.08.06	CBAier	
6099	<i>M. tarantus</i>	CB-06-32	3.330	101.760	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	roadside	08.08.06	CBAier	
6100	<i>M. tarantus</i>	CB-06-33	3.330	101.760	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	roadside	08.08.06	CBAier	
6101	<i>M. tarantus</i>	CB-06-34	3.330	101.760	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	roadside	08.08.06	CBAier	
6102	<i>M. tarantus</i>	CB-06-35	3.330	101.760	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	roadside	08.08.06	CBAier	
6103	<i>M. tarantus</i>	CB-06-36	3.330	101.760	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	roadside	08.08.06	CBAier	
6104	<i>M. tarantus</i>	CB-06-37	3.330	101.760	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	roadside	08.08.06	CBAier	
6105	<i>M. tarantus</i>	CB-06-38	3.330	101.760	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	roadside	08.08.06	CBAier	
6106	<i>M. tarantus</i>	CB-06-39	3.330	101.760	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	roadside	08.08.06	CBAier	
6107	<i>M. tarantus</i>	CB-06-40	3.330	101.760	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	roadside	08.08.06	CBAier	
6108	<i>M. tarantus</i>	CB-06-41	3.330	101.760	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	roadside	08.08.06	CBAier	
6109	<i>M. tarantus</i>	CB-06-42	3.330	101.760	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	roadside	08.08.06	CBAier	
6110	<i>M. tarantus</i>	CB-06-43	3.330	101.760	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	roadside	08.08.06	CBAier	
6111	<i>M. tarantus</i>	CB-06-44	3.330	101.760	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	roadside	08.08.06	CBAier	GAT-6395
6086	<i>M. tarantus</i>	CB-06-01	3.310	101.740	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	roadside	08.08.06	CBAier	
6069	<i>M. tarantus</i>	CB-06-02	3.310	101.740	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	roadside	08.08.06	CBAier	
6070	<i>M. tarantus</i>	CB-06-03	3.310	101.740	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	roadside	08.08.06	CBAier	
6071	<i>M. tarantus</i>	CB-06-04	3.310	101.740	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	roadside	08.08.06	CBAier	
6072	<i>M. tarantus</i>	CB-06-05	3.310	101.740	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	roadside	08.08.06	CBAier	GAT-6394
6073	<i>M. tarantus</i>	CB-06-06	3.310	101.740	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	roadside	08.08.06	CBAier	GAT-6392
6074	<i>M. tarantus</i>	CB-06-07	3.310	101.740	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	roadside	08.08.06	CBAier	
6075	<i>M. tarantus</i>	CB-06-08	3.310	101.740	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	roadside	08.08.06	CBAier	
6077	<i>M. tarantus</i>	CB-06-10	3.310	101.740	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	roadside	08.08.06	CBAier	
6078	<i>M. tarantus</i>	CB-06-11	3.310	101.740	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	roadside	08.08.06	CBAier	
6079	<i>M. tarantus</i>	CB-06-12	3.310	101.740	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	roadside	08.08.06	CBAier	
6080	<i>M. tarantus</i>	CB-06-13	3.310	101.740	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	roadside	08.08.06	CBAier	
6081	<i>M. tarantus</i>	CB-06-14	3.310	101.740	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	roadside	08.08.06	CBAier	
6082	<i>M. tarantus</i>	CB-06-15	3.310	101.740	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	roadside	08.08.06	CBAier	
41	<i>M. tarantus</i>	BF0757	3.729	101.750	Malaysia, Pahang, Fraser's Hill		09.08.38	UMaschwitz	
6001	<i>M. tarantus</i>	BF42406	4.800	114.650	Brunei, Tutong, between Tutong and T.Merimbun, close to Kg. Maya	roadside	30.08.06	BFfiala	
6002	<i>M. tarantus</i>	BF42506	4.800	114.650	Brunei, Tutong, between Tutong and T.Merimbun, close to Kg. Maya	roadside	30.08.06	BFfiala	
6929	<i>M. tarantus</i>	BF0762	4.876	114.879	Brunei, road BSB-Seria, Liang, km 64	roadside	30.08.07	BFfiala	
6930	<i>M. tarantus</i>	BF0763	4.876	114.879	Brunei, road BSB-Seria, Liang, km 64	roadside	31.08.07	BFfiala	
6931	<i>M. tarantus</i>	BF0764	4.876	114.879	Brunei, road BSB-Seria, Liang, km 64	roadside	31.08.07	BFfiala	
28	<i>M. tarantus</i>	M50	4.941	114.949	Brunei, Bandar Seri Begawan	roadside	17.09.98	UMaschwitz	
6922	<i>M. tarantus</i>	BF0757	4.862	115.406	Malaysia, Sarawak, 15 km to Lawas	roadside	29.08.07	BFfiala	
6924	<i>M. tarantus</i>	BF0759	4.862	115.406	Malaysia, Sarawak, 15 km to Lawas	roadside	29.08.07	BFfiala	
5232	<i>M. tarantus</i>	DG06_325	5.731	115.652	Malaysia, Borneo, Sabah, Pulau Tiga Island	along trails in forest	06.09.06	DGuicking	
5233	<i>M. tarantus</i>	DG06_326	5.731	115.652	Malaysia, Borneo, Sabah, Pulau Tiga Island	along trails in forest	06.09.06	DGuicking	
5234	<i>M. tarantus</i>	DG06_327	5.731	115.652	Malaysia, Borneo, Sabah, Pulau Tiga Island	along trails in forest	06.09.06	DGuicking	
5235	<i>M. tarantus</i>	DG06_328	5.731	115.652	Malaysia, Borneo, Sabah, Pulau Tiga Island	along trails in forest	06.09.06	DGuicking	
5236	<i>M. tarantus</i>	DG06_329	5.731	115.652	Malaysia, Borneo, Sabah, Pulau Tiga Island	along trails in forest	06.09.06	DGuicking	
5237	<i>M. tarantus</i>	DG06_330	5.731	115.652	Malaysia, Borneo, Sabah, Pulau Tiga Island	along trails in forest	06.09.06	DGuicking	
5238	<i>M. tarantus</i>	DG06_331	5.731	115.652	Malaysia, Borneo, Sabah, Pulau Tiga Island	along trails in forest	06.09.06	DGuicking	
5239	<i>M. tarantus</i>	DG06_332	5.731	115.652	Malaysia, Borneo, Sabah, Pulau Tiga Island	along trails in forest	06.09.06	DGuicking	
5240	<i>M. tarantus</i>	DG06_333	5.731	115.652	Malaysia, Borneo, Sabah, Pulau Tiga Island	along trails in forest	06.09.06	DGuicking	
5241	<i>M. tarantus</i>	DG06_334	5.731	115.652	Malaysia, Borneo, Sabah, Pulau Tiga Island	along trails in forest	06.09.06	DGuicking	
5242	<i>M. tarantus</i>	DG06_335	5.731	115.652	Malaysia, Borneo, Sabah, Pulau Tiga Island	along trails in forest	06.09.06	DGuicking	
5243	<i>M. tarantus</i>	DG06_336	5.731	115.652	Malaysia, Borneo, Sabah, Pulau Tiga Island	along trails in forest	06.09.06	DGuicking	
5244	<i>M. tarantus</i>	DG06_337	5.731	115.652	Malaysia, Borneo, Sabah, Pulau Tiga Island	along trails in forest	06.09.06	DGuicking	
6190	<i>M. tarantus</i>	CB-06-122	5.180	116.590	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasia	roadside	21.08.06	CBAier	
6191	<i>M. tarantus</i>	CB-06-123	5.180	116.590	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasia	roadside	21.08.06	CBAier	
6192	<i>M. tarantus</i>	CB-06-124	5.180	116.590	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasia	roadside	21.08.06	CBAier	
6193	<i>M. tarantus</i>	CB-06-125	5.180	116.590	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasia	roadside	21.08.06	CBAier	
6194	<i>M. tarantus</i>	CB-06-126	5.180	116.590	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasia	roadside	21.08.06	CBAier	
6195	<i>M. tarantus</i>	CB-06-127	5.180	116.590	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasia	roadside	21.08.06	CBAier	
6196	<i>M. tarantus</i>	CB-06-128	5.180	116.590	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasia	roadside	21.08.06	CBAier	GAT-6369
6197	<i>M. tarantus</i>	CB-06-129	5.180	116.590	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasia	roadside	21.08.06	CBAier	
6198	<i>M. tarantus</i>	CB-06-130	5.180	116.590	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasia	roadside	21.08.06	CBAier	
6199	<i>M. tarantus</i>	CB-06-131	5.180	116.590	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasia	roadside	21.08.06	CBAier	
6176	<i>M. tarantus</i>	CB-06-108	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	20.08.06	CBAier	GAT-6366 / 6375
6177	<i>M. tarantus</i>	CB-06-109	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	20.08.06	CBAier	
6178	<i>M. tarantus</i>	CB-06-110	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	20.08.06	CBAier	
6179	<i>M. tarantus</i>	CB-06-111	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	20.08.06	CBAier	
6180	<i>M. tarantus</i>	CB-06-112	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	20.08.06	CBAier	
6181	<i>M. tarantus</i>	CB-06-113	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	20.08.06	CBAier	
6182	<i>M. tarantus</i>	CB-06-114	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	20.08.06	CBAier	
6183	<i>M. tarantus</i>	CB-06-115	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	20.08.06	CBAier	
6184	<i>M. tarantus</i>	CB-06-116	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	20.08.06	CBAier	
6185	<i>M. tarantus</i>	CB-06-117	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	20.08.06	CBAier	
6186	<i>M. tarantus</i>	CB-06-118	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	20.08.06	CBAier	
6187	<i>M. tarantus</i>	CB-06-119	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	20.08.06	CBAier	
6188	<i>M. tarantus</i>	CB-06-120	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	20.08.06	CBAier	GAT-6370
6189	<i>M. tarantus</i>	CB-06-121	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	20.08.06	CBAier	
6200	<i>M. tarantus</i>	CB-06-132	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	21.08.06	CBAier	GAT-6379
6201	<i>M. tarantus</i>	CB-06-133	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	21.08.06	CBAier	
6202	<i>M. tarantus</i>	CB-06-134	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	21.08.06	CBAier	
6203	<i>M. tarantus</i>	CB-06-135	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	21.08.06	CBAier	
6204	<i>M. tarantus</i>	CB-06-136	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	21.08.06	CBAier	
6205	<i>M. tarantus</i>	CB-06-137	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	21.08.06	CBAier	
6206	<i>M. tarantus</i>	CB-06-138	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	21.08.06	CBAier	
6207	<i>M. tarantus</i>	CB-06-139	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	21.08.06	CBAier	
6208	<i>M. tarantus</i>	CB-06-140	5.210	116.570	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	roadside	21.08.06	CBAier	
6226	<i>M. tarantus</i>	CB-06-158	5.200	116.560	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasia	roadside	23.08.06	CBAier	GAT-6386
6227	<i>M. tarantus</i>	CB-06-159	5.200	116.560	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasia	roadside	23.08.06	CBAier	

Plant ID Number	Species	Field number	Latitude	Longitude	Location	Habitat / Ecology	Collection		Herbarium (Number)
							Date (dd.mm.yy)	Collector	
6402	<i>M. tanarius</i>	CB-06-334	6.510	116.750	Malaysia, Borneo, Sabah, from KK to Ranau, stop 2	roadside	02.09.06	CBaier	
6440	<i>M. tanarius</i>	CB-06-372	6.500	116.750	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6441	<i>M. tanarius</i>	CB-06-373	6.500	116.850	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6442	<i>M. tanarius</i>	CB-06-374	6.500	116.850	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6439	<i>M. tanarius</i>	CB-06-371	6.500	116.750	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6433	<i>M. tanarius</i>	CB-06-365	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6434	<i>M. tanarius</i>	CB-06-366	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6436	<i>M. tanarius</i>	CB-06-367	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6435	<i>M. tanarius</i>	CB-06-368	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6437	<i>M. tanarius</i>	CB-06-369	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6438	<i>M. tanarius</i>	CB-06-370	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6443	<i>M. tanarius</i>	CB-06-375	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6444	<i>M. tanarius</i>	CB-06-376	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6445	<i>M. tanarius</i>	CB-06-377	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6446	<i>M. tanarius</i>	CB-06-378	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6447	<i>M. tanarius</i>	CB-06-379	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6448	<i>M. tanarius</i>	CB-06-380	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6450	<i>M. tanarius</i>	CB-06-382	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6451	<i>M. tanarius</i>	CB-06-383	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6452	<i>M. tanarius</i>	CB-06-384	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6453	<i>M. tanarius</i>	CB-06-385	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6457	<i>M. tanarius</i>	CB-06-389	6.500	117.200	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6449	<i>M. tanarius</i>	CB-06-381	6.500	117.210	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6454	<i>M. tanarius</i>	CB-06-386	6.500	117.210	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6455	<i>M. tanarius</i>	CB-06-387	6.500	117.210	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6456	<i>M. tanarius</i>	CB-06-388	6.500	117.210	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6458	<i>M. tanarius</i>	CB-06-390	6.500	117.210	Malaysia, Borneo, Sabah, outskirts of Ranau	roadside	03.09.06	CBaier	
6030	<i>M. tanarius</i>	BF45376	6.070	116.720	Malaysia, Borneo, Sabah, Poring, staff quarters	area around staff quarters	13.08.06	BFiala	
6025	<i>M. tanarius</i>	BF44906	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	roadside	12.08.06	BFiala	
6027	<i>M. tanarius</i>	BF45006	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	next to river	12.08.06	BFiala	
6033	<i>M. tanarius</i>	BF45906	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	next to river	12.08.06	BFiala	
6034	<i>M. tanarius</i>	BF45006	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	next to river	12.08.06	BFiala	
6035	<i>M. tanarius</i>	BF45906	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	next to river	12.08.06	BFiala	
6036	<i>M. tanarius</i>	BF45906	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	next to river	12.08.06	BFiala	
6037	<i>M. tanarius</i>	BF46006	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	next to river	12.08.06	BFiala	
6040	<i>M. tanarius</i>	BF46006	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	very recent logging site/road	12.08.06	BFiala	
6043	<i>M. tanarius</i>	BF46606	6.070	116.720	Malaysia, Borneo, Sabah, Poring, Langinan	trail in forest	17.08.06	BFiala	
6031	<i>M. tanarius</i>	BF45406	6.070	116.720	Malaysia, Borneo, Sabah, Poring, Hot springs area	roadside	13.08.06	BFiala	
6029	<i>M. tanarius</i>	BF45206	6.070	116.720	Malaysia, Borneo, Sabah, Poring, Camp site	roadside	13.08.06	BFiala	
6032	<i>M. tanarius</i>	BF45206	6.070	116.720	Malaysia, Borneo, Sabah, Poring, Camp site	roadside	14.08.06	BFiala	
6134	<i>M. tanarius</i>	BF 917?	5.850	117.210	Malaysia, Borneo, Sabah, Telup, Jln. Microwave	roadside	28.08.05	BFiala	
4442	<i>M. tanarius</i>	CB-06-74	5.050	117.760	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	roadside	15.08.06	CBaier	
6143	<i>M. tanarius</i>	CB-06-75	5.050	117.760	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	roadside	15.08.06	CBaier	
6144	<i>M. tanarius</i>	CB-06-76	5.050	117.760	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	roadside	15.08.06	CBaier	
6145	<i>M. tanarius</i>	CB-06-77	5.050	117.760	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	roadside	15.08.06	CBaier	
6148	<i>M. tanarius</i>	CB-06-80	5.050	117.760	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	roadside	15.08.06	CBaier	
6149	<i>M. tanarius</i>	CB-06-81	5.050	117.760	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	roadside	15.08.06	CBaier	
6150	<i>M. tanarius</i>	CB-06-82	5.050	117.760	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	roadside	15.08.06	CBaier	
6151	<i>M. tanarius</i>	CB-06-83	5.050	117.760	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	roadside	15.08.06	CBaier	
6152	<i>M. tanarius</i>	CB-06-84	5.050	117.760	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	roadside	15.08.06	CBaier	
6161	<i>M. tanarius</i>	CB-06-93	4.990	117.960	Malaysia, Borneo, Sabah, Danum Valley, DV/C, east	primary forest	03.09.06	CBaier	
5211	<i>M. tanarius</i>	DG06_304	4.990	117.960	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5212	<i>M. tanarius</i>	DG06_305	4.990	117.960	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5213	<i>M. tanarius</i>	DG06_306	4.990	117.960	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5214	<i>M. tanarius</i>	DG06_307	4.990	117.960	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5215	<i>M. tanarius</i>	DG06_308	4.990	117.960	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5216	<i>M. tanarius</i>	DG06_309	4.990	117.960	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5217	<i>M. tanarius</i>	DG06_310	4.990	117.960	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5218	<i>M. tanarius</i>	DG06_311	4.990	117.960	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5219	<i>M. tanarius</i>	DG06_312	4.990	117.960	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5220	<i>M. tanarius</i>	DG06_313	4.990	117.960	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5221	<i>M. tanarius</i>	DG06_314	4.990	117.960	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5222	<i>M. tanarius</i>	DG06_315	4.990	117.960	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
4302	<i>M. tanarius</i>	BF 57	5.310	118.840	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Resort	open area	25.08.05	BFiala	
4306	<i>M. tanarius</i>	BF 61	5.310	118.840	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Resort	open area	27.08.05	BFiala	
5119	<i>M. tanarius</i>	DG06_212	4.390	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	edge of oil palm plantation and secondary forest	29.08.06	DGuicking	
5120	<i>M. tanarius</i>	DG06_213	4.390	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	edge of oil palm plantation and secondary forest	29.08.06	DGuicking	
5121	<i>M. tanarius</i>	DG06_214	4.390	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	edge of oil palm plantation and secondary forest	29.08.06	DGuicking	
5123	<i>M. tanarius</i>	DG06_216	4.390	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	edge of oil palm plantation and secondary forest	29.08.06	DGuicking	
5124	<i>M. tanarius</i>	DG06_217	4.390	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	edge of oil palm plantation and secondary forest	29.08.06	DGuicking	
5125	<i>M. tanarius</i>	DG06_218	4.390	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	edge of oil palm plantation and secondary forest	29.08.06	DGuicking	
5126	<i>M. tanarius</i>	DG06_221	4.390	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	edge of oil palm plantation and secondary forest	29.08.06	DGuicking	
5129	<i>M. tanarius</i>	DG06_222	4.390	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	edge of oil palm plantation and secondary forest	29.08.06	DGuicking	
5130	<i>M. tanarius</i>	DG06_223	4.390	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	edge of oil palm plantation and secondary forest	29.08.06	DGuicking	
5131	<i>M. tanarius</i>	DG06_224	4.390	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	edge of oil palm plantation and secondary forest	29.08.06	DGuicking	
5132	<i>M. tanarius</i>	DG06_225	4.390	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	edge of oil palm plantation and secondary forest	29.08.06	DGuicking	
5133	<i>M. tanarius</i>	DG06_226	4.390	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	edge of oil palm plantation and secondary forest	29.08.06	DGuicking	
5134	<i>M. tanarius</i>	DG06_227	4.390	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	edge of oil palm plantation and secondary forest	29.08.06	DGuicking	
5135	<i>M. tanarius</i>	DG06_228	4.390	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	edge of oil palm plantation and secondary forest	29.08.06	DGuicking	
305	<i>M. tanarius</i>		-7.855	110.723	Indonesia, Java	edge of oil palm plantation and secondary forest	02.10.00	UMSchwartz	
1531	<i>M. tanarius</i>	M644	-0.980	116.930	Indonesia, Borneo, E-Kalimantan, Samboja	burned 18 and 3 years ago	11.12.01	FSiik	
1532	<i>M. tanarius</i>	M693	-0.980	116.930	Indonesia, Borneo, E-Kalimantan, Samboja	burned 18 and 3 years ago	11.12.01	FSiik	
1533	<i>M. tanarius</i>	M705	-0.980	116.930	Indonesia, Borneo, E-Kalimantan, Samboja	burned 18 and 3 years ago	13.12.01	FSiik	
6713	<i>M. winkleri</i>	CB-07-248	1.463	111.560	Malaysia, Borneo, Sarawak, Bt. Saban Resort to Beting	edge of gravel path to Paku	05.08.07	CBaier	
7056	<i>M. winkleri</i>	CB-07-225	2.190	113.060	Malaysia, Borneo, Sarawak, Pelagus Resort	near hotel	20.07.07	CBaier	
7078	<i>M. winkleri</i>	CB-07-11	2.190	113.060	Malaysia, Borneo, Sarawak, Pelagus Resort	next to creek in forest	19.07.07	CBaier	
7102	<i>M. winkleri</i>	CB-07-35	2.190	113.060	Malaysia, Borneo, Sarawak, Pelagus Resort	near hotel	20.07.07	CBaier	
7079	<i>M. winkleri</i>	CB-07-59	2.190	113.060	Malaysia, Borneo, Sarawak, Pelagus Resort	near hotel	20.07.07	CBaier	
7087	<i>M. winkleri</i>	CB-07-20	2.190	113.060	Malaysia, Borneo, Sarawak, Pelagus Resort	next to creek in forest	20.07.07	CBaier	
7088	<i>M. winkleri</i>	CB-07-22	2.190	113.060	Malaysia, Borneo, Sarawak, Pelagus Resort	near hotel	20.07.07	CBaier	
7088	<i>M. winkleri</i>	CB-07-21	2.190	113.060	Malaysia, Borneo, Sarawak, Pelagus Resort	next to creek in forest	20.07.07	CBaier	
7098	<i>M. winkleri</i>	CB-07-31	2.190	113.060	Malaysia, Borneo, Sarawak, Pelagus Resort	next to creek in forest	20.07.07	CBaier	
7093	<i>M. winkleri</i>	CB-07-26	2.190	113.060	Malaysia, Borneo, Sarawak, Pelagus Resort	next to creek in forest	20.07.07	CBaier	
6670	<i>M. winkleri</i>	CB-07-205	3.350	113.440	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu, street to Tubau	close to a small creek	31.07.07	CBaier	GAT-6403
6676	<i>M. winkleri</i>								

Plant ID Number	Species	Field number	Latitude	Longitude	Location	Habitat / Ecology	Collection		Herbarium (Number)
							Date (dd.mm.yy)	Collector	
6423	M. winkleri	CB-06-355	6.330	116.720	Malaysia, Borneo, Sabah, from KK to Ranau, stop 6, 55 km to Ranau	roadside	02.09.06	Cbaier	
6405	M. winkleri	CB-06-337	6.400	116.580	Malaysia, Borneo, Sabah, from KK to Ranau, near Kg Manangkob	roadside, edge of small banana plantation	02.09.06	Cbaier	
6407	M. winkleri	CB-06-339	6.400	116.580	Malaysia, Borneo, Sabah, from KK to Ranau, near Kg Manangkob	roadside, edge of small banana plantation	02.09.06	Cbaier	
6408	M. winkleri	CB-06-340	6.400	116.580	Malaysia, Borneo, Sabah, from KK to Ranau, near Kg Manangkob	roadside, edge of small banana plantation	02.09.06	Cbaier	
6406	M. winkleri	CB-06-338	6.400	116.580	Malaysia, Borneo, Sabah, from KK to Ranau, near Kg Manangkob	roadside, edge of small banana plantation	02.09.06	Cbaier	
6404	M. winkleri	CB-06-336	6.400	116.580	Malaysia, Borneo, Sabah, from KK to Ranau, near Kg Manangkob	roadside, edge of small banana plantation	02.09.06	Cbaier	
6403	M. winkleri	CB-06-335	6.400	116.580	Malaysia, Borneo, Sabah, from KK to Ranau, near Kg Manangkob	roadside, edge of small banana plantation	02.09.06	Cbaier	
6420	M. winkleri	CB-06-352	6.400	116.830	Malaysia, Borneo, Sabah, from KK to Ranau, stop 5	roadside	02.09.06	Cbaier	
6419	M. winkleri	CB-06-351	6.400	116.830	Malaysia, Borneo, Sabah, from KK to Ranau, stop 5	roadside	02.09.06	Cbaier	
6421	M. winkleri	CB-06-353	6.400	116.830	Malaysia, Borneo, Sabah, from KK to Ranau, stop 5	roadside	02.09.06	Cbaier	
6417	M. winkleri	CB-06-349	6.400	116.830	Malaysia, Borneo, Sabah, from KK to Ranau, stop 5	roadside	02.09.06	Cbaier	
6409	M. winkleri	CB-06-341	6.400	116.580	Malaysia, Borneo, Sabah, from KK to Ranau, near Kg Manangkob	roadside, edge of small banana plantation	02.09.06	Cbaier	
2119	M. winkleri	DG04_25	6.060	116.690	Malaysia, Borneo, Sabah, Poring, Langanan trail, ca km 1.6	primary forest	01.08.04	BFlala/DGuicking	
510	M. winkleri	582001	6.060	116.690	Malaysia, Borneo, Sabah, Poring, Langanan trail	primary forest	16.04.01	BFlala	
505	M. winkleri	532001	6.050	116.700	Malaysia, Borneo, Sabah, Poring, canopy walkway	behind path, canopy walkway	12.04.01	BFlala	
6044	M. winkleri	BH46706	6.070	116.720	Malaysia, Borneo, Sabah, Poring, walkway	walkway	13.08.06	BFlala	
6047	M. winkleri	BF47006	6.070	116.720	Malaysia, Borneo, Sabah, Poring, Langanan	trail	17.08.06	BFlala	
6046	M. winkleri	BF46906	6.070	116.720	Malaysia, Borneo, Sabah, Poring, Langanan	trail	17.08.06	BFlala	
6053	M. winkleri	BF48106	6.070	116.720	Malaysia, Borneo, Sabah, Poring, Langanan	trail	17.08.06	BFlala	
6054	M. winkleri	BF48206	6.070	116.720	Malaysia, Borneo, Sabah, Poring, Langanan	trail	17.08.06	BFlala	
6045	M. winkleri	BF46806	6.070	116.720	Malaysia, Borneo, Sabah, Poring, Langanan	trail	17.08.06	BFlala	
5667	M. winkleri	BF1506	6.070	116.720	Malaysia, Borneo, Sabah, Poring, Langanan	trail	13.08.06	BFlala	
5669	M. winkleri	BH1706	6.070	116.720	Malaysia, Borneo, Sabah, Poring, Langanan	trail	13.08.06	BFlala	
5674	M. winkleri	BF2206	6.070	116.720	Malaysia, Borneo, Sabah, Poring, Langanan	trail	13.08.06	BFlala	
5665	M. winkleri	BF1106	6.070	116.720	Malaysia, Borneo, Sabah, Poring, Langanan	trail	13.08.06	BFlala	
5666	M. winkleri	BF1300b	6.070	116.720	Malaysia, Borneo, Sabah, Poring, Langanan	trail	13.08.06	BFlala	
5660	M. winkleri	BF0500b	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	12.08.06	BFlala	
5662	M. winkleri	BF0300b	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	12.08.06	BFlala	
5663	M. winkleri	BF0306	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	12.08.06	BFlala	
5659	M. winkleri	BF0400b	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	12.08.06	BFlala	
5657	M. winkleri	BF0200b	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	12.08.06	BFlala	
5661	M. winkleri	BF0300b	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	12.08.06	BFlala	
6038	M. winkleri	BF46106	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	12.08.06	BFlala	
2323	M. winkleri	DG04_229	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	old logging road	12.08.04	DGuicking	
2351	M. winkleri	DG04_257	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	old logging road	12.08.04	BFlala	
5663	M. winkleri	BF1300b	6.070	116.720	Malaysia, Borneo, Sabah, Poring	path to canopy walkway in primary forest	13.08.06	BFlala	
5664	M. winkleri	BF1006	6.070	116.720	Malaysia, Borneo, Sabah, Poring	path to canopy walkway in primary forest	13.08.06	BFlala	
4744	M. winkleri		6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	31.03.06	HFeldhaar	
4742	M. winkleri	HF 56-58	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	31.03.06	HFeldhaar	
4743	M. winkleri	HF 6-55	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	31.03.06	HFeldhaar	
4749	M. winkleri	HF 6-66	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	31.03.06	HFeldhaar	
4754	M. winkleri	HF 6-73	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	31.03.06	HFeldhaar	
4751	M. winkleri	HF 6-63	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	31.03.06	HFeldhaar	
4753	M. winkleri	HF 6-72	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	31.03.06	HFeldhaar	
4748	M. winkleri	HF 6-65	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	31.03.06	HFeldhaar	
4755	M. winkleri	HF 6-71	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	31.03.06	HFeldhaar	
4756	M. winkleri	HF 6-69	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	31.03.06	HFeldhaar	
4750	M. winkleri	HF 6-61	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	31.03.06	HFeldhaar	
4747	M. winkleri	HF 6-67	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	31.03.06	HFeldhaar	
4745	M. winkleri	HF 6-70	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	31.03.06	HFeldhaar	
4752	M. winkleri	HF 6-76	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	31.03.06	HFeldhaar	
4746	M. winkleri	HF 6-69	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	31.03.06	HFeldhaar	
4757	M. winkleri	HF 6-60	6.070	116.720	Malaysia, Borneo, Sabah, Poring, logging road	logging road	31.03.06	HFeldhaar	
2337	M. winkleri	DG04_243	6.080	116.730	Malaysia, Borneo, Sabah, Poring, logging road	new logging road	12.08.04	DGuicking	
2581	M. winkleri	DG04_491	5.890	116.980	Malaysia, Borneo, Sabah, Bukit Tavau, stop 7	roadside	20.08.04	DGuicking	
2485	M. winkleri	DG04_391	5.890	116.980	Malaysia, Borneo, Sabah, Bukit Tavau, stop 1	roadside	20.08.04	DGuicking	
2478	M. winkleri	DG04_384	5.890	116.980	Malaysia, Borneo, Sabah, Bukit Tavau, stop 1	roadside	20.08.04	DGuicking	
112	M. winkleri	16000	5.330	117.330	Malaysia, Borneo, Sabah, Deramakot Forest Reserve	roadside	10.04.00	BFlala	
118	M. winkleri	22000	5.230	117.330	Malaysia, Borneo, Sabah, Deramakot Forest Reserve	roadside	11.04.00	BFlala	
4043	M. winkleri	DG05-1319	5.866	117.967	Malaysia, Borneo, Sabah, Sepilok, trail to birdwatching tower	primary forest	28.08.05	DGuicking	
4044	M. winkleri	DG05-1320	5.866	117.967	Malaysia, Borneo, Sabah, Sepilok, trail to birdwatching tower	primary forest	28.08.05	DGuicking	
4045	M. winkleri	DG05-1321	5.866	117.967	Malaysia, Borneo, Sabah, Sepilok, waterhole	primary forest	28.08.05	DGuicking	
4049	M. winkleri	DG05-1325	5.866	117.967	Malaysia, Borneo, Sabah, Sepilok, waterhole	primary forest	28.08.05	DGuicking	
2829	M. winkleri	DG05-105	5.110	117.600	Malaysia, Borneo, Sabah, Danum Valley, logging road near Malua	logging road	30.07.05	DGuicking	
2830	M. winkleri	DG05-106	5.110	117.600	Malaysia, Borneo, Sabah, Danum Valley, logging road near Malua	logging road	30.07.05	DGuicking	
2831	M. winkleri	DG05-107	5.110	117.600	Malaysia, Borneo, Sabah, Danum Valley, logging road near Malua	logging road	30.07.05	DGuicking	
2854	M. winkleri	DG05-130	5.110	117.600	Malaysia, Borneo, Sabah, Danum Valley, logging road near Malua	logging road	30.07.05	DGuicking	
2866	M. winkleri	DG05-142	5.110	117.600	Malaysia, Borneo, Sabah, Danum Valley, logging road near Malua	logging road	30.07.05	DGuicking	
2867	M. winkleri	DG05-143	5.110	117.600	Malaysia, Borneo, Sabah, Danum Valley, logging road near Malua	logging road	30.07.05	DGuicking	
3545	M. winkleri	DG05-821	5.100	117.650	Malaysia, Borneo, Sabah, Danum Valley, Malua, new logging road	logging road	17.08.05	DGuicking	
3663	M. winkleri	DG05-939	5.100	117.650	Malaysia, Borneo, Sabah, Danum Valley, Malua, new logging road	logging road	17.08.05	DGuicking	
3664	M. winkleri	DG05-940	5.100	117.650	Malaysia, Borneo, Sabah, Danum Valley, Malua, new logging road	logging road	17.08.05	DGuicking	
3740	M. winkleri	DG05-1016	5.100	117.650	Malaysia, Borneo, Sabah, Danum Valley, Malua, new logging road	logging road	17.08.05	DGuicking	
3661	M. winkleri	DG05-937	5.100	117.650	Malaysia, Borneo, Sabah, Danum Valley, Malua, new logging road	logging road	17.08.05	DGuicking	
3662	M. winkleri	DG05-938	5.100	117.650	Malaysia, Borneo, Sabah, Danum Valley, Malua, new logging road	logging road	17.08.05	DGuicking	
3222	M. winkleri	DG05-498	5.080	117.740	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	07.08.05	DGuicking	
3253	M. winkleri	DG05-497	5.080	117.740	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	07.08.05	DGuicking	
3415	M. winkleri	DG05-691	5.090	117.650	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	10.08.05	DGuicking	
3414	M. winkleri	DG05-690	5.090	117.650	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	10.08.05	DGuicking	
6155	M. winkleri	CB-06-87	5.070	117.720	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	15.08.06	Cbaier	
6157	M. winkleri	CB-06-89	5.070	117.720	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	20.08.06	Cbaier	
6158	M. winkleri	CB-06-90	5.070	117.720	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	15.08.06	Cbaier	
6156	M. winkleri	CB-06-88	5.070	117.720	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	15.08.06	Cbaier	
6160	M. winkleri	CB-06-92	5.070	117.720	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	15.08.06	Cbaier	GAT-6388
3815	M. winkleri	DG05-1091	5.070	117.730	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	17.08.05	DGuicking	
3816	M. winkleri	DG05-1092	5.070	117.730	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	17.08.05	DGuicking	
3221	M. winkleri	DG05-497	5.080	117.740	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	07.08.05	DGuicking	
3330	M. winkleri	DG05-605	5.080	117.750	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	07.08.05	DGuicking	
3331	M. winkleri	DG05-607	5.080	117.750	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	07.08.05	DGuicking	
3332	M. winkleri	DG05-608	5.080	117.750	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	07.08.05	DGuicking	KAS
3333	M. winkleri	DG05-609	5.080	117.750	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	07.08.05	DGuicking	
3334	M. winkleri	DG05-610	5.080	117.750	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	07.08.05	DGuicking	KAS
3329	M. winkleri	DG05-605	5.080	117.750	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	07.08.05	DGuicking	
3254	M. winkleri	DG05-530	5.050	117.760	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	07.08.05	DGuicking	
3232	M. winkleri	DG05-568	5.050	117.760	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	07.08.05	DGuicking	
3293	M. winkleri	DG05-569	5.050	117.760	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	07.08.05	DGuicking	
3294	M. winkleri	DG05-570	5.050	117.760	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	07.08.05	DGuicking	
3878	M. winkleri	DG05-1154	5.000	117.800	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside	17.08.05	DGuicking	
3982	M. winkleri	DG05-1158	5.000	117.800	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	roadside			

Plant ID Number	Species	Field number	Latitude	Longitude	Location	Habitat / Ecology	Collection		Herbarium (Number)
							Date (dd.mm.yy)	Collector	
4656	<i>M. winkleri</i>	B06/174	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, Elephant Ridge trail E15	river vegetation, sapling uninhabited	19.03.06	BFlala	
4655	<i>M. winkleri</i>	BF06/173	4.960	117.850	Malaysia, Borneo, Sabah, Danum Valley, Elephant Ridge trail,	sapling, uninhabited	19.03.06	BFlala	
3959	<i>M. winkleri</i>	DG05-1235	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Sg. Segama, Elephant Ridge trail	primary forest	19.08.05	DGuicking	
4507	<i>M. winkleri</i>	BF06/40	4.980	117.800	Malaysia, Borneo, Sabah, Danum Valley, east grid E14-15	primary forest, uninhabited plant	10.03.06	BFlala	
3203	<i>M. winkleri</i>	DG05-479	4.980	117.870	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	roadside	06.08.05	DGuicking	
3011	<i>M. winkleri</i>	DG05-287	4.970	117.940	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	abandoned logging road	03.08.05	DGuicking	
3039	<i>M. winkleri</i>	DG05-315	4.970	117.940	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	abandoned logging road	03.08.05	DGuicking	
3040	<i>M. winkleri</i>	DG05-316	4.970	117.940	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	abandoned logging road	03.08.05	DGuicking	
3041	<i>M. winkleri</i>	DG05-317	4.970	117.940	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	abandoned logging road	03.08.05	DGuicking	
3010	<i>M. winkleri</i>	DG05-286	4.970	117.940	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	abandoned logging road	03.08.05	DGuicking	
3042	<i>M. winkleri</i>	DG05-318	4.970	117.940	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	abandoned logging road	03.08.05	DGuicking	
3013	<i>M. winkleri</i>	DG05-289	4.970	117.940	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	abandoned logging road	03.08.05	DGuicking	
3038	<i>M. winkleri</i>	DG05-314	4.970	117.940	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	abandoned logging road	03.08.05	DGuicking	
2968	<i>M. winkleri</i>	DG05-244	4.960	117.950	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	abandoned logging road	03.08.05	DGuicking	
2987	<i>M. winkleri</i>	DG05-263	4.960	117.950	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	abandoned logging road	03.08.05	DGuicking	
3061	<i>M. winkleri</i>	DG05-337	5.010	118.040	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	roadside	03.08.05	DGuicking	
2985	<i>M. winkleri</i>	DG05-264	4.960	117.950	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	abandoned logging road	03.08.05	DGuicking	
5224	<i>M. winkleri</i>	DG06_317	4.990	117.960	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5227	<i>M. winkleri</i>	DG06_320	4.990	117.960	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5228	<i>M. winkleri</i>	DG06_318	4.990	117.960	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5226	<i>M. winkleri</i>	DG06_319	4.990	117.960	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5228	<i>M. winkleri</i>	DG06_321	4.990	117.960	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5231	<i>M. winkleri</i>	DG06_324	4.990	117.960	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5230	<i>M. winkleri</i>	DG06_323	4.990	117.960	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5223	<i>M. winkleri</i>	DG06_316	4.990	117.960	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
5229	<i>M. winkleri</i>	DG06_322	4.990	117.960	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	very recent logging site/road	03.09.06	DGuicking	
2185	<i>M. winkleri</i>	DG04_91	4.970	117.950	Malaysia, Borneo, Sabah, Danum Valley, road Lahad Datu to DVFC, 25 km to DVFC	logged area	05.08.04	BFlala/DGuicking	
2148	<i>M. winkleri</i>	DG04_134	4.970	117.950	Malaysia, Borneo, Sabah, Danum Valley, road Lahad Datu to DVFC, 5 km to DVFC	roadside	03.08.04	BFlala/DGuicking	
2206	<i>M. winkleri</i>	DG04_112	4.970	117.940	Malaysia, Borneo, Sabah, Danum Valley, road Lahad Datu to DVFC, 23 km to DVFC	roadside	05.08.04	BFlala/DGuicking	
3385	<i>M. winkleri</i>	DG05-661	4.970	117.820	Malaysia, Borneo, Sabah, Danum Valley, 1-2km to DVFC	secondary forest	09.08.05	DGuicking	
3386	<i>M. winkleri</i>	DG05-662	4.970	117.820	Malaysia, Borneo, Sabah, Danum Valley, 1-2km to DVFC	secondary forest	09.08.05	DGuicking	KAS
3284	<i>M. winkleri</i>	DG05-660	4.950	117.830	Malaysia, Borneo, Sabah, Danum Valley, Lahad Datu to DVFC, junction to DVFC	roadside	03.08.06	BFlala/DGuicking	
4616	<i>M. winkleri</i>	BF06/139	4.980	117.800	Malaysia, Borneo, Sabah, Danum Valley, DVFC, gap close to office	gap, sapling	17.03.06	BFlala	
4618	<i>M. winkleri</i>	BF06/141	4.980	117.800	Malaysia, Borneo, Sabah, Danum Valley, DVFC, gap close to office	gap, sapling	17.03.06	BFlala	
4617	<i>M. winkleri</i>	BF06/140	4.980	117.800	Malaysia, Borneo, Sabah, Danum Valley, DVFC, gap close to office	gap, sapling	17.03.06	BFlala	
4620	<i>M. winkleri</i>	BF06/143	4.980	117.800	Malaysia, Borneo, Sabah, Danum Valley, DVFC, gap close to office	gap, sapling	17.03.06	BFlala	
4615	<i>M. winkleri</i>	BF06/138	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, DVFC, gap close to office	gap, sapling	17.03.06	BFlala	
4619	<i>M. winkleri</i>	BF06/142	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, DVFC, gap close to office	gap, sapling	17.03.06	BFlala	
6122	<i>M. winkleri</i>	CB-06-55	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6123	<i>M. winkleri</i>	CB-06-56	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6126	<i>M. winkleri</i>	CB-06-59	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6125	<i>M. winkleri</i>	CB-06-58	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6127	<i>M. winkleri</i>	CB-06-60	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6124	<i>M. winkleri</i>	CB-06-57	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6136	<i>M. winkleri</i>	CB-06-69	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6133	<i>M. winkleri</i>	CB-06-66	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6129	<i>M. winkleri</i>	CB-06-62	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6134	<i>M. winkleri</i>	CB-06-67	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6135	<i>M. winkleri</i>	CB-06-68	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6132	<i>M. winkleri</i>	CB-06-65	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6117	<i>M. winkleri</i>	CB-06-50	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6137	<i>M. winkleri</i>	CB-06-70	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6119	<i>M. winkleri</i>	CB-06-52	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6138	<i>M. winkleri</i>	CB-06-72	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6120	<i>M. winkleri</i>	CB-06-53	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6121	<i>M. winkleri</i>	CB-06-54	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6130	<i>M. winkleri</i>	CB-06-63	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6128	<i>M. winkleri</i>	CB-06-61	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6138	<i>M. winkleri</i>	CB-06-71	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6131	<i>M. winkleri</i>	CB-06-64	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, riverside	13.08.06	CBaier	
6112	<i>M. winkleri</i>	CB-06-45	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, plant growing on trunk in river	13.08.06	CBaier	
6114	<i>M. winkleri</i>	CB-06-47	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, plant growing on trunk in river	13.08.06	CBaier	
6113	<i>M. winkleri</i>	CB-06-46	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, plant growing on trunk in river	13.08.06	CBaier	
6116	<i>M. winkleri</i>	CB-06-49	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, plant growing on trunk in river	13.08.06	CBaier	
6115	<i>M. winkleri</i>	CB-06-48	4.950	117.800	Malaysia, Borneo, Sabah, Danum Valley, Tembelang trail	primary forest, plant growing on trunk in river	13.08.06	CBaier	
6106	<i>M. winkleri</i>	DG06-382	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembelang trail	primary forest	04.08.06	DGuicking	
4593	<i>M. winkleri</i>	BF06/118	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembelang trail, waterfall	primary forest	16.03.06	BFlala	
4592	<i>M. winkleri</i>	B06/122	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembelang trail, waterfall	primary forest	16.03.06	BFlala	
4607	<i>M. winkleri</i>	B06/127	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembelang trail, waterfall	primary forest, uninhabited small saplings	16.03.06	BFlala	
4600	<i>M. winkleri</i>	B06/125	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembelang trail, waterfall	primary forest, uninhabited small saplings	16.03.06	BFlala	
4599	<i>M. winkleri</i>	B06/124	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembelang trail, waterfall	primary forest, uninhabited small saplings	16.03.06	BFlala	
4601	<i>M. winkleri</i>	B06/126	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembelang trail, waterfall	primary forest, uninhabited small saplings	16.03.06	BFlala	
4598	<i>M. winkleri</i>	DG06-22	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembelang trail, waterfall	primary forest, uninhabited small saplings	16.03.06	BFlala	
4595	<i>M. winkleri</i>	B06/120	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembelang trail, waterfall	primary forest	16.03.06	BFlala	
4596	<i>M. winkleri</i>	BF06/121	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembelang trail, waterfall	primary forest	16.03.06	BFlala	
4612	<i>M. winkleri</i>	B06/136	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembelang trail, waterfall	primary forest	16.03.06	BFlala	
4485	<i>M. winkleri</i>	BF06/23	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembelang trail, Chris plot 5	primary forest	10.03.06	BFlala	
4495	<i>M. winkleri</i>	BF06/31	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembelang trail, Chris plot 5	primary forest	10.03.06	BFlala	
4487	<i>M. winkleri</i>	BF06/23	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembelang trail, Chris plot 5	primary forest	10.03.06	BFlala	
4594	<i>M. winkleri</i>	BF06/119	4.950	117.810	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembelang trail, Christoph 6	primary forest	16.03.06	BFlala	
4286	<i>M. winkleri</i>	BF 42	5.310	118.840	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Lipad trail, gap	good secondary forest	25.08.05	BFlala	
4290	<i>M. winkleri</i>	BF 44	5.310	118.840	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Lipad trail, gap	good secondary forest	25.08.05	BFlala	
4291	<i>M. winkleri</i>	BF 45	5.310	118.840	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Lipad trail, gap	good secondary forest	25.08.05	BFlala	
2051	<i>M. winkleri</i>	BF 091-03	4.630	117.380	Malaysia, Borneo, Sabah, Lussang	picnic area	03.09.03	BFlala	
5093	<i>M. winkleri</i>	DG06_186	4.400	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, picnic area	picnic area	28.08.06	DGuicking	
5094	<i>M. winkleri</i>	DG06_187	4.400	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, picnic area	picnic area	28.08.06	DGuicking	
5096	<i>M. winkleri</i>	DG06_189	4.400	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, picnic area	picnic area	28.08.06	DGuicking	
5095	<i>M. winkleri</i>	DG06_188	4.400	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, picnic area	picnic area	28.08.06	DGuicking	
5159	<i>M. winkleri</i>	DG06_252	4.400	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs	water catchment reserve	29.08.06	DGuicking	
5175	<i>M. winkleri</i>	DG06_268	4.400	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs	water catchment reserve	29.08.06	DGuicking	
5194	<i>M. winkleri</i>	DG06_287	4.400	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs	water catchment reserve	29.08.06	DGuicking	
5196	<i>M. winkleri</i>	DG06_289	4.400	117.890	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs	water catchment reserve	29.08.06		

Appendix D *Macaranga winkleri* individuals and outgroups included in the TCS haplotype network calculation, with corresponding haplotypes, HT groups, origin and collector.

Plant ID Number	HT		Population		Species	Collector	Location
	HT ¹	Groups ¹	Circles ²				
5139	1	1	1a	<i>M. winkleri</i>	DGuicking	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation 'Golden Hope', trail to Bt. Bombalai	
5140	1	1	1a	<i>M. winkleri</i>	DGuicking	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation 'Golden Hope', trail to Bt. Bombalai	
5142	1	1	1a	<i>M. winkleri</i>	DGuicking	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation 'Golden Hope', trail to Bt. Bombalai	
5159	1	1	1b	<i>M. winkleri</i>	DGuicking	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs, 0 to 2.6 km	
5194	1	1	1b	<i>M. winkleri</i>	DGuicking	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs, 0 to 2.6 km	
2051	1	1	1c	<i>M. winkleri</i>	BFiala	Malaysia, Borneo, Sabah, Luasong	
2478	1	1	1d	<i>M. winkleri</i>	DGuicking	Malaysia, Borneo, Sabah, Bukit Taviu, stop 1	
2485	1	1	1d	<i>M. winkleri</i>	DGuicking	Malaysia, Borneo, Sabah, Bukit Taviu, stop 1	
2581	1	1	1d	<i>M. winkleri</i>	DGuicking	Malaysia, Borneo, Sabah, Bukit Taviu, stop 7	
3857	1	1	1e	<i>M. winkleri</i>	DGuicking	Malaysia, Borneo, Sabah, Danum Valley, Borneo rainforest lodge	
3860	1	1	1e	<i>M. winkleri</i>	DGuicking	Malaysia, Borneo, Sabah, Danum Valley, Borneo rainforest lodge	
4286	1	1	1f	<i>M. winkleri</i>	BFiala	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Lipad trail	
4291	1	1	1f	<i>M. winkleri</i>	BFiala	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Lipad trail, gap	
5655	1	1	1g	<i>M. winkleri</i>	BFiala	Malaysia, Borneo, Sabah, Poring, Langanan	
5667	1	1	1g	<i>M. winkleri</i>	BFiala	Malaysia, Borneo, Sabah, Poring, Langanan	
5669	1	1	1g	<i>M. winkleri</i>	BFiala	Malaysia, Borneo, Sabah, Poring, Langanan	
5196	2	1	1b	<i>M. winkleri</i>	DGuicking	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs, 0 to 2.6 km	
6146	3	2	2a	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to Borneo rainforest lodge	
6154	3	2	2a	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to Borneo rainforest lodge	
6153	3	2	2a	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to Borneo rainforest lodge	
4733	3	2	2b	<i>M. winkleri</i>	BFiala	Malaysia, Borneo, Sabah, Danum Valley, junction to Borneo rainforest lodge	
4734	3	2	2b	<i>M. winkleri</i>	BFiala	Malaysia, Borneo, Sabah, Danum Valley, junction to Borneo rainforest lodge	
4736	3	2	2b	<i>M. winkleri</i>	BFiala	Malaysia, Borneo, Sabah, Danum Valley, junction to Borneo rainforest lodge	
6112	3	2	2c	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	
6129	3	2	2c	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	
6130	3	2	2c	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	
4290	3	2	2d	<i>M. winkleri</i>	BFiala	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Lipad trail, gap	
5058	3	2	2e	<i>M. winkleri</i>	DGuicking	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	
5065	3	2	2e	<i>M. winkleri</i>	DGuicking	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	
5066	3	2	2e	<i>M. winkleri</i>	DGuicking	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	
4615	4	2	2f	<i>M. winkleri</i>	BFiala	Malaysia, Borneo, Sabah, Danum Valley, DVFC, big gap close to office, trail into forest	
6407	5	3	3a	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, Jalan Hulan, near Kunung Manangkob, stop 3	
6408	5	3	3a	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, Jalan Hulan, near Kunung Manangkob, stop 3	
6412	5	3	3b	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 4	
6414	5	3	3b	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 4	
6420	5	3	3c	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 5	
6421	5	3	3c	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 5	
6424	5	3	3d	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 6, 55 km to Ranau	
6427	5	3	3d	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 6, 55 km to Ranau	
6462	5	3	3e	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, Ranau to Kota Kinabalu	
6417	5	3	3c	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 5	
6403	5	3	3a	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, Jalan Hulan, near Kunung Manangkob, stop 3	
6468	5	3	3e	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, Ranau to Kota Kinabalu	
6469	6	3	3e	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, Ranau to Kota Kinabalu	
6426	7	3	3d	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 6, 55 km to Ranau	
6411	8	3	3b	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 4	
4396	9	4	4	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Temburong, Kuala Belalong	
5	10	5	5a	<i>M. winkleri</i>	UMaschwitz	Borneo, Brunei, Temburong, Belalong	
5828	10	5	5b	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Temburong, Bukit Patoi	
6873	10	5	5c	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Belait, Wong Kadi waterfall	
6897	10	5	5b	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Temburong, Bukit Patoi	
6898	10	5	5b	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Temburong, Bukit Patoi	
5723	11	5	5a	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Temburong, Belalong	
5700	11	5	5b	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Temburong, Bukit Patoi	
6895	12	5	5b	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Temburong, Bukit Patoi	
5829	13	5	5b	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Temburong, Bukit Patoi	
5810	14	5	5a	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Temburong, Belalong	
4391	15	5	5c	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Temburong, Kuala Belalong	
5763	16	5	5b	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Temburong, Bukit Patoi	
5855	17	5	5b	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Temburong, Bukit Patoi	
7060	18	6	6	<i>M. winkleri</i>	BFiala	Malaysia, Borneo, Sarawak, Puni	
6656	19	7	7a	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	
6658	19	7	7a	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	
6561	20	7	7b	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sarawak, Lambir National Park	
6562	20	7	7b	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sarawak, Lambir National Park	
6657	21	7	7c	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	
6659	22	7	7c	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	
6061	23	8	8a	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Belait, Labi	
244	23	8	8a	<i>M. winkleri</i>	UMoog	Borneo, Brunei, Belait, Labi road (southern part of the road)	
5803	23	8	8b	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Belait, Tereja	
5962	23	8	8b	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Belait, Tereja	
5970	23	8	8b	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Belait, Tereja	
5974	23	8	8b	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Belait, Tereja	
6874	23	8	8c	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Belait, Wong Kadi waterfall	
6962	23	8	8c	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Belait, Wong Kadi waterfall	
6963	23	8	8c	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Belait, Wong Kadi waterfall	
5983	24	8	8b	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Belait, Tereja	
5918	25	8	8a	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Belait, Labi	
6875	26	8	8c	<i>M. winkleri</i>	BFiala	Borneo, Brunei, Belait, Wong Kadi waterfall	
6678	27	9	9a	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	
6679	27	9	9a	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	
7078	27	9	9b	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sarawak, Pelagus Resort	
7089	27	9	9b	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sarawak, Pelagus Resort	
7126	27	9	9b	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sarawak, Pelagus Resort	
6673	28	9	9a	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	
6713	29	10	10	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sarawak, between Bukit Saban Resort and Betong	
6566	30	11	11	<i>M. winkleri</i>	CBAier	Malaysia, Borneo, Sarawak, Lambir National Park	
396	31	12	12a	<i>M. winkleriella</i>	BFiala	Malaysia, Borneo, Sarawak, Mulu, Clearwatercave, Melliau Gorge	
397	31	12	12a	<i>M. winkleriella</i>	BFiala	Malaysia, Borneo, Sarawak, Mulu, Clearwatercave, trail	
398	31	12	12a	<i>M. winkleriella</i>	BFiala	Malaysia, Borneo, Sarawak, Mulu, Clearwatercave, trail	
399	31	12	12a	<i>M. winkleriella</i>	BFiala	Malaysia, Borneo, Sarawak, Mulu, Clearwatercave, trail	
400	31	12	12a	<i>M. winkleriella</i>	BFiala	Malaysia, Borneo, Sarawak, Mulu, Clearwatercave, trail	
401	31	12	12a	<i>M. winkleriella</i>	BFiala	Malaysia, Borneo, Sarawak, Mulu, Clearwatercave, trail	
403	31	12	12a	<i>M. winkleriella</i>	BFiala	Malaysia, Borneo, Sarawak, Mulu, Clearwatercave, trail	
523	31	12	12b	<i>M. winkleriella</i>	BFiala	Malaysia, Borneo, Sarawak, Mulu	
7137	31	12	12b	<i>M. winkleriella</i>	BFiala	Malaysia, Borneo, Sarawak, Mulu National Park	
7138	31	12	12b	<i>M. winkleriella</i>	BFiala	Malaysia, Borneo, Sarawak, Mulu National Park	
6984	32	12	12b	<i>M. winkleriella</i>	BFiala	Malaysia, Sarawak, Mulu	
6985	32	12	12b	<i>M. winkleriella</i>	BFiala	Malaysia, Sarawak, Mulu	
6986	32	12	12b	<i>M. winkleriella</i>	BFiala	Malaysia, Sarawak, Mulu	
201	33	13	13	<i>M. gigantea</i>	UMaschwitz	Malaysia, Selangor	
203	34	14	14	<i>M. gigantea</i>	UMaschwitz / HHeckroth	Malaysia, Selangor	
202	35	15	15	<i>M. pruinosa</i>	UMaschwitz	Malaysia, Selangor	
205	36	16	16	<i>M. diepenhorstii</i>	UMoog	Malaysia, Selangor	

1. The HT corresponds to the numbering in Figure 2-5.

2. The matching number/letter combinations indicate that the individuals are grouped together in one population circle in figure 2-6.

Appendix F *Macaranga tanarius* individuals included in the TCS haplotype network calculation, with corresponding haplotypes, population circles, locations and collectors.

Plant ID number	HT ¹	Population circles ²	Species	Collector	Location
6367	2	1	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel
5864	4	2	<i>M. tanarius</i>	BFiala	Malaysia, Sabah, 5 km to Kuala Penyu
227	5	3	<i>M. tanarius</i>	UMoog	Indonesia, Sumatra, Jambi, road from Sungaipenuh to Bangko ca. 70 km to Bangko
216	7	4	<i>M. tanarius</i>	ASchwarzbach	Australia
28	1a	5	<i>M. tanarius</i>	UMaschwitz	Borneo, Brunei, Bandar Seri Begawan
6927	1a	5	<i>M. tanarius</i>	BFiala	Borneo, Brunei, road BSB-S. Liang, km 64
6928	1a	5	<i>M. tanarius</i>	BFiala	Borneo, Brunei, road BSB-S. Liang, km 64
6929	1a	5	<i>M. tanarius</i>	BFiala	Borneo, Brunei, road BSB-S. Liang, km 64
6001	1a	6	<i>M. tanarius</i>	BFiala	Borneo, Brunei, Tutong
6002	1a	6	<i>M. tanarius</i>	BFiala	Borneo, Brunei, Tutong
5215	1a	7	<i>M. tanarius</i>	DGuicking	Malaysia, Borneo, Sabah, Danum Valley, logging site 2006, north of road to Lahad Datu
5217	1a	7	<i>M. tanarius</i>	DGuicking	Malaysia, Borneo, Sabah, Danum Valley, logging site 2006, north of road to Lahad Datu
5218	1a	7	<i>M. tanarius</i>	DGuicking	Malaysia, Borneo, Sabah, Danum Valley, logging site 2006, north of road to Lahad Datu
6144	1a	8	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL
6145	1a	8	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL
6149	1a	8	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL
6396	1a	9	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 1
6397	1a	9	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 1
6398	1a	9	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 1
6400	1a	10	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 2
6351	1a	11	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, from Kota Kinabalu towards Kota Belud
6352	1a	11	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, from Kota Kinabalu towards Kota Belud
6353	1a	11	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, from Kota Kinabalu towards Kota Belud
6387	1a	12	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Belud, direction Kudat
6388	1a	12	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Belud, direction Kudat
6389	1a	12	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Belud, direction Kudat
6360	1a	13	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel
6361	1a	13	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel
6362	1a	13	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel
6363	1a	13	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel
6364	1a	13	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel
6366	1a	13	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel
6325	1a	14	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang
6326	1a	14	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang
6327	1a	14	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang
6328	1a	14	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang
6329	1a	14	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang
6330	1a	14	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang
6265	1a	15	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery of KK
6266	1a	15	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery of KK
6267	1a	15	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery of KK
6292	1a	16	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya
6293	1a	16	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya
6294	1a	16	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya
6436	1a	17	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, outskirts of Ranau
6443	1a	17	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, outskirts of Ranau
6450	1a	17	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, outskirts of Ranau
6451	1a	17	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, outskirts of Ranau
6257	1a	18	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, periphery of Beaufort
6043	1a	19	<i>M. tanarius</i>	BFiala	Malaysia, Borneo, Sabah, Poring, Langanan
6026	1a	19	<i>M. tanarius</i>	BFiala	Malaysia, Borneo, Sabah, Poring, logging road
6033	1a	19	<i>M. tanarius</i>	BFiala	Malaysia, Borneo, Sabah, Poring, logging road
5239	1a	20	<i>M. tanarius</i>	DGuicking	Malaysia, Borneo, Sabah, Pulau Tiga Island
5240	1a	20	<i>M. tanarius</i>	DGuicking	Malaysia, Borneo, Sabah, Pulau Tiga Island
5241	1a	20	<i>M. tanarius</i>	DGuicking	Malaysia, Borneo, Sabah, Pulau Tiga Island
6356	1a	21	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, South of Kota Belud
6357	1a	21	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, South of Kota Belud
6359	1a	21	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, South of Kota Belud
5127	1a	22	<i>M. tanarius</i>	DGuicking	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation
5128	1a	22	<i>M. tanarius</i>	DGuicking	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation
5129	1a	22	<i>M. tanarius</i>	DGuicking	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation
6220	1a	23	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasa
6223	1a	23	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasa
6224	1a	23	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasa
6225	1a	23	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasa
6227	1a	23	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasa
6181	1a	24	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera
6182	1a	24	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera
6183	1a	24	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera
6195	1a	24	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Tenom, Jalan Tumentalik, near river Pegalan
6197	1a	24	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Tenom, Jalan Tumentalik, near river Pegalan
6198	1a	24	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Tenom, Jalan Tumentalik, near river Pegalan
6922	1a	25	<i>M. tanarius</i>	BFiala	Malaysia, Borneo, Sarawak, Lawas
6923	1a	25	<i>M. tanarius</i>	BFiala	Malaysia, Borneo, Sarawak, Lawas
6924	1a	25	<i>M. tanarius</i>	BFiala	Malaysia, Borneo, Sarawak, Lawas
6925	1a	25	<i>M. tanarius</i>	BFiala	Malaysia, Borneo, Sarawak, Lawas
6926	1a	25	<i>M. tanarius</i>	BFiala	Malaysia, Borneo, Sarawak, Lawas
1531	1b	26	<i>M. tanarius</i>	FSilk	Indonesia, Borneo, E-Kalimantan, Samboja
1532	1b	26	<i>M. tanarius</i>	FSilk	Indonesia, Borneo, E-Kalimantan, Samboja
1533	1b	26	<i>M. tanarius</i>	FSilk	Indonesia, Borneo, E-Kalimantan, Samboja
4334	1c	27	<i>M. tanarius</i>	BFiala	Malaysia, Borneo, Sabah, Telupid, Jln. Microwave
6365	3a	28	<i>M. tanarius</i>	CBaier	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel
305	3b	29	<i>M. tanarius</i>	UMaschwitz	Indonesia, Java
448	6a	30	<i>M. tanarius</i>	UMoog	Malaysia, Peninsula, Pahang, Cameron Highlands, Tanah Rata, road to Tanah Rata
6073	6a	30	<i>M. tanarius</i>	CBaier	Malaysia, Peninsula, Selangor, alte Genting road, 20 km to K.L.
6076	6a	30	<i>M. tanarius</i>	CBaier	Malaysia, Peninsula, Selangor, alte Genting road, 20 km to K.L.
6077	6a	30	<i>M. tanarius</i>	CBaier	Malaysia, Peninsula, Selangor, alte Genting road, 20 km to K.L.
6078	6a	30	<i>M. tanarius</i>	CBaier	Malaysia, Peninsula, Selangor, alte Genting road, 20 km to K.L.
6079	6a	30	<i>M. tanarius</i>	CBaier	Malaysia, Peninsula, Selangor, alte Genting road, 20 km to K.L.
6080	6a	30	<i>M. tanarius</i>	CBaier	Malaysia, Peninsula, Selangor, alte Genting road, 20 km to K.L.
6106	6a	31	<i>M. tanarius</i>	CBaier	Malaysia, Peninsula, Selangor, alte Genting road, 25 km to K.L.
6107	6a	31	<i>M. tanarius</i>	CBaier	Malaysia, Peninsula, Selangor, alte Genting road, 25 km to K.L.
6108	6a	31	<i>M. tanarius</i>	CBaier	Malaysia, Peninsula, Selangor, alte Genting road, 25 km to K.L.
6086	6a	32	<i>M. tanarius</i>	CBaier	Malaysia, Peninsula, Selangor, alte Genting road, after pass, 50 km to K.L.
6087	6a	32	<i>M. tanarius</i>	CBaier	Malaysia, Peninsula, Selangor, alte Genting road, after pass, 50 km to K.L.
6088	6a	32	<i>M. tanarius</i>	CBaier	Malaysia, Peninsula, Selangor, alte Genting road, after pass, 50 km to K.L.
6092	6a	32	<i>M. tanarius</i>	CBaier	Malaysia, Peninsula, Selangor, alte Genting road, after pass, 50 km to K.L.
2682	6a	32	<i>M. tanarius</i>	UMaschwitz	Malaysia, Peninsula, Selangor, Gombak Valley
6070	6b	33	<i>M. tanarius</i>	CBaier	Malaysia, Peninsula, Selangor, alte Genting road, 20 km to K.L.
43	6b	33	<i>M. tanarius</i>	UMaschwitz	Malaysia, Peninsula, Selangor, Kuala Lumpur

1. The HT corresponds to the numbering in Figure 2-3.

2. Matching numbers indicate that individuals are grouped together in one population circle in Figure 2-4.

Appendix G Chloroplast regions checked for the possibility of amplification and sequencing and sequence variation and corresponding primer sequences.

Locus Name	Primer Name	Direction	Primer Sequence (5' - 3')
ccmp1 ¹	ccmp1F	forward	CAGGTAAACTTCTCAACGGA
	ccmp1R	reverse	CCGAAGTCAAAAGAGCGATT
ccmp2 ¹	ccmp2F	forward	GATCCCGGACGTAATCCTG
	ccmp2R	reverse	ATCGTACCGAGGGTTCTGAAT
ccmp3 ¹	ccmp3F	forward	CAGACCAAAGCTGACATAG
	ccmp3R	reverse	GTTTCATTCTGGCTCCTTTAT
ccmp4 ¹	ccmp4F	forward	AATGCTGAATCGAYGACCTA
	ccmp4R	reverse	CCAAAATATTBGGAGGACTCT
ccmp5 ¹	ccmp5F	forward	TGTTCCAATATCTTCTTGTCAATTT
	ccmp5R	reverse	AGGTTCCATCGGAACAATTAT
ccmp6 ¹	ccmp6F	forward	CGATGCATATGTAGAAAGCC
	ccmp6R	reverse	CATTACGTGCGACTATCTCC
ccmp7 ¹	ccmp7F	forward	CAACATATACTACTGTCAAG
	ccmp7R	reverse	ACATCATTATTGTATACTCTTTC
ccmp10 ¹	ccmp10F	forward	TTTTTTTTTAGTGAACGTGTCA
	ccmp10R	reverse	TTCGTCGDCGTAGTAAATAG
<i>atpB-rbcL</i> ²	<i>atpB-rbcL</i> -F	forward	GAAGTAGTAGGATTGATTCTC
	<i>atpB-rbcL</i> -R	reverse	CAACACTTGCTTTAGTCTCTG
<i>trnL-trnF</i> ³	<i>trnL-trnF</i> -F	forward	GGAAATGGGGATATGGCG
	<i>trnL-trnF</i> -R	reverse	ATTTGAACTGGTGACACGAG
<i>rpL16</i> ⁴	<i>rpL16F71</i> ⁴	forward	GCTATGCTTAGTGTGTGACTCGTTG
	<i>RpL16-F2-PCR</i> ⁵	forward	CTCATCGCTTTGCATTATCTGG
	<i>rpL16R1516</i> ⁴	reverse	CCCTTCATTCTTCTCTATGTTG
<i>trnD</i> ^{GUC} - <i>trnT</i> ^{GGU} ⁶	<i>trnD</i> ^{GUC}	forward	ACCAATTGAACTACAATCCC
	<i>trnT</i> ^{GGU}	reverse	CTACCACTGAGTTAAAAGGG
<i>trnS</i> ^{UGA} - <i>trnM</i> ^{CAU} ⁶	<i>trnS</i> ^{UGA}	forward	GAGAGAGAGGGATTCTGAACC
	<i>trnM</i> ^{CAU}	reverse	CATAACCTTGAGGTCACGGG

¹ Chloroplast markers, Weising & Gardner 1999; Vogel et al. 2003.

² Samuel et al. 1997.

³ Taberlet et al. 1991, Forwardard primer nested from Jakob & Blattner 2006.

⁴ Small et al. 1998; Shaw et al. 2005.

⁵ Self-designed.

⁶ Demesure et al. 1995; Shaw et al. 2005.

Appendix H Individuals included in the haplotype network calculation of *M. winkleri* and other *Macaranga* species with corresponding microsatellite sequence information based on *atpB-rbcL* intergenic spacer sequences (this study and database).

Plant ID Number	HT Species	Location	Database accession number	1st SSR in atpB-rbcL	Letter for motif	2nd SSR in atpB-rbcL	Letter for motif	3rd SSR in atpB-rbcL	Letter for motif	4th SSR in atpB-rbcL	Letter for motif	5th SSR in atpB-rbcL	Letter for motif
4396	1 <i>M. winkleri</i>	Borneo, Brunei, Kuala Belalong		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
2478	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Bukit Tavu, stop 1		TTTTTTTT	F	TTTTTTTT	A	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
2485	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Bukit Tavu, stop 1		TTTTTTTT	F	TTTTTTTT	A	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
2581	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Bukit Tavu, stop 7		TTTTTTTT	F	TTTTTTTT	A	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
3857	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, Borneo rainforest lodge		TTTTTTTT	F	TTTTTTTT	B	TTTTTTTT	B	TTTTTTTT	B	AAAAAAAA	B
3860	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, Borneo rainforest lodge		TTTTTTTT	F	TTTTTTTT	B	TTTTTTTT	B	TTTTTTTT	B	AAAAAAAA	B
4615	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, DVFC, big gap close to office, trail into forest		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
4733	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, junction to Borneo rainforest lodge		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
4734	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, junction to Borneo rainforest lodge		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
4736	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, junction to Borneo rainforest lodge		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6154	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to Borneo rainforest lodge		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6146	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to Borneo rainforest lodge		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6153	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to Borneo rainforest lodge		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6130	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6112	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6129	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
5066	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
5058	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
5065	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6403	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, from KK to Ranau, Jalan Hulian, near Gunung Manangkob, stop 3		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6407	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, from KK to Ranau, Jalan Hulian, near Gunung Manangkob, stop 3		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6408	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, from KK to Ranau, Jalan Hulian, near Gunung Manangkob, stop 3		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6412	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, from KK to Ranau, stop 4		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6414	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, from KK to Ranau, stop 4		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6411	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, from KK to Ranau, stop 4		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6417	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, from KK to Ranau, stop 5		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6420	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, from KK to Ranau, stop 5		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6421	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, from KK to Ranau, stop 5		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6424	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, from KK to Ranau, stop 6, 55 km to Ranau		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6426	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, from KK to Ranau, stop 6, 55 km to Ranau		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6427	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, from KK to Ranau, stop 6, 55 km to Ranau		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
2051	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Luasong		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
5955	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Poring, Langanan		TTTTTTTT	F	TTTTTTTT	B	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
5667	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Poring, Langanan		TTTTTTTT	F	TTTTTTTT	B	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
5669	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Poring, Langanan		TTTTTTTT	F	TTTTTTTT	B	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6462	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Ranau to KK		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6469	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Ranau to KK		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6468	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Ranau to KK		TTTTTTTT	E	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
4286	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Lipad trail		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
4291	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Lipad trail, gap		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
4290	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Lipad trail, gap		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
5139	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tawau Hills Park		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
5140	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tawau Hills Park		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
5142	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tawau Hills Park		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
5159	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs, 0 to 2.6 km		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
5196	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs, 0 to 2.6 km		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
5194	1 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs, 0 to 2.6 km		TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
6679	1 <i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu		TTTTTTTT	D	TTTTTTTT	D	TTTTTTTT	D	TTTTTTTT	D	AAAAAAAA	B
6673	1 <i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu		TTTTTTTT	D	TTTTTTTT	D	TTTTTTTT	D	TTTTTTTT	D	AAAAAAAA	B
6678	1 <i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu		TTTTTTTT	D	TTTTTTTT	D	TTTTTTTT	D	TTTTTTTT	D	AAAAAAAA	B
7076	1 <i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Pelagus Resort		TTTTTTTT	D	TTTTTTTT	D	TTTTTTTT	D	TTTTTTTT	D	AAAAAAAA	B
7399	1 <i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Pelagus Resort		TTTTTTTT	D	TTTTTTTT	D	TTTTTTTT	D	TTTTTTTT	D	AAAAAAAA	B
7126	1 <i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Pelagus Resort		TTTTTTTT	D	TTTTTTTT	D	TTTTTTTT	D	TTTTTTTT	D	AAAAAAAA	B
6713	1 <i>M. winkleri</i>	Malaysia, Borneo, Sarawak, between Bukit Saban Resort and Betong		TTTTTTTT	D	TTTTTTTT	D	TTTTTTTT	D	TTTTTTTT	D	AAAAAAAA	B
6061	2 <i>M. winkleri</i>	Borneo, Brunei, Belait, Labi		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	C	AAAAAAAAA	A
244	2 <i>M. winkleri</i>	Borneo, Brunei, Belait, Labi road (southern part of the road)		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	D	AAAAAAAAA	A
5803	2 <i>M. winkleri</i>	Borneo, Brunei, Belait, Teraja		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	C	AAAAAAAAA	A
5862	2 <i>M. winkleri</i>	Borneo, Brunei, Belait, Teraja		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	C	AAAAAAAAA	A
5970	2 <i>M. winkleri</i>	Borneo, Brunei, Belait, Teraja		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	C	AAAAAAAAA	A
5974	2 <i>M. winkleri</i>	Borneo, Brunei, Belait, Teraja		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	C	AAAAAAAAA	A
5983	2 <i>M. winkleri</i>	Borneo, Brunei, Belait, Teraja		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	C	AAAAAAAAA	A
6873	2 <i>M. winkleri</i>	Borneo, Brunei, Belait, Wong Kadi waterfall		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAAA	A
6874	2 <i>M. winkleri</i>	Borneo, Brunei, Belait, Wong Kadi waterfall		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	C	AAAAAAAAA	A
6875	2 <i>M. winkleri</i>	Borneo, Brunei, Belait, Wong Kadi waterfall		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	C	AAAAAAAAA	A
6962	2 <i>M. winkleri</i>	Borneo, Brunei, Belait, Wong Kadi waterfall		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	C	AAAAAAAAA	A
6963	2 <i>M. winkleri</i>	Borneo, Brunei, Belait, Wong Kadi waterfall		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	C	AAAAAAAAA	A
5700	2 <i>M. winkleri</i>	Borneo, Brunei, Temburong, Belalong		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAAA	A
5723	2 <i>M. winkleri</i>	Borneo, Brunei, Temburong, Belalong		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAAA	A
5	2 <i>M. winkleri</i>	Borneo, Brunei, Temburong, Belalong		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAAA	A
6955	2 <i>M. winkleri</i>	Borneo, Brunei, Temburong, Bukit Patoi		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAAA	A
6897	2 <i>M. winkleri</i>	Borneo, Brunei, Temburong, Bukit Patoi		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAAA	A
5855	2 <i>M. winkleri</i>	Borneo, Brunei, Temburong, Bukit Patoi		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAAA	A
6898	2 <i>M. winkleri</i>	Borneo, Brunei, Temburong, Bukit Patoi		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAAA	A
5763	2 <i>M. winkleri</i>	Borneo, Brunei, Temburong, Bukit Patoi		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAAA	A
5828	2 <i>M. winkleri</i>	Borneo, Brunei, Temburong, Bukit Patoi		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAAA	A
5829	2 <i>M. winkleri</i>	Borneo, Brunei, Temburong, Bukit Patoi		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAAA	A
6656	2 <i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	D	AAAAAAAAA	A
6657	2 <i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	D	AAAAAAAAA	A
6658	2 <i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	D	AAAAAAAAA	A
6659	2 <i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	D	AAAAAAAAA	A
6661	2 <i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Lambir National Park		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	D	AAAAAAAAA	A
6662	2 <i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Lambir National Park		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	D	AAAAAAAAA	A
6566	2 <i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Lambir National Park		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	D	AAAAAAAAA	A
7060	2 <i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Puri		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAAA	A
5918	3 <i>M. winkleri</i>	Borneo, Brunei, Belait, Labi		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	A	TTTTTTTT	C	AAAAAAAAA	A
5810	3 <i>M. winkleri</i>	Borneo, Brunei, Temburong, Belalong		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAAA	A
202	4 <i>M. prunosa</i>	Malaysia, Selangor		TTTTTTTT	B	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAA	B
201	5 <i>M. gigantea</i>	Malaysia, Selangor		TTTTTTTT	B	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAA	B
205	6 <i>M. clepanthostylis</i>	Malaysia, Selangor		TTTTTTTT	D	TTTTTTTT	E	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAA	B
523	7 <i>M. winkleriella</i>	Malaysia, Borneo, Sarawak, Mulu		TTTTTTTT	E	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	F	AAAAAAAA	B
6984	7 <i>M. winkleriella</i>	Malaysia, Borneo, Sarawak, Mulu		TTTTTTTT	E	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	F	AAAAAAAA	B
6985	7 <i>M. winkleriella</i>	Malaysia, Borneo, Sarawak, Mulu		TTTTTTTT	E	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	F	AAAAAAAA	B
6986	7 <i>M. winkleriella</i>	Malaysia, Borneo, Sarawak, Mulu		TTTTTTTT	E	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	F	AAAAAAAA	B
7137	7 <i>M. winkleriella</i>	Malaysia, Borneo, Sarawak, Mulu National Park		TTTTTTTT	E	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	F	AAAAAAAA	B
7138	7 <i>M. winkleriella</i>	Malaysia, Borneo, Sarawak, Mulu National Park		TTTTTTTT	E	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	F	AAAAAAAA	B
396	7 <i>M. winkleriella</i>	Malaysia, Borneo, Sarawak, Mulu, Clearwatercave, Mellau Gorge		TTTTTTTT	E	TTTTTTTT	E	TTTTTTTT	B	TTTTTTTT	F	AAAAAAAA	B
397	7 <i>M. winkleriella</i>	Malaysia, Borneo, Sarawak, Mulu, Clearwatercave, trail		TTTTTTTT	E	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	F	AAAAAAAA	B
398	7 <i>M. winkleriella</i>	Malaysia, Borneo, Sarawak, Mulu, Clearwatercave, trail		TTTTTTTT	E	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	F	AAAAAAAA	B
399	7 <i>M. winkleriella</i>	Malaysia, Borneo, Sarawak, Mulu, Clearwatercave, trail		TTTTTTTT	E	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	F	AAAAAAAA	B
400	7 <i>M. winkleriella</i>	Malaysia, Borneo, Sarawak, Mulu, Clearwatercave, trail		TTTTTTTT	E	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	F	AAAAAAAA	B
401	7 <i>M. winkleriella</i>	Malaysia, Borneo, Sarawak, Mulu, Clearwatercave, trail		TTTTTTTT	E	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	F	AAAAAAAA	B
403	7 <i>M. winkleriella</i>	Malaysia, Borneo, Sarawak, Mulu, Clearwatercave, trail		TTTTTTTT	E	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	F	AAAAAAAA	B
4391	8 <i>M. winkleri</i>	Borneo, Brunei, Temburong, Kuala Belalong		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAAA	A
12	9 <i>M. winkleri</i>	Borneo, Brunei, Temburong, Belalong		TTTTTTTT	C	TTTTTTTT	D	TTTTTTTT	B	TTTTTTTT	D	AAAAAAAAA	A
118	10 <i>M. winkleri</i>	Malaysia, Borneo, Sabah, Deramakot Forest Reserve	DQ358245	TTTTTTTT	F	TTTTTTTT	C	TTTTTTTT	B	TTTTTTTT	A	AAAAAAAA	B
136	11 <i>M. recurvata</i>	Malaysia, Borneo, Sabah, Tawau Forest Reserve	DQ358244	TTTTTTTT	A	TTTTTTTA	F	TTTTTTTT	A	TTTTTTTT	D	AAAAAAAA	

Appendix I Order of the *M. winkleri* individuals in the bar plots of the chloroplast assignment analysis.

Individual (1 bar)	Plant ID Number	Species	Location
1	2478	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Bukit Taviu, stop 1
2	2485	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Bukit Taviu, stop 1
3	2581	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Bukit Taviu, stop 7
4	3857	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, Borneo rainforest lodge
5	3860	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, Borneo rainforest lodge
6	4615	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, DVFC, big gap close to office, trail into forest
7	4733	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, junction to Borneo rainforest lodge
8	4734	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, junction to Borneo rainforest lodge
9	4736	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, junction to Borneo rainforest lodge
10	6112	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail
11	6129	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail
12	6130	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail
13	6146	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to Borneo rainforest lodge
14	6154	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to Borneo rainforest lodge
15	6153	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to Borneo rainforest lodge
16	5058	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5
17	5065	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5
18	5066	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5
19	6407	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, Jalan Hulan, near Kunung Manangkob
20	6408	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, Jalan Hulan, near Kunung Manangkob
21	6403	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, Jalan Hulan, near Kunung Manangkob
22	6412	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 4
23	6414	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 4
24	6411	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 4
25	6420	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 5
26	6421	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 5
27	6417	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 5
28	6424	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 6, 55 km to Ranau
29	6426	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 6, 55 km to Ranau
30	6427	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, from Kota Kinabalu to Ranau, stop 6, 55 km to Ranau
31	2051	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Luasong
32	5665	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Poring, Langanan
33	5667	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Poring, Langanan
34	5669	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Poring, Langanan
35	6462	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Ranau to Kota Kinabalu
36	6469	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Ranau to Kota Kinabalu
37	6468	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Ranau to Kota Kinabalu
38	4286	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Lipad trail
39	4290	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Lipad trail, gap
40	4291	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Lipad trail, gap
41	5139	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation 'Golden Hope'
42	5140	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation 'Golden Hope'
43	5142	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation 'Golden Hope'
44	5159	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs, 0 bis 2.6 km
45	5194	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs, 0 bis 2.6 km
46	5196	<i>M. winkleri</i>	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs, 0 bis 2.6 km
47	6713	<i>M. winkleri</i>	Malaysia, Borneo, Sarawak, between Bukit Saban Resort and Betong
48	6656	<i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Jalan Miri -Bintulu
49	6657	<i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Jalan Miri -Bintulu
50	6658	<i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Jalan Miri -Bintulu
51	6659	<i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Jalan Miri -Bintulu
52	6673	<i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Jalan Miri -Bintulu
53	6678	<i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Jalan Miri -Bintulu
54	6679	<i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Jalan Miri -Bintulu
55	6561	<i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Lambir National Park
56	6562	<i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Lambir National Park
57	6566	<i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Lambir National Park
58	7078	<i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Pelagus Resort
59	7089	<i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Pelagus Resort
60	7126	<i>M. winkleri</i>	Malaysia, Borneo, Sarawak, Pelagus Resort
61	7060	<i>M. winkleri</i>	Malaysia, Sarawak, Puni
62	5	<i>M. winkleri</i>	Borneo, Brunei, Belalong
63	6061	<i>M. winkleri</i>	Borneo, Brunei, Belait, Labi
64	244	<i>M. winkleri</i>	Borneo, Brunei, Belait, Labi road (southern part of the road)
65	5918	<i>M. winkleri</i>	Borneo, Brunei, Belait, Labi
66	5803	<i>M. winkleri</i>	Borneo, Brunei, Belait, Tereja
67	5962	<i>M. winkleri</i>	Borneo, Brunei, Belait, Tereja
68	5970	<i>M. winkleri</i>	Borneo, Brunei, Belait, Tereja
69	5974	<i>M. winkleri</i>	Borneo, Brunei, Belait, Tereja
70	5983	<i>M. winkleri</i>	Borneo, Brunei, Belait, Tereja
71	6873	<i>M. winkleri</i>	Borneo, Brunei, Belait, Wong Kadi waterfall
72	6874	<i>M. winkleri</i>	Borneo, Brunei, Belait, Wong Kadi waterfall
73	6875	<i>M. winkleri</i>	Borneo, Brunei, Belait, Wong Kadi waterfall
74	6962	<i>M. winkleri</i>	Borneo, Brunei, Belait, Wong Kadir waterfall
75	6963	<i>M. winkleri</i>	Borneo, Brunei, Belait, Wong Kadir waterfall
76	4391	<i>M. winkleri</i>	Borneo, Brunei, Kuala Belalong
77	4396	<i>M. winkleri</i>	Borneo, Brunei, Kuala Belalong
78	5723	<i>M. winkleri</i>	Borneo, Brunei, Temburong, Belalong
79	5700	<i>M. winkleri</i>	Borneo, Brunei, Temburong, Belalong
80	5810	<i>M. winkleri</i>	Borneo, Brunei, Temburong, Belalong
81	6895	<i>M. winkleri</i>	Borneo, Brunei, Temburong, Bukit Patoi
82	6897	<i>M. winkleri</i>	Borneo, Brunei, Temburong, Bukit Patoi
83	6898	<i>M. winkleri</i>	Borneo, Brunei, Temburong, Bukit Patoi
84	5855	<i>M. winkleri</i>	Borneo, Brunei, Tutong, Bukit Patoi
85	5763	<i>M. winkleri</i>	Borneo, Brunei, Tutong, Bukit Patoi
86	5828	<i>M. winkleri</i>	Borneo, Brunei, Tutong, Bukit Patoi
87	5829	<i>M. winkleri</i>	Borneo, Brunei, Tutong, Bukit Patoi

Appendix J Order of the *M. winkleri* individuals for all bar plots created for both STRUCTURE and INSTRUCT analyses using the microsatellite data, and percentages with which individuals are assigned to each cluster for $K = 3$ (STRUCTURE).

Plant ID	Individual	Percent of individual assigned to			Location	Latitude	Longitude		
		Number	Species	(1 bar)				Cluster K=1	Cluster K=2
6713	<i>M. winkleri</i>	1		99.3%	0.5%	0.3%	Malaysia, Borneo, Sarawak, Bt. Saban Resort to Betong	1.463	111.560
7092	<i>M. winkleri</i>	2		93.7%	3.3%	3.0%	Malaysia, Borneo, Sarawak, Pelagus Resort	2.190	113.060
7078	<i>M. winkleri</i>	3		70.1%	29.4%	0.6%	Malaysia, Borneo, Sarawak, Pelagus Resort	2.190	113.060
7102	<i>M. winkleri</i>	4		98.7%	0.7%	0.6%	Malaysia, Borneo, Sarawak, Pelagus Resort	2.190	113.060
7126	<i>M. winkleri</i>	5		89.3%	10.4%	0.3%	Malaysia, Borneo, Sarawak, Pelagus Resort	2.190	113.060
7087	<i>M. winkleri</i>	6		92.7%	6.5%	0.8%	Malaysia, Borneo, Sarawak, Pelagus Resort	2.190	113.060
7089	<i>M. winkleri</i>	7		99.3%	0.4%	0.2%	Malaysia, Borneo, Sarawak, Pelagus Resort	2.190	113.060
7088	<i>M. winkleri</i>	8		99.3%	0.5%	0.2%	Malaysia, Borneo, Sarawak, Pelagus Resort	2.190	113.060
7098	<i>M. winkleri</i>	9		95.3%	4.4%	0.3%	Malaysia, Borneo, Sarawak, Pelagus Resort	2.190	113.060
7093	<i>M. winkleri</i>	10		94.4%	5.2%	0.4%	Malaysia, Borneo, Sarawak, Pelagus Resort	2.190	113.060
6670	<i>M. winkleri</i>	11		99.4%	0.4%	0.3%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.350	113.440
6676	<i>M. winkleri</i>	12		98.5%	1.2%	0.3%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.350	113.440
6669	<i>M. winkleri</i>	13		94.0%	1.0%	5.1%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.350	113.440
6675	<i>M. winkleri</i>	14		98.7%	1.0%	0.3%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.350	113.440
6668	<i>M. winkleri</i>	15		90.0%	0.5%	9.5%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.350	113.440
6674	<i>M. winkleri</i>	16		99.4%	0.4%	0.2%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.350	113.440
6667	<i>M. winkleri</i>	17		94.0%	5.4%	0.7%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.350	113.440
6680	<i>M. winkleri</i>	18		98.8%	0.9%	0.3%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.350	113.440
6679	<i>M. winkleri</i>	19		99.3%	0.4%	0.3%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.350	113.440
6678	<i>M. winkleri</i>	20		99.2%	0.5%	0.2%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.350	113.440
6673	<i>M. winkleri</i>	21		99.2%	0.6%	0.3%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.350	113.440
6671	<i>M. winkleri</i>	22		99.3%	0.5%	0.3%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.350	113.440
6677	<i>M. winkleri</i>	23		98.8%	0.8%	0.4%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.350	113.440
6672	<i>M. winkleri</i>	24		98.4%	1.1%	0.5%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.350	113.440
6659	<i>M. winkleri</i>	25		98.7%	0.5%	0.8%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.680	113.750
6658	<i>M. winkleri</i>	26		99.3%	0.4%	0.3%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.680	113.750
6657	<i>M. winkleri</i>	27		99.3%	0.4%	0.4%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.680	113.750
6664	<i>M. winkleri</i>	28		99.1%	0.6%	0.3%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.680	113.750
6656	<i>M. winkleri</i>	29		99.1%	0.6%	0.3%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.680	113.750
6663	<i>M. winkleri</i>	30		99.2%	0.6%	0.3%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.680	113.750
6655	<i>M. winkleri</i>	31		99.3%	0.5%	0.2%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.680	113.750
6662	<i>M. winkleri</i>	32		99.2%	0.5%	0.3%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.680	113.750
6654	<i>M. winkleri</i>	33		99.2%	0.5%	0.2%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.680	113.750
6661	<i>M. winkleri</i>	34		98.7%	0.7%	0.6%	Malaysia, Borneo, Sarawak, Jalan Miri - Bintulu	3.680	113.750
6557	<i>M. winkleri</i>	35		99.4%	0.3%	0.2%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6559	<i>M. winkleri</i>	36		99.3%	0.4%	0.2%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6551	<i>M. winkleri</i>	37		99.1%	0.4%	0.5%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6560	<i>M. winkleri</i>	38		99.2%	0.5%	0.2%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
7136	<i>M. winkleri</i>	39		99.3%	0.5%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6552	<i>M. winkleri</i>	40		99.3%	0.5%	0.2%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6561	<i>M. winkleri</i>	41		98.4%	1.2%	0.4%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6553	<i>M. winkleri</i>	42		99.0%	0.7%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6562	<i>M. winkleri</i>	43		92.5%	7.2%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
7124	<i>M. winkleri</i>	44		99.1%	0.5%	0.4%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6554	<i>M. winkleri</i>	45		98.3%	1.5%	0.2%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6566	<i>M. winkleri</i>	46		98.6%	0.7%	0.7%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
7125	<i>M. winkleri</i>	47		99.3%	0.4%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6555	<i>M. winkleri</i>	48		99.3%	0.4%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6567	<i>M. winkleri</i>	49		99.0%	0.6%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6556	<i>M. winkleri</i>	50		99.3%	0.4%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6568	<i>M. winkleri</i>	51		99.2%	0.4%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6608	<i>M. winkleri</i>	52		99.0%	0.7%	0.2%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6605	<i>M. winkleri</i>	53		99.3%	0.4%	0.2%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6604	<i>M. winkleri</i>	54		99.3%	0.5%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6607	<i>M. winkleri</i>	55		94.9%	4.8%	0.4%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6606	<i>M. winkleri</i>	56		99.2%	0.4%	0.4%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6615	<i>M. winkleri</i>	57		96.8%	2.8%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6614	<i>M. winkleri</i>	58		98.6%	0.8%	0.6%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6613	<i>M. winkleri</i>	59		98.7%	0.8%	0.4%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6612	<i>M. winkleri</i>	60		99.2%	0.5%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6620	<i>M. winkleri</i>	61		98.5%	0.8%	0.7%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6611	<i>M. winkleri</i>	62		98.8%	0.8%	0.4%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6618	<i>M. winkleri</i>	63		99.2%	0.5%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6610	<i>M. winkleri</i>	64		98.3%	1.4%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
7135	<i>M. winkleri</i>	65		99.3%	0.4%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
7134	<i>M. winkleri</i>	66		95.8%	1.6%	2.7%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
7133	<i>M. winkleri</i>	67		99.4%	0.3%	0.2%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
7130	<i>M. winkleri</i>	68		99.3%	0.4%	0.2%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
7129	<i>M. winkleri</i>	69		99.1%	0.7%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
7128	<i>M. winkleri</i>	70		98.8%	0.8%	0.4%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
7127	<i>M. winkleri</i>	71		99.4%	0.4%	0.2%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
7132	<i>M. winkleri</i>	72		99.4%	0.3%	0.2%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6599	<i>M. winkleri</i>	73		92.9%	6.6%	0.5%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6597	<i>M. winkleri</i>	74		99.3%	0.5%	0.2%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6596	<i>M. winkleri</i>	75		99.4%	0.3%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6980	<i>M. winkleri</i>	76		99.2%	0.6%	0.2%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6941	<i>M. winkleri</i>	77		99.2%	0.6%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6942	<i>M. winkleri</i>	78		99.4%	0.4%	0.2%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6943	<i>M. winkleri</i>	79		99.3%	0.4%	0.2%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6903	<i>M. winkleri</i>	80		99.1%	0.6%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
7110	<i>M. winkleri</i>	81		99.4%	0.4%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6583	<i>M. winkleri</i>	82		99.4%	0.4%	0.2%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6582	<i>M. winkleri</i>	83		93.2%	0.4%	6.4%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6584	<i>M. winkleri</i>	84		99.3%	0.4%	0.4%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6617	<i>M. winkleri</i>	85		98.3%	1.4%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6616	<i>M. winkleri</i>	86		98.5%	0.7%	0.8%	Malaysia, Borneo, Sarawak, Lambir National Park	4.226	114.035
6579	<i>M. winkleri</i>	87		96.4%	3.4%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.225	114.037
6577	<i>M. winkleri</i>	88		98.5%	1.1%	0.4%	Malaysia, Borneo, Sarawak, Lambir National Park	4.225	114.037
6576	<i>M. winkleri</i>	89		99.2%	0.5%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.225	114.037
6575	<i>M. winkleri</i>	90		99.2%	0.5%	0.3%	Malaysia, Borneo, Sarawak, Lambir National Park	4.225	114.037
6966	<i>M. winkleri</i>	91		93.2%	3.3%	3.6%	Borneo, Brunei, Belait, Wong Kadir waterfall	4.375	114.459
6962	<i>M. winkleri</i>	92		98.0%	0.7%	1.3%	Borneo, Brunei, Belait, Wong Kadir waterfall	4.375	114.459
6963	<i>M. winkleri</i>	93		99.2%	0.5%	0.2%	Borneo, Brunei, Belait, Wong Kadir waterfall	4.375	114.459
6964	<i>M. winkleri</i>	94		99.2%	0.5%	0.4%	Borneo, Brunei, Belait, Wong Kadir waterfall	4.375	114.459
6965	<i>M. winkleri</i>	95		95.0%	4.6%	0.5%	Borneo, Brunei, Belait, Wong Kadir waterfall	4.375	114.459
6875	<i>M. winkleri</i>	96		98.8%	0.6%	0.6%	Borneo, Brunei, Belait, Wong Kadir waterfall	4.375	114.459
6873	<i>M. winkleri</i>	97		97.5%	2.1%	0.4%	Borneo, Brunei, Belait, Wong Kadir waterfall	4.375	114.459

Plant ID	Individual Number	Species	Individual (1 bar)	Percent of individual assigned to			Location	Latitude	Longitude
				Cluster K=1	Cluster K=2	Cluster K=3			
6874	M. winkleri	98	99.1%	0.5%	0.4%	Borneo, Brunei, Belait, Wong Kadir waterfall	4.375	114.459	
5975	M. winkleri	99	79.2%	17.6%	3.2%	Borneo, Brunei, Belait, Tereja	4.460	114.470	
5957	M. winkleri	100	93.9%	2.9%	3.2%	Borneo, Brunei, Belait, Tereja	4.460	114.470	
5986	M. winkleri	101	98.6%	1.0%	0.4%	Borneo, Brunei, Belait, Tereja	4.460	114.470	
5952	M. winkleri	102	81.0%	0.7%	18.3%	Borneo, Brunei, Belait, Tereja	4.460	114.470	
5802	M. winkleri	103	91.6%	8.1%	0.3%	Borneo, Brunei, Belait, Tereja	4.460	114.470	
5803	M. winkleri	104	95.8%	2.8%	1.5%	Borneo, Brunei, Belait, Tereja	4.460	114.470	
5974	M. winkleri	105	99.3%	0.5%	0.3%	Borneo, Brunei, Belait, Tereja	4.460	114.470	
5983	M. winkleri	106	98.2%	1.2%	0.5%	Borneo, Brunei, Belait, Tereja	4.460	114.470	
5962	M. winkleri	107	92.8%	2.6%	4.7%	Borneo, Brunei, Belait, Tereja	4.460	114.470	
5970	M. winkleri	108	90.7%	0.4%	8.9%	Borneo, Brunei, Belait, Tereja	4.460	114.470	
6061	M. winkleri	109	98.7%	0.9%	0.3%	Borneo, Brunei, Belait, Labi	4.460	114.470	
5918	M. winkleri	110	93.6%	1.2%	5.2%	Borneo, Brunei, Belait, Labi	4.460	114.470	
244	M. winkleri	111	95.5%	2.9%	1.6%	Borneo, Brunei, Belait, Labi road	4.460	114.470	
7060	M. winkleri	112	97.9%	0.6%	1.4%	Malaysia, Borneo, Sarawak, Puni	4.715	115.032	
5701	M. winkleri	113	57.1%	42.5%	0.3%	Borneo, Brunei, Temburong, Belalong	4.717	115.067	
5700	M. winkleri	114	79.2%	19.5%	1.3%	Borneo, Brunei, Temburong, Belalong	4.717	115.067	
5697	M. winkleri	115	97.1%	1.2%	1.7%	Borneo, Brunei, Temburong, Belalong	4.717	115.067	
5711	M. winkleri	116	89.5%	10.1%	0.3%	Borneo, Brunei, Temburong, Belalong	4.717	115.067	
5713	M. winkleri	117	49.3%	50.3%	0.4%	Borneo, Brunei, Temburong, Belalong	4.717	115.067	
5716	M. winkleri	118	97.9%	1.7%	0.4%	Borneo, Brunei, Temburong, Belalong	4.717	115.067	
5694	M. winkleri	119	77.3%	22.1%	0.6%	Borneo, Brunei, Temburong, Belalong	4.717	115.067	
5723	M. winkleri	120	50.2%	49.1%	0.7%	Borneo, Brunei, Temburong, Belalong	4.717	115.067	
5810	M. winkleri	121	99.2%	0.5%	0.3%	Borneo, Brunei, Temburong, Belalong	4.717	115.067	
5693	M. winkleri	122	98.8%	0.9%	0.3%	Borneo, Brunei, Temburong, Belalong	4.717	115.067	
6902	M. winkleri	123	93.2%	4.7%	2.0%	Borneo, Brunei, Temburong, 10 km before Bangar	4.712	115.079	
6899	M. winkleri	124	98.0%	0.8%	1.3%	Borneo, Brunei, Temburong, 10 km before Bangar	4.712	115.079	
6900	M. winkleri	125	96.4%	3.2%	0.4%	Borneo, Brunei, Temburong, 10 km before Bangar	4.712	115.079	
6901	M. winkleri	126	78.2%	21.1%	0.7%	Borneo, Brunei, Temburong, 10 km before Bangar	4.712	115.079	
5	M. winkleri	127	92.4%	5.3%	2.4%	Borneo, Brunei, Belalong	4.550	115.133	
4391	M. winkleri	128	74.6%	6.0%	19.4%	Borneo, Brunei, Kuala Belalong	4.566	115.151	
4396	M. winkleri	129	96.7%	2.9%	0.3%	Borneo, Brunei, Kuala Belalong	4.566	115.151	
5760	M. winkleri	130	78.3%	19.8%	1.9%	Borneo, Brunei, Tutong, Bukit Patoi	4.760	115.180	
5855	M. winkleri	131	76.2%	23.3%	0.5%	Borneo, Brunei, Tutong, Bukit Patoi	4.760	115.180	
5764	M. winkleri	132	40.3%	59.4%	0.3%	Borneo, Brunei, Tutong, Bukit Patoi	4.760	115.180	
5762	M. winkleri	133	78.0%	21.5%	0.5%	Borneo, Brunei, Tutong, Bukit Patoi	4.760	115.180	
6008	M. winkleri	134	70.1%	29.6%	0.3%	Borneo, Brunei, Tutong, Bukit Patoi	4.760	115.180	
6012	M. winkleri	135	87.4%	10.3%	2.3%	Borneo, Brunei, Tutong, Bukit Patoi	4.760	115.180	
5852	M. winkleri	136	70.7%	28.8%	0.5%	Borneo, Brunei, Tutong, Bukit Patoi	4.760	115.180	
5853	M. winkleri	137	99.3%	0.4%	0.3%	Borneo, Brunei, Tutong, Bukit Patoi	4.760	115.180	
5828	M. winkleri	138	99.1%	0.6%	0.3%	Borneo, Brunei, Tutong, Bukit Patoi	4.760	115.180	
5763	M. winkleri	139	99.3%	0.5%	0.2%	Borneo, Brunei, Tutong, Bukit Patoi	4.760	115.180	
5829	M. winkleri	140	98.4%	1.3%	0.3%	Borneo, Brunei, Tutong, Bukit Patoi	4.760	115.180	
6011	M. winkleri	141	96.4%	3.1%	0.5%	Borneo, Brunei, Tutong, Bukit Patoi	4.760	115.180	
5850	M. winkleri	142	84.7%	14.9%	0.5%	Borneo, Brunei, Tutong, Bukit Patoi	4.760	115.180	
6894	M. winkleri	143	99.1%	0.4%	0.5%	Borneo, Brunei, Temburong, Bukit Patoi	4.760	115.180	
6895	M. winkleri	144	96.5%	3.2%	0.3%	Borneo, Brunei, Temburong, Bukit Patoi	4.760	115.180	
6897	M. winkleri	145	96.4%	3.3%	0.3%	Borneo, Brunei, Temburong, Bukit Patoi	4.760	115.180	
6898	M. winkleri	146	95.6%	0.5%	3.9%	Borneo, Brunei, Temburong, Bukit Patoi	4.760	115.180	
482	M. winkleri	147	1.4%	98.3%	0.3%	Malaysia, Borneo, Sabah, Crocker Range	5.899	116.225	
6463	M. winkleri	148	0.5%	44.8%	54.7%	Malaysia, Borneo, Sabah, Ranau to KK	6.090	116.750	
6460	M. winkleri	149	1.9%	97.7%	0.4%	Malaysia, Borneo, Sabah, Ranau to KK, Kinabalu view	6.110	116.840	
6459	M. winkleri	150	1.2%	98.5%	0.3%	Malaysia, Borneo, Sabah, Ranau to KK, Kinabalu view	6.110	116.840	
6462	M. winkleri	151	11.2%	88.5%	0.4%	Malaysia, Borneo, Sabah, Ranau to KK	6.160	116.970	
6461	M. winkleri	152	14.9%	84.7%	0.4%	Malaysia, Borneo, Sabah, Ranau to KK, 44 km to Tuaran	6.160	116.970	
6468	M. winkleri	153	3.9%	95.8%	0.4%	Malaysia, Borneo, Sabah, Ranau to KK	6.180	116.610	
6469	M. winkleri	154	1.0%	98.5%	0.5%	Malaysia, Borneo, Sabah, Ranau to KK	6.180	116.610	
6414	M. winkleri	155	12.5%	87.2%	0.3%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 4	6.190	116.860	
6410	M. winkleri	156	1.0%	98.7%	0.3%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 4	6.190	116.860	
6412	M. winkleri	157	4.8%	95.1%	0.4%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 4	6.190	116.860	
6416	M. winkleri	158	0.8%	97.7%	1.5%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 4	6.190	116.860	
6411	M. winkleri	159	27.9%	71.7%	0.4%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 4	6.190	116.860	
6415	M. winkleri	160	31.4%	66.7%	1.9%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 4	6.190	116.860	
5766	M. winkleri	161	2.4%	97.3%	0.3%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
5780	M. winkleri	162	2.1%	52.5%	45.4%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
5767	M. winkleri	163	1.6%	98.1%	0.4%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
5771	M. winkleri	164	0.5%	70.6%	28.9%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
5778	M. winkleri	165	2.0%	97.4%	0.5%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
5772	M. winkleri	166	1.8%	97.7%	0.5%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
5779	M. winkleri	167	1.3%	98.1%	0.6%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
5777	M. winkleri	168	0.5%	98.5%	1.0%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
6022	M. winkleri	169	0.7%	99.0%	0.4%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
6020	M. winkleri	170	0.7%	99.0%	0.3%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
6021	M. winkleri	171	0.4%	99.3%	0.3%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
6025	M. winkleri	172	0.7%	99.0%	0.3%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
5770	M. winkleri	173	0.7%	98.6%	0.7%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
5788	M. winkleri	174	0.5%	99.2%	0.3%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
5774	M. winkleri	175	2.5%	97.2%	0.3%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
5781	M. winkleri	176	1.5%	96.5%	2.0%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
5775	M. winkleri	177	1.0%	98.4%	0.6%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
5765	M. winkleri	178	0.6%	99.1%	0.3%	Malaysia, Sabah, road KK-Ranau, ca km 60	6.330	116.720	
6426	M. winkleri	179	2.7%	96.9%	0.4%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 6, 55 km to Ranau	6.330	116.720	
6429	M. winkleri	180	19.8%	79.8%	0.4%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 6, 55 km to Ranau	6.330	116.720	
6430	M. winkleri	181	2.2%	97.5%	0.3%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 6, 55 km to Ranau	6.330	116.720	
6427	M. winkleri	182	0.7%	38.6%	60.7%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 6, 55 km to Ranau	6.330	116.720	
6424	M. winkleri	183	2.0%	96.9%	1.1%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 6, 55 km to Ranau	6.330	116.720	
6432	M. winkleri	184	3.5%	96.1%	0.3%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 6, 55 km to Ranau	6.330	116.720	
6422	M. winkleri	185	0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 6, 55 km to Ranau	6.330	116.720	
6428	M. winkleri	186	37.9%	61.8%	0.3%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 6, 55 km to Ranau	6.330	116.720	
6431	M. winkleri	187	23.7%	75.9%	0.4%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 6, 55 km to Ranau	6.330	116.720	
6423	M. winkleri	188	1.1%	98.6%	0.3%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 6, 55 km to Ranau	6.330	116.720	
6405	M. winkleri	189	1.1%	91.4%	7.5%	Malaysia, Borneo, Sabah, from KK to Ranau, near Kg Manangkob	6.400	116.580	
6407	M. winkleri	190	3.6%	96.0%	0.3%	Malaysia, Borneo, Sabah, from KK to Ranau, near Kg Manangkob	6.400	116.580	
6408	M. winkleri	191	1.0%	89.0%	10.0%	Malaysia, Borneo, Sabah, from KK to Ranau, near Kg Manangkob	6.400	116.580	
6406	M. winkleri	192	2.6%	96.9%	0.5%	Malaysia, Borneo, Sabah, from KK to Ranau, near Kg Manangkob	6.400	116.580	
6404	M. winkleri	193	6.7%	92.8%	0.5%	Malaysia, Borneo, Sabah, from KK to Ranau, near Kg Manangkob	6.400	116.580	
6403	M. winkleri	194	2.5%	97.2%	0.3%	Malaysia, Borneo, Sabah, from KK to Ranau, near Kg Manangkob	6.400	116.580	

Plant ID	Individual	Percent of individual assigned to			Location	Latitude	Longitude		
		Number	Species	(1 bar)				Cluster K=1	Cluster K=2
6420	<i>M. winkleri</i>	195		8.5%	91.1%	0.4%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 5	6.400	116.830
6419	<i>M. winkleri</i>	196		7.0%	92.3%	0.7%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 5	6.400	116.830
6421	<i>M. winkleri</i>	197		19.8%	79.5%	0.6%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 5	6.400	116.830
6417	<i>M. winkleri</i>	198		0.4%	98.8%	0.8%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 5	6.400	116.830
6409	<i>M. winkleri</i>	199		2.1%	97.6%	0.3%	Malaysia, Borneo, Sabah, from KK to Ranau, near Kg Manangkob	6.400	116.580
2119	<i>M. winkleri</i>	200		0.9%	98.8%	0.3%	Malaysia, Borneo, Sabah, Poring, Langanan trail, ca km 1.6	6.060	116.690
510	<i>M. winkleri</i>	201		12.9%	83.7%	3.4%	Malaysia, Borneo, Sabah, Poring, Langanan trail	6.060	116.690
505	<i>M. winkleri</i>	202		3.4%	95.1%	1.5%	Malaysia, Borneo, Sabah, Poring, canopy walkway	6.050	116.700
6044	<i>M. winkleri</i>	203		1.0%	98.7%	0.3%	Malaysia, Borneo, Sabah, Poring, walkway	6.070	116.720
6047	<i>M. winkleri</i>	204		1.5%	98.2%	0.3%	Malaysia, Borneo, Sabah, Poring, Langanan	6.070	116.720
6046	<i>M. winkleri</i>	205		0.8%	98.8%	0.4%	Malaysia, Borneo, Sabah, Poring, Langanan	6.070	116.720
6053	<i>M. winkleri</i>	206		0.6%	99.0%	0.4%	Malaysia, Borneo, Sabah, Poring, Langanan	6.070	116.720
6054	<i>M. winkleri</i>	207		0.6%	97.3%	2.2%	Malaysia, Borneo, Sabah, Poring, Langanan	6.070	116.720
6045	<i>M. winkleri</i>	208		0.7%	99.0%	0.3%	Malaysia, Borneo, Sabah, Poring, Langanan	6.070	116.720
5667	<i>M. winkleri</i>	209		0.5%	99.3%	0.3%	Malaysia, Borneo, Sabah, Poring, Langanan	6.070	116.720
5669	<i>M. winkleri</i>	210		5.3%	94.3%	0.3%	Malaysia, Borneo, Sabah, Poring, Langanan	6.070	116.720
5674	<i>M. winkleri</i>	211		1.4%	98.3%	0.3%	Malaysia, Borneo, Sabah, Poring, Langanan	6.070	116.720
5665	<i>M. winkleri</i>	212		1.6%	98.1%	0.3%	Malaysia, Borneo, Sabah, Poring, Langanan	6.070	116.720
5666	<i>M. winkleri</i>	213		0.8%	98.9%	0.3%	Malaysia, Borneo, Sabah, Poring, Langanan	6.070	116.720
5660	<i>M. winkleri</i>	214		11.9%	89.9%	18.2%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
5662	<i>M. winkleri</i>	215		0.6%	98.9%	0.5%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
5658	<i>M. winkleri</i>	216		0.4%	99.2%	0.4%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
5659	<i>M. winkleri</i>	217		0.4%	99.3%	0.3%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
5657	<i>M. winkleri</i>	218		0.4%	98.8%	0.8%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
5661	<i>M. winkleri</i>	219		0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
6038	<i>M. winkleri</i>	220		5.8%	89.6%	4.6%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
2323	<i>M. winkleri</i>	221		0.4%	99.1%	0.4%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
2351	<i>M. winkleri</i>	222		0.7%	99.0%	0.3%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
5663	<i>M. winkleri</i>	223		0.7%	97.4%	1.9%	Malaysia, Borneo, Sabah, Poring	6.070	116.720
5664	<i>M. winkleri</i>	224		1.1%	98.6%	0.3%	Malaysia, Borneo, Sabah, Poring	6.070	116.720
4744	<i>M. winkleri</i>	225		1.6%	98.0%	0.3%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
4742	<i>M. winkleri</i>	226		2.8%	96.8%	0.4%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
4743	<i>M. winkleri</i>	227		12.8%	86.6%	0.6%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
4749	<i>M. winkleri</i>	228		0.8%	98.6%	0.6%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
4754	<i>M. winkleri</i>	229		0.8%	99.0%	0.3%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
4751	<i>M. winkleri</i>	230		0.4%	98.8%	0.8%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
4753	<i>M. winkleri</i>	231		16.0%	83.6%	0.4%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
4748	<i>M. winkleri</i>	232		0.4%	99.2%	0.3%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
4755	<i>M. winkleri</i>	233		0.4%	98.9%	0.7%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
4756	<i>M. winkleri</i>	234		21.2%	76.3%	2.5%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
4750	<i>M. winkleri</i>	235		1.0%	98.7%	0.3%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
4747	<i>M. winkleri</i>	236		0.6%	99.2%	0.3%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
4745	<i>M. winkleri</i>	237		53.5%	45.9%	0.6%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
4752	<i>M. winkleri</i>	238		0.7%	99.1%	0.3%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
4746	<i>M. winkleri</i>	239		10.4%	89.3%	0.3%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
4757	<i>M. winkleri</i>	240		0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
2337	<i>M. winkleri</i>	241		0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Poring, logging road	6.060	116.730
2581	<i>M. winkleri</i>	242		1.4%	98.1%	0.5%	Malaysia, Borneo, Sabah, Bukit Taviu, stop 7	5.680	116.940
2485	<i>M. winkleri</i>	243		0.6%	97.9%	1.5%	Malaysia, Borneo, Sabah, Bukit Taviu, stop 1	5.690	116.980
2478	<i>M. winkleri</i>	244		0.9%	98.8%	0.3%	Malaysia, Borneo, Sabah, Bukit Taviu, stop 1	5.690	116.980
112	<i>M. winkleri</i>	245		3.6%	93.8%	2.6%	Malaysia, Borneo, Sabah, Deramakot Forest Reserve	5.330	117.330
118	<i>M. winkleri</i>	246		0.9%	96.9%	2.2%	Malaysia, Borneo, Sabah, Deramakot Forest Reserve	5.330	117.330
4043	<i>M. winkleri</i>	247		3.8%	1.1%	95.0%	Malaysia, Borneo, Sabah, Sepilok, trail to birdwatching tower	5.866	117.967
4044	<i>M. winkleri</i>	248		0.9%	0.8%	98.3%	Malaysia, Borneo, Sabah, Sepilok, trail to birdwatching tower	5.866	117.967
4048	<i>M. winkleri</i>	249		2.2%	1.7%	96.1%	Malaysia, Borneo, Sabah, Sepilok, waterhole	5.866	117.967
4049	<i>M. winkleri</i>	250		0.5%	0.8%	98.7%	Malaysia, Borneo, Sabah, Sepilok, waterhole	5.866	117.967
2829	<i>M. winkleri</i>	251		41.0%	29.2%	29.8%	Malaysia, Borneo, Sabah, Danum Valley, logging road near Malua	5.110	117.600
2830	<i>M. winkleri</i>	252		0.4%	97.1%	2.5%	Malaysia, Borneo, Sabah, Danum Valley, logging road near Malua	5.110	117.600
2831	<i>M. winkleri</i>	253		0.6%	99.0%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, logging road near Malua	5.110	117.600
2854	<i>M. winkleri</i>	254		0.9%	98.5%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, logging road near Malua	5.110	117.600
2866	<i>M. winkleri</i>	255		0.6%	99.0%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, logging road near Malua	5.110	117.600
2867	<i>M. winkleri</i>	256		1.0%	98.6%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, logging road near Malua	5.110	117.600
3545	<i>M. winkleri</i>	257		1.2%	97.8%	1.0%	Malaysia, Borneo, Sabah, Danum Valley, Malua, new logging road	5.100	117.650
3663	<i>M. winkleri</i>	258		0.5%	99.0%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, Malua, new logging road	5.100	117.650
3664	<i>M. winkleri</i>	259		0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Malua, new logging road	5.100	117.650
3740	<i>M. winkleri</i>	260		0.6%	96.7%	2.8%	Malaysia, Borneo, Sabah, Danum Valley, Malua, new logging road	5.100	117.650
3661	<i>M. winkleri</i>	261		1.0%	7.3%	91.7%	Malaysia, Borneo, Sabah, Danum Valley, Malua, new logging road	5.100	117.650
3662	<i>M. winkleri</i>	262		0.4%	0.3%	99.3%	Malaysia, Borneo, Sabah, Danum Valley, Malua, new logging road	5.100	117.650
3222	<i>M. winkleri</i>	263		3.6%	15.1%	81.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.060	117.740
3253	<i>M. winkleri</i>	264		1.0%	4.0%	95.0%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.050	117.760
3415	<i>M. winkleri</i>	265		1.5%	98.1%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.090	117.650
3414	<i>M. winkleri</i>	266		1.4%	98.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.090	117.650
6155	<i>M. winkleri</i>	267		19.7%	79.8%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.070	117.720
6157	<i>M. winkleri</i>	268		0.6%	99.0%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.070	117.720
6158	<i>M. winkleri</i>	269		9.4%	90.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.070	117.720
6156	<i>M. winkleri</i>	270		0.9%	98.8%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.070	117.720
6160	<i>M. winkleri</i>	271		0.3%	99.4%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.070	117.720
6159	<i>M. winkleri</i>	272		0.4%	99.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.070	117.720
3815	<i>M. winkleri</i>	273		0.4%	99.4%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.070	117.730
3816	<i>M. winkleri</i>	274		0.5%	98.7%	0.8%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.070	117.730
3221	<i>M. winkleri</i>	275		0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.060	117.740
3330	<i>M. winkleri</i>	276		1.2%	98.5%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.060	117.750
3331	<i>M. winkleri</i>	277		1.5%	97.7%	0.8%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.060	117.750
3332	<i>M. winkleri</i>	278		0.8%	98.5%	0.8%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.060	117.750
3333	<i>M. winkleri</i>	279		5.6%	94.0%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.060	117.750
3334	<i>M. winkleri</i>	280		1.9%	94.7%	3.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.060	117.750
3329	<i>M. winkleri</i>	281		1.0%	84.8%	14.2%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.060	117.750
3254	<i>M. winkleri</i>	282		0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.050	117.760
3292	<i>M. winkleri</i>	283		0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.050	117.760
3293	<i>M. winkleri</i>	284		1.4%	98.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.050	117.760
3294	<i>M. winkleri</i>	285		1.0%	98.7%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.050	117.760
3878	<i>M. winkleri</i>	286		0.4%	99.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.000	117.800
3882	<i>M. winkleri</i>	287		0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.000	117.800
3883	<i>M. winkleri</i>	288		2.3%	97.4%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.000	117.800
3936	<i>M. winkleri</i>	289		0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.000	117.800
3937	<i>M. winkleri</i>	290		0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua	5.000	117.800
6154	<i>M. winkleri</i>	291		25.8%	73.7%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	5.050	117.760

Plant ID	Individual Number	Species	Individual (1 bar)	Percent of individual assigned to			Location	Latitude	Longitude
				Cluster K=1	Cluster K=2	Cluster K=3			
6153	M. winkleri	292	2.9%	96.3%	0.8%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	5.050	117.760	
6147	M. winkleri	293	2.4%	73.1%	24.5%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	5.050	117.760	
6141	M. winkleri	294	1.0%	98.7%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	5.050	117.760	
6146	M. winkleri	295	1.5%	52.8%	45.7%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	5.050	117.760	
4732	M. winkleri	296	0.8%	98.9%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, junction to BRL	4.950	117.810	
4733	M. winkleri	297	1.1%	95.8%	3.1%	Malaysia, Borneo, Sabah, Danum Valley, junction to BRL	4.950	117.810	
4734	M. winkleri	298	0.9%	98.9%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, junction to BRL	4.950	117.810	
4735	M. winkleri	299	0.5%	98.9%	0.6%	Malaysia, Borneo, Sabah, Danum Valley, junction to BRL	4.950	117.810	
4736	M. winkleri	300	1.1%	98.3%	0.6%	Malaysia, Borneo, Sabah, Danum Valley, junction to BRL	4.950	117.810	
4737	M. winkleri	301	0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, junction to BRL	4.950	117.810	
3857	M. winkleri	302	0.8%	96.1%	3.1%	Malaysia, Borneo, Sabah, Danum Valley, BRL	5.020	117.750	
3860	M. winkleri	303	0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, BRL	5.020	117.750	
3861	M. winkleri	304	0.7%	25.7%	73.6%	Malaysia, Borneo, Sabah, Danum Valley, BRL	5.020	117.750	
3078	M. winkleri	305	0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Main Line North	5.040	118.040	
4642	M. winkleri	306	1.0%	98.7%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Sg. Kailsun trail	5.010	118.070	
3443	M. winkleri	307	0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Sg. Kailsun trail	5.010	118.070	
4988	M. winkleri	308	1.4%	97.4%	1.2%	Malaysia, Borneo, Sabah, Danum Valley, Sg. Kailsun	5.010	118.070	
4987	M. winkleri	309	0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Sg. Kailsun	5.010	118.070	
4989	M. winkleri	310	0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Sg. Kailsun	5.010	118.070	
4726	M. winkleri	311	0.5%	99.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Sg. Kailsun trail	5.010	118.070	
4807	M. winkleri	312	0.7%	92.2%	7.2%	Malaysia, Borneo, Sabah, Danum Valley, Kailsun	4.950	117.810	
3462	M. winkleri	313	4.1%	93.5%	2.4%	Malaysia, Borneo, Sabah, Danum Valley, Sg. Purut trail	4.950	117.800	
2233	M. winkleri	314	0.9%	89.9%	9.2%	Malaysia, Borneo, Sabah, Danum Valley, Westambling trail, waterfall	4.980	117.800	
5083	M. winkleri	315	1.5%	98.0%	0.6%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W13,1N5	4.980	117.800	
5082	M. winkleri	316	0.5%	99.0%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W15N3	4.980	117.800	
4550	M. winkleri	317	0.6%	98.1%	1.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid W15 N1.5	4.980	117.800	
4551	M. winkleri	318	9.5%	90.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid W15 N1.5	4.980	117.800	
4544	M. winkleri	319	1.3%	87.9%	10.8%	Malaysia, Borneo, Sabah, Danum Valley, west grid W15 N1.5	4.980	117.800	
4555	M. winkleri	320	23.2%	76.5%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid W15 N1.5	4.980	117.800	
3478	M. winkleri	321	4.9%	94.8%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid N1W15	4.980	117.800	
3479	M. winkleri	322	0.6%	98.1%	1.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid N1W15	4.980	117.800	
4662	M. winkleri	323	0.8%	98.6%	0.6%	Malaysia, Borneo, Sabah, Danum Valley, west grid W12	4.980	117.800	
4668	M. winkleri	324	1.0%	98.7%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid W12	4.980	117.800	
4669	M. winkleri	325	0.4%	99.1%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid W12	4.980	117.800	
4664	M. winkleri	326	1.1%	96.7%	2.2%	Malaysia, Borneo, Sabah, Danum Valley, west grid W12	4.980	117.800	
4667	M. winkleri	327	1.1%	98.5%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid W12	4.980	117.800	
4671	M. winkleri	328	0.4%	98.3%	1.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid W12	4.950	117.810	
4672	M. winkleri	329	0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid W12	4.950	117.810	
4661	M. winkleri	330	1.2%	98.4%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid W12	4.950	117.810	
4663	M. winkleri	331	0.3%	0.3%	99.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid W12	4.980	117.800	
4666	M. winkleri	332	0.5%	99.1%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid W12	4.980	117.800	
4670	M. winkleri	333	83.3%	12.4%	4.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid W12	4.980	117.800	
4688	M. winkleri	334	0.5%	99.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid W11	4.980	117.800	
5202	M. winkleri	335	0.3%	99.4%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W11	4.980	117.800	
5201	M. winkleri	336	0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W11	4.980	117.800	
4693	M. winkleri	337	0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid W11	4.980	117.800	
4473	M. winkleri	338	0.6%	98.6%	0.8%	Malaysia, Borneo, Sabah, Danum Valley, west grid W10 N3	4.980	117.800	
5043	M. winkleri	339	0.3%	0.3%	99.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1 25	4.980	117.800	
5059	M. winkleri	340	32.2%	67.3%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5063	M. winkleri	341	29.0%	70.5%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5048	M. winkleri	342	1.7%	98.0%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5050	M. winkleri	343	0.8%	98.3%	0.9%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5055	M. winkleri	344	0.5%	99.1%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5071	M. winkleri	345	0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5061	M. winkleri	346	0.9%	98.8%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5060	M. winkleri	347	0.7%	88.8%	10.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5072	M. winkleri	348	0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5056	M. winkleri	349	0.8%	98.8%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5062	M. winkleri	350	1.0%	98.7%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5075	M. winkleri	351	0.3%	76.9%	22.8%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5051	M. winkleri	352	8.2%	91.4%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5064	M. winkleri	353	0.6%	63.2%	36.2%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5054	M. winkleri	354	0.7%	99.0%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5068	M. winkleri	355	0.9%	98.9%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5057	M. winkleri	356	0.9%	98.8%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5069	M. winkleri	357	0.4%	66.7%	33.0%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5070	M. winkleri	358	1.0%	98.1%	0.9%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5073	M. winkleri	359	0.8%	99.0%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5045	M. winkleri	360	0.7%	99.0%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5046	M. winkleri	361	0.6%	99.0%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5067	M. winkleri	362	1.0%	98.8%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5049	M. winkleri	363	0.7%	99.1%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5078	M. winkleri	364	0.3%	99.4%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5077	M. winkleri	365	0.3%	99.2%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5076	M. winkleri	366	5.6%	94.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5080	M. winkleri	367	1.6%	97.6%	0.8%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5079	M. winkleri	368	0.7%	99.0%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5066	M. winkleri	369	1.9%	96.5%	1.6%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5058	M. winkleri	370	0.6%	93.8%	5.6%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5065	M. winkleri	371	0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5081	M. winkleri	372	1.0%	98.7%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5044	M. winkleri	373	0.3%	93.0%	6.7%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5047	M. winkleri	374	0.4%	99.4%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5053	M. winkleri	375	1.5%	89.5%	9.0%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5052	M. winkleri	376	46.8%	1.8%	51.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.5	4.980	117.800	
5086	M. winkleri	377	0.9%	98.6%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S1.10	4.980	117.800	
5084	M. winkleri	378	0.4%	99.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W10S3.6	4.980	117.800	
4728	M. winkleri	379	0.8%	98.9%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, upper rhino ridge trail, R51	5.100	117.650	
4729	M. winkleri	380	0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, upper rhino ridge trail, R51	5.100	117.650	
4727	M. winkleri	381	0.7%	99.0%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Rhino ridge trail, R13-R14	5.100	117.650	
5085	M. winkleri	382	0.7%	99.0%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W8S5	4.980	117.800	
2137	M. winkleri	383	0.3%	99.1%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, main trail W8	4.980	117.800	
4981	M. winkleri	384	0.4%	99.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, creek at R1	4.980	117.800	
4979	M. winkleri	385	1.0%	98.8%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, creek at R1	4.980	117.800	
4982	M. winkleri	386	0.5%	99.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, creek at R1	4.980	117.800	
4980	M. winkleri	387	0.4%	99.0%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, creek at R1	4.950	117.810	
4978	M. winkleri	388	0.5%	97.3%	2.2%	Malaysia, Borneo, Sabah, Danum Valley, west grid, before R1	4.980	117.800	

Plant ID	Species	Individual (1 bar)	Percent of individual assigned to			Location	Latitude	Longitude
			Cluster K=1	Cluster K=2	Cluster K=3			
4984	<i>M. winkleri</i>	389	1.0%	98.5%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, creek at R1	4.980	117.800
5037	<i>M. winkleri</i>	390	0.3%	0.4%	99.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5036	<i>M. winkleri</i>	391	0.6%	0.6%	98.8%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5040	<i>M. winkleri</i>	392	0.3%	0.3%	99.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5023	<i>M. winkleri</i>	393	0.2%	0.2%	99.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5030	<i>M. winkleri</i>	394	0.2%	0.4%	99.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5033	<i>M. winkleri</i>	395	0.6%	0.4%	99.1%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5031	<i>M. winkleri</i>	396	0.3%	0.3%	99.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5027	<i>M. winkleri</i>	397	0.5%	12.7%	86.7%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5028	<i>M. winkleri</i>	398	0.4%	0.4%	99.2%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5039	<i>M. winkleri</i>	399	0.3%	0.3%	99.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5034	<i>M. winkleri</i>	400	0.3%	0.4%	99.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5029	<i>M. winkleri</i>	401	0.2%	0.3%	99.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5035	<i>M. winkleri</i>	402	0.3%	0.3%	99.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5032	<i>M. winkleri</i>	403	0.3%	0.4%	99.2%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5024	<i>M. winkleri</i>	404	0.4%	0.5%	99.1%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5025	<i>M. winkleri</i>	405	1.0%	0.5%	98.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5026	<i>M. winkleri</i>	406	0.6%	0.8%	98.7%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5041	<i>M. winkleri</i>	407	0.7%	0.6%	98.7%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
5042	<i>M. winkleri</i>	408	0.2%	0.3%	99.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W7.8	4.980	117.800
3466	<i>M. winkleri</i>	409	0.4%	99.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid W7.5	4.980	117.800
3467	<i>M. winkleri</i>	410	0.4%	99.4%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid W7.5	4.980	117.800
3468	<i>M. winkleri</i>	411	0.5%	99.0%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid W7.5	4.980	117.800
5022	<i>M. winkleri</i>	412	1.2%	2.4%	96.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W5.8	4.980	117.800
5013	<i>M. winkleri</i>	413	0.2%	0.2%	99.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W5N5.3	4.980	117.800
5015	<i>M. winkleri</i>	414	1.1%	0.4%	98.6%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W5N5.3	4.980	117.800
5016	<i>M. winkleri</i>	415	1.3%	0.6%	98.2%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W5N5.3	4.980	117.800
5014	<i>M. winkleri</i>	416	0.3%	0.9%	98.9%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W5N5.3	4.980	117.800
5021	<i>M. winkleri</i>	418	0.3%	0.3%	99.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid, near W5	4.980	117.800
3998	<i>M. winkleri</i>	417	2.4%	28.1%	69.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid W5S5.3	4.980	117.800
6140	<i>M. winkleri</i>	419	0.3%	0.4%	99.3%	Malaysia, Borneo, Sabah, Danum Valley, West grid, Plot 4	4.980	117.800
6163	<i>M. winkleri</i>	420	22.5%	33.1%	44.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W4	4.980	117.800
6169	<i>M. winkleri</i>	421	33.9%	5.2%	60.9%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W4	4.980	117.800
6171	<i>M. winkleri</i>	422	7.8%	14.9%	77.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W4	4.980	117.800
6168	<i>M. winkleri</i>	423	22.3%	0.7%	77.0%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W4	4.980	117.800
6170	<i>M. winkleri</i>	424	14.1%	19.4%	66.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W4	4.980	117.800
6164	<i>M. winkleri</i>	425	36.2%	6.9%	56.9%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W4	4.980	117.800
6167	<i>M. winkleri</i>	426	8.4%	19.0%	72.6%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W4	4.980	117.800
6172	<i>M. winkleri</i>	427	19.7%	20.9%	59.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W3.5N5	4.980	117.800
6173	<i>M. winkleri</i>	428	26.8%	8.3%	65.0%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W3.5N5	4.980	117.800
6162	<i>M. winkleri</i>	429	0.2%	0.3%	99.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W3.5N5	4.980	117.800
6165	<i>M. winkleri</i>	430	5.8%	31.2%	63.0%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W2.5	4.980	117.800
6166	<i>M. winkleri</i>	431	25.9%	1.4%	72.7%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W2.5	4.980	117.800
5198	<i>M. winkleri</i>	432	0.2%	0.3%	99.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W2	4.980	117.800
5200	<i>M. winkleri</i>	433	0.3%	0.3%	99.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W2	4.980	117.800
5199	<i>M. winkleri</i>	434	0.3%	0.3%	99.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W2	4.980	117.800
4959	<i>M. winkleri</i>	435	0.2%	0.3%	99.5%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W0N13	4.980	117.800
4961	<i>M. winkleri</i>	436	4.8%	94.9%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W0N13	4.980	117.800
4958	<i>M. winkleri</i>	437	1.0%	98.7%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W0N13	4.980	117.800
4957	<i>M. winkleri</i>	438	6.3%	88.0%	5.8%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W0N13	4.980	117.800
4960	<i>M. winkleri</i>	439	0.7%	97.3%	2.1%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W0N13	4.980	117.800
4956	<i>M. winkleri</i>	440	0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid, W0N13	4.980	117.800
4533	<i>M. winkleri</i>	441	0.4%	96.3%	3.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid W0 nach N12	4.980	117.800
4533b	<i>M. winkleri</i>	442	0.4%	98.1%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid W0 nach N12	4.980	117.800
4533e	<i>M. winkleri</i>	443	0.5%	98.6%	0.9%	Malaysia, Borneo, Sabah, Danum Valley, west grid W0 nach N12	4.980	117.800
4533f	<i>M. winkleri</i>	444	1.7%	97.7%	0.6%	Malaysia, Borneo, Sabah, Danum Valley, west grid W0 nach N12	4.980	117.800
4533c	<i>M. winkleri</i>	445	2.4%	96.4%	1.2%	Malaysia, Borneo, Sabah, Danum Valley, west grid W0 nach N12	4.980	117.800
4533a	<i>M. winkleri</i>	446	2.4%	75.8%	21.8%	Malaysia, Borneo, Sabah, Danum Valley, west grid W0 nach N12	4.980	117.800
5009	<i>M. winkleri</i>	447	0.3%	0.3%	99.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid, von W0N7	4.980	117.800
5008	<i>M. winkleri</i>	448	0.5%	0.7%	98.8%	Malaysia, Borneo, Sabah, Danum Valley, west grid, von W0N7	4.980	117.800
5007	<i>M. winkleri</i>	449	0.7%	0.3%	99.0%	Malaysia, Borneo, Sabah, Danum Valley, west grid, von W0N7	4.980	117.800
5010	<i>M. winkleri</i>	450	0.3%	0.3%	99.4%	Malaysia, Borneo, Sabah, Danum Valley, west grid, von W0N7	4.980	117.800
5011	<i>M. winkleri</i>	451	0.7%	98.4%	0.9%	Malaysia, Borneo, Sabah, Danum Valley, west grid, von W0N7	4.980	117.800
4531	<i>M. winkleri</i>	452	0.4%	99.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, west grid W0 N5 after N10	4.980	117.800
4656	<i>M. winkleri</i>	453	0.5%	99.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Elephant Ridge trail E15	4.950	117.810
4655	<i>M. winkleri</i>	454	0.5%	99.1%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, Elephant Ridge trail,	4.980	117.800
3959	<i>M. winkleri</i>	455	0.8%	98.9%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Sg. Segama, Elephant Ridge trail	4.950	117.800
4507	<i>M. winkleri</i>	456	0.8%	98.8%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, east grid E14-15	4.980	117.800
3203	<i>M. winkleri</i>	457	22.6%	70.4%	7.0%	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	4.980	117.870
3011	<i>M. winkleri</i>	458	25.2%	74.5%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	4.970	117.940
3039	<i>M. winkleri</i>	459	0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	4.970	117.940
3040	<i>M. winkleri</i>	460	3.5%	91.8%	4.7%	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	4.970	117.940
3041	<i>M. winkleri</i>	461	0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	4.970	117.940
3010	<i>M. winkleri</i>	462	0.4%	99.4%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	4.970	117.940
3042	<i>M. winkleri</i>	463	0.9%	98.5%	0.6%	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	4.970	117.940
3013	<i>M. winkleri</i>	464	4.9%	94.8%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	4.970	117.940
3038	<i>M. winkleri</i>	465	1.2%	98.5%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	4.970	117.940
2968	<i>M. winkleri</i>	466	1.0%	32.1%	67.0%	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	4.960	117.950
2987	<i>M. winkleri</i>	467	0.7%	98.8%	0.6%	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	4.960	117.950
3061	<i>M. winkleri</i>	468	0.5%	99.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	5.010	118.040
2988	<i>M. winkleri</i>	469	0.4%	99.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road to Lahad Datu	4.960	117.950
5224	<i>M. winkleri</i>	470	0.9%	98.8%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	4.990	117.960
5227	<i>M. winkleri</i>	471	0.9%	97.7%	1.5%	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	4.990	117.960
5225	<i>M. winkleri</i>	472	0.7%	99.0%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	4.990	117.960
5226	<i>M. winkleri</i>	473	0.4%	99.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	4.990	117.960
5228	<i>M. winkleri</i>	474	0.6%	98.9%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	4.990	117.960
5231	<i>M. winkleri</i>	475	1.7%	91.6%	6.7%	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	4.990	117.960
5230	<i>M. winkleri</i>	476	1.1%	98.6%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	4.990	117.960
5223	<i>M. winkleri</i>	477	0.9%	98.8%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	4.990	117.960
5229	<i>M. winkleri</i>	478	0.9%	98.8%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, north of road to Lahad Datu	4.990	117.960
2185	<i>M. winkleri</i>	479	0.4%	98.4%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road Lahad Datu to DVFC, 25 km to DVFC	4.970	117.950
2148	<i>M. winkleri</i>	480	0.3%	89.0%	10.7%	Malaysia, Borneo, Sabah, Danum Valley, road Lahad Datu to DVFC, 6 km to DVFC	4.970	117.950
2206	<i>M. winkleri</i>	481	0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, road Lahad Datu to DVFC, 23 km to DVFC	4.970	117.940
3385	<i>M. winkleri</i>	482	0.3%	99.4%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, 1-2km to DVFC	4.970	117.820
3386	<i>M. winkleri</i>	483	3.8%	95.1%	1.1%	Malaysia, Borneo, Sabah, Danum Valley, 1-2km to DVFC	4.970	117.820
2224	<i>M. winkleri</i>	484	1.0%	98.6%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, road Lahad Datu to DVFC, junction to DVFC	4.990	117.890
4616	<i>M. winkleri</i>	485	0.7%	99.0%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, DVFC, gap close to office	4.980	117.800

Plant ID Number	Species	Individual (1 bar)	Percent of individual assigned to			Location	Latitude	Longitude
			Cluster K=1	Cluster K=2	Cluster K=3			
4618	<i>M. winkleri</i>	486	0.7%	97.9%	1.4%	Malaysia, Borneo, Sabah, Danum Valley, DVFC, gap close to office	4.980	117.800
4617	<i>M. winkleri</i>	487	0.4%	99.4%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, DVFC, gap close to office	4.980	117.800
4620	<i>M. winkleri</i>	488	0.4%	99.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, DVFC, gap close to office	4.980	117.800
4615	<i>M. winkleri</i>	489	0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, DVFC, gap close to office	4.950	117.810
4619	<i>M. winkleri</i>	490	0.4%	99.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, DVFC, gap close to office	4.950	117.810
6122	<i>M. winkleri</i>	491	27.2%	70.6%	2.3%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6123	<i>M. winkleri</i>	492	0.7%	98.7%	0.6%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6126	<i>M. winkleri</i>	493	0.8%	98.3%	0.9%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6125	<i>M. winkleri</i>	494	0.6%	98.7%	0.7%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6127	<i>M. winkleri</i>	495	1.0%	98.7%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6124	<i>M. winkleri</i>	496	0.4%	98.8%	0.8%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6136	<i>M. winkleri</i>	497	1.0%	94.2%	4.8%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6133	<i>M. winkleri</i>	498	0.4%	99.3%	0.2%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6129	<i>M. winkleri</i>	499	1.4%	98.0%	0.7%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6134	<i>M. winkleri</i>	500	0.7%	98.3%	1.0%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6135	<i>M. winkleri</i>	501	4.3%	95.4%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6132	<i>M. winkleri</i>	502	0.4%	99.1%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6117	<i>M. winkleri</i>	503	1.0%	98.5%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6137	<i>M. winkleri</i>	504	0.7%	98.9%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6119	<i>M. winkleri</i>	505	0.3%	99.1%	0.6%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6139	<i>M. winkleri</i>	506	0.8%	98.7%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6120	<i>M. winkleri</i>	507	0.4%	97.7%	1.9%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6121	<i>M. winkleri</i>	508	0.5%	99.1%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6130	<i>M. winkleri</i>	509	0.4%	98.6%	1.0%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6128	<i>M. winkleri</i>	510	0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6138	<i>M. winkleri</i>	511	0.4%	98.3%	1.3%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6131	<i>M. winkleri</i>	512	0.8%	98.6%	0.6%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6112	<i>M. winkleri</i>	513	0.8%	98.9%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6114	<i>M. winkleri</i>	514	0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6113	<i>M. winkleri</i>	515	0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6116	<i>M. winkleri</i>	516	0.5%	99.1%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
6115	<i>M. winkleri</i>	517	1.1%	98.4%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, Tembaling trail	4.950	117.800
3106	<i>M. winkleri</i>	518	0.6%	95.1%	4.3%	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembaling trail	4.950	117.810
4593	<i>M. winkleri</i>	519	0.9%	98.6%	0.6%	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembaling trail	4.950	117.810
4597	<i>M. winkleri</i>	520	5.4%	94.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembaling trail, waterfall	4.950	117.810
4602	<i>M. winkleri</i>	521	0.7%	99.0%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembaling trail, waterfall	4.950	117.810
4600	<i>M. winkleri</i>	522	0.7%	99.0%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembaling trail, waterfall	4.950	117.810
4599	<i>M. winkleri</i>	523	0.5%	98.2%	1.3%	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembaling trail, waterfall	4.950	117.810
4601	<i>M. winkleri</i>	524	0.8%	98.9%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembaling trail, waterfall	4.950	117.810
4598	<i>M. winkleri</i>	525	1.4%	98.3%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembaling trail, waterfall	4.950	117.810
4595	<i>M. winkleri</i>	526	0.4%	98.6%	1.0%	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembaling trail, waterfall	4.950	117.810
4596	<i>M. winkleri</i>	527	0.5%	99.2%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembaling trail, waterfall	4.950	117.810
4612	<i>M. winkleri</i>	528	0.6%	98.6%	0.8%	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembaling trail, waterfall	4.950	117.810
4486	<i>M. winkleri</i>	529	0.4%	97.8%	1.8%	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembaling trail, Chris plot 5	4.950	117.810
4495	<i>M. winkleri</i>	530	2.4%	97.3%	0.3%	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembaling trail, Chris plot 5	4.950	117.810
4487	<i>M. winkleri</i>	531	0.4%	98.0%	1.6%	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembaling trail, Chris plot 5	4.950	117.810
4594	<i>M. winkleri</i>	532	0.5%	98.6%	0.9%	Malaysia, Borneo, Sabah, Danum Valley, Kuala Tembaling trail, Chrisplot 6	4.950	117.810
4286	<i>M. winkleri</i>	533	1.0%	98.7%	0.3%	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Lipad trail	5.310	118.840
4290	<i>M. winkleri</i>	534	0.7%	99.0%	0.3%	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Lipad trail, gap	5.310	118.840
4291	<i>M. winkleri</i>	535	3.8%	95.9%	0.3%	Malaysia, Borneo, Sabah, Tabin Wildlife Reserve, Lipad trail, gap	5.310	118.840
2051	<i>M. winkleri</i>	536	0.3%	54.0%	45.7%	Malaysia, Borneo, Sabah, Luasong	4.630	117.380
5093	<i>M. winkleri</i>	537	4.8%	94.9%	0.3%	Malaysia, Borneo, Sabah, Tawau Hills Park, picnic area	4.400	117.890
5094	<i>M. winkleri</i>	538	1.3%	98.4%	0.3%	Malaysia, Borneo, Sabah, Tawau Hills Park, picnic area	4.400	117.890
5096	<i>M. winkleri</i>	539	0.6%	98.9%	0.4%	Malaysia, Borneo, Sabah, Tawau Hills Park, picnic area	4.400	117.890
5095	<i>M. winkleri</i>	540	0.7%	99.0%	0.3%	Malaysia, Borneo, Sabah, Tawau Hills Park, picnic area	4.400	117.890
5159	<i>M. winkleri</i>	541	47.3%	49.3%	3.4%	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs	4.400	117.890
5175	<i>M. winkleri</i>	542	23.3%	75.2%	1.5%	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs	4.400	117.890
5194	<i>M. winkleri</i>	543	1.7%	97.9%	0.5%	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs	4.400	117.890
5196	<i>M. winkleri</i>	544	0.8%	98.9%	0.3%	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs	4.400	117.890
5181	<i>M. winkleri</i>	545	0.6%	99.1%	0.3%	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs	4.400	117.890
5195	<i>M. winkleri</i>	546	1.6%	98.2%	0.3%	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to hot springs	4.400	117.890
5186	<i>M. winkleri</i>	547	0.7%	99.0%	0.3%	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to waterfall Galas	4.400	117.890
5185	<i>M. winkleri</i>	548	0.6%	98.8%	0.6%	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to waterfall Galas	4.400	117.890
5187	<i>M. winkleri</i>	549	1.1%	98.6%	0.3%	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to waterfall Galas	4.400	117.890
5184	<i>M. winkleri</i>	550	0.5%	95.3%	4.1%	Malaysia, Borneo, Sabah, Tawau Hills Park, trail to waterfall Galas	4.400	117.890
5140	<i>M. winkleri</i>	551	1.0%	59.2%	39.8%	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	4.390	117.890
5142	<i>M. winkleri</i>	552	1.5%	98.2%	0.3%	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	4.390	117.890
5143	<i>M. winkleri</i>	553	3.2%	96.4%	0.3%	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	4.390	117.890
5139	<i>M. winkleri</i>	554	3.1%	96.6%	0.3%	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	4.390	117.890
5141	<i>M. winkleri</i>	555	0.4%	99.3%	0.3%	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	4.390	117.890
5144	<i>M. winkleri</i>	556	1.5%	98.1%	0.4%	Malaysia, Borneo, Sabah, Tawau Hills Park, edge of oil palm plantation	4.390	117.890
1964	<i>M. winkleri</i>	557	0.005	0.991	0.003	Malaysia, Borneo, Sabah, Tawau Hills, Bukit Tawau	4.33	118
479	<i>M. winkleri</i>	558	0.006	0.99	0.004	Malaysia, Borneo, Sabah, Tawau Hills	4.33	118
1986	<i>M. winkleri</i>	559	0.008	0.99	0.003	Malaysia, Borneo, Sabah, Tawau Hills	4.33	118
1985	<i>M. winkleri</i>	560	0.004	0.993	0.003	Malaysia, Borneo, Sabah, Tawau Hills	4.33	118

Appendix K Order of *M. tanarius* individuals for all bar plots created for both STRUCTURE and INSTRUCT analyses, and percentages with which individuals are assigned to each cluster for K = 6 (STRUCTURE).

Plant ID	Number	Species	Individual (1 bar)	Geographic Identifier 1	East/West of Crocker Range ²	Percent of individual assigned to cluster						Location	Latitude	Longitude
						K=1	K=2	K=3	K=4	K=5	K=6			
448	<i>M. tanarius</i>	1	Malay Peninsula			1.4%	1.2%	1.2%	94.5%	0.9%	0.8%	Malaysia, Peninsula, Pahang, Cameron Highlands, Tanah Rata	4.450	101.370
2734	<i>M. tanarius</i>	2	Malay Peninsula			0.9%	1.2%	0.9%	95.9%	0.5%	0.5%	Malaysia, Peninsula, Selangor, FRIM, forest road	3.239	101.633
2743	<i>M. tanarius</i>	3	Malay Peninsula			1.1%	0.7%	0.8%	94.5%	0.6%	2.2%	Malaysia, Peninsula, Selangor, FRIM, forest road	3.239	101.633
43	<i>M. tanarius</i>	3	Malay Peninsula			0.8%	3.6%	0.4%	94.4%	0.4%	0.3%	Malaysia, Peninsula, Selangor, Kuala Lumpur	3.148	101.711
2682	<i>M. tanarius</i>	5	Malay Peninsula			0.3%	0.4%	0.4%	98.2%	0.3%	0.4%	Malaysia, Peninsula, Selangor, Gombak Valley	3.320	101.750
6083	<i>M. tanarius</i>	6	Malay Peninsula			0.5%	0.6%	0.3%	97.9%	0.3%	0.3%	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	3.340	101.820
6084	<i>M. tanarius</i>	7	Malay Peninsula			2.3%	3.4%	2.3%	87.9%	1.5%	2.8%	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	3.340	101.820
6085	<i>M. tanarius</i>	8	Malay Peninsula			0.3%	0.4%	0.3%	97.9%	0.7%	0.4%	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	3.340	101.820
6086	<i>M. tanarius</i>	9	Malay Peninsula			0.7%	1.3%	0.9%	95.5%	0.7%	0.9%	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	3.340	101.820
6087	<i>M. tanarius</i>	10	Malay Peninsula			0.3%	0.5%	0.4%	97.4%	0.6%	0.8%	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	3.340	101.820
6088	<i>M. tanarius</i>	11	Malay Peninsula			0.4%	0.5%	0.5%	97.5%	0.6%	0.4%	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	3.340	101.820
6089	<i>M. tanarius</i>	12	Malay Peninsula			0.4%	0.6%	0.4%	91.7%	0.9%	5.7%	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	3.340	101.820
6090	<i>M. tanarius</i>	13	Malay Peninsula			0.6%	2.4%	0.6%	62.4%	0.5%	33.6%	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	3.340	101.820
6092	<i>M. tanarius</i>	14	Malay Peninsula			0.5%	1.5%	1.4%	94.2%	0.6%	1.8%	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	3.340	101.820
6093	<i>M. tanarius</i>	15	Malay Peninsula			1.3%	1.1%	0.8%	95.0%	1.1%	0.8%	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	3.340	101.820
6094	<i>M. tanarius</i>	16	Malay Peninsula			2.4%	1.2%	0.7%	92.6%	2.5%	0.6%	Malaysia, Peninsula, Selangor, old Genting road, after pass 50 km to K.L.	3.340	101.820
6095	<i>M. tanarius</i>	17	Malay Peninsula			0.6%	0.4%	1.3%	96.6%	0.5%	0.5%	Malaysia, Peninsula, Selangor, old Genting road, 43 km to K.L.	3.330	101.770
6096	<i>M. tanarius</i>	18	Malay Peninsula			0.6%	0.5%	0.5%	96.8%	0.7%	0.5%	Malaysia, Peninsula, Selangor, old Genting road, 43 km to K.L.	3.330	101.770
6097	<i>M. tanarius</i>	19	Malay Peninsula			0.5%	0.7%	0.8%	96.0%	1.1%	0.3%	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	3.330	101.780
6098	<i>M. tanarius</i>	20	Malay Peninsula			0.2%	0.3%	0.3%	98.6%	0.3%	0.3%	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	3.330	101.760
6099	<i>M. tanarius</i>	21	Malay Peninsula			0.2%	0.3%	0.3%	98.6%	0.3%	0.3%	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	3.330	101.760
6100	<i>M. tanarius</i>	22	Malay Peninsula			0.5%	0.4%	0.4%	98.0%	0.5%	0.3%	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	3.330	101.760
6101	<i>M. tanarius</i>	23	Malay Peninsula			0.4%	1.1%	0.3%	96.9%	0.7%	0.6%	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	3.330	101.760
6102	<i>M. tanarius</i>	24	Malay Peninsula			2.6%	0.6%	1.1%	93.3%	1.4%	0.9%	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	3.330	101.760
6103	<i>M. tanarius</i>	25	Malay Peninsula			0.5%	3.1%	0.6%	83.3%	7.3%	5.2%	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	3.330	101.760
6104	<i>M. tanarius</i>	26	Malay Peninsula			0.4%	0.3%	0.3%	96.2%	0.5%	0.2%	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	3.330	101.760
6105	<i>M. tanarius</i>	27	Malay Peninsula			0.7%	0.4%	0.3%	98.1%	0.3%	0.3%	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	3.330	101.760
6106	<i>M. tanarius</i>	28	Malay Peninsula			2.3%	1.5%	0.6%	94.7%	0.5%	0.3%	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	3.330	101.760
6107	<i>M. tanarius</i>	29	Malay Peninsula			0.3%	0.6%	0.9%	97.3%	0.4%	0.5%	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	3.330	101.760
6108	<i>M. tanarius</i>	30	Malay Peninsula			1.1%	1.5%	1.2%	93.8%	1.9%	0.5%	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	3.330	101.760
6109	<i>M. tanarius</i>	31	Malay Peninsula			0.3%	0.3%	0.4%	98.4%	0.3%	0.3%	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	3.330	101.760
6110	<i>M. tanarius</i>	32	Malay Peninsula			0.6%	0.6%	0.3%	97.5%	0.6%	0.4%	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	3.330	101.760
6111	<i>M. tanarius</i>	33	Malay Peninsula			0.4%	0.3%	0.4%	97.8%	0.7%	0.4%	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	3.330	101.760
6069	<i>M. tanarius</i>	34	Malay Peninsula			0.3%	0.4%	0.3%	98.4%	0.3%	0.3%	Malaysia, Peninsula, Selangor, old Genting road, 25 km to K.L.	3.310	101.740
6069	<i>M. tanarius</i>	35	Malay Peninsula			0.4%	0.5%	0.6%	95.3%	2.9%	0.3%	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	3.310	101.740
6070	<i>M. tanarius</i>	36	Malay Peninsula			3.6%	1.1%	0.3%	94.2%	0.4%	0.5%	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	3.310	101.740
6071	<i>M. tanarius</i>	37	Malay Peninsula			0.8%	3.3%	0.4%	81.1%	4.5%	9.9%	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	3.310	101.740
6072	<i>M. tanarius</i>	38	Malay Peninsula			5.0%	0.8%	0.6%	92.8%	0.5%	0.3%	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	3.310	101.740
6073	<i>M. tanarius</i>	39	Malay Peninsula			0.2%	0.3%	0.3%	98.7%	0.3%	0.2%	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	3.310	101.740
6074	<i>M. tanarius</i>	40	Malay Peninsula			0.3%	0.4%	0.3%	98.5%	0.3%	0.3%	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	3.310	101.740
6075	<i>M. tanarius</i>	41	Malay Peninsula			0.8%	0.5%	0.2%	97.6%	0.7%	0.2%	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	3.310	101.740
6077	<i>M. tanarius</i>	42	Malay Peninsula			0.5%	1.5%	0.2%	96.7%	0.4%	0.3%	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	3.310	101.740
6078	<i>M. tanarius</i>	43	Malay Peninsula			1.7%	0.8%	0.4%	96.0%	0.5%	0.6%	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	3.310	101.740
6079	<i>M. tanarius</i>	44	Malay Peninsula			0.4%	0.3%	0.3%	98.3%	0.4%	0.3%	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	3.310	101.740
6080	<i>M. tanarius</i>	45	Malay Peninsula			0.6%	0.6%	1.3%	96.3%	0.8%	0.4%	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	3.310	101.740
6081	<i>M. tanarius</i>	46	Malay Peninsula			0.3%	1.2%	0.6%	95.1%	0.6%	2.3%	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	3.310	101.740
6082	<i>M. tanarius</i>	47	Malay Peninsula			4.7%	1.3%	1.3%	90.1%	1.6%	1.0%	Malaysia, Peninsula, Selangor, old Genting road, 20 km to K.L.	3.310	101.740
41	<i>M. tanarius</i>	48	Malay Peninsula			0.3%	0.5%	0.4%	98.2%	0.3%	0.2%	Malaysia, Peninsula, Pahang, Fraser's Hill	3.720	101.750
6306	<i>M. tanarius</i>	49		West		39.2%	7.2%	4.7%	6.6%	47.8%	3.3%	Brunei, Tutong	4.800	114.650
6002	<i>M. tanarius</i>	50		West		97.7%	0.5%	0.6%	0.4%	0.4%	0.5%	Brunei, Tutong	4.800	114.650
6929	<i>M. tanarius</i>	51		West		77.8%	3.7%	13.2%	0.5%	1.1%	3.7%	Brunei, road BSB-S, Liang, km 64	4.876	114.879
6930	<i>M. tanarius</i>	52		West		95.6%	0.8%	0.9%	0.4%	0.9%	1.4%	Brunei, road BSB-S, Liang, km 64	4.876	114.879
6931	<i>M. tanarius</i>	53		West		5.0%	0.8%	2.9%	0.4%	53.7%	37.2%	Brunei, road BSB-S, Liang, km 64	4.876	114.879
28	<i>M. tanarius</i>	54		West		13.3%	1.3%	53.1%	0.8%	30.5%	1.0%	Brunei, Bandar Seri Begawan	4.941	114.949
6922	<i>M. tanarius</i>	55		West		94.1%	1.4%	0.8%	0.4%	2.7%	0.6%	Malaysia, Sarawak, Lawas	4.862	115.406
6924	<i>M. tanarius</i>	56		West		34.1%	45.9%	0.8%	0.4%	17.3%	1.5%	Malaysia, Sarawak, Lawas	4.862	115.406
5232	<i>M. tanarius</i>	57		West		0.6%	2.1%	2.8%	0.1%	90.3%	3.8%	Malaysia, Borneo, Sabah, Pulau Tiga Island	5.731	115.652
5233	<i>M. tanarius</i>	58		West		4.9%	48.8%	2.2%	0.5%	40.8%	2.8%	Malaysia, Borneo, Sabah, Pulau Tiga Island	5.731	115.652
5234	<i>M. tanarius</i>	59		West		0.4%	92.0%	2.6%	2.3%	2.0%	0.7%	Malaysia, Borneo, Sabah, Pulau Tiga Island	5.731	115.652
5235	<i>M. tanarius</i>	60		West		1.7%	84.1%	1.5%	0.3%	7.5%	4.8%	Malaysia, Borneo, Sabah, Pulau Tiga Island	5.731	115.652
5236	<i>M. tanarius</i>	61		West		1.3%	0.9%	20.6%	1.1%	7.2%	68.9%	Malaysia, Borneo, Sabah, Pulau Tiga Island	5.731	115.652
5237	<i>M. tanarius</i>	62		West		1.5%	57.8%	1.4%	0.5%	33.0%	5.7%	Malaysia, Borneo, Sabah, Pulau Tiga Island	5.731	115.652
5238	<i>M. tanarius</i>	63		West		9.3%	71.6%	3.1%	1.1%	12.8%	2.0%	Malaysia, Borneo, Sabah, Pulau Tiga Island	5.731	115.652
5239	<i>M. tanarius</i>	64		West		0.8%	46.1%	7.1%	6.1%	34.4%	5.5%	Malaysia, Borneo, Sabah, Pulau Tiga Island	5.731	115.652
5240	<i>M. tanarius</i>	65		West		5.6%	74.8%	0.9%	0.4%	17.4%	0.9%	Malaysia, Borneo, Sabah, Pulau Tiga Island	5.731	115.652
5241	<i>M. tanarius</i>	66		West		1.2%	3.1%	49.4%	0.3%	6.2%	39.9%	Malaysia, Borneo, Sabah, Pulau Tiga Island	5.731	115.652
5242	<i>M. tanarius</i>	67		West		1.5%	31.7%	1.3%	0.7%	61.3%	3.6%	Malaysia, Borneo, Sabah, Pulau Tiga Island	5.731	115.652
5243	<i>M. tanarius</i>	68		West		0.7%	3.3%	4.7%	0.3%	5.1%	85.9%	Malaysia, Borneo, Sabah, Pulau Tiga Island	5.731	115.652
5244	<i>M. tanarius</i>	69		West		1.3%	23.4%	7.9%	0.6%	57.2%	9.6%	Malaysia, Borneo, Sabah, Pulau Tiga Island	5.731	115.652
6190	<i>M. tanarius</i>	70		East		77.2%	9.6%	8.6%	0.5%	3.6%	0.5%	Malaysia, Borneo, Sabah, Tenom, Jalan Tumbatilik, near river Pegalan	5.180	116.590
6191	<i>M. tanarius</i>	71		East		87.8%	6.5%	1.1%	1.1%	0.9%	2.6%	Malaysia, Borneo, Sabah, Tenom, Jalan Tumbatilik, near river Pegalan	5.180	116.590
6192	<i>M. tanarius</i>	72		East		99.9%	4.2%	0.8%	0.3%	0.9%	0.7%	Malaysia, Borneo, Sabah, Tenom, Jalan Tumbatilik, near river Pegalan	5.180	116.590
6193	<i>M. tanarius</i>	73		East		94.7%	0.8%	0.6%	0.3%	0.7%	2.9%	Malaysia, Borneo, Sabah, Tenom, Jalan Tumbatilik, near river Pegalan	5.180	116.590
6194	<i>M. tanarius</i>	74		East		96.1%	0.6%	1.5%	0.6%	0.7%	0.5%	Malaysia, Borneo, Sabah, Tenom, Jalan Tumbatilik, near river Pegalan	5.180	116.590
6195	<i>M. tanarius</i>	75		East		86.0%	1.0%	0.6%	0.3%	2.8%	9.4%	Malaysia, Borneo, Sabah, Tenom, Jalan Tumbatilik, near river Pegalan	5.180	116.590
6196	<i>M. tanarius</i>	76		East		91.6%	0.8%	1.1%	0.5%	5.5%	0.5%	Malaysia, Borneo, Sabah, Tenom, Jalan Tumbatilik, near river Pegalan	5.180	116.590
6197	<i>M. tanarius</i>	77		East		95.9%	1.0%	0.9%	0.3%	1.2%	0.7%	Malaysia, Borneo, Sabah, Tenom, Jalan Tumbatilik, near river Pegalan	5.180	116.590
6198	<i>M. tanarius</i>	78		East		96.7%	0.5%	1.0%	0.3%	1.0%	0.5%	Malaysia, Borneo, Sabah, Tenom, Jalan Tumbatilik, near river Pegalan	5.180	116.590
6199	<i>M. tanarius</i>	79		East		28.9%	3.4%	20.5%	0.4%	10.9%	28.0%	Malaysia, Borneo, Sabah, Tenom, Jalan Tumbatilik, near river Pegalan	5.180	116.590
6176	<i>M. tanarius</i>	80		East		96.9%	0.8%	1.0%	0.3%	1.0%	0.8%	Malaysia, Borneo, Sabah, Tenom, Jalan Tumbatilik, near river Pegalan	5.210	116.570
6177	<i>M. tanarius</i>	81		East		87.3%	1.0%	7.2%	0.5%	2.1%	2.0%	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	5.210	116.570
6178	<i>M. tanarius</i>	82		East		96.2%	1.0%	0.7%	0.2%	0.9%	1.0%	Malaysia, Borneo, Sabah, Tenom, Jalan Bukit Bendera	5.210	116.570
6179	<i>M. tanarius</i>	83</												

Plant ID	Number	Species	Individual (1 bar)	Geographic Identifier	East / West of Crocker Range	Percent of individual assigned to cluster						Location	Latitude	Longitude
						K=1	K=2	K=3	K=4	K=5	K=6			
6215	M. tanarius	121	3	East	89.0%	1.4%	7.5%	0.3%	0.6%	1.2%	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasas	5.210	116.560	
6216	M. tanarius	122	3	East	97.2%	0.7%	0.5%	0.4%	0.6%	0.5%	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasas	5.210	116.560	
6217	M. tanarius	123	3	East	97.1%	0.7%	0.5%	0.4%	0.7%	0.6%	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasas	5.210	116.560	
6218	M. tanarius	124	3	East	92.2%	0.5%	0.6%	0.3%	1.7%	4.7%	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasas	5.210	116.560	
6220	M. tanarius	125	3	East	97.0%	0.4%	0.4%	0.3%	0.7%	1.3%	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasas	5.210	116.560	
6221	M. tanarius	126	3	East	95.1%	0.7%	0.9%	1.3%	1.5%	0.6%	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasas	5.210	116.560	
6222	M. tanarius	127	3	East	95.9%	1.1%	1.0%	0.4%	0.8%	0.8%	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasas	5.210	116.560	
6223	M. tanarius	128	3	East	82.0%	0.6%	0.5%	15.7%	0.5%	0.7%	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasas	5.210	116.560	
6224	M. tanarius	129	3	East	94.6%	2.1%	0.8%	0.6%	1.3%	0.6%	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasas	5.210	116.560	
6225	M. tanarius	130	3	East	91.3%	2.8%	2.1%	0.4%	2.0%	1.3%	Malaysia, Borneo, Sabah, Tenom, Hill near Hotel Perkasas	5.210	116.560	
6257	M. tanarius	131	4	West	4.4%	81.9%	10.1%	1.8%	0.4%	1.3%	Malaysia, Borneo, Sabah, periphery of Beaufort	5.570	116.230	
5863	M. tanarius	132	4	West	0.5%	51.8%	1.7%	10.7%	34.4%	0.9%	Malaysia, Sabah, 5 km to Kuala Penyu	5.564	115.600	
5864	M. tanarius	133	4	West	0.8%	61.1%	3.7%	12.3%	20.7%	0.9%	Malaysia, Sabah, 5 km to Kuala Penyu	5.564	115.600	
6290	M. tanarius	134	5	West	0.7%	0.9%	97.2%	0.3%	0.5%	0.5%	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya	6.020	116.080	
6291	M. tanarius	135	5	West	0.9%	0.5%	96.7%	0.6%	0.5%	0.7%	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya	6.020	116.080	
6292	M. tanarius	136	5	West	0.8%	3.0%	28.8%	1.8%	64.6%	1.0%	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya	6.020	116.080	
6293	M. tanarius	137	5	West	2.1%	11.8%	82.0%	2.7%	0.7%	0.7%	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya	6.020	116.080	
6294	M. tanarius	138	5	West	27.1%	2.5%	31.9%	1.4%	34.2%	2.9%	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya	6.020	116.080	
6295	M. tanarius	139	5	West	1.7%	21.4%	61.6%	0.4%	7.5%	7.3%	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya	6.020	116.080	
6296	M. tanarius	140	5	West	0.4%	6.8%	90.4%	1.2%	0.6%	0.6%	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya	6.020	116.080	
6297	M. tanarius	141	5	West	0.9%	39.8%	52.5%	4.9%	0.6%	1.2%	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya	6.020	116.080	
6298	M. tanarius	142	5	West	1.0%	8.8%	86.1%	0.4%	1.1%	2.6%	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya	6.020	116.080	
6299	M. tanarius	143	5	West	0.8%	1.5%	95.1%	0.3%	0.8%	1.4%	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya	6.020	116.080	
6300	M. tanarius	144	5	West	2.7%	17.8%	77.6%	0.4%	0.2%	0.2%	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya	6.020	116.080	
6301	M. tanarius	145	5	West	2.0%	4.2%	87.5%	0.7%	1.6%	3.9%	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya	6.020	116.080	
6302	M. tanarius	146	5	West	0.7%	41.1%	47.2%	0.4%	9.8%	0.8%	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya	6.020	116.080	
6303	M. tanarius	147	5	West	0.5%	5.0%	91.1%	0.4%	1.5%	1.4%	Malaysia, Borneo, Sabah, near Kota Kinabalu, Pulau Gaya	6.020	116.080	
6342	M. tanarius	148	5	West	2.1%	0.9%	93.3%	1.3%	0.8%	1.6%	Malaysia, Borneo, Sabah, Putera Jaya	6.120	116.310	
6343	M. tanarius	149	5	West	3.7%	28.6%	59.9%	0.4%	1.7%	5.7%	Malaysia, Borneo, Sabah, Putera Jaya	6.120	116.310	
6258	M. tanarius	150	5	West	0.6%	0.9%	97.0%	0.3%	0.7%	0.4%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6259	M. tanarius	151	5	West	1.6%	0.7%	90.2%	4.7%	1.5%	1.3%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6260	M. tanarius	152	5	West	0.7%	3.3%	85.0%	0.8%	2.0%	8.2%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6261	M. tanarius	153	5	West	61.6%	8.9%	21.5%	0.3%	3.3%	4.4%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6262	M. tanarius	154	5	West	0.5%	0.5%	90.7%	0.3%	0.6%	0.5%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6263	M. tanarius	155	5	West	0.5%	0.5%	97.7%	0.3%	0.6%	0.5%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6264	M. tanarius	156	5	West	0.4%	0.5%	97.3%	0.2%	0.4%	1.1%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6265	M. tanarius	157	5	West	2.2%	34.4%	22.0%	0.3%	1.0%	40.0%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6266	M. tanarius	158	5	West	0.9%	0.5%	97.0%	0.3%	0.7%	0.6%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6267	M. tanarius	159	5	West	0.8%	0.5%	95.8%	0.3%	1.4%	1.2%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6268	M. tanarius	160	5	West	0.6%	0.5%	97.0%	0.3%	0.7%	0.9%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6269	M. tanarius	161	5	West	2.0%	0.7%	95.4%	0.3%	0.6%	0.9%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6270	M. tanarius	162	5	West	1.1%	87.7%	6.8%	2.1%	0.6%	1.8%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6271	M. tanarius	163	5	West	0.4%	0.5%	98.1%	0.2%	0.4%	0.4%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6272	M. tanarius	164	5	West	0.8%	0.7%	96.7%	0.4%	0.8%	0.6%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6273	M. tanarius	165	5	West	0.6%	0.8%	95.4%	0.4%	1.7%	1.1%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6274	M. tanarius	166	5	West	1.0%	1.5%	94.6%	1.8%	0.6%	0.6%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6275	M. tanarius	167	5	West	9.5%	3.5%	84.8%	0.4%	1.0%	0.8%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6276	M. tanarius	168	5	West	0.6%	13.7%	47.9%	0.3%	0.8%	36.6%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6277	M. tanarius	169	5	West	2.4%	0.9%	91.4%	1.5%	3.1%	0.7%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6278	M. tanarius	170	5	West	3.1%	1.9%	91.7%	0.4%	0.7%	2.2%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6279	M. tanarius	171	5	West	0.4%	0.6%	97.5%	0.2%	0.4%	0.9%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6280	M. tanarius	172	5	West	1.1%	2.0%	94.2%	0.4%	1.2%	1.1%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6281	M. tanarius	173	5	West	1.1%	0.8%	95.3%	0.4%	1.0%	1.5%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6282	M. tanarius	174	5	West	1.3%	12.4%	83.8%	0.6%	1.3%	0.7%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6283	M. tanarius	175	5	West	1.3%	2.6%	90.5%	0.3%	1.0%	4.3%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6284	M. tanarius	176	5	West	9.9%	2.3%	85.2%	1.2%	0.8%	0.5%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6285	M. tanarius	177	5	West	1.5%	6.3%	33.2%	8.9%	43.7%	6.5%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6286	M. tanarius	178	5	West	0.4%	0.6%	97.7%	0.4%	0.4%	0.5%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6287	M. tanarius	179	5	West	2.0%	2.7%	73.3%	0.4%	15.7%	5.9%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6288	M. tanarius	180	5	West	0.4%	1.5%	96.7%	0.3%	0.5%	0.6%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6289	M. tanarius	181	5	West	5.3%	0.8%	89.0%	0.6%	3.0%	1.4%	Malaysia, Borneo, Sabah, Kota Kinabalu, periphery	6.640	116.130	
6317	M. tanarius	182	5	West	1.1%	3.8%	92.2%	0.7%	1.5%	0.7%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.080	
6318	M. tanarius	183	5	West	1.0%	0.9%	91.8%	0.6%	2.0%	3.6%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.080	
6319	M. tanarius	184	5	West	1.2%	0.9%	95.3%	0.4%	1.3%	0.9%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.080	
6320	M. tanarius	185	5	West	1.0%	3.3%	91.2%	0.4%	0.8%	3.3%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.080	
6321	M. tanarius	186	5	West	1.2%	6.8%	95.4%	0.3%	1.1%	3.0%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6308	M. tanarius	187	5	West	0.9%	17.2%	73.3%	6.8%	1.5%	1.4%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6309	M. tanarius	188	5	West	9.6%	6.7%	78.8%	0.4%	1.8%	2.7%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6310	M. tanarius	189	5	West	1.2%	14.1%	67.9%	0.6%	1.2%	15.0%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6311	M. tanarius	190	5	West	0.5%	1.0%	42.2%	4.4%	51.4%	0.5%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6312	M. tanarius	191	5	West	7.1%	1.9%	88.5%	0.3%	0.9%	1.3%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6313	M. tanarius	192	5	West	3.3%	23.9%	71.0%	0.3%	0.8%	0.6%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6314	M. tanarius	193	5	West	3.3%	57.4%	29.8%	1.0%	5.3%	3.1%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6315	M. tanarius	194	5	West	3.8%	1.9%	92.5%	0.3%	0.8%	0.7%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6316	M. tanarius	195	5	West	1.7%	0.8%	95.4%	0.4%	1.0%	0.7%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6321	M. tanarius	196	5	West	0.6%	63.1%	30.9%	1.4%	1.1%	2.8%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6322	M. tanarius	197	5	West	0.5%	1.2%	86.6%	1.1%	29.0%	0.5%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6323	M. tanarius	198	5	West	1.0%	1.0%	94.9%	0.6%	2.2%	0.5%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6324	M. tanarius	199	5	West	12.8%	3.4%	79.0%	0.4%	1.3%	3.1%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6325	M. tanarius	200	5	West	0.6%	0.8%	97.4%	0.3%	0.5%	0.4%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6326	M. tanarius	201	5	West	1.4%	44.4%	17.6%	0.2%	0.4%	36.0%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6327	M. tanarius	202	5	West	1.6%	1.4%	88.9%	0.4%	6.9%	0.7%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6328	M. tanarius	203	5	West	5.1%	2.4%	89.5%	0.5%	1.6%	0.9%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6329	M. tanarius	204	5	West	4.2%	1.9%	90.6%	0.3%	2.4%	0.6%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6330	M. tanarius	205	5	West	0.6%	7.8%	88.6%	1.6%	0.6%	0.8%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6331	M. tanarius	206	5	West	0.6%	3.1%	92.3%	1.4%	1.8%	0.8%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6332	M. tanarius	207	5	West	0.6%	1.0%	95.4%	0.3%	1.1%	0.6%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6333	M. tanarius	208	5	West	2.6%	2.4%	93.1%	0.3%	0.5%	0.8%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6334	M. tanarius	209	5	West	2.3%	7.6%	83.1%	0.3%	5.1%	1.6%	Malaysia, Borneo, Sabah, Kota Kinabalu, near Padang	6.640	116.130	
6335	M. tanarius													

Plant ID Number	Species	Individual (1 bar)	Geographic Identifier ¹	East / West of Crocker Range ²	Percent of individual assigned to cluster						Location	Latitude	Longitude
					K=1	K=2	K=3	K=4	K=5	K=6			
6360	<i>M. tanarius</i>	241	6	West	4.7%	90.9%	1.7%	0.3%	1.2%	1.1%	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel	6.630	116.680
6361	<i>M. tanarius</i>	242	6	West	15.9%	65.3%	6.5%	0.4%	9.3%	0.7%	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel	6.630	116.680
6362	<i>M. tanarius</i>	243	6	West	58.4%	7.5%	0.5%	2.0%	2.7%	28.9%	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel	6.630	116.680
6363	<i>M. tanarius</i>	244	6	West	84.6%	7.5%	1.9%	3.8%	1.4%	0.9%	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel	6.630	116.680
6364	<i>M. tanarius</i>	245	6	West	27.9%	18.8%	50.9%	0.4%	1.5%	0.6%	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel	6.630	116.680
6365	<i>M. tanarius</i>	246	6	West	1.8%	77.5%	17.3%	0.3%	0.5%	2.5%	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel	6.630	116.680
6366	<i>M. tanarius</i>	247	6	West	25.0%	9.2%	9.9%	0.6%	51.5%	3.8%	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel	6.630	116.680
6367	<i>M. tanarius</i>	248	6	West	1.8%	7.5%	1.6%	0.6%	86.1%	2.3%	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel	6.630	116.680
6369	<i>M. tanarius</i>	249	6	West	0.5%	79.2%	8.5%	0.9%	6.3%	4.8%	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel	6.630	116.680
6376	<i>M. tanarius</i>	250	6	West	3.3%	12.7%	2.2%	0.3%	67.9%	13.5%	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel	6.630	116.680
6379	<i>M. tanarius</i>	251	6	West	91.5%	3.3%	2.6%	0.6%	0.9%	1.0%	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel	6.640	116.680
6380	<i>M. tanarius</i>	252	6	West	25.0%	34.2%	3.5%	0.3%	3.1%	33.9%	Malaysia, Borneo, Sabah, Kota Belud, near Siu Motel	6.640	116.680
6387	<i>M. tanarius</i>	253	6	West	7.4%	79.6%	0.7%	0.4%	2.1%	94.1%	Malaysia, Borneo, Sabah, Kota Belud, direction Kudat	6.600	116.650
6384	<i>M. tanarius</i>	254	6	West	2.1%	17.2%	18.1%	0.6%	2.5%	59.3%	Malaysia, Borneo, Sabah, Kota Belud, direction Kudat	6.600	116.680
6385	<i>M. tanarius</i>	255	6	West	1.6%	60.5%	7.2%	1.3%	2.1%	27.2%	Malaysia, Borneo, Sabah, Kota Belud, direction Kudat	6.600	116.680
6394	<i>M. tanarius</i>	256	6	West	36.4%	40.1%	10.2%	2.1%	2.0%	9.2%	Malaysia, Borneo, Sabah, Kota Belud, direction Kudat	6.630	116.680
6382	<i>M. tanarius</i>	257	6	West	0.7%	94.1%	3.5%	0.3%	0.5%	0.9%	Malaysia, Borneo, Sabah, Kota Belud, direction Kudat	6.600	116.750
6383	<i>M. tanarius</i>	258	6	West	3.4%	91.7%	1.5%	0.3%	1.2%	1.9%	Malaysia, Borneo, Sabah, Kota Belud, direction Kudat	6.600	116.750
6388	<i>M. tanarius</i>	259	6	West	2.8%	9.8%	0.9%	0.4%	17.0%	69.1%	Malaysia, Borneo, Sabah, Kota Belud, direction Kudat	6.600	116.750
6389	<i>M. tanarius</i>	260	6	West	2.6%	83.9%	3.2%	3.3%	0.6%	6.3%	Malaysia, Borneo, Sabah, Kota Belud, direction Kudat	6.600	116.750
6390	<i>M. tanarius</i>	261	6	West	8.8%	56.4%	1.7%	0.4%	26.3%	6.6%	Malaysia, Borneo, Sabah, Kota Belud, direction Kudat	6.600	116.750
6391	<i>M. tanarius</i>	262	6	West	1.6%	68.0%	4.9%	2.7%	21.8%	0.9%	Malaysia, Borneo, Sabah, Kota Belud, direction Kudat	6.600	116.750
6393	<i>M. tanarius</i>	263	6	West	53.4%	25.9%	9.3%	0.9%	4.8%	5.7%	Malaysia, Borneo, Sabah, Kota Belud, direction Kudat	6.600	116.750
6395	<i>M. tanarius</i>	264	6	West	3.0%	90.4%	2.9%	0.3%	1.3%	1.6%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 1	6.280	116.700
6396	<i>M. tanarius</i>	265	6	West	4.4%	55.9%	15.8%	0.7%	7.2%	16.0%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 1	6.280	116.500
6397	<i>M. tanarius</i>	266	6	West	4.8%	83.9%	1.8%	0.7%	3.6%	5.2%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 1	6.280	116.500
6398	<i>M. tanarius</i>	267	6	West	0.8%	92.4%	1.9%	1.4%	1.8%	1.6%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 1	6.280	116.660
6399	<i>M. tanarius</i>	268	6	West	6.8%	39.8%	46.5%	1.1%	3.5%	2.4%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 2	6.510	116.650
6400	<i>M. tanarius</i>	269	6	West	3.7%	94.1%	0.8%	0.3%	0.5%	0.5%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 2	6.510	116.650
6401	<i>M. tanarius</i>	270	6	West	1.4%	79.3%	14.6%	0.6%	1.9%	2.3%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 2	6.510	116.750
6402	<i>M. tanarius</i>	271	6	West	0.6%	89.1%	0.8%	0.3%	1.0%	8.1%	Malaysia, Borneo, Sabah, from KK to Ranau, stop 2	6.510	116.750
6440	<i>M. tanarius</i>	272	7	East	0.5%	0.8%	2.4%	0.9%	2.7%	92.8%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	116.650
6441	<i>M. tanarius</i>	273	7	East	1.1%	1.2%	0.5%	0.4%	1.5%	95.4%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	116.650
6452	<i>M. tanarius</i>	274	7	East	0.9%	0.6%	0.7%	0.4%	0.1%	97.3%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	116.650
6439	<i>M. tanarius</i>	275	7	East	0.7%	0.9%	0.7%	0.3%	0.7%	96.6%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	116.750
6433	<i>M. tanarius</i>	276	7	East	5.8%	80.1%	0.7%	2.2%	3.6%	7.4%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6434	<i>M. tanarius</i>	277	7	East	0.7%	0.5%	0.9%	0.4%	0.5%	96.9%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6435	<i>M. tanarius</i>	278	7	East	9.8%	1.5%	1.4%	1.2%	1.0%	85.0%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6436	<i>M. tanarius</i>	279	7	East	0.8%	1.1%	1.2%	0.6%	0.5%	95.9%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6437	<i>M. tanarius</i>	280	7	East	2.8%	85.5%	1.2%	0.8%	8.2%	1.6%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6438	<i>M. tanarius</i>	281	7	East	0.5%	0.7%	0.5%	0.1%	0.6%	93.6%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6443	<i>M. tanarius</i>	282	7	East	1.0%	0.7%	0.7%	0.4%	1.0%	96.2%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6444	<i>M. tanarius</i>	283	7	East	1.4%	59.0%	0.7%	1.1%	36.8%	1.0%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6445	<i>M. tanarius</i>	284	7	East	0.4%	0.6%	0.9%	1.4%	0.5%	96.2%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6446	<i>M. tanarius</i>	285	7	East	1.0%	10.5%	2.9%	0.3%	1.3%	81.9%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6447	<i>M. tanarius</i>	286	7	East	1.0%	8.1%	1.8%	0.4%	3.5%	85.1%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6448	<i>M. tanarius</i>	287	7	East	2.0%	4.0%	3.5%	0.5%	2.3%	87.7%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6450	<i>M. tanarius</i>	288	7	East	0.8%	1.8%	4.1%	1.5%	1.0%	90.7%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6451	<i>M. tanarius</i>	289	7	East	0.5%	0.8%	9.8%	0.3%	0.8%	87.8%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6452	<i>M. tanarius</i>	290	7	East	0.6%	0.6%	0.9%	0.3%	0.7%	96.8%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6453	<i>M. tanarius</i>	291	7	East	0.7%	1.6%	0.7%	0.9%	0.7%	95.4%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6457	<i>M. tanarius</i>	292	7	East	0.7%	0.8%	4.5%	0.9%	0.5%	92.6%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.200
6449	<i>M. tanarius</i>	293	7	East	1.1%	2.1%	0.4%	0.3%	1.1%	95.0%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.210
6454	<i>M. tanarius</i>	294	7	East	0.5%	0.4%	0.6%	0.2%	0.4%	97.8%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.210
6455	<i>M. tanarius</i>	295	7	East	5.6%	3.2%	2.3%	1.0%	0.6%	87.3%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.210
6456	<i>M. tanarius</i>	296	7	East	0.4%	0.6%	0.6%	0.5%	0.4%	97.4%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.210
6458	<i>M. tanarius</i>	297	7	East	1.0%	17.1%	1.1%	8.6%	3.2%	68.9%	Malaysia, Borneo, Sabah, outskirts of Ranau	6.500	117.210
6030	<i>M. tanarius</i>	298	7	East	1.0%	0.8%	1.2%	0.3%	1.4%	95.3%	Malaysia, Borneo, Sabah, Poring, staff quarters	6.070	116.720
6026	<i>M. tanarius</i>	299	7	East	0.4%	0.6%	0.9%	0.3%	0.5%	97.4%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
6027	<i>M. tanarius</i>	300	7	East	1.1%	1.1%	0.5%	1.8%	2.6%	92.9%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
6033	<i>M. tanarius</i>	301	7	East	0.6%	0.6%	0.5%	0.4%	0.9%	97.0%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
6034	<i>M. tanarius</i>	302	7	East	0.7%	0.4%	0.5%	0.2%	1.7%	96.5%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
6035	<i>M. tanarius</i>	303	7	East	0.4%	0.6%	1.2%	0.4%	0.6%	96.7%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
6036	<i>M. tanarius</i>	304	7	East	0.6%	0.8%	0.8%	0.3%	0.7%	96.8%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
6037	<i>M. tanarius</i>	305	7	East	0.4%	0.6%	13.5%	1.3%	0.4%	83.2%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
6046	<i>M. tanarius</i>	306	7	East	0.7%	1.8%	0.8%	0.3%	0.2%	95.4%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
6043	<i>M. tanarius</i>	307	7	East	0.4%	0.6%	1.1%	1.8%	0.8%	95.3%	Malaysia, Borneo, Sabah, Poring, logging road	6.070	116.720
6031	<i>M. tanarius</i>	308	7	East	0.7%	1.4%	1.1%	0.3%	1.1%	95.4%	Malaysia, Borneo, Sabah, Poring, Hot springs area	6.070	116.720
6029	<i>M. tanarius</i>	309	7	East	0.7%	0.7%	0.6%	0.3%	0.7%	97.0%	Malaysia, Borneo, Sabah, Poring, Camp site	6.070	116.720
6032	<i>M. tanarius</i>	310	7	East	1.9%	2.4%	2.1%	1.3%	0.7%	91.5%	Malaysia, Borneo, Sabah, Poring, Camp site	6.070	116.720
4334	<i>M. tanarius</i>	311	8	East	4.0%	21.3%	5.3%	0.3%	67.5%	1.6%	Malaysia, Borneo, Sabah, Telupid, Jln. Microwave	5.650	117.210
6142	<i>M. tanarius</i>	312	9	East	0.7%	1.5%	1.1%	0.9%	95.1%	0.7%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	5.050	117.760
6143	<i>M. tanarius</i>	313	9	East	0.8%	0.7%	1.7%	0.2%	93.8%	2.8%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	5.050	117.760
6144	<i>M. tanarius</i>	314	9	East	3.7%	2.0%	26.7%	0.5%	57.0%	10.1%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	5.050	117.760
6145	<i>M. tanarius</i>	315	9	East	1.6%	0.4%	0.6%	0.3%	96.7%	0.4%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	5.050	117.760
6148	<i>M. tanarius</i>	316	9	East	0.3%	95.4%	0.3%	0.3%	2.6%	1.1%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	5.050	117.760
6149	<i>M. tanarius</i>	317	9	East	0.4%	0.6%	1.3%	0.4%	93.4%	0.8%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	5.050	117.760
6150	<i>M. tanarius</i>	318	9	East	0.9%	0.5%	0.6%	0.4%	96.7%	0.9%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	5.050	117.760
6151	<i>M. tanarius</i>	319	9	East	0.6%	0.4%	0.5%	4.9%	93.1%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	5.050	117.760
6152	<i>M. tanarius</i>	320	9	East	19.0%	0.6%	0.9%	0.4%	78.6%	0.5%	Malaysia, Borneo, Sabah, Danum Valley, road to Malua, junction to BRL	5.050	117.760
6161	<i>M. tanarius</i>	321	9	East	2.6%	36.7%	30.7%	1.6%	23.6%	4.8%	Malaysia, Borneo, Sabah, Danum Valley, DVFC, exit	4.950	117.810
5211	<i>M. tanarius</i>	322	9	East	0.7%	0.6%	0.8%	0.4%	96.8%	0.8%	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	4.990	117.960
5212	<i>M. tanarius</i>	323	9	East	5.0%	1.3%	1.3%	1.0%	90.9%	0.5%	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	4.990	117.960
5213	<i>M. tanarius</i>	324	9	East	0.6%	0.4%	0.6%	1.6%	95.6%	1.2%	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	4.990	117.960
5214	<i>M. tanarius</i>	325	9	East	0.6%	0.4%	0.8%	0.3%	96.8%	1.1%	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	4.990	117.960
5215	<i>M. tanarius</i>	326	9	East	0.8%	1.0%	1.1%	0.3%	68.1%	28.7%	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	4.990	117.960
5216	<i>M. tanarius</i>	327	9	East	0.9%	0.5%	0.7%	0.3%	96.8%	1.0%	Malaysia, Borneo, Sabah, DV, logging site 2006, north of road to Lahad Datu	4.990	117.960
5217	<												

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- Baier, C., Guicking, D., Prinz, K., Fey-Wagner, C., Wöhrmann, T., Weising, K., Debener, T., Schie, S. & Blattner, F. R. 2009. Isolation and characterization of 11 new microsatellite markers for *Macaranga* (Euphorbiaceae). *Molecular Ecology Resources*, 9, 1049-1052.
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- Baier, C. & Blattner, F.R.: Comparative Phylogeography of Bornean myrmecophytic and non-myrmecophytic species of *Macaranga* (Euphorbiaceae), Vortrag auf der PSSC 2009, 23-26.06.2009
- Marchelli, P., Baier, C.; Mengel, C; Ziegenhagen, B; Gallo, L. Historia biogeográfica de *Araucaria araucana* (Molina) K. Koch e implicancias para su conservación, Poster auf dem XXXVII Congreso Argentino de Genética. Tandil, Argentina, 19-24. 09. 2008
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- Baier, C. & Blattner, F.R.: Genetic structure in and among populations of the Southeast Asian tropical ant-plants of *Macaranga* (Euphorbiaceae), Poster auf der Botany 2008, Vancouver, 26-30.07.2008
- Baier, C. & Blattner, F.R.: Genetic structure in and among populations of the Southeast Asian tropical ant-plants of *Macaranga* (Euphorbiaceae); Poster auf der Plant Science Student Conference 2008, Gatersleben, 01-04.07.2008
- Baier, C. & Blattner, F.R.: Analysis of the genetic structure of two Southeast Asian tropical antplants – *Macaranga winkleri* and *M. tanarius* (Euphorbiaceae); Poster auf der Systematics 2008, Göttingen, 07-11.04.2008
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Gatersleben, den 28.03.2011

Christina Baier

Eigenständigkeitserklärung

Hiermit erkläre ich, dass diese Arbeit bisher weder der Naturwissenschaftlichen Fakultät der Martin-Luther-Universität Halle Wittenberg noch irgendeiner anderen wissenschaftlichen Einrichtung zum Zweck der Promotion vorgelegt wurde.

Ich erkläre, dass ich mich bisher noch nie um einen Doktorgrad beworben habe.

Ferner erkläre ich, dass ich die vorliegende Arbeit selbständig und ohne fremde Hilfe verfasst habe. Es wurden keine anderen als die angegebenen Quellen und Hilfsmittel benutzt, und die den benutzten Werken wörtlich oder inhaltlich entnommenen Stellen wurden als solche kenntlich gemacht.

Gatersleben, den 28.03.2011

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