DIVERSITY OF WILD BANANA (*Musa acuminata* Colla)
IN THE LOWER NORTH OF THAILAND

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DOCTER OF PHILOSOPHY

IN BIOLOGICAL SCIENCES

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ความหลากหลายของกล้วยป่า (Musa acuminata Colla) บริเวณ ภาคเหนือตอนล่างของประเทศไทย

DIVERSITY OF WILD BANANA (*Musa acuminata* Colla) IN THE LOWER NORTH OF THAILAND

เดช วัฒนชัยยิ่งเจริญ

วิทยานิพนธ์นี้เสนอต่อมหาวิทยาลัยแม่ฟ้าหลวง เพื่อเป็นส่วนหนึ่ง
ของการศึกษาตามหลักสูตรปริญญาปรัชญาดุษฎีบัณฑิต
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มหาวิทยาลัยแม่ฟ้าหลวง

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DIVERSITY OF WILD BANANA (*Musa acuminata* Colla)

IN THE LOWER NORTH OF THAILAND

DET WATTANACHAIYINGCHAROEN

THIS THESIS HAS BEEN APPROVED

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ABSTRACT

This research was conducted in six study sites, scattered in lower northern Thailand during 2001 - 2007. Three hundred and twenty six samples of wild bananas were collected and identified with 20 characteristics through classical taxonomy into 3 subspecies and others. They were ssp. *malaccensis* (Ridl.) Simmonds, *burmannica* Simmonds, *siamea* Simmonds and hybrid (ssp. *siamea x burmannica*). Others had characters of *(1.)* ssp. *burmannica, siamea* Simmonds and *M. rubra* and *(2.)* ssp. *malaccensis* (Ridl.) Simmonds and *M. flaviflora* N. W. Simmonds. Hierarchical cluster and Discriminant analyses re-examined group separation indicated that ssp. *siamea*, ssp. *burmanica* and hybrid (ssp. *siamea x burmannica*) were in the same group and clearly isolated from ssp. *malaccensis*. In addition, the outliers or others should be the mutants or hybrids. Outgroup specimens from Chantaburi, Trang and Kanchanaburi were also identified and reconfirmed the subspecies through previous methods. Moreover, accessions from all groups and outgroup taxa were sequenced and re - determined by polymorphisms in chloroplast with four cp - markers loci (*rpl* 16, *ndh* A introns, *psa* A - *ycf* 3 and *pet* A - *psb* J – *psb* L – *psb* F intergenic spacers) using PCR – RF - SSCP. The phylogenetic and network analyses indicated various kind relations of different genomes may strongly introduced with their parental genetic materials and hybridizations. In addition, classical taxonomy was practically improved by the statistical applications and molecular techniques. Adding more morphological characteristics and more banana accessions from various locations are required to explain the banana complex. These understanding will promote the sustainable utilization and conservation of wild banana.

Keywords : Banana / *Musa /* Morphological Variations / Genetic Variations / Taxonomy / Environment / Diversity

ชื่อเรื่องวิทยานิพนธ์ ความหลากหลายของกล้วยป่า (*Musa acuminata* Colla) บริเวณภาคเหนือตอนล่างของประเทศไทย

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บทคัดย่อ

การศึกษาในพื้นที่ป่า 7 แห่ง เขตภาคเหนือตอนล่าง ระหว่างปี 2545 - 2550 จัดจำแนกแบบ Classical taxonomy กล้วยป่า 326 ตัวอย่างใช้ 20 ลักษณะทางสัณฐานวิทยา ได้เป็น 3 subspecies และกลุ่มย่อย คือ ssp. *malaccensis* (Ridl.) Simmonds, *burmannica* Simmonds และ *siamea* Simmonds และ *siamea* ส่วน outlier *(1.)* มีลักษณะร่วมของ ssp. *burmannica, siamea* Simmonds and *M. rubra*. และ *(2.)* มีลักษณะร่วมของ ssp. *malaccensis* and *M. flaviflora* N. W. Simmonds จากการตรวจสอบด้วยวิธี Hierarchical cluster และ Discriminant analyses พบว่า ssp. *siamea*, ssp. *burmanica* เป็นกลุ่มเดียวกัน นอกจากนั้น outlier มีลักษณะผ่าเหล่าหรือลูกผสม (the mutants or hybrids) ให้ผลสอดคล้องกับการนำตัวอย่างนอกพื้นที่ อาทิ จันทบุรี ตรังและกาญจนบุรี มาทดสอบจัดจำแนกตามวิธีการข้างต้น ส่วนการศึกษา Polymorphisms ใน Chloroplast ด้วย 4 cp - markers (*rpl* 16, *ndh* A introns, *psa* A - *ycf* 3 and *pet* A - *psb* J – *psb*L - *psb*F intergenic spacers) ใช้ PCR – RF - SSCP และจากการวิเคราะห์ความสัมพันธ์เครือญาติและเครือข่าย พบว่าทุกวิธีการให้ผลสอดคล้องกันและแสดงความสัมพันธ์ระหว่าง ความแตกต่างกันจากสารพันธุกรรมจากพ่อแม่และการเกิดลูกผสม การจัดจำแนกแบบ Classical taxonomy นั้นสามารถพัฒนาใช้ประกอบกับเทคนิคทางสถิติและในระดับโมเลกุล หากมีการเพิ่มการศึกษาลักษณะทางสรีรวิทยาที่ละเอียดมากขึ้นและมีจำนวนตัวอย่างจากกลุ่มต่างๆที่หลากหลายจะก่อให้เกิดคำอธิบายที่ชัดเจนต่อ ความ

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คำสำคัญ : กล้วย / ความผันแปรทางสัณฐานวิทยา / ความผันแปรทางพันธุกรรม / อนุกรมวิธาน สิ่งแวดล้อม

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CHAPTER 1

INTRODUCTION

Banana and plantains are among the most important tropical fruit crops. All banana species and cultivars are believed to originate from South and Southeast Asia (Stover & Simmonds, 1987). The most likely wild ancestor of cultivated bananas and plantains are *M. acuminata* and *M. balbisiana* (Benchamas & Chalongchai, 1987, 1983).

Cheesman (1947a, 1947b) mentioned that *M. acuminata* Colla's distribution was in Assam, Burma, Indochina, Indonesia, Siam, Malaya Peninsula and the Philippines with very great variations even within each country. It occurred mainly in forest areas with various ecological conditions and predominantly in the secondary forests (Cheesman, 1947b). The bananas growing in these isolated areas for a long time could have generated variations in some characters such as size and shape of the bunch and bud or vegetative characters (Cheesman, 1947a).

The edible domesticated varieties must have originated from this center of diversity (Hancock, 1992; Simmonds, 1979). However, a more precise origin within the *Musa acuminata* complex is rather difficult (Cheesman, 1948a, 1978b; Simmonds 1953a, 1956, 1960; Benchamas & Chalongcha, 1983, 1987) due to inadequate taxonomic information of the species (Argent, 2000). Insufficient information on morphological variations of wild bananas and their relationships to environmental factors under natural conditions are considered major limiting factors for their future utilization and for conservation programs. Variations in natural populations with natural selection are the outcome of natural selection and the foundation of diversity in living organisms (Morin, 1999).

This research focused on the diversity of wild banana and their habitat conditions in the natural forest. Speculations are advanced for the future exploration that will stimulate further investigation *M. acuminata* and subspecies diversity. This research explored the diversity and analyzed it with, classical and numerical taxonomy at the intra species level, and using molecular identification. So far, information on morphological and genetic variations of wild bananas with their ecological conditions is scanty. The main hypothesis is that the subspecies of wild banana (*M. acuminata*) in lower northern Thailand also occur and that *M. siamea* cannot be reliably differentiated from *M. balbisiana.*

There are three main reasons to study.

(i) To classify *M. acuminata* diversity and classification: It is currently difficult to recognize and identify wild bananas as subspecies, since only few studies have considered diversity in natural environment.

(ii.) Natural habitat: To understand the distribution and diversity of banana in relation to their habitat conditions. Researches in the past usually overlooked ecological factors influencing on wild banana populations and rarely studied morphological and genetic variations in various ecological conditions.

(iii.) Exploration of new genetic material: Results from this study will benefit future banana breeding, utilization, diversity studies and identifications.

1.1 Objectives of the Research

This research aims to; *(i)* explore morphological variations, classification and genetic variations within and among populations of *M. acuminata* in lower northern Thailand, *(ii)* provide a better understanding of their habitat and major environmental factors determining the distribution of wild banana, (*iii*) describe some the results of variations by DNA analysis.

1.2 Anticipated Benefits of This Research

Information of the wild banana *M. acuminata* especially concerning morphological and genetical variations, classification status and their habitat preference will be gained and used for future conservation, preservation, utilization and management programs.

1.3 Definitions

Wild banana in this study refers to *Musa acuminata* Colla.

Habitat is the natural growing place of wild banana.

Lower northern Thailand is the area between the upper north and central region of Thailand. It comprises the provinces of Tak, Kamphaengphet, Nakornsawan, Phitsanulok, Uttaradit, Sukhothai, Phetchabun and Phichit.

Environmental factors are the ecological factors of the wild banana habitat.

CHAPTER 2

LITERATURE REVIEWS

2.1 Utilization and Demand on Banana Germplasm

Bananas and plantains are the staple food for at least 400 million people throughout the world. Only about 10% of the more than 80 million tons of produced annually are exported and served as desserts (Sharrock & Frison, 1998; Schoofs *et al*., 1999; FAO, 2003). Economic and food securities of some countries rely upon their banana production and export. In fact, banana is ranked as the fourth of world food crop, after rice, milk and wheat (Sharrock & Frison, 1998; FAO, 2003). Banana is one of the most common fruit crops in Thailand that plays an important role in economic, cultural and social life.

Most edible bananas are sterile diploid or triploid plants. Past outbreaks of *Fusarium* wilt, black sigatoka, banana bunchy top virus (BBTV) and banana streak virus (BSV) have caused serious destructions with devastating effects on world banana production and industry (Sharrock & Frison, 1998; Schoofs *et al*., 1999). The existing control methods of these diseases are economically expensive and environmentally hazardous (Valmayor, 2001). These factors increase the need for new banana genetic materials. New promising diploid male parents of *M. acuminata* are urgently required for banana improvement and breeding programs to ensure food security (Simmonds, 1986).

Banana hybridization programs are expected to be the solution of many problems of cultivated banana's weaknesses, *i.e.* susceptible to several pests and diseases. Many research and development activities have indicated the success of the utilization of promising resistance genes from wild diploid bananas (Sagi *et al*., 1998; Swennen *et al*., 1998; Sagi, 2000). In addition, every time when a serious epidemic problem occurs, an international banana breeding program is launched to find a solution for those problems. A crucial part of any banana improvement program is a collection of germplasm, which can provide genetic sources for resistance genes. The favorite donors are genes from the wild relatives *M. acuminata* and *M. balbisiana* that thrive under adverse conditions (Valmayor, 2001). A cultivated *Musa* collecting expedition in Tanzania in 1999 was motivated by *(i)* the serious lack of knowledge about banana genetic materials in the highlands of East - Africa, and *(ii)* the growing risk of deforestation. Potentially important materials for genetic improvement could be lost due to changing of agricultural practices in the region (Italienews, 2001).

Most banana collection missions have been done in Southeast Asia, the center of origin and diversity of bananas (Valmayor, 2001). Unfortunately, the rich diversity of wild species and primitive banana cultivars of the world have rapidly diminished (Pascua & Espino, 1986) and are subject to genetic erosion (Silayoi & Chomchalow, 1986) due to the pressures of deforestation, agriculture and technology development.

2.2 Banana Ecology and Environment

The most probably center of *M. acuminata* is the region of Burma and Siam as well as Indochina (Cheesman, 1947b). Wild bananas can be found in moist areas of tropical and subtropical environments. Bananas provide important ecological services such as soil conservation, food production as well as numerous useful secondary products (Simmonds, 1986).

M. acuminata is one of the major pioneer species that play an important role in succession stage after forest fires or deforestations. Fertile fruit and mature seeds require four months of development after the fertilization (Marod, 1995). Wild banana, especially *M. acuminata* Colla ssp. *malaccensis* (Ridl.) Simmonds synonym *M. malaccensis* Ridl., was the most common, particularly in jungle clearings and along riverbanks in Peninsular Malaya (Howes, 1928). It appears to favor richer granite soils and is one of the pioneer species on newly cleared land, where it is sometimes found completely dominant or as a pure stand population in the forest. The ripe fruit is consumed and distributed by birds, monkeys and other fruit eating animals (Howes, 1928).

Wild *M. acuminata*'s seeds germinate easily after fire and grow rapidly. High numbers of seedling establishment will remove the habitat of *Eupatorium odoratum* Linn. (สาบเสือ) and *Imperata cylindrica* P. Beauv. (หญ้าคา) (Chirdsak, 1996). *Musa* provide more fertile soil and higher water holding capacity conditions for other successor trees such as *Croton oblongifolius* Roxb. (เปล้าหลวง), *Ficus hispida* Linn. f. (มะเดื่อปล้อง), *Bauhinia viridescens* Desv. var. *viridescens* (เสี้ยวฟ่อม), *Sterculia macrophylla* Vent. (เกล็ดแรด, ปอพัดโบก), and *Lagerstroemia tomentosa* Presl. (เสลา) (Marod, 1995). Rainfall, light intensity, temperature, water and nutrient in soil are the most important factors for banana growth and succession stages (Chirdsak, 1996).

Fruit and seed formation of wild banana (*M. acuminata*) were investigated, which showed that hand- and insect pollinations induced mature long fruits with numerous fertile seeds. The fertilization and seed development depend upon the flowering time, which is influenced by environmental conditions. *Trigona* spp. (ชันโรง), *Apis cerana* Fabricius (ผึ้งโพรง), and *A. florea* Fabricius (ผึ้งมิ้ม), birds and bats are important for pollen transfer (Chirdsak, 1996).

There is an interesting study on the growth and development of *M. angustigemma* Simmonds, responding to different environments in Trinidad field conditions. Different environments in the wild conditions resulted in poor growth, a more slender pseudostem, reddish sap, narrower bud and smaller seeds. Different growth conditions also introduced different banana morphological characteristics in *M. angustigemma* Simmonds (Simmonds, 1953b). Moreover, irregularities in some morphological characteristics of *Musa* ssp. and *Ensete* ssp. were caused by different growing conditions such as altitudes, soil conditions, climates and habitats. For example, many *Ensete* species were adapted to cooler and drier environments better than most *Musa* species. In addition, most *Musa* ssp. are distributed commonly in rain – forest countries. While, *M. itinerans* Cheesman with long rhizomes distributes in evergreen forests, which create scattered population distribution pattern (Cheesman, 1949a).

2.3 Banana Morphology and Taxonomy

The evolution of edible bananas arose through morphological variations in development from seedy, to seedless and parthenocarpic forms (Simmonds & Weatherup, 1988). All edible and commercial banana cultivars were believed to have originated in Southeast Asia from the seedy species, *M. acuminata* Colla (genome defined as AA) and *M. balbisiana* Colla (genome defined as BB) (Simmonds & Weatherup, 1988). *M. acuminata* was considered to be the ancestral parent and probably the first domesticated cultivar due to its diploid AA genome. Furthermore, most of parthenocarpic bananas were regulated by several complementary dominant genes of the wild *M. acuminata* (Simmonds, 1979; Hancock, 1992). These AA cultivars were also crossed with wild *M. balbisiana* (Simmonds, 1986). They provide new edible hybrid cultivars for future needs with AB, AAB, ABB, BBA, ABBB, AABB and AAAB genome constitutions.

J. G. Baker separated the genus *Musa* into three subgenera as follows: subgenus *Physocaulis* or giant bananas (*M. ensete*), of which the major characters are bottle–shaped stem, many flowers on a bract, usually tricuspidate petal and not edible fruit; subgenus *Eumusa* or banana with fleshy fruit (*M. sapientum*), of which its major characters are cylindrical stem, many flowers on a bract, ovate petal – acuminate, bracts green, brown or dull violet, fruit as both edible and not edible. Major characters of the subgenus *Rhodochlamys* or ornamental banana with upright inflorescences and brightly colored bracts are cylindrical stem, few flowers on a bract, linear petal, fruit usually not edible, bright – colored bracts and often red bracts (Cheesman, 1947b).

However, Cheesman (1947b) separated *Ensete* (subgenus *Physocaulis* sensu Baker) from *Musa* and classified *Musa* L. into 4 sections: *Eumusa, Rhodochlamys, Australimusa* and *Callimusa.* He confirmed the true bananas as *Eumusa*. The two most common and widely ranging species in the sections are *M. acuminata* Colla and *M. balbisiana* Colla.

M. acuminata and *M. balbisiana* are present throughout Thailand. Hybridization of these two species resulted in the following genome combinations of edible diploids (AA, AB), triploids (AAB, ABB) and tetraploids (AAAB, AABB, ABBB) (Simmonds & Shepherd, 1955). Preliminary morphological study of Thai bananas had been made based on characters such as fruit, petiole canal, stem color and so on, as laid out in the IBPGR "Minimum List of Descriptors" (Benchamas & Chalongchai, 1983, 1986, 1987). Morphological and cytotaxonomic studies were conducted by Benchamas & Chalongchai (1986) with 15 morphological characters scored on 137 accessions following Simmonds & Shepherd's (1955). The cytological determinations of the chromosome number together with scoring of 15 morphological characters give a clear picture of the classification of cultivated bananas (Table 2.1).

Table 2.1 Genomic constitution and chromosome numbers of Thai cultivars

Score	Genomic Constitution	Xn	No Accessions in Thailand
15-25 1/	AA	22	37
15-25 1/	AAA	33	25
26-46	AAB	33	29
59-63	ABB	33	33
67-69 2/	ABBB	44	3
70-75 3/	BB	22	9
70-75 3/	BBB	33	1

Score have been modified form the original scheme as follows: 1/ original: 15-23, 2/ original: 67, 3/ original: not given. Source: Silayoi and Chomchalow

However, Benchamas and Chalongchai (1986) recommended that the scoring method using 15 characteristics following the procedure of Simmonds and Shepherd's (1955) should be modified due to some variations of environmental conditions and the ambiguous situations when there were naturally no male bud in some plants. This genomic scoring system had been developed for cultivars. Thus wild bananas could not be taxonomically identified to recognize their variations at the species and subspecies levels. In addition, it is not easy or practically for a person to repeat the identification precisely with this general scoring procedure.

Taxonomic classification of the Philippines banana cultivars is also based on IBPGR scoring system. Moreover, cluster analysis was employed to classify the Philippines bananas with 12 quantitative characters such as pseudostem height and diameter, leaf length, width and its ratio, bunch weight, number of the fingers / hands, finger length and diameter, number of flowering days, number of harvesting days. The result showed that the diploid cultivars (AA) were mixed up in the various groups and clusters. It really becomes difficult to distinguish them. Thus, these quantitative characters could not be used to distinguish and group various Philippines bananas (Pascua & Espino, 1986).

The ultimate goal in taxonomic classification of banana is to develop a reliable index in distinguishing the various cultivars and species both at the vegetative and reproductive stages of growth (Pascua & Espino, 1986).

Some agronomic characters were evaluated in banana breeding program such as bunch, fruit orientation, fruit apex and shape. Crop selection was emphasised on the potentiality of perennial production, female fertility and economic return (Swennen & Vuylsteke, 1986). These results did not bring any further development in wild banana taxonomy as most of the works concentrated only on domesticated cultivars and banana yield production.

Morphological taxonomy of *Musa* clones in Eastern Africa focused on the male flowers especially the compound tepal, its lobes, the free tepal, filament, anthers or staminodes, style and stigma of pistil. It was also the strong emphasis on agricultural utilization that grouped bananas into sweet bananas, flour plantains, beer and boiling bananas (Sebasigari, 1986). In contrast, several *Musa* species have been taxonomically described from fruit specimens and recorded in literature. There were no record from visiting sites and natural living plants. In fact, characteristics of banana should be critically identified especially from seedling stage until flowering stage in natural fields (Cheesman, 1947a). Ortiz (1997) and Tenkouano (2000) reported on the remarkable taxonomic variations of *Musa* in Africa such as the presence or absence of hermaphrodite flowers and the persistence of the male flower.

Recent progress in *Musa* classification is focused on the comparison of classical or conventional techniques and modern methods. Quantitative data from 15 characters such as number of days from flowering to harvest, plant high (m), pseudostem girth (cm), number of suckers, number of leaves, leaf length (m), leaf width (cm), bunch length (cm), number of hands, number of fingers, bunch weight (Kg), finger length (cm), finger girth (cm), finger weight (g), and TSS (Brix) were recorded on 28 samples of *Musa* species and cultivars (reference). Numerical analysis separated them into five clusters using cluster analysis with D^2 statistics.

These five clusters were significantly different from the hierarchical cluster analysis using RAPD markers, which classified the samples into more than 20 groups. This case showed that these quantitative characters should not be reasonable to apply (Rekha *et al.,* 2001).

2.4 Importance of the Banana Exploration

Banana exploration and collection is the fastest way to discover new genetic materials. Former wild banana exploration missions primarily covered some areas of Malaysia, Thailand and Myanmar concentrating on the wild *M. acuminata* (Valmayor, 2001). The determination of *Musa* species and banana varieties depends on descriptions and drawings with various qualities. Unfortunately, numerous errors have crept into literature due to the differences in criteria and understandings of the researchers within the region. So that, living materials were the only satisfactory materials for *Musa* classification (Cheesman, 1947b).

New wild materials of *M. acuminata* might be found in relatively inaccessible places where collection opportunities for foreign explorers were rare. The complete data from natural specimens within the sites was the most important information of the banana classification. Unfortunately, many wild bananas are not in the suitable stages for the complete taxonomic description in the survey conditions. Suckers or seeds are worthwhile to bring back and grow to obtain important information. Generally, detailed descriptions from herbarium specimen are vital information in the biosystematic research. However, the herbariums of banana specimens are not convenient and useful due to the large size of the plants and thus the necessary fragmentation which after laborious drying could not represent the characteristics of the living plant (Cheesman, 1947b).

The vast area on searching and survey of new plant materials with systematic exploration would bring better knowledge in diversity and taxonomy. For example, *M. lolodensis* Cheesman from Halmahera Island, Indonesia was firstly reported by Fairchild in 1940. This had been taken a long time to identify and name by Cheesman in 1950; while *M. salaccensis* Zoll from Java, Indonesia, was firstly reported by Zollinger in 1854. Many researchers believed that both species had gone extinct due to timber industry and forest clearing. But, they were rediscovered in 1982, after those areas were being revisited and studied. This encouraged the understanding on its adaptation in the changing environment. Both species turned out to be widely distributed and survived in the open spaces of the new habitats of lowland and secondary forest at the altitude range from 300 m to 1,200 m above sea level (Nasution, 1993).

Recently, survey equipment and technology such as GIS (Geographic Information System), GPS (Global Positioning System), remote sensing, digital image and computerized information database have been used. Data has been collected directly in the natural habitat conditions (Frohn, 1998). These modern survey techniques with management of information system are important vehicles to induce the understanding on environment of living plant and more useful for further biological conservation. They also fill up some fragmentary knowledge of the species and provide easier revisiting and future studying.

2.5 *Musa acuminata* Colla Identification

Cheesman (1948) classified wild banana (*M. acuminata*) specimens from Southeast Asia into several "forms" such as Buitenzorg, Selangor, Annam, Kedah, Mariani, and Tavoy. Simmonds (1956; 1960) re-examined these forms by using 15 morphological characters. He reviewed and recognized five intra - specific taxa within *M. acuminata*. They were ssp. *malaccensis* (Ridl) Simmonds, ssp. *siamea* Simmonds, ssp. *burmanica* Simmonds, ssp. *banksii* (F. Muell.) Simmonds, and ssp. *microcarpa* (Becc.) Simmonds. He also recognized *M. acuminata* ssp. *truncata*.

***M. acuminata* Colla ssp. *banksii* (F. Muell.) Simmonds** (syn: *M. banksii* F. V. Mueller; *M. paradisiaca* ssp. *seminifera* (Lour.); *M. banksii* var. *muelleriana* Domin.), had been collected from Samoa, Queensland and New Guinea. Simmonds (1956) concluded taxonomic characterisation and comparison. The diagnostic features of the subspecies were the predominantly brown pseudostems and the slight development of wax on leaves. The bunch is large and sometimes more or less ageotropic. The fruits are long – pedicellate and obtuse or very shortly acuminate. Non – imbricate male buds with bracts are often yellow. All flowers show some degrees of male fertility, which effect the position of inflorescence. In addition, the normal basal female flowers are not function and hermaphrodite.

The large fruit is the major characteristic of subspecies. These results are due to the large seed contents and high ovule numbers with high number of seeds. The reproductive parts of the plant have been used as the significant identification information to classify subspecies (Simmonds, 1956).

***M. acuminata* Colla ssp. *malaccensis* (Ridl.) Simmonds** (syn: *M. malaccensis* Ridley; *M. acuminata* Colla (the Selangor form); *M. flava* Ridl.) specimen were analyzed and collected from Malaysia and the South of Thailand. Subspecies characteristics are slender plants that are usually strongly waxy with midribs commonly (but not always) bright red underneath and horizontal bunch and bright red non – imbricate male bracts (Simmonds, 1956). Wild ssp. *malaccensis* Ridl is most common particularly in jungle clearings and along riverbanks in Malay Peninsular (Howes, 1928).

***M. acuminata* Colla ssp. *siamea* Simmonds** (syn: *M. acuminata* Colla, the Annam and Kedah forms) specimens were collected from Malaya, Thailand and Indochina. This ssp. *siamea* is the closest ssp. to ssp. *malaccensis* (Simmonds, 1956). Their characteristics are the plants commonly shorter stature, less black and brown smudging on pseudostems. Peduncle is often glabrous, commonly smaller fruits, imbricate male buds, paler bracts and more purple in tone often slightly yellow – streaked, and pale yellowish tips. The distribution and ecology of ssp. *malaccensis* are in the equatorial Malaya, where ssp. *siamea* is in the monsoon lands of Northern Malaya, Thailand and Indochina (Simmonds, 1956).

***M. acuminata* Colla ssp. *microcarpa* (Beccari) Simmonds** (syn: *M. microcarpa* Beccari; *M. truncata* Ridley; *M. acuminata* Colla or the Camerons form) specimens were collected from Malaya, Borneo and Thailand. This ssp., *microcarpa*, is characterized by the yellowish tinge and virtual waxlessness of the foliage, the intense chocolate brown pigmentation of sheaths, midribs often fading purple flush on the peduncle and male rachis. Plump non - imbricate male bud has purple bracts with pale red underneath, which are weakly something and rolling at the time of falling. Fruits have variable sizes. They are most commonly short and slender. Bunch is usually horizontal and sometime oblique (Simmonds, 1956). Additional distinguishing characters of ssp. *microcarpa* are green - yellow, shiny pseudostem, petiole margin spreading and petiole canal open, male bud intermediate - to - plump - top, pale red internal bract, pendulous rachis position, not - prominent bract scars, sharply curved fruit and 10-20 mm fruit pedicel length (Hakkinen & De Langhe, 2001).

***M. acuminata* Colla. ssp. *truncata* Ridley** (syn*: M. truncata* Ridley; *M. microcarpa* Beccari; *M. acuminata* Colla ssp. *microcarpa* (Beccari) Simmonds (Simmonds, 1956). Simmonds (1956) reduced *M. truncata* Ridley under *M. acuminata* Colla ssp. *microcarpa* (Beccari) Simmonds. This name is applied to a distinct population in Borneo (West Malaysia). In addition, Hotta (1989) mentioned ssp. *truncata* as distinct highland form.

***M. acuminata* Colla ssp. *burmanica* Simmonds** (syn: *M. acuminata* Colla. (Tavoy form) and *M. acuminata* Colla ssp. *microcarpa*) specimens were collected from Burma, and Thailand, and were identified by Simmonds (1956). The ssp. *burmanica* is distinguished by its yellowish and waxless foliage, light brown markings on the pseudostem, compact pendulous bunch, and strongly imbricate purple bracts. The ssp. *burmanica* is mentioned as highly genetically different from the ssp. *malaccensis* (Simmonds, 1956). In addition, the ssp. *burmannica* was also chosen for its vigour and pendulous bunch and used in banana breeding program (Simmonds, 1956). Moreover, Simmonds (1960) introduced an interesting *M. acuminata* Colla from Ceylon, which is remarkably similar to the ssp. *burmanica* only that the basal flowers are functionally female.

Simmonds (1960) also concluded that there were 5 subspecies of *M. acuminata* in Burma, Thailand, Malaysia and Indochina. They were ssp. *malaccensis* (Ridl.) Simmonds, ssp. *siamea* Simmonds, ssp. *burmannica* Simmonds, ssp. *microcarpa* (Becc.) Simmonds, and ssp. *banksii* (F. v. Muell.) Simmonds. These description concepts have been accepted and have been used as the references since then.

New species of banana, *M. acuminata* Colla. ssp. *errans* (Blanco) R. Valmayor*, M. alinsanaya* R. Valmayor, and *Musella exotica* R. Valmayor, were botanically described in 2001. The perfect basal flower clusters, fruit and flower characteristics of ssp. *errans* were revealed to be different from ssp. *banksii*. These characteristics of ssp. *Errans* that distinguish from ssp. *banksii* are the presence of hermaphrodite basal flowers rather than of female flowers as commonly observed in the other *Musa* species (Valmayor, 2001).

Recently, *M. acuminata* exploration in North Borneo has been conducted in searching for subspecies; *microcarpa, truncata, siamea, burmanica* by Markku Hakkinen and Edmond De Langhe. A number of accessions were characterized and focused on moderately to strongly imbricated male bud and tendency of bract colors from pink to red and purple. Male bud with visibly imbricate bract was a characteristic in the ssp. *siamea* and ssp. *burmanica* (*Musa*News, 2002). Hakkinen and De Langhe (2001) found the co - characteristics of subspecies *burmanica, siamea, malaccensis, zebrina* and *banksii* in Northern Borneo, which are the male buds with visibly imbricate bracts. These are characteristics of the subspecies *siamea* and *burmanica*.

In Thailand, the common names of wild banana (*M. acuminata*) are changed upon some morphology and phenotypic characters as well as local culture. For example, some bananas with lots of wax on the pseudostem and dorsal of leaves are called "Kluai Hmon". While, "Kluai Daeng" presents the characteristic of the fading red flush on the petiole and leaf blades. However, this is a common way to recognise the local banana's name, which induces much more confusion due to various native languages and diversity. For instance, ssp. *malaccensis* was recorded on its distribution in the south of Thailand, and north of Malaysia. Moreover, ssp. *microcarpa* was mentions to be found in Songkhla and Pattani provinces which are in the lower south of Thailand. But both subspecies are also called "Kluai Tuan" by native people. Ssp. *siamea* Simmonds also reported its existence in the north and lower southern part of Thailand, where it is also called Kluai Tuan, Kluai Pa, Kluai Ling, and Kluai Hmon (Chote, 1978). However, ssp. *microcarpa* is never found in Thailand in any scientific reports. Furthermore, Silayoi and Chomchalow (1983) recorded the distribution of *M. acuminata* throughout Thailand. Unfortunately, there were no subspecies identifications. However, De Langhe *et al.* (1998) explored and reported these subspecies distributions in northern Thailand. Their distribution range from low lands to high altitude (Figure 2.1)

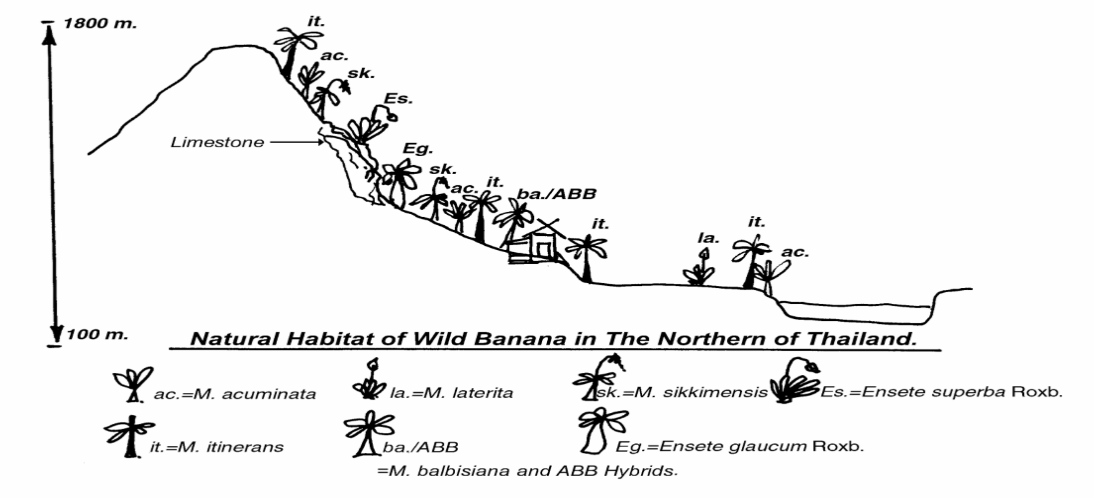


Figure 2.1 Wild bananas in northern Thailand distributed at various elevations and habitats (De Langhe *et al.,* 1998)

2.6 Other *Musa* spp. in Thailand

There are several other species of wild *Musa* in Thailand. Their taxonomic determination is sometimes uncertain. Some examples of wild banana species which normally be found or reported to be found in Thailand are as follow:

***M. itinerans* Cheesman** bract is pale yellow and shiny inside, dark reddish purple outside and commonly with a yellow margin. Fruit shape is either oblong – turbinate or ovoid, widest near the apex with truncate acumen and narrowing gradually into a long pedicel. *M itinerans* has running rhizomes (Cheesman, 1949a). This species is common in northern and rare in eastern Thailand. The major *M. itinerans* characters were significantly different from other ssp. *of acuminata* having long rhizomes, thus individual stems, not clumps.

***M. laterita* Cheesman** firstly found in Burma was described as having a slender pseudostem 1–2 m. in length. The inflorescence is erect and having ovate male bud in advanced blooming. The bracts are slightly imbricate at the tip with bright - brick red. The bunch is very compact with the fruits almost appressed to the rachis. The fruits are usually in a single row per hand. An individual fruit is about 8 – 10 cm. long, 2 cm. in diameter on a very short pedicel (0.5 cm.) with pronounced acumen (Cheesman, 1949c).

M. rubra N. Wallich ex W. S. Kurz. was reported to be found in India, China, Myanmar and

Thailand. Pseudostem is dark purple with 1.5 – 2.4 m. Infloresence is erect and rachis is brown vilous. Bracts are pink and lanceolate. Compound tepal is golden yellow. Fruits are reddish and cylindric. Rhizome is tuberous.

M. balbisiana Colla. (syn: *M. sapientum* ssp. *seminifera* form *pruinosa* King MSS ex Baker and *M. sapientum* var. *pruinosa* King MSS ex Cowan and Cowan) cultivated around Thailand for the leaves which are used for wrapping, the young fruits which are pickled and the male buds which are eaten as a vegetable. The specimens record in Thailand were collected in temple grove, Nan and Bangkok. It is also called Kluai Pa or Kluai Tani and Kluai Tani – Pa (Simmonds,1956).

2.7 Morphological Variations and Ecological Factors

Kobayashi (1984) published a paper on the Geological History of Thailand and West Malaysia. The paper explores the strong tectonic relation between northern Thailand to the west of Malaysia. It indicated the strong variations in geology, palaeontology of lower northern Thailand, and showed the initial points of environmental variations and ecological diversity, which induce various ecological habitat conditions. Thailand is the interception area of three floristic elements. They were Indo - Burmese, Indo – Chinese and Malaysian elements (EPA, 1995). These biospheres are covering the area of wild banana distribution in the northern of Thailand over such period of time.

M. acuminata is naturally widely distributed from India to the Philippines, Thailand and via Southern China (Simmonds & Shepherd, 1955). However, the native banana populations in Thailand have been changed due to increasing of agriculture activities, deforestation and road construction. So, these populations are needed to study. Chirdsak (1996) mentioned that rainfall, light intensity, temperature, water and nutrient in soil are the most important factors for wild banana growth and succession stages.

Environmental factors such as temperature, rainfall and soil conditions have also been studied for seedling establishment and growth of four tree species: (*Hopea odorata* Roxb., *Litsea cubeba* (Lour.) Pers, *Holarrhena pubescens* (Buch.-Ham.) Wall. ex G. Don. and *Terminalia mucronata* Craib et Hutch. (Baker, 1997). These trees are distributed across evergreen or deciduous forests mosaic in western Thailand. These indicates that: *(i)* habitat conditions induced growth and survival dynamics and reflected the community - level patterns, *(ii)* environmental factors, fire and seeds dispersion generated the patterns of forest types across the landscape (Baker, 1997).

In Honshu, Japan, morphological variations among 20 populations of *Corydalis* (Fumariaceae) were analyzed quantitatively with 8 reproductive system parameters. Qualitative data of pollen grains and ovule fertility, size and volume could clearly separate *Corydalis orthoceras* from *C. lineariloba*. It was found that ecological and geographical differentiations were significantly correlated with their morphological variations (Fukuhara, 2000).

Numerical classification has been employed to provide a better understanding of morphological variations and classifications. At IRRI, 9 qualitative and 20 quantitative traits of both vegetative and reproductive characters in wild rice species complex, *Oryza meyeriana* were analyzed. The objectives were to investigate the variations, taxonomic status and biosystematic relationship. It was found that traditionally used characters such as spikelet length do not contribute significantly to the grouping of the studied samples. Moreover, the authors suggested that *O. granulata* and *O. meyeriana* do not warrant separate species and recommend that they should be combined as *O. granulata* (Gong *et al.,* 2000).

Banziger and Hansen (2000) revised the taxonomy of the species in the genus *Rhizanthes* Dumortier (Rafflesiaceae) using numerical taxonomy. Re - evaluation and recombination of old and new characters of flower were obtained from extensive field research in Southeast Asia and herbarium specimens, then analyzed by morphometric techniques. The result indicated that *Rhizanthes* actually consisted of at least four species: *R. zippeli* (Blume) Spach., *R. lowiii* (Beccari) Harms., *R. deceptor* sp.n., and *R. infaniticida* sp.n.

A moss species, *Sphagnum majus*, was geologically surveyed and collected from Norway, Newfoundland and New York. UPGMA - analysis and cluster analysis were successfully employed for identification and population structure. Correspondent analysis classified these mosses in to 7 groups according to ecological differences (Sastad *et al.*, 2000).

A transect survey and cluster analysis techniques have been used to study differences in topography, soil and microclimate of monsoon forest in Doi Suthep Pui National Park in order to investigate species diversity, distribution of forest associations related to ecological gradients and forest profile (Elliott *et al.,* 1989). Large variations in topography, soil and microclimate have been thought to be responsible for the high tree species richness as 90 species per hectare. From the study, cluster analysis divided the transect into two main associations. The first one is a deciduous association, in which 88.2% of trees were deciduous, occurred mostly on xeric sites at lower elevations or along the ridges at higher elevations. The second one is a mixed evergreen - deciduous association, in which 49.6% of trees were deciduous and 43% were evergreen, occurred on the more mesic parts of the transect at higher elevations or along seasonal streams at lower elevations (Elliott *et al.,* 1989).

Bunyavejchewin (1983) determined the characteristics of the dominance - type of the tropical dry deciduous forests of Thailand. Quantitative characteristics of various trees were collected under various topographic features and soil properties. The analysis of tropical dry deciduous forests in Thailand indicated that *Tectona grandis* forest – subtype *Xylia kerrii,* and subtype *Xylia kerrii* - *Terminalia mucronata* were found in different sites under different environmental factors. *T. grandis* – subtype *Xylia kerrii*, occured from 150-650 m above sea level and established in deep slightly acid sandy clay loam. Whilst, *T. grandis* – subtype *Xylia kerrii* - *Terminalia mucronata* were smaller and had shorter stem than those of the previous subtypes and grew well in slightly shallower sandy loam. Vegetation and environment relationships were analyzed with multiple regressions using stepwise method to explain the distribution of plant response to environmental factors, such as topography and soil gradients, in tropical dry deciduous forests of Thailand. It was found that the distribution of dominant tree species appeared highly correlated to the environment factors such as elevations and soil bulk density. In the study, the best example was teak, *Tectona grandis* L. f. distributed in soil with high levels of calcium and phosphorus. In contrast, *Lagerstroemia calyculata* Kurz was found on soil with low levels of calcium, phosphorus and potassium content (Bunyavejchewin, 1985). The natural distribution of teak (*T. grandis* L. f.) was strongly correlated with environmental factors such as rainfall (1,270-3,800 mm / annum), temperature (13 - 40^{o}C), and 75 - 95 % of full daylight. The most suitable soil for teak's growth was usually derived from rock of volcanic origin such as trap, basalt and granitic – gneisses, pH 6.5 - 7.5 and Ca mineral elements in soil (Kaosa - ard, 1989).

2.8 DNA analysis

The chloroplast sequences from various individuals of *Lithocapus* were used to determine

geographical distribution of Asian stone oaks (*Lithocapus*) and their genetic diversity. The result indicated that one clade was confined to the island of Borneo, and the other was widespread (Cannon *et al.*, 2003).

Concerning genetic diversity studies, AFLP technique is being widely used because it reveals significant polymorphism and reliable as well as robust genetic molecular marker assay with high potential to understand *Musa* genetic and germplasm analysis (Crouch *et al*., 1998a; Swennen et al., 1999; Ude *et al*., 2002b).

Moreover, twenty eight accessions of *M. acuminata* (AA) Colla, *M. balbisiana* (BB) Colla and their natural hybrids were assessed for their genetic diversity and relationships using AFLP markers. The results indicated four major clusters and closely corresponding with the accessions genome composition. These genetic diversity study indicated that more than one subspecies may be involved in the origin of triploid AAA edible bananas (Ude *et al*., 2002a).

DNA markers are now more widely used than morphological characters in *Musa* genetic diversity studies due to them being free from environmental influence (Jarret *et al*., 1993; Kaemmer *et al*., 1997; Crouch *et al*., 1999; Pillay *et al*., 2001; Ude *et al*., 2002a). Restriction fragment Length Polymorphism (RFLP) has not been popularly used in *Musa* diversity studies. This technique is expensive and highly demanding (Crouch *et al*., 1998a; Ude *et al*., 2002b)

Therefore, most of *Musa* genetic researchers have focused more on the application of PCR - based markers such as Random Amplified Polymorphic DNA (RAPD), Simple Sequence Repeates (SSRs), and Amplified Fragment Length Polymorphism (AFLP) (Ude *et al*., 2002b).

Chloroplast DNA sequence analysis was used in genealogical relationship of one wild population of *M. balbisiana* to investigated that *M. balbisiana* is native to Thailand. However, new accessions of *M. balbisiana* are required in the future works on morphology and DNA analyses for further determination of accurate relationship (Swangpol *et al*., 2006).

CHAPTER 3

GENERAL MATERIALS AND METHODS

Morphological and environmental data of wild banana specimens were collected from 6 sites in lower northern Thailand.

The research methodology consisted of 5 steps. *(i.)* The locations and site structure details were determined their forest types by GIS for survey preparation. *(ii.)* Banana samples and environmental data were collected along line transects in the study sites and the locations of each sample was recorded with a GPS receiver. *(iii.)* The taxonomic status was evaluated by multivariate morphometric analyses such as cluster and discriminant analyses. These accessions were then compared to accessions from three other areas of Thailand. Meanwhile, the results were compared to identification of wild bananas used classical taxonomy with a checklist. *(iv.)* Environmental variables of wild bananas habitat were recorded. The relationships between morphological variations and ecological factors were investigated using statistic techniques such as multivariate analysis. *(v.)* Phylogeny of some accessions was determined using DNA sequences and compared with other *M. acuminata* and cultivated bananas.

3.1 Location, Site Structure and Sample Collection

Sites were selected from 6 protected areas in lower northern Thailand. These were *(i.)* Namnaow National Park (Nw), Phetchabun Province, *(ii.)* Thung Salaeng Luang National Park (Tl), Phitsanulok Province, *(iii.)* Lumnamnan National Park (Ln), Uttaradit Province, *(iv.)* Umphang Wildlife Sanctuary (Up), Tak Province, *(v.)* Mae Wong National Park (Mw), Khamphangphet Province, and *(vi.)* Phu Hin Rong Kla National Park (Ph), Phitsanulok Province (Figure 3.1). Wild banana samples were collected along line transects which passed through several forest types located in the six study sites. The collection sites were surveyed and mapped on 1:50,000 maps. Taxonomy identification and laboratory work were carried out at the study sites, and at the Princess Sirindhorn Plants Herbarium of Bangkok Herbarium, at Mae Fah Luang University, Chulalongkorn University and Naresuan University.

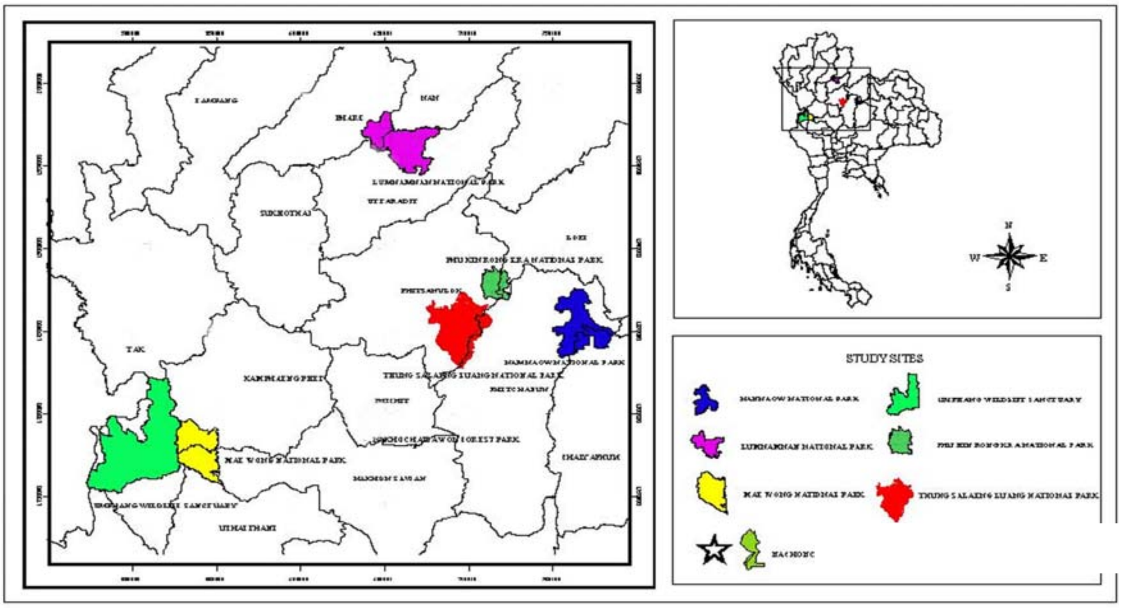


Figure 3.1 The six study sites in lower northern Thailand

Banana plants within a distance of 10 m from the main route of the survey lines were collected (Krebs, 1999). The position of each collected specimen was recorded with GPS (Krebs, 1999). Morphological characters were recorded according to the Plant Sample Descriptor Technique (IPGRI/INIBAP/CIRAD, 1997) (Appendix A). The determinations of intra - specific taxa of wild banana was carried out following the descriptions of Cheesman (1947a, 1947b, 1948a, 1948b, 1949a, 1949b, 1949c, 1950a, 1950b), Simmonds (1953a, 1953b, 1956 1960), Simmonds and Shepherd (1955), De Langhe *et al.* (1998). Identification and classification conclusions were reported.

Additionally, wild banana samples were collected from three reference areas, western (Kanchanaburi), eastern (Chanthaburi), and southern Thailand (Trang). They were compared to all specimens from the six studied sites in lower northern Thailand.

3.2 Morphological Study and Identifications

Morphological data was collected from living plants with digital photographs. All details and data were studied according to the *Musa* description, identification, and classification techniques (Simmonds, 1956, 1959, 1960, 1979; Simmonds & Shepherd, 1955; Simmonds & Weatherup, 1988; Cheesman, 1948a; IPGRI/INIBAP/CIRAD, 1997; De Langhe *et al.,* 1998). Twenty characteristics were used to identify the samples into subspecies as follow.

(1.) Pseudostem height (m.) was recorded from the base of pseudostem to emerging point of the peduncle.

(2.) Pseudostem appearance was recorded as 1. Dull (waxy) or 2. Shiny (not waxy).

(3.) Blotches at petiole base were recorded as 1. Sparse blotching, 2.Small blotch, 3. Large blotch, 4. Extensive pigmentation, or 5. Without pigmentation.

(4.) Blotch color recorded as 1. Brown, 2. Dark brown, 3. Brown-black, 4. Black-purple, and Other (specify).

(5.) Petiole cannel at leaf III was recorded as 1. Open with margins spreading, 2. Wide with erect margins, 3. Straight with erect margins, 4. Margins curved inward, or 5. Margins overlapping.

(6.) Wax on leaves (lower surface) was recorded as 1. Very little or no visible sign of wax 2. Few wax 3. Moderately waxy, or 4. Very waxy.

(7.) Peduncle hairiness was recorded as 1. Hairless, 2. Slightly hairy, 3. Very hairy, short hairs (similar to velvet touch), or 4. Very hairy, long hairs (> 2mm.).

(8.) Bunch position (of the fruit-bearing part) and angle from vertical to the general axis of the bunch was recorded as 1. Hanging vertically, 2. Slightly angled, 3. Hanging at angle 45^{o}, 4. Horizontal or 5. Erect.

(9.) Rachis position after the bunch was recorded as 1. Falling vertically, 2. At an angle, 3. With a curve, 4. Horizontal, or 5 Erect.

(10.) Male bud shape was recorded as1. Like a top, 2. Lanceolate, 3. Intermediate, 4. Ovoid, or 5. Rounded.

(11.) Bract imbrication (alignment of bracts at the apex of the male bud) was recorded as 1. outer bract covers the underlying bracts at the apex of bud (like ssp. *malaccensis*), 2. Young bracts slightly protruding, 3. Young bracts greatly protruding (like ssp. *burmanica*).

(12.) Color of the bract external face was recorded as 1. Yellow, 2. Green, 3. Red, 4. Red-purple, 5.Purple-brown, 6. Purple, 7. Blue, 8. Pink-purple, 9. Orange-red, or 10. Other (specify) (Figure 3.3: Chart A).

(13.) Color of the bract internal face was recorded as 1. Whitish, 2. Yellow or Green, 3. Orange red, 4. Red, 5. Purple, 6. Purple brown, 7. Pink-purple, 8. Other (specify) (Figure 3.3: Chart A).

(14.) Wax on the bract was recorded as 1. Very little or no visible sign of wax, 2. Few wax, 3. Moderately waxy, or 4. Very waxy.

(15.) Compound tepal basic color was recorded as 1. White, 2. Cream, 3.Yellow, 4. Orange, 5. Pink / Pink-purple, or 6. Other (specify) (Figure 3.3; Chart B).

(16.) Lobe color of compound tepal was recorded as 1. Cream, 2.Yellow, 3. Orange, 5. Green, or 6. Other (specify) (Figure 3.3; Chart B).

(17.) Color on the bract apex (External) was recorded as 1. Tinted with yellow (Discolored), or 2. Not tinted with yellow (Color is uniform until apex).

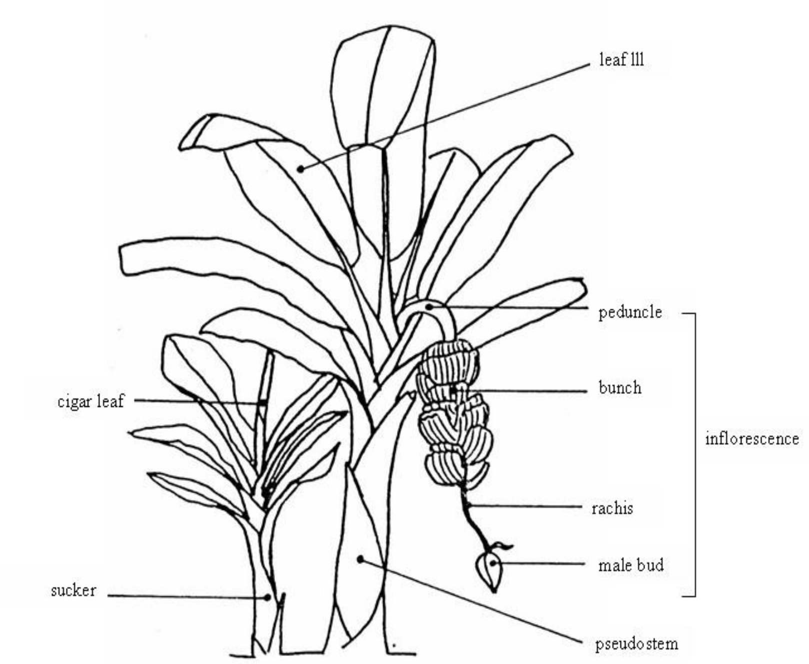
(18.) Color stripe on the bract was recorded as 1. Without discolor lines (Not ridges) on the external face, or 2. With lines of discoloration or stripes on the external face.

(19.) Fruit apex was recorded as 1. Pointed, 2. Lengthily pointed, 3. Blunt-tipped, 4. Bottle-necked, or 5. Rounded.

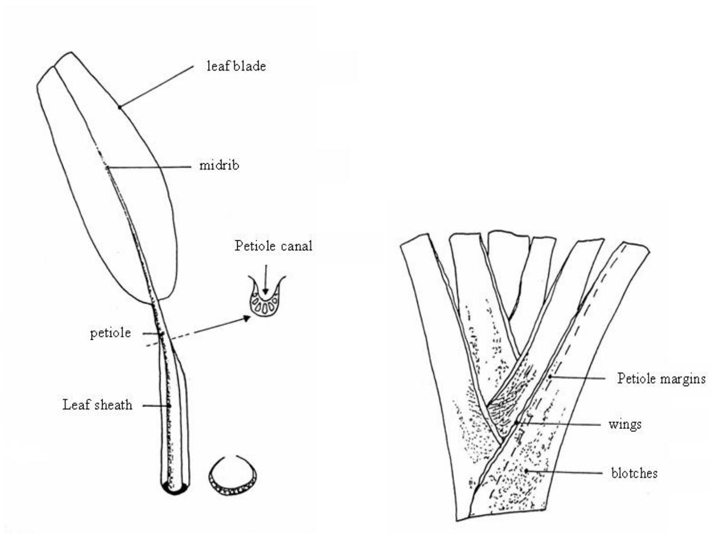
(20.) Fusion of pedicel was recorded as 1. Very partially or no visible sign of fusion, or 2. Partially fused, or 3. Totally fused.

The details of characteristic criteria and color chart to measure these various variables are in the Figure 3.2 - 3.3.

A summary key of Simmonds (1956) with the additional information from the work of Cheesman (1947a, 1947b, 1948a, 1948b, 1949a, 1949b) was used to classify the collected plants into five subspecies (Table 3.1). Specimens were analyzed and compared to the herbarium (No. SN 244333, SN 244335, SN 244340, SN 244338, SN 244347, and SN 244339) at Princess Sirindhorn Plant Herbarium of Bangkok Herbarium. All samples were kept in Faculty of Agriculture, Natural Resources and Environment, Naresuan University and at Bangkok Herbarium, Department of Agriculture.

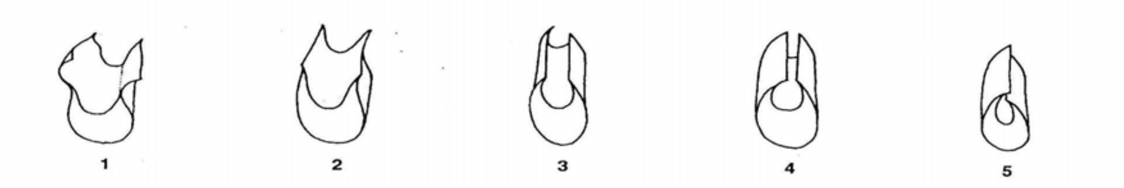


Banana Pseudostem

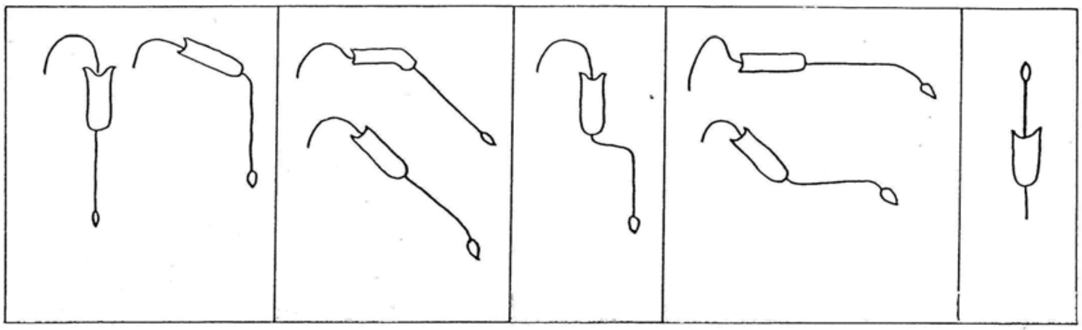


Petiole/Midrib/Leaf

Figure 3.2 Morphological Characteristic (IPGRI/INIBAP/CIRAD, 1997)



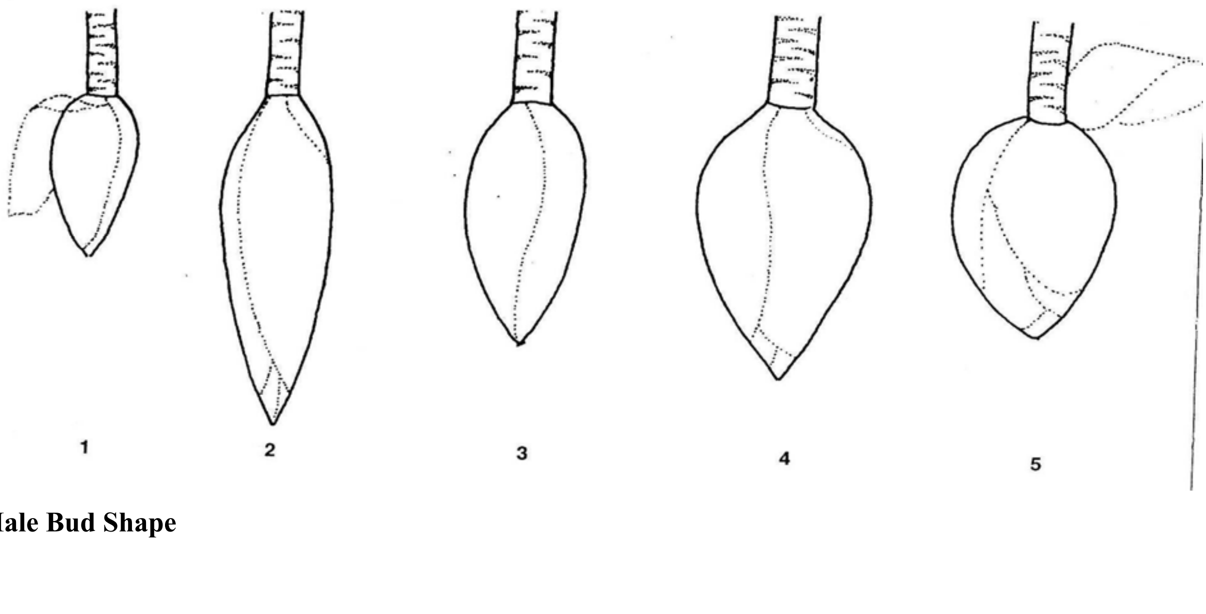
Petiole Cannel at Leaf III



1. **2.** **3.** **4.**

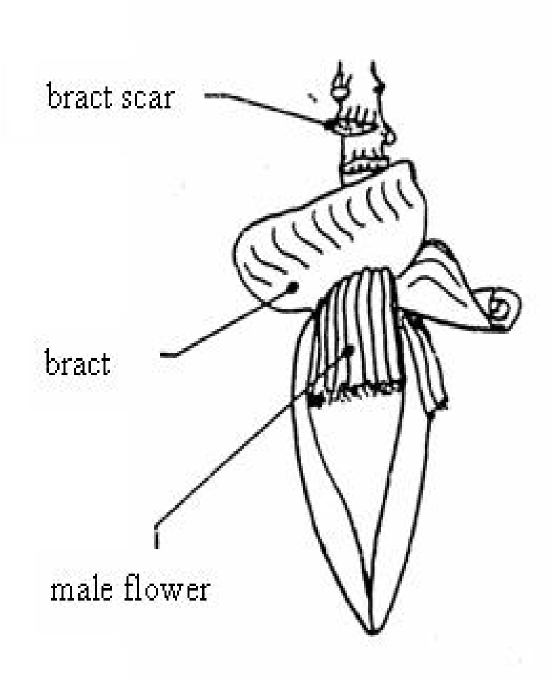
5.

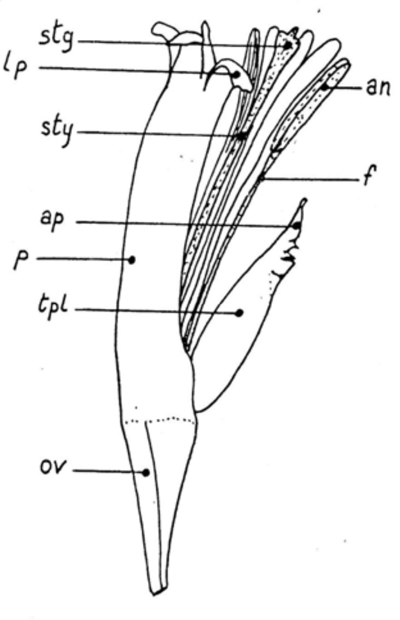
Rachis Position



Male Bud Shape

Figure 3.2 Morphological Characteristic (IPGRI/INIBAP/CIRAD, 1997) (Cont.)





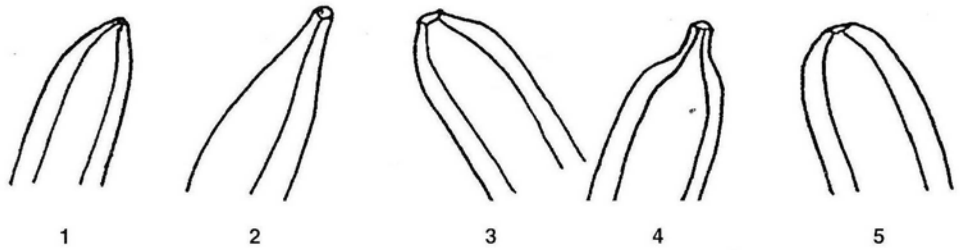
Male Bud and Flower

Figure 3.2 Morphological Characteristic (IPGRI/INIBAP/CIRAD, 1997**)** (Cont.)

stg : Stigma; **lp** : Lobes of Compound Tepal; **sty** : Style; **ap** : Apex;

p : Compound Tepal; **tpl** : Free Tepal; **ov** : Ovary; an : Anthers;

f : Filament



Fruit Apex

Figure 3.2 Morphological Characteristic (IPGRI/INIBAP/CIRAD, 1997) (Cont.)

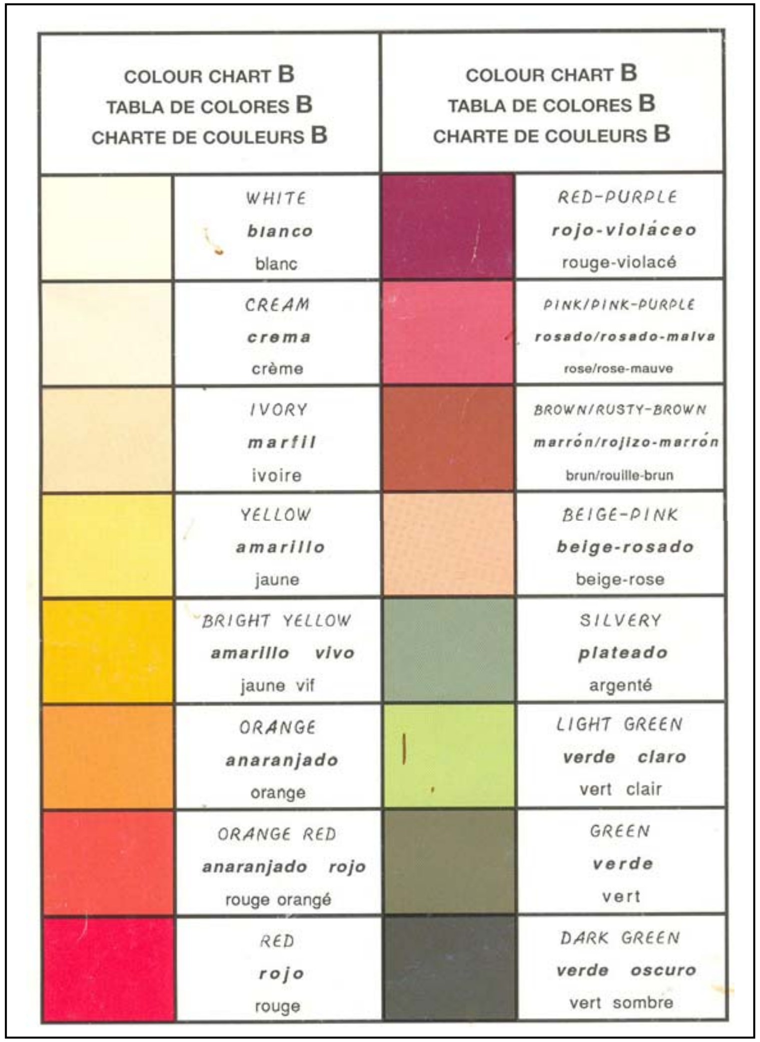


Figure 3.3 Color charts (A) and (B) for characterizations and classifications of *Musa acuminata* Colla (IPGRI/INIBAP/CIRAD, 1996)

Table 3.1 Identification key for the five subspecies of *M. acuminata* Colla (Simmonds, 1956)

---

1. Sheaths: Waxless except in young suckers ……….………..………….....…………………….2.
   Sheaths: Waxless or little wax.……………………………………..………..…….………3.
2. Pseudostems: intensely brown - pigmented (brown - purple) #;
   (6 m high), male bud: plump, and not imbricate, male bracts pale red on the internal face………………………………………………………………………….**ssp. *microcarpa***
   Pseudostems: lightly pigmented; (3 - 5 m high) #,
   (male bud shape: advance blooming acute) #,
   male bracts crimson red on the internal face, imbricate……………………….**ssp. *burmanica***
3. Sheaths: lightly waxy; female flowers, at least the upper ones, male-fertile; fruits subobtuse; ovules more than 200 per ovary; bracts yellow or dirty dull red on the bract internal face…………………………….………………………………………….**...ssp. *banksii***
   Sheaths: waxy; female flowers male-sterile; fruits acuminate; ovules fewer than 200 per ovary; bracts bright red or purplish red on the bract internal face ……………………….4.
4. Bracts: bright red on the bract external face, quickly deciduous, non-imbricate (red beneath and often purplish above also, petiole margin induplicate) #..………………..**ssp. *malaccensis***
   Bract: purplish red on the bract external face, with yellowish tips, often slightly persistent, usually imbricate in the young bud (petiole margin yellowish green; erect) # ……**ssp. *siamea***

Remark: #: The character in the parenthesis (-) are additional information from the work of Cheesman (1947a, 1947b, 1948a, 1948b, 1949a, 1949b); More details are in the Appendix A

3.3 Morphological Identification of Wild Banana (*Musa acuminata* Colla) Using Classical Taxonomy and Cluster Analysis Technique

Twenty morphological characters were recorded on 326 specimens. The samples were tentatively classified using the key in the Table 3.1. The pseudostem height at flowering stage is quantitative data but it is not normally distributed. The 19 other characteristics of the specimens were ordinal, nominal or ranking scales which were qualitative data. All data were transformed to stabilize the variance using standardization by logarithmic or square root equations depending upon their skewness or kurtosis (Snedecor & Cochran, 1982; SPSS, 1993). After that all data were analyzed by hierarchical cluster analysis with Between - Group Linkage or Average Linkage Between Group or Unweighted Pair - Group Method using Arithmetic Average, UPGMA (Vanitbuncha, 2000). The distance values were calculated using Euclidean Distance (SPSS, 1993). After that all data were analyzed by hierarchical cluster analysis with Between - Group Linkage or Average Linkage Between Group or Unweighted Pair - Group Method using Arithmetic Average, UPGMA (Vanitbuncha, 2000). Agglomerative hierarchical cluster analysis or agglomerative schedule was used for combining clusters. The results were presented in a hierarchical dendrogram (SPSS, 1993). Cluster analyses were repeated with the additional specimens of ssp. *siamea* (Chanthaburi), ssp. *malaccensis* (Trang), ssp. *burmanica* (Kanchanaburi), and dummy type description of Simmonds (1956) for ssp. *siamea* and ssp. *burmanica* were included in the same data set.

Relationships or correlation of classical taxonomy with cluster analysis techniques were statistically analyzed by Pearson correlation (SPSS, 1993). Discriminant analysis was tested for cluster analysis with the original and cross - validated methods to accept the predictions of the cluster and grouping (SPSS, 1993). The flowchart of the research procedure was shown in Figure 3.4.

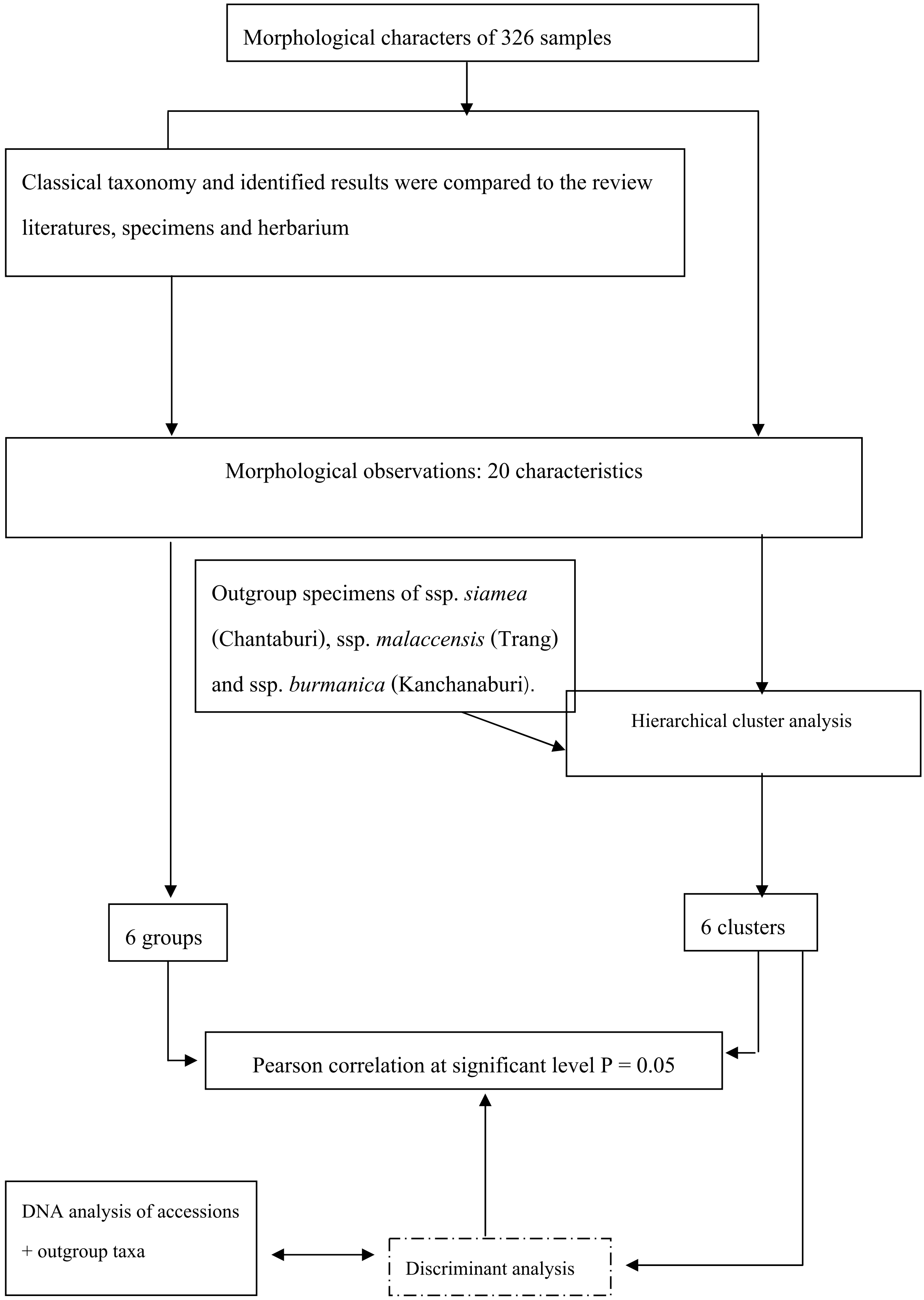


Figure 3.4 Flowchart of the analysis research procedure

3.4 Habitat of Wild Banana (*Musa acuminata* Colla)

Environmental factors of samples at the 6 study sites were collected from the field conditions (Griffiths, 1994). The aims are to gain the baseline information of the habitat and understand the primary environmental conditions. They were altitude, relative humidity (%RH), air temperature, light intensity, elevation, soil texture, soil pH, and soil Water Holding Capacity (%WHC) using the methods derived from Bunyavejchewin (1983) and Gliessman (2000). For soil analysis, three soil samples were taken at 0 - 30 cm. depth across the banana mat and analysed as a composite sample (Gliessman, 2000). Soil type (texture) was determined by using the hydrometer method. Soil pH was determined using a pH meter. Water Holding Capacity (%) of soil was determined by weighing samples of known volume before and after oven dried at 105^{o}C for 48 hours (Bunyavejchewin, 1983; Gliessman, 2000). The relative humidity, air temperature and light intensity were measured at the ground surface under the canopy of the specimens and at an open space outside the habitat. The ratios between the canopy and open area measurements were statistically analysed. These provide fundamental microclimate information with the wild banana dispersal. Other additional habitat information such as forest types, annual temperatures, annual rainfalls, daylight periods and elevations of the study areas were taken from the national parks information centre and meteorological stations of lower northern Thailand to understand their macro - ecological conditions. All data were analyzed following the methods of Ludwig and Reynolds (1988), ASEAN (1990), Jones (1992), Griffiths (1994), Petersen (1994), Jorgensen *et al.* (1996), Kaosa – ard (1989), Kimmins (1997), Morin (1999), and Gliessman (2000). Plant community profiles were recorded and were redrawn on profile diagram using the method derived from Elliott *et al.* (1989). The forest ecology and distribution of wild banana samples were graphically presented on geographic maps (Bunyavejchewin, 1983). After that, information and details were overlayed as multi - data layers. The survey lines, sample locations and zoning of the different forest types were analyzed on GIS framework using ARCVIEW 3.2 (Haines-Young *et al*., 1993; Frohn, 1998).

The relationships of the morphological groups from classical taxonomy and environmental factors were statistically analyzed using multivariate analyses (Conover, 1980; Snedecor & Cochran, 1982; Griffiths, 1994; Petersen, 1994; Jorgensen *et al.,* 1996; Baker, 1997). Statistical analysis with SPSS was used to test the differences of the environmental factors among all samples of different wild banana groups such as regression analysis, analysis of variance (ANOVA) and others (Baker, 1997). The distributions of each morphological group were presented on GIS map (Ludwig & Reynolds, 1988; Haines-Young *et. al*., 1993; Kearsey & Pooni, 1996; Frohn, 1998). Their morphological and environmental data of sample's collection within the habitat are presented in the Figure 3.5 below.

Figure 3.5 Demonstration on morphological and environmental data of wild bananas (*M. acuminata* Colla) sample's collection within the habitat.

❶ Light intensity, temperature and relative humidity percentage (%RH) were recorded at the ground surface under the banana canopy (under canopy). Soil samples were collected and then analyzed for its pH and %WHC.

❷ Morphological characters of wild banana samples were recorded as the checklist (IPGRI/INIBAP/CIRAD, 1997). The sampling positions and elevations were recorded with GPS.

❸ Light intensity, air temperature and %RH were measured at the top of the banana canopies.

❹ Light intensity, air temperature and %RH were measured at open space outside the sampling area without banana trees (open space). The ratios of environmental factors between under canopy between outside the sampling areas were determined.

3.5 Phylogeny of *Musa acuminata* Colla and its Related Cultivars on DNA Analysis

DNA sequences were obtained from thirty - six accessions of *M. acuminata* (Musa section Eumusa, 11 chromosomes) representing different locations in Thailand (Table 3.2). These DNA sequences were analysed as phylogentic trees and network.

DNA Sequences Analysis

DNA of the 36 accessions was extracted from banana buds using DNeasy Plant Minikit. Sixteen accessions of *M. acuminata* from the lower northern Thailand were selected, representing the different groups identified by classical and numerical taxonomy. They were AAw_LN20, AAw_MW10, AAw_MW20, AAw_MW31, AAw_NW22, AAw_NW33, AAw_NW38, AAw_NW41, AAw_PH04, AAw_PH05, AAw_TL18, AAw_UP16, AAw_UP18, AAw_UP25, AAw_UP36 and AAw_UP37 (Appendix 4). 10 more accessions of *M. acuminata* were selected from 3 other regions of Thailand. They were AAw_Chanthaburi1, AAw_Chanthaburi2, AAw_Chanthaburi3 and AAw_Chanthaburi4 as representing ssp. *siamea,* AAw_Kanchanaburi1, AAw_Kanchanaburi2 and AAw_Kanchanaburi3 representing ssp. *burmanica,* and AAw_Trang1, AAw_Trang2 and AAw_Trang3 representing ssp. *malaccensis*. In addition, nine individual accessions of wild *M. acuminata* were also introduced from different parts of Thailand, which were AAw_MaeYom, AAw_Ranong, AAw_Salaween, AAw_Chanthaburi, AAw_Yala, AAw_PrachuabKhiriKhan, AAw_Rayong, AAw_Mukdahan, AAw_Trang. *M. schizocarpa* was used as an outgroup accession.

These extracted DNA samples were kindly provided by Dr. Hugo Volkaert, Centre of Agricultural Biotechnology (CAB), Kasetsart University Kamphaengsaen Campus. Four chloroplast DNA fragments containing mostly non – coding regions were amplified by PCR: the intron of the *rpl*16 gene; the intron of the *ndh*A gene; the intergenic region between *psa*A and…, and; a fragment from the 3'end of the *pet*A gene to the *pet*F gene, containing the short *psb*J and … genes and all intergenic regions in between. The amplified fragments were separated on polyacrylamide gel using SSCP conditions (Orita *et al.,* 1989; Jordan *et al.*, 1998; Sato & Nishio 2002) following a previous study by Swangpol (2003) and Swangpol *et al*., (2007) (Appendix D). PCR was conducted in a total reaction mixture of 10 microL. Formamide loading dye was added to the digested products and the reactions were denatured for 10 min at 95°C and cooled down to stabilize single strands. Then 3.5 ml aliquots were loaded on non - denaturing polyacrylamide gel and electrophoresis was performed with a constant power of 10W at a temperature of 4C. The fragments were revealed by silver staining using standard procedure (Bassam *et al.,* 1991). Accessions showing polymorphic bands were grouped as haplotypes and were selected for cloning and sequencing or sequenced directly.

For cloning and sequencing, undigested PCR fragments were purified using MinElute PCR Purification Kit (Qiagen), ligated into either TOPO TA Cloning kit (Invitrogen) or pGEM-T Vector System (Promega) and transformed into *E. coli* 'DH10B' using electroporation. Plasmids were extracted using the Wizard® *Plus* SV miniprep DNA Purification System (Promega) and sent for sequencing (Macrogen, Inc, Seoul, South Korea) (Appendix D).

The nucleotide sequences were aligned with the GeneDoc program version 2.6.002 (Nicholas & Nicholas, 1997; Swangpol, 2003; Swangpol; *et al.,* 2007). The base compositions were determined by the analysis of aligned matrix using the DnaSP program version 4 (Rozas *et al*., 2003; Swangpol, 2003; Swangpol *et al*., 2007). After that, all cpDNA sequences were analyses and compared.

Phylogenetic and Network Analyses

Phylogenetic analyses of the relationships among *Musa* cpDNA were inferred using the program MrBayes 3.1.2. M_schizocarpa_ITC was included as an outgroup in both phylogenetic and network analyses.

The Bayesian trees were created with all characters weighted equally for phylogenetic analyses. The general time reversible model of nucleotide substitutions was used with gamma distribution of rates of substitution and a proportion of invariants. The Markov Chains were run for 1,000,000 generations after a burn-in of 250,000 generation. The 50% majority consensus tree was then calculated for all saved trees. Bayesian posterior probabilities were indicated.

Gene genealogies were estimated on the accessions by parsimony haplotype network reconstruction using statistical parsimony algorithm (Templeton *et al*., 1992) as implemented in the program TCS 1.13 (Clement *et al*., 2000) which calculates unrooted cladograms of a high probability (>95%). Insertion deletions were counted as one mutational event irrespective of their length and analysed as fifth state (Swangpol, 2003; Swangpol *et al*., 2007). *Musa* accessions, origins and sources of accessions are shown in Table 3.2

Table 3.2 List of *Musa* accessions, origins and sources of accessions.

No.	Code	Origin [a]	Source [b]	Species/Cultivar
1	AAw_LN20 *	Lumnamnam, Uttaradit, Thailand	DW	Wild *M. acuminata* Colla
2	AAw_MW10 *	Mae Wong, Khamphagphet, Thailand	DW	Wild *M. acuminata* Colla
3	AAw_MW20 *	Mae Wong, Khamphagphet, Thailand	DW	Wild *M. acuminata* Colla
4	AAw_MW31 *	Mae Wong, Khamphagphet, Thailand	DW	Wild *M. acuminata* Colla
5	AAw_NW22 *	Namnaow, Phetchabun, Thailand	DW	Wild *M. acuminata* Colla
6	AAw_NW33 *	Namnaow, Phetchabun, Thailand	DW	Wild *M. acuminata* Colla
7	AAw_NW38 *	Namnaow, Phetchabun, Thailand	DW	Wild *M. acuminata* Colla
8	AAw_NW41 *	Namnaow, Phetchabun, Thailand	DW	Wild *M. acuminata* Colla
9	AAw_PH04 *	Phu Hin Rong Kla, Phitsanulok, Thailand	DW	Wild *M. acuminata* Colla
10	AAw_PH05 *	Phu Hin Rong Kla, Phitsanulok, Thailand	DW	Wild *M. acuminata* Colla

Table 3.2 List of *Musa* accessions, origins and sources of accessions. (Cont.)

No.	Code	Origin [a]	Source [b]	Species/Cultivar
11	AAw_TL18 *	Thung Salaeng Luang, Phitsanulok, Thailand	DW	Wild *M. acuminata* Colla
12	AAw_UP16 *	Umphang, Tak, Thailand	DW	Wild *M. acuminata* Colla
13	AAw_UP18 *	Umphang, Tak, Thailand	DW	Wild *M. acuminata* Colla
14	AAw_UP25 *	Umphang, Tak, Thailand	DW	Wild *M. acuminata* Colla
15	AAw_UP36 *	Umphang, Tak, Thailand	DW	Wild *M. acuminata* Colla
16	AAw_UP37 *	Umphang, Tak, Thailand	DW	Wild *M. acuminata* Colla
17	AAw_Chanthaburi1 *	Chanthaburi, Thailand	DW	Wild ssp. *siamea*
18	AAw_Chanthaburi2 *	Chanthaburi, Thailand	DW	Wild ssp. *siamea*
19	AAw_Chanthaburi3 *	Chanthaburi, Thailand	DW	Wild ssp. *siamea*
20	AAw_Chanthaburi4 *	Chanthaburi, Thailand	DW	Wild ssp. *siamea*
21	AAw_Kanchanaburi1 *	Kanchanaburi, Thailand	DW	Wild ssp. *burmanica*
22	AAw_Kanchanaburi2 *	Kanchanaburi, Thailand	DW	Wild ssp. *burmanica*
23	AAw_ Kanchanaburi3 *	Kanchanaburi , Thailand	DW	Wild ssp. *burmanica*
24	AAw_Trang1 *	Trang, Thailand	DW	Wild ssp. *malaccensis*
25	AAw_Trang2 *	Trang , Thailand	DW	Wild ssp. *malaccensis*
26	AAw_Trang3 *	Trang, Thailand	DW	Wild ssp. *malaccensis*
27	AAw_MaeYom**	LomDong, MaeYom, Phrae, Thailand	CAB, KU	Wild ssp. *siamea*
28	AAw_Ranong **	Ranong, Thailand	CAB, KU	Wild ssp. *malaccensis*
29	AAw_Chanthaburi **	Chanthaburi, Thailand	CAB, KU	Wild ssp. *siamea*
30	AAw_Yala **	Betong, Yala, Thailand	CAB, KU	Wild ssp. *malaccensis*
31	AAw_PrachuabKhiriKhan**	PrachuabKhiriKhan, Thailand	CAB, KU	Wild ssp. *burmanica*

Table 3.2 List of *Musa* accessions, origins and sources of accessions. (Cont.)

32	AAw_Rayong **	Rayong, Thailand	CAB, KU	Wild ssp. *siamea*
33	AAw_Mukdahan **	Mukdahan, Thailand	CAB, KU	Wild ssp. *siamea*
34	AAw_Trang **	Trang, Thailand	CAB, KU	Wild ssp. *malaccensis*
35	AAw_Salaween **	Salaween, MaeHongSon, Thailand	CAB, KU	Wild ssp. *malaccensis*
36	M_schizocarpa_ITC ***	?	ITC	*M. schizocarpa*

In this Table, * = accessions from the field survey; ** additional samples from other parts of Thailand; *** = The outgroup accession for Phylogenetic and Network analyses, **a** = Indicates known origins; **b =** indicates sources of accessions; **DW** = Field Collection by Det Wattanachaiyingcharoen; **CAB, KU** = Center of Agricultural Biotechnology, Kasetsart University Kamphaengsaen Campus; **ITC** = International Transit Center, International Network for the Improvement of Banana and Plantain (INIBAP), Leuven, Belgium.

CHAPTER 4

MORPHOLOGICAL VARIATIONS OF WILD BANANA

(Musa acuminata Colla) IN THAILAND

SUMMARY

Three hundred and twenty six specimens of wild banana were collected in five national parks and one wildlife sanctuary of lower northern of Thailand during March 2002 to March 2006. In addition, 13 accessions each were collected from Chantaburi and Kanchanaburi, and 12 accessions from Trang. Canonical discriminant scored for twenty morphological characteristics showed a separation into two major groups with a few scattered accessions. The two groups corresponded to *(i.)* ssp. *malaccensis*, and *(ii.)* ssp. *siamea* and ssp. *burmanica*. In addition, cluster analyses of outgroup specimens of ssp. *siamea* (Chantaburi), ssp. *malaccensis* (Trang) and ssp. *burmanica* (Kanchanaburi) were also precisely classified into their groups. Hierarchical analyses as numerical taxonomy confirmed the same separation at 23 units of rescaled distance. In contrast, classical taxonomy classified all accessions into 3 subspecies of ssp. *siamea*, ssp. *malaccensis*, ssp. *burmanica* and some outliers. However, the statistical classification strongly indicated that ssp. *siamea* and ssp. *burmanica* were in the same group and clearly isolated from ssp. *malaccensis*. The few outliers may be mutants or hybrids. Further study has to focus on the current key and banana classifications of Simmonds (1956), which may not cover the new characters of new specimens and has to be reviewed.

Keywords: Wild Banana, *Musa acuminata* Colla, Identification, Cluster Analysis

INTRODUCTION

Wild bananas (*M. acuminata* Colla) grow naturally in Southeast Asia including Thailand (Benchamas & Chalongchai, 1983). Thai common names are Kluai Kae, Kluai Paa (Northern Thai), Kluai Tuan (Southern Thai), Kluai Ling (Uttaradit), Kluai Hmon (Chiang Mai) (Suvatti, 1978). There are found in natural forests through Thailand (Suvatti, 1978; Benchamas & Chalongchai, 1983). Four subspecies were identified through classical taxonomy and primary reported in Thailand. They were *(i.)* ssp. *siamea* Simmonds, *(ii.)* ssp. *burmanica* Simmonds, *(iii.)* ssp. *malaccensis* (Ridl.) Simmonds, and *(iv.)* ssp. *microcarpa* (Becc.) Simmonds (Simmonds, 1956). After banana genomes and scoring techniques were developed, they encouraged the demand on germplasm utilization for industry and breeding programs. Classification of banana cultivars has been achieved by applying morphological scoring techniques. By these techniques, 15 characteristics were used to classify those bananas (Simmonds & Shepherd, 1955; Benchamas & Chalongchai, 1983). These techniques roughly supported primary varieties and cultivars identification. In addition, large numbers of accessions were not clearly classified nor created genomic and taxonomic confusing. Other techniques were also introduced to reconfirm and correct the scoring results. Cytology and chromosome counting (Benchamas & Chalongchai, 1983; Jong & Argent, 2001), molecular chemistry and DNA techniques (Rekha *et al.,* 2001) were also successfully applied to identify genome groups of cultivated banana, especially the hybridization of *M. acuminata* (AA genome) and / or *M. balbisiana* (BB genome) (Swennen & Vuylsteke, 1986; Simmonds & Weatherup, 1988). However, molecular techniques required high expertise and laboratory works, which were not practical for a person to identify banana in the field (Argent, 2000). Numerical statistics techniques, then have been popularly used as a tool to investigate the difference in a sampled population (Fielding, 2007). However, the classical taxonomy is still suitable to support fieldwork and complement to rapidly identification results (Simmonds & Shepherd, 1955; Valmayor & Pascua, 1985; Valmayor, 2001). The classical taxonomy and identification of subspecies should be used to harmonize with the other modern taxonomy trends (Nasution, 1993). Numerical taxonomy technique could enhance the efficiency utilization of classical taxonomy and for other techniques (Argent, 2001). However, these are so many numerical techniques for the cluster and classification. Fortunately, the appropriate testing data methods were standardize and give the similar results and classification accuracy such as Re – substitution, Hold out, Cross – validation, Jack – knife, Bootstrapping, Out – of – bag estimates, and Reject rates (Fielding, 2007). Canonical discriminant analysis and hierarchical cluster analysis which cover some of the testing data methods are used in this study. The objectives of this research are to investigate the application of numerical taxonomy techniques on exploration of new wild banana materials, and to clarify the subspecies variation of *M. acuminata.*

MATERIALS AND METHODS

1. The study sites were selected to cover the lower northern, Thailand. Three hundred and twenty six samples were collected along line transects and morphological data was recorded from living plants. The outgroup specimens of ssp. *siamea* (from Chantaburi), ssp. *malaccensis* (from Trang) and ssp. *burmanica* (from Kanchanaburi) were also collected and data was recorded. These characteristics were pseudostem height, pseudostem appearance, blotch at petiole base, blotch color, petiole canal leaf, wax on leaf, peduncle hairiness, bunch position, rachis position, male bud shape, bract imbrication, color of the bract external face, color of the bract internal face, wax on the bract, compound tepal basic color, lobe color of compound tepal, color on the bract apex, color stripe on the bract, fruit apex, and fusion of pedicel. The details of measurement, color chart and characteristic criteria to measure these various variables are in the Chapter3 and Appendix A

2. Canonical discriminant analysis of all data was conducted with SPSS version 13. The aim was to search diversity within this population. After that, all samples were grouped into subspecies using classical taxonomy technique. The discriminant analysis was tested for cluster analysis with the original and cross - validated methods to accept the predictions of the cluster and grouping (SPSS, 1993).

3. These 20 characteristics of specimens were analyzed by hierarchical cluster analysis with Between - Group Linkage or Average Linkage Between Group or Unweighted Pair - Group Method using Arithmetic Average, UPGMA (Vanitbuncha, 2000). The distance and similarity value were calculated using Euclidean Distance (SPSS, 1993). In addition, agglomerative hierarchical cluster analysis or agglomerative schedule was a method for

combining clusters. The results were presented in hierarchical dendrogram (SPSS, 1993). In addition, cluster analyses were repeated on classical taxonomy and the outgroup specimens.

4. Twenty characteristics were used to identify the samples into subspecies. Classical taxonomy was studied according to the *Musa* description, identification, and classification techniques (Simmonds, 1956; 1959; 1960; 1979; Simmonds & Shepherd, 1955; Simmonds & Weatherup, 1988; Cheesman, 1948a; IPGRI/INIBAP/CIRAD, 1997; De Langhe *et al*., 1998).

5. Comparison between numerical taxonomy and classical taxonomy will be conducted. Relationships or correlation of classical taxonomy with cluster analysis techniques were statistically analyzed by Pearson correlation (SPSS, 1993).

6. Habitat Environment of Wild Banana (*Musa acuminata* Colla) Groups were analyzed following the methods of Ludwig and Reynolds (1988), ASEAN (1990), Jones (1992), Griffiths (1994), Petersen (1994), Jorgensen *et al.* (1996), Kaosa – ard (1989), Kimmins (1997), Morin (1999), and Gliessman (2000)

RESULTS

1. Exploration Results

Three hundred and twenty six samples were collected from six study sites as shown in Table 4.1 and Figure 4.1 Other 13 specimens each were collected from Chantaburi and Kanchanaburi. In addition, 12 specimens were collected from Trang.

Table 4.1 Sampling locations and sample numbers of *M. acuminata* Colla in the 6 study sites with

three outgroup specimen from three locations

Sites	Collector Number	Total Number
Umphang Wildlife Sanctuary, Tak	Up1 - Up48	48
Thung Salaeng Luang National Park, Phitsanulok	Tl1 - Tl55	55
Mae Wong National Park, Nakhon Sawan	Mw1 - Mw59	59
Phu Hin Rong Kra National Park, Phitsanulok	Ph1 - Ph61	61
Lumnamnan National Park, Uttaradit	Ln1 - Ln55	55
Namnaow National Park, Petchabun	Nw1 - Nw48	48
Total	-	326
Outgroup: Chantaburi (ssp. *siamea*)	C1 – C13	13
Outgroup: Trang (ssp. *malaccensis*)	T1 – T12	12
Outgroup: Kanchanaburi (ssp. *burmanica*)	K1 – K13	13
Grand Total	-	364

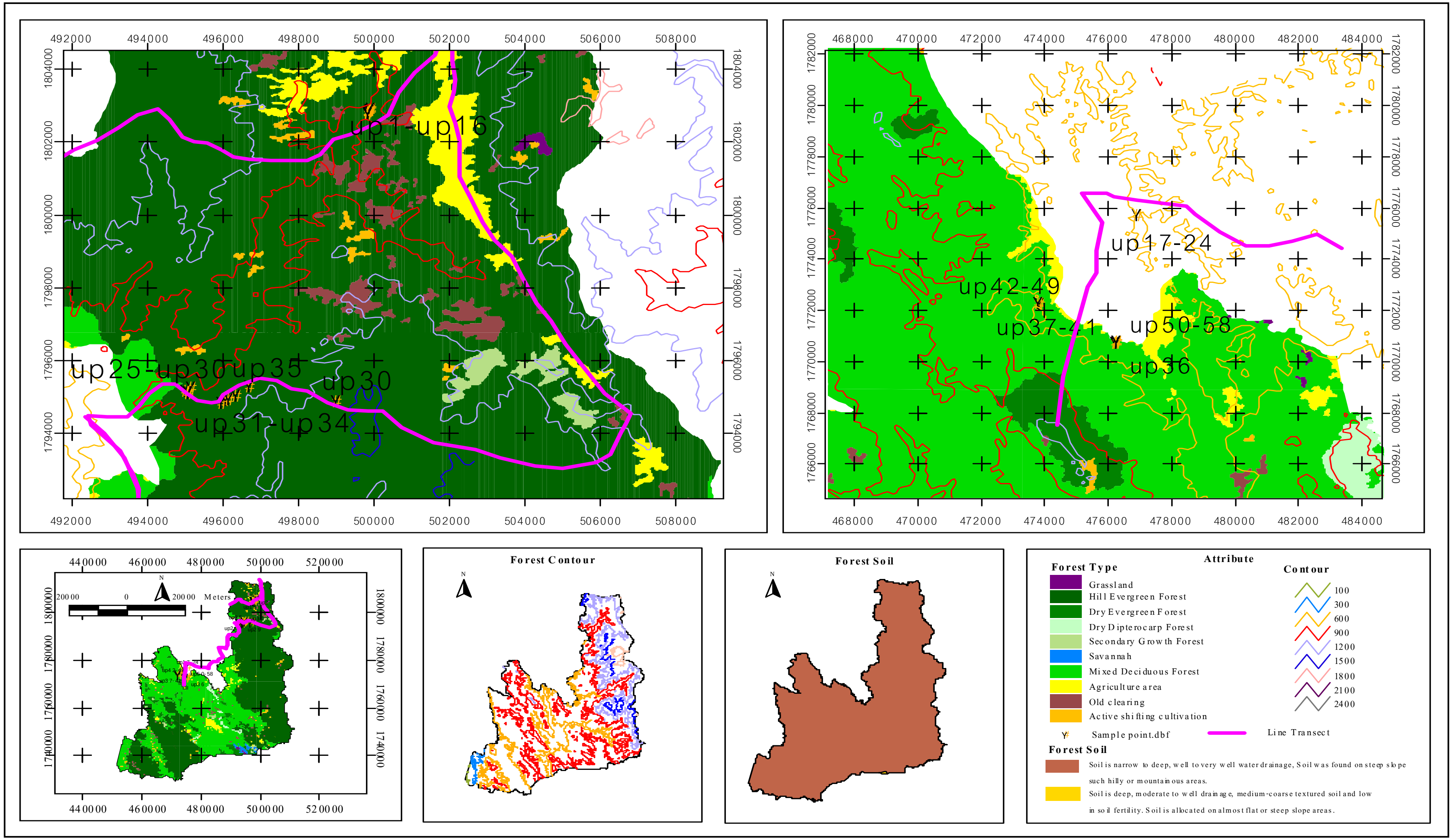


Figure 4.1 (A.) GIS map of wild bananas survey in Umphang Wildlife Sanctuary indicated forest types, forest contour (elevation), forest soil types, samples distribution, line transect and information

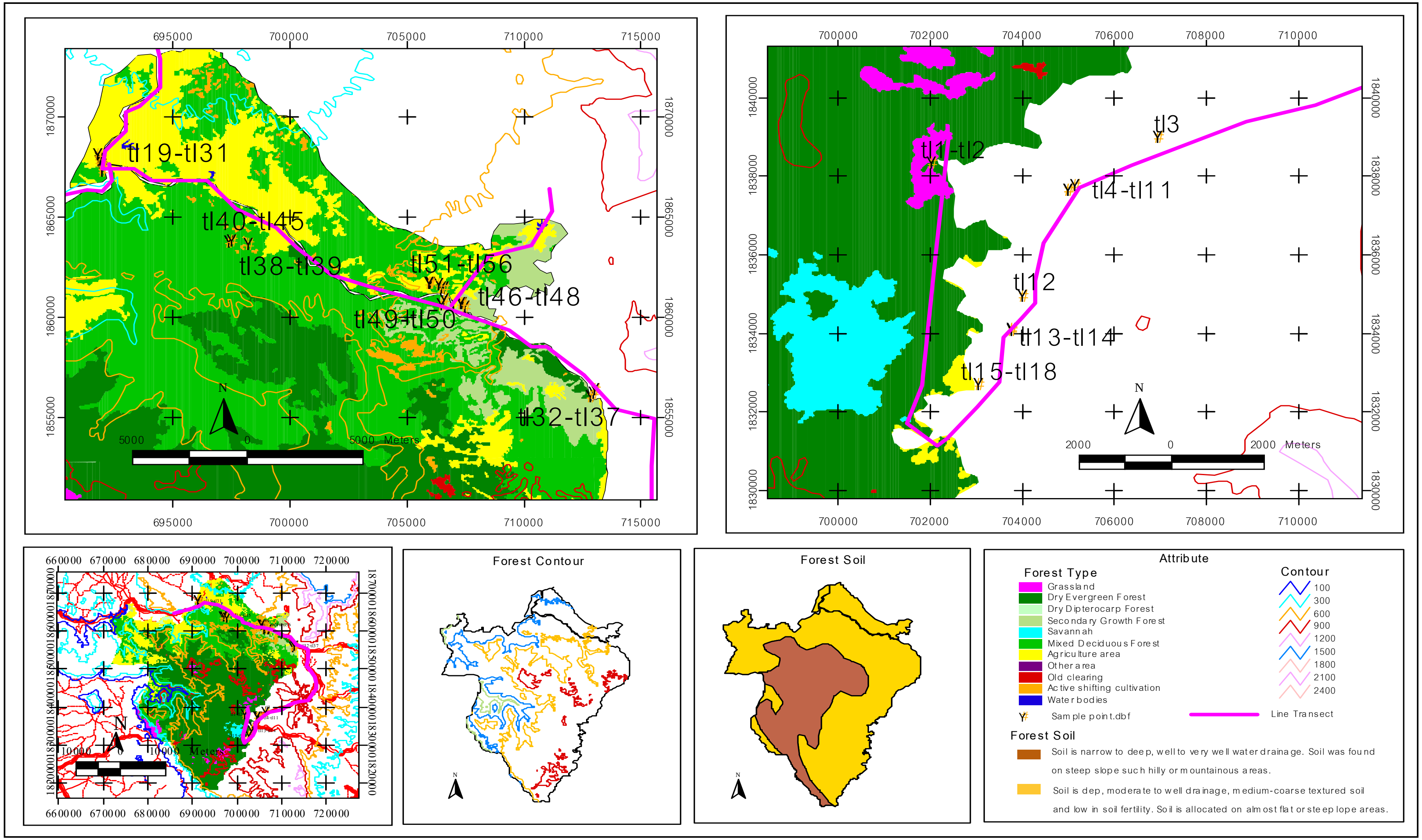


Figure 4.1 (B) GIS map of wild bananas survey in Thung Saleang Luang National Park indicated forest types, forest contour (elevation), forest soil types, samples distribution, line transect and information

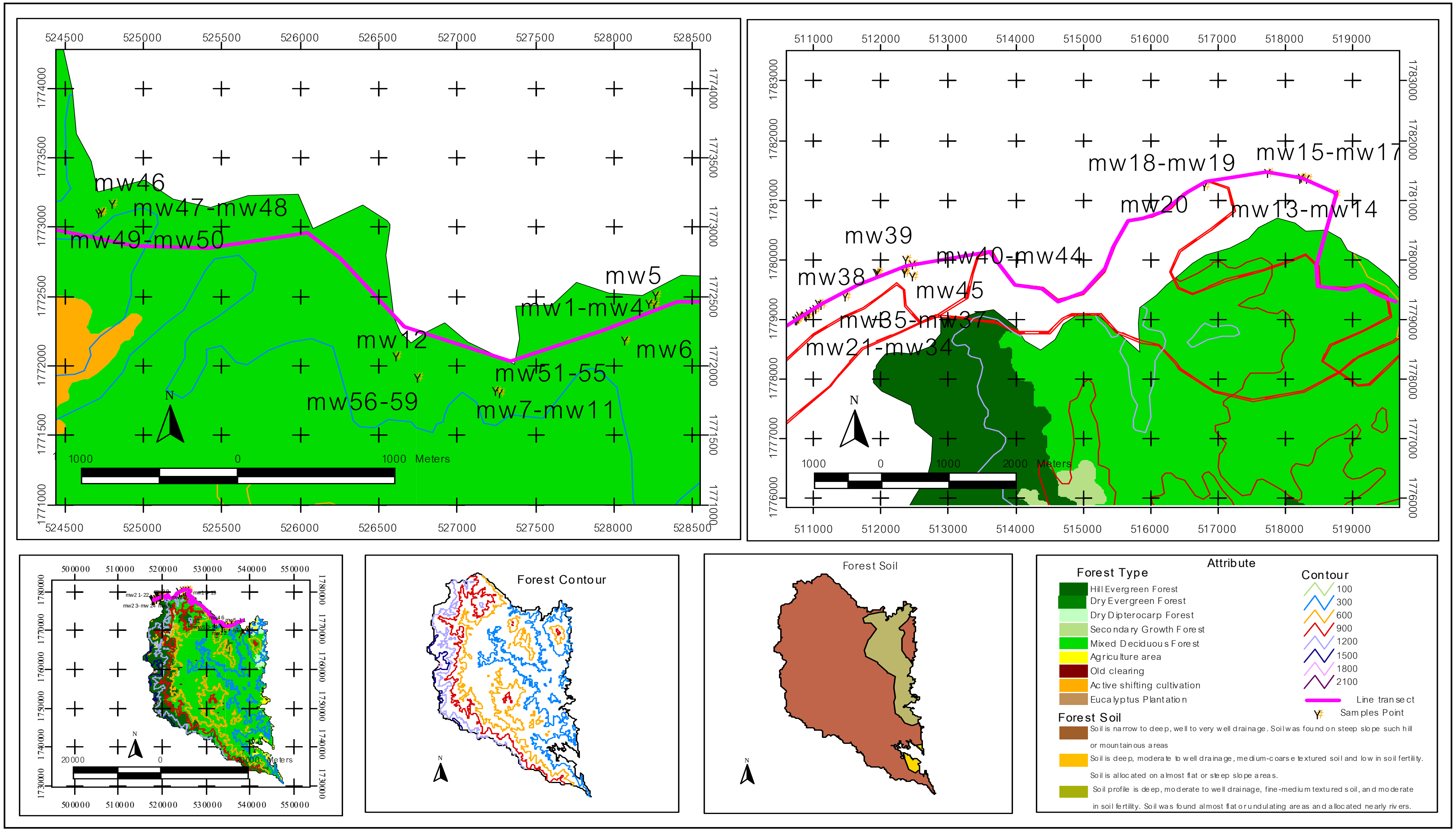


Figure 4.1 (C) GIS map of wild bananas survey in Mae Wong National Park indicated forest types, forest contour (elevation), forest soil types, samples distribution, line transect and information

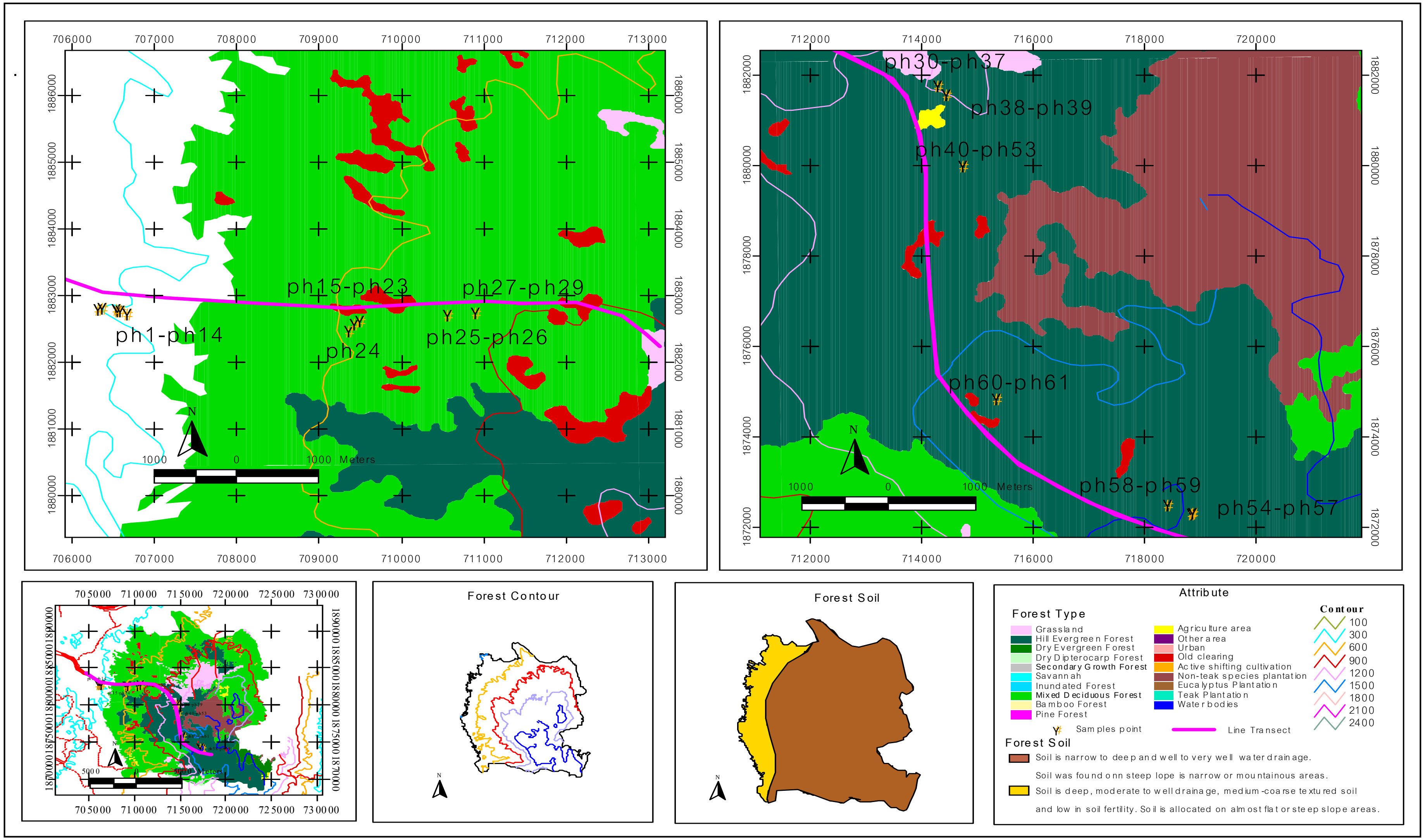


Figure 4.1 (D) GIS map of wild bananas survey in Phu Hin Rong Kra National Park indicated forest types, forest contour (elevation), forest soil types, samples distribution, line transect and information

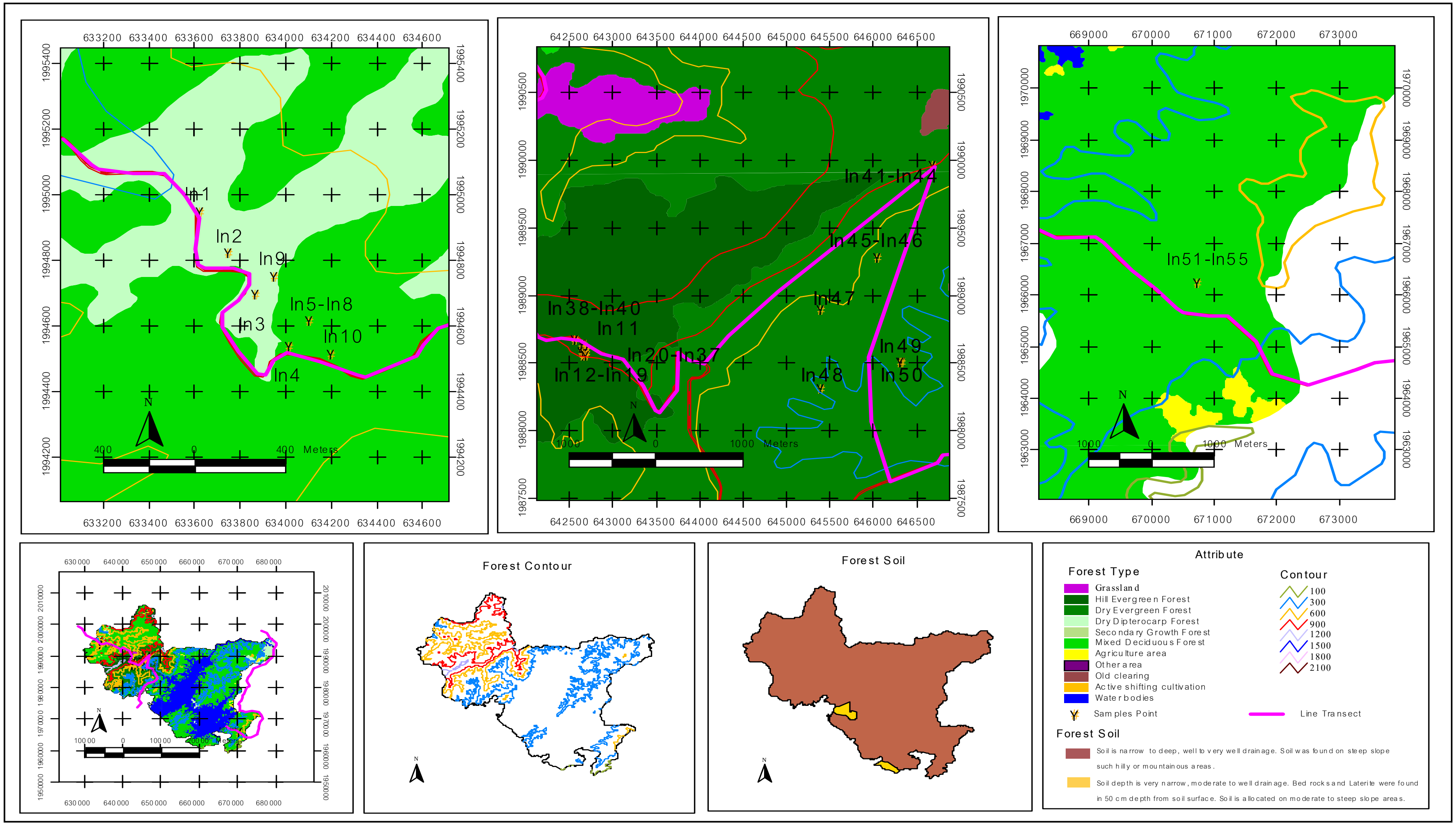


Figure 4.1 (E) GIS map of wild bananas survey in Lumnamnan National Park indicated forest types, forest contour (elevation), forest soil types, samples distribution, line transect and information

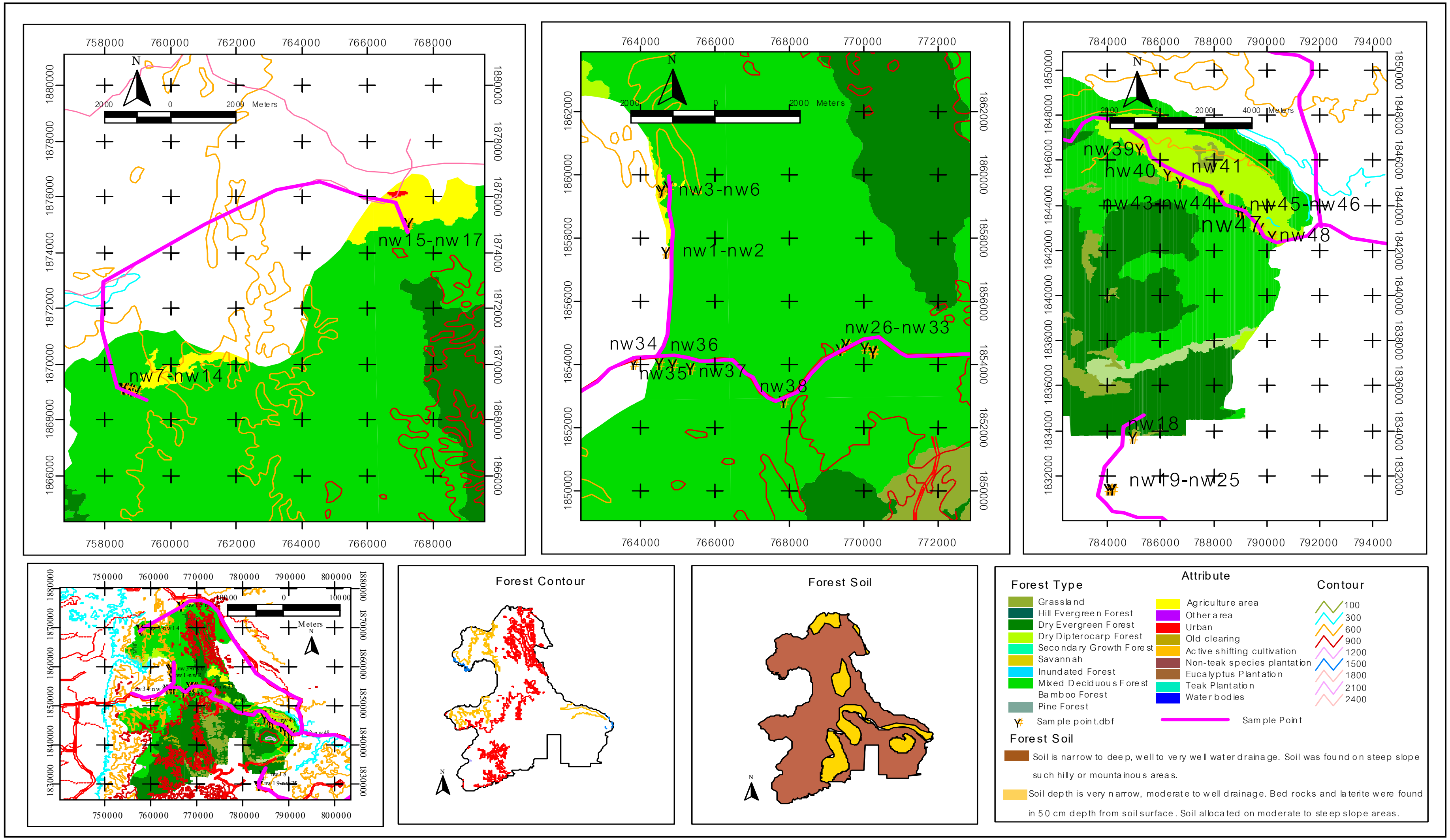


Figure 4.1 (F) GIS map of wild bananas survey in Namnaow National Park indicated forest types, forest contour (elevation), forest soil types, samples distribution, line transect and information

2. Discriminant Analysis

Canonical Discriminant analysis of all accessions was conducted. The aim was to search diversity within this population. The group means were calculated. Then, test of equality of group means were analyzed by Discriminant analysis. Canonical Discriminant Function was conducted. There were 2 functions and were selected due to their high Eigenvalue with high % of variance and higher cumulative % of variance higher canonical correlation. Classification results predicted group membership into two groups by Original and Cross-validated value. The result indicated that there were two major groups and a few intermediate individuals (Figure 4.2; Table 4.2 – 4.7) There was a difference within sample population. An interesting question is "what are these two groups"? The hypothesis was that there were two major groups of variations within this population, which were classified differently from classical taxonomy classification.

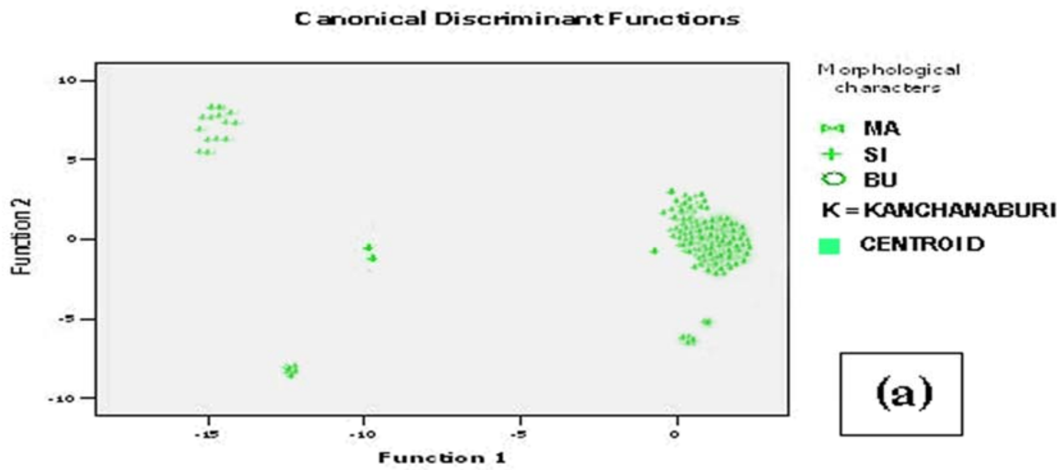


Figure 4.2 Scatter plot of all accessions by canonical discriminant functions

The mean values of 20 morphological characters of both groups were compared (Table 4.2 – 4.7) Both groups were significantly different due to the result of equality of group means test (Table 4.2 - 4.3)

Table 4.2 The mean values of 20 morphological characteristics of all accessions

Morphological characters	Mean	Std. Dev.	Group1		Group2	
			Mean	Std. Dev.	Mean	Std. Dev.
Pseudostem height	2.16	.768	2.43	.788	2.12	.777
Pseudostem appearance	1.93	.262	1.00	.000	1.99	.079
Blotch at the petiole base	2.50	.950	1.96	1.022	2.33	1.021
Blotch color	3.38	1.051	3.48	.511	3.20	1.180
Petiole canal leaf	2.73	.729	4.39	.583	2.56	.750
Wax on leaves	1.29	.640	4.00	.000	1.19	.397
Peduncle hairiness	1.63	.719	1.48	.511	1.57	.732
Bunch position	3.40	.819	3.43	.662	3.49	.824
Rachis position	1.25	.516	3.04	1.022	1.46	.907
Male bud shape	1.39	.655	2.13	.968	1.38	.607
Bract imbrication	1.89	.613	1.00	.000	2.00	.618
Color of the bract external face	6.30	.895	3.39	.499	6.24	.636
Color of the bract internal face	6.89	1.949	3.57	1.502	6.99	1.781
Color on the bract apex	1.08	.267	1.04	.209	1.12	.321
Color stripes on bract	1.07	.262	1.52	.511	1.08	.265
Wax on the bract	1.58	.665	1.00	.000	1.59	.666
Compound tepal basic color	2.39	.543	2.09	.288	2.33	.600
Lobe color of compound tepal	2.40	.816	2.04	.209	2.21	.450
Fruit apex	3.97	.233	3.30	.635	3.98	.177
Fusion of pedicel	2.20	.754	1.30	.635	2.19	.762

Table 4.3 Tests of Equality of Group Means

Tests of Equality of Group Means

	Wilks' Lambda	F	df1	df2	Sig.
Pseudostem height	.984	2.904	2	361	.056
Pseudostem appearance	.238	577.321	2	361	.000
Blotch at the petiole base	.967	6.117	2	361	.002
Blotch color	.991	1.576	2	361	.208
Petiole canal leaf	.702	76.573	2	361	.000
Wax on leaves	.225	621.807	2	361	.000
Peduncle hairiness	.999	.231	2	361	.794
Bunch position	.981	3.485	2	361	.032
Rachis position	.824	38.515	2	361	.000
Male bud shape	.908	18.262	2	361	.000
Bract imbrication	.834	35.993	2	361	.000
Color of the bract external face	.356	326.644	2	361	.000
Color of the bract internal face	.668	89.839	2	361	.000
Color on the bract apex	.989	2.046	2	361	.131
Color stripes on bract	.861	29.160	2	361	.000
Wax on the bract	.951	9.369	2	361	.000
Compound tepal basic color	.920	15.796	2	361	.000
Lobe color of compound tepal	.369	309.059	2	361	.000
Fruit apex	.654	95.406	2	361	.000
Fusion of pedicel	.916	16.593	2	361	.000

According to the Wilk's Lambda and F values (Table 4.3) there were significant differences between the two identified clusters for most characters: Pseudostem height, Pseudostem appearance, Blotch color, Petiole canal leaf, Wax on leaves, Peduncle hairiness , Bunch position, Rachis position, Male bud shape, Bract imbrication, Color of the bract external face, Color of the bract internal face, Color on the bract apex, Wax on the bract, Compound tepal basic color, Lobe color of compound tepal, Fruit apex, and Fusion of pedicel (Table 4.3) There was no significant difference between the groups for color stripes on the bract and for the presence of blotches at the petiole base. When correlation values of each pair of character was higher than 0.5, it indicated the strong relationships after Pooled Within - Groups Matrices and Covariance Matrix (Appendix B).

So, only both characters indicated non - significant correlation in separation of both groups. Eigenvalues of canonical Discriminant Functions were shown in Table 4.4. The function

1 and 2 were suitable sufficient to be used as canonical discriminant functions with (eigenvalues higher than 1 (13.4993.821 and 3.673) and together explained 100 % of cumulative variance (78.5 and 21.5% respectively) (Table 4.4)

If the centroids of sample population and outgroup accessions were not significantly different with the functions, the accessions were in the same groups. Moreover, if the canonical discriminant function coefficient was high, that character was an important parameter to explain the differences among sample populations (Table 4.5; 4.6) Wax on leaves was the most important parameter in the function 1. The character of Pseudostem appearance was the most important parameters in the function 2, respectively. Wax on leaves was 0.506 that indicated strong correlation between this variable and the canonical variable (Table 4.6) While for Lobe color of compound tepal was – 0.667 in function 2, respectively. The Canonical Discriminant Functions 1 and 2 were employed to explain the population separation into groups (Table 4.7 and Figure 4.5 – 4.8) There were two major groups and some scattered individuals. The details of all two canonical discriminant functions were shown in Table 4.7 Scatter plots of canonical discriminant functions showing all accessions and the outgroup were presented in Figure 4.8

Table 4.4 Eigenvalues of canonical discriminant functions and test of functions with Wilks' Lambda

Summary of Canonical Discriminant Functions

Eigenvalues

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	13.449[a]	78.5	78.5	.965
2	3.673[a]	21.5	100.0	.887

a. First 2 canonical discriminant functions were used in the analysis.

Wilks' Lambda

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1 through 2	.015	1480.646	40	.000
2	.214	541.926	19	.000

Table 4.5 Standardized Canonical Discriminant Function Coefficients

Standardized Canonical Discriminant Function Coefficients

	Function	
	1	2
Pseudostem height	.164	-.128
Pseudostem appearance	-.653	.539
Blotch at the petiole base	.025	-.099
Blotch color	.256	-.044
Petiole canal leaf	.340	.050
Wax on leaves	.845	.238
Peduncle hairiness	-.249	.169
Bunch position	-.021	.098
Rachis position	.335	-.026
Male bud shape	.068	-.109
Bract imbrication	.125	-.097
Color of the bract external face	-.317	-.205
Color of the bract internal face	-.110	.235
Color on the bract apex	-.117	.312
Color stripes on bract	.006	.068
Wax on the bract	.027	-.246
Compound tepal basic color	.027	-.103
Lobe color of compound tepal	-.370	-.837
Fruit apex	-.209	.115
Fusion of pedicel	-.136	.090

Table 4.6 Structure Matrix

Structure Matrix

	Function	
	1	2
Wax on leaves	.506*	-.013
Color of the bract external face	-.333*	-.293
Fruit apex	-.198*	.021
Petiole canal leaf	.175*	.056
Rachis position	.124*	.047
Color stripes on bract	.109*	.017
Fusion of pedicel	-.076*	.061
Wax on the bract	-.061*	.024
Lobe color of compound tepal	-.076	-.667*
Pseudostem appearance	-.419	.477*
Color of the bract internal face	-.107	.306*
Compound tepal basic color	-.039	-.135*
Bract imbrication	-.104	.120*
Male bud shape	.067	-.104*
Blotch at the petiole base	-.031	-.075*
Bunch position	.001	.072*
Color on the bract apex	-.012	.051*
Pseudostem height	.024	-.048*
Blotch color	.019	.033*
Peduncle hairiness	-.008	.010*

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions

Variables ordered by absolute size of correlation within function.

*. Largest absolute correlation between each variable and any discriminant function

Table 4.7 Canonical Discriminant Function Coefficients

Canonical Discriminant Function Coefficients

	Function	
	1	2
Pseudostem height	.211	-.166
Pseudostem appearance	-4.461	3.685
Blotch at the petiole base	.025	-.099
Blotch color	.219	-.038
Petiole canal leaf	.471	.069
Wax on leaves	2.274	.640
Peduncle hairiness	-.351	.238
Bunch position	-.026	.124
Rachis position	.377	-.030
Male bud shape	.102	-.164
Bract imbrication	.211	-.163
Color of the bract external face	-.513	-.332
Color of the bract internal face	-.062	.134
Color on the bract apex	-.382	1.023
Color stripes on bract	.023	.244
Wax on the bract	.042	-.386
Compound tepal basic color	.048	-.181
Lobe color of compound tepal	-.778	-1.759
Fruit apex	-.916	.506
Fusion of pedicel	-.184	.122
(Constant)	12.060	-4.860

Unstandardized coefficients

The Canonical Discriminant Function Coefficients

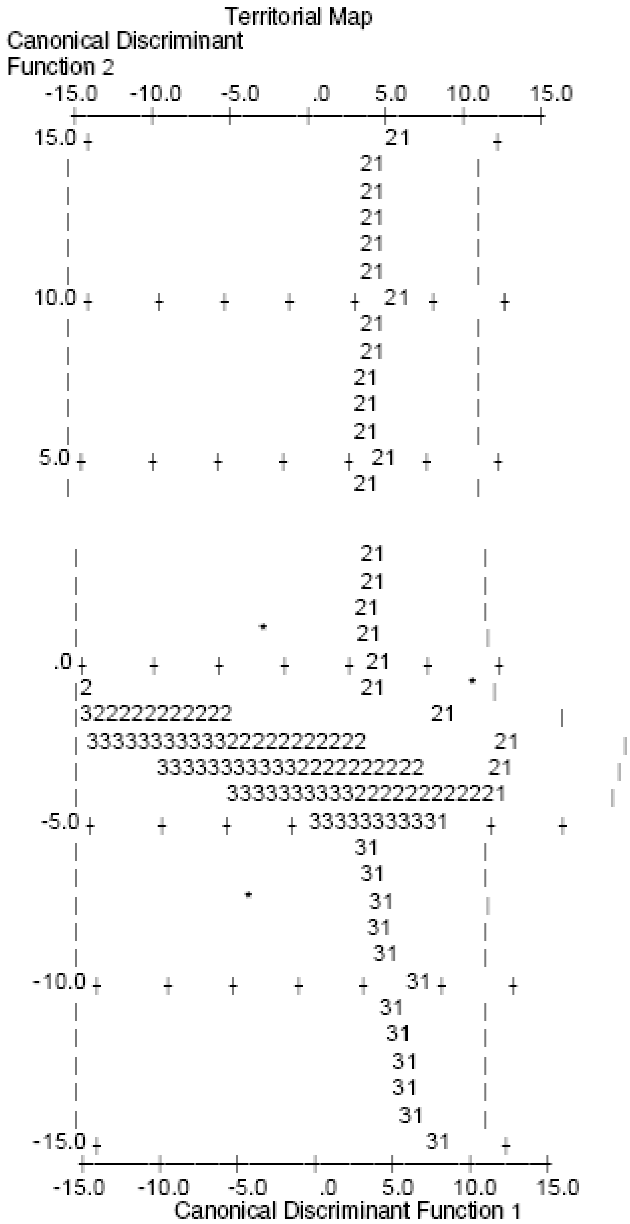
There were two Canonical Discriminant Function Coefficients in Table 4.7

(1) 12.060+(0.211) Pseudostem height +(-4.461) Pseudostem appearance +(0.025) Blotch at the petiole base +(0.219) Blotch color +(0.471) Petiole canal leaf +(2.274) Wax on leaves+(-0.351) Peduncle hairiness +(-0.026) Bunch position +(0.377) Rachis position +(0.102) Male bud shape +(0.211) Bract imbrication +(-0.513) Color of the bract external face +(-0.062) Color of the bract internal face +(-0.382) Color on the bract apex +(0.023) Color stripes on bract +(0.042) Wax on the bract +(0.048) Compound tepal basic color +(-0.778) Lobe color of compound tepal +(-0.916) Fruit apex +(-0.184)Fusion of pedicel

(2) -4.860 +(-0.166) Pseudostem height +(3.685) Pseudostem appearance +(-0.099) Blotch at the petiole base +(-0.038) Blotch color +(0.069) Petiole canal leaf +(0.640) Wax on leaves+(0.238) Peduncle hairiness +(0.124) Bunch position +(-0.030) Rachis position +(-0.164) Male bud shape +(-0.163) Bract imbrication +(-0.332) Color of the bract external face +(0.134) Color of the bract internal face +(1.023) Color on the bract apex +(0.244) Color stripes on bract +(-0.386) Wax on the bract +(-0.181) Compound tepal basic color +(-1.759) Lobe color of compound tepal +(0.506) Fruit apex +(0.122) Fusion of pedicel.

Two Canonical Discriminant Functions classified all specimens into two groups and a few intermediate individuals. After, all specimens were labeled with their subspecies from classical taxonomy (Figure 4.5 -4.7) The outgroup specimens of Trang as ssp. *malaccensis*, Kanchanaburi as ssp. *burmanica* and Chanthaburi as ssp. *siamea* were also classified into two groups. The first group were Trang specimens, while, Kanchanaburi and Chanthaburi specimens were in the second group (Figure 4.4) In addition, all specimens were also reclassified into two groups (Figure 4.5) They were *(i.)* ssp. *malaccensis*, *(ii.)* ssp. *siamea* and ssp. *burmanica*, and scattering of outliers. The crosscheck using outergroup and the character of three subspecies from classical taxonomy as Tested accessions were rerun through these canonical discriminant functions and also give the same results (Figure 4.6 and 4.7) Tested accessions of ssp. *siamea* and ssp. *burmanica* were clearly classified into the group of ssp. *siamea* and ssp. *burmanica*. In addition, tested accessions of ssp. *malaccensis* was also classified into the group of ssp. *malaccensis* (Figure 4.6-4.7) The outgroup specimens of Trang, Kanchanaburi and Chanthaburi specimens were also classified into these two groups. Trang were in the same group with ssp. *malaccensis*, while Kanchanaburi and Chanthaburi were in the same group with ssp. *siamea* and ssp. *burmanica,* respectively (Figure 4.5 and Table 4.8-4.9)

All samples were reconfirmed their separation into two groups and outliers (called “Others” in classical taxonomy) with territorial map using canonical discriminant functions (Figure 4.3) The number indicated their territorial and boundary.



Symbol Group Label: 1 = Group 1; 2 = Group 2 ; 3 = Ungrouped cases; * = a group centroid

Figure 4.3 Territorial Map of group separation of canonical discriminant functions

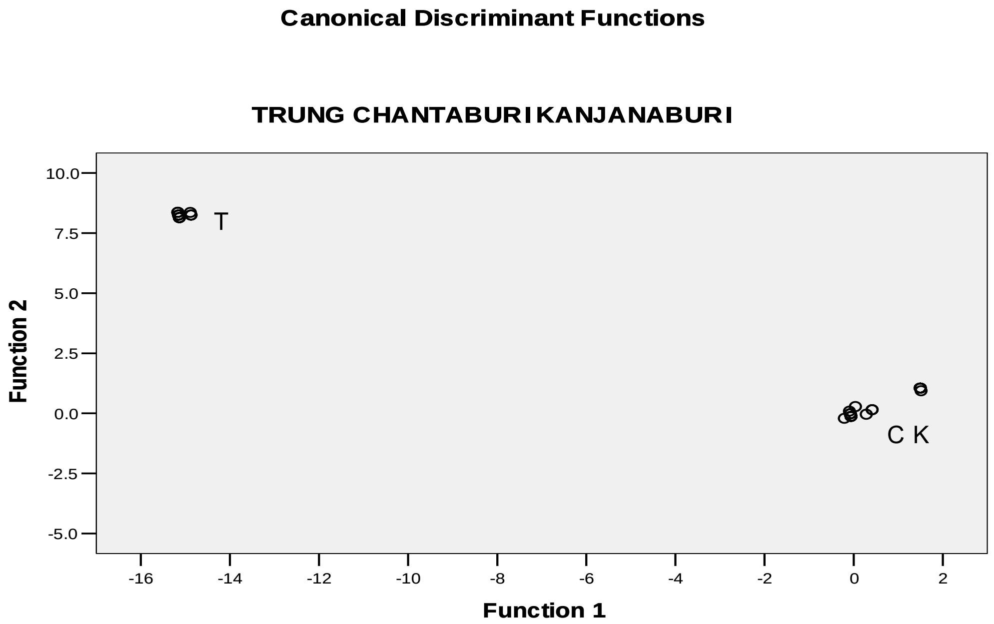
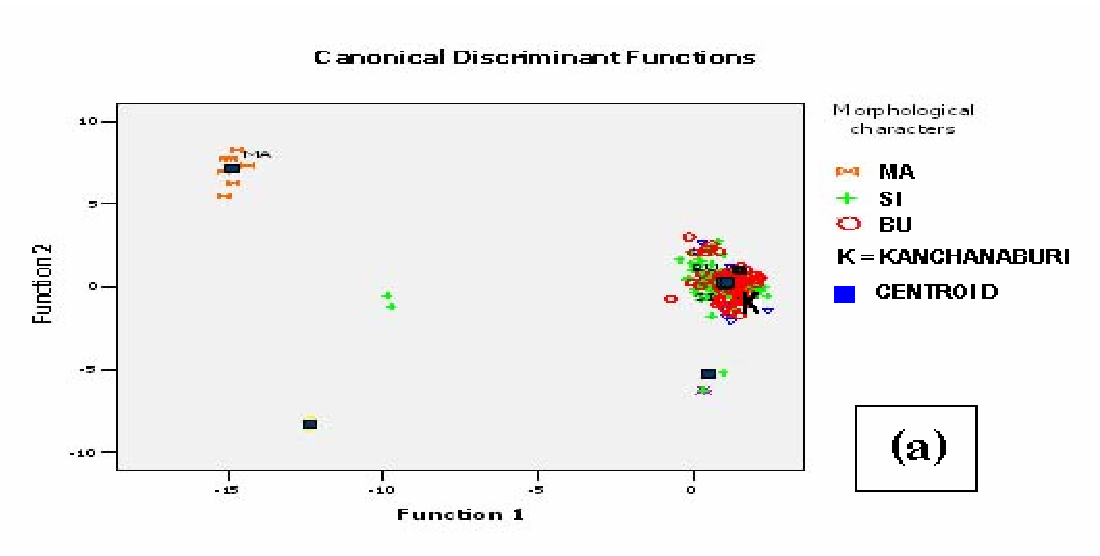
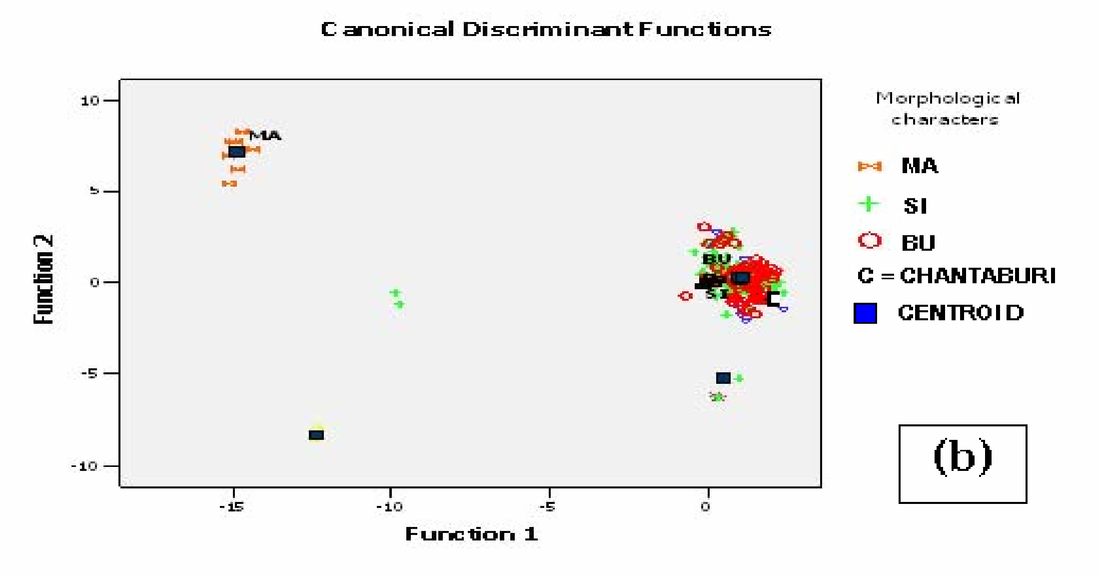


Figure 4.4 Scatter plot of Trang (T), Chantaburi (C) and Kanchanaburi (K) in canonical discriminant function

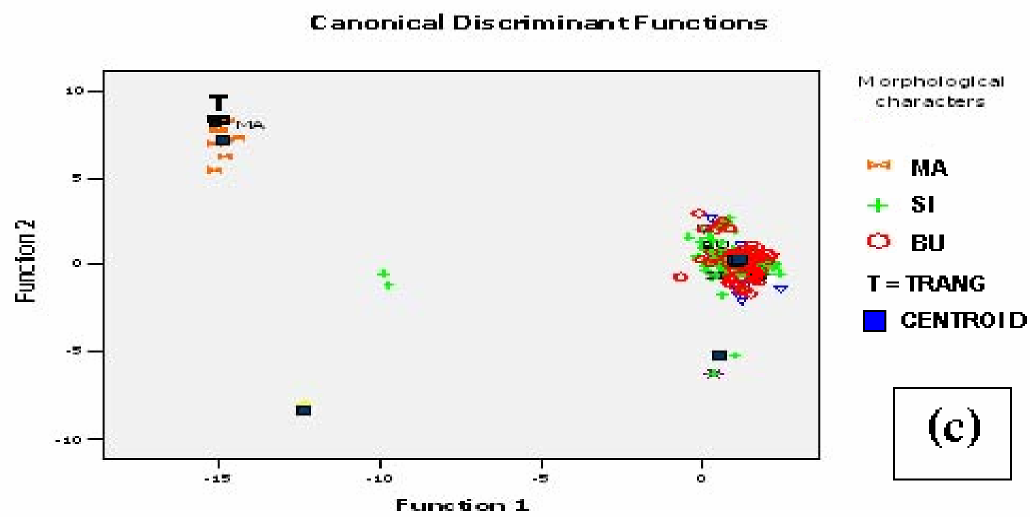


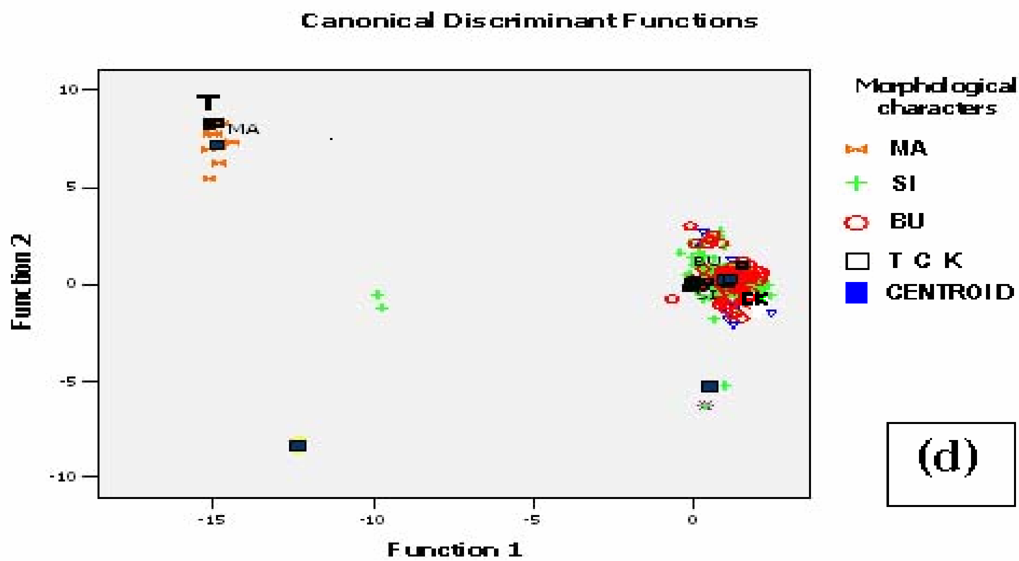


SI = ssp. *siamea*, MA = ssp. *malaccensis*, BU = ssp. *burmanica*, T = Trang, C = Chantaburi,

K = Kanchanaburi from classical taxonomy

Figure 4.5 Centroid and scatter plot of all accession in canonical discriminant function **(a)** Kanchanaburi; **(b)** Chantaburi





SI = ssp. *siamea*, MA = ssp. *malaccensis*, BU = ssp. *burmanica*, T = Trang, C = Chantaburi,

K = Kanchanaburi from classical taxonomy

Figure 4.5 Centroid and scatter plot of all accession in canonical discriminant function (Cont.)

(c) Trang; **(d)** Kanchanaburi and Chantaburi and Trang

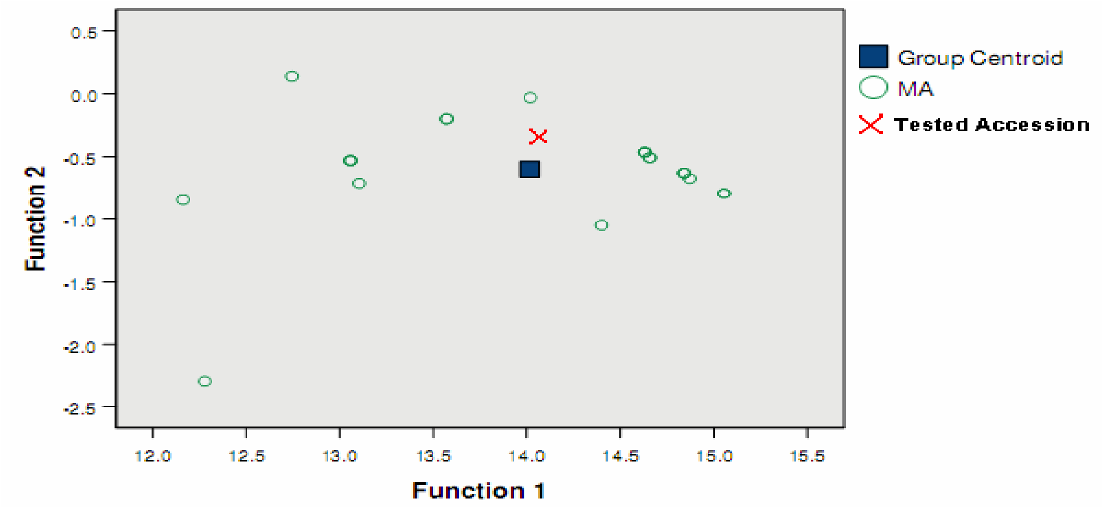


Figure 4.6 Centroid and scatter plot of tested accession of ssp. *malaccensis* within the population of ssp. *malaccensis* (MA) using canonical discriminant function

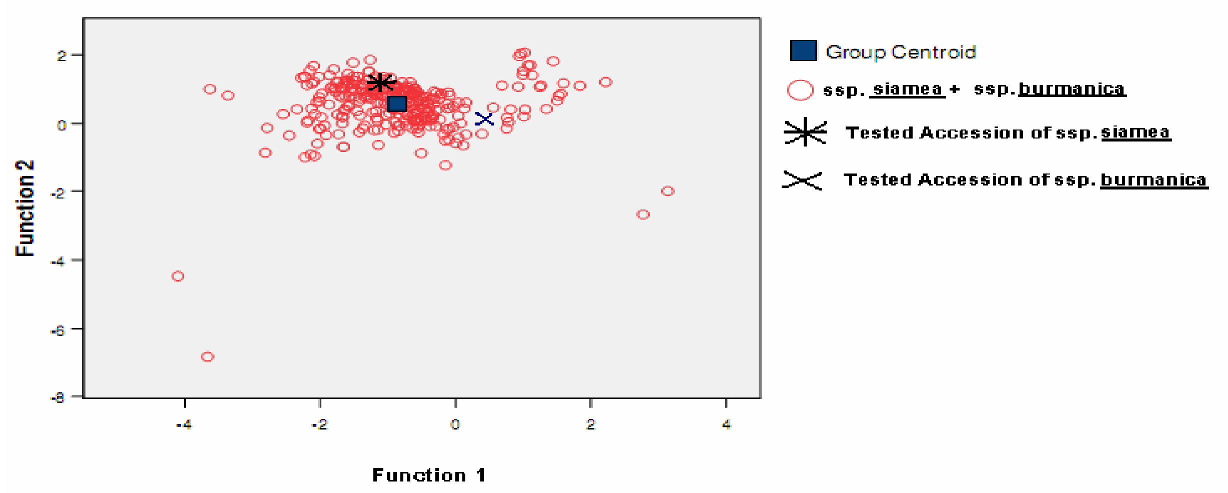


Figure 4.7 Centroid and scatter plot of tested accession of ssp. *siamea* and ssp. *burmanica* within the population of ssp. *siamea* and ssp. *burmanica* from classical taxonomy using canonical discriminant function

Table 4.8 Classification Functions Coefficients of two groups, MA = ssp. *malaccensis* and trang, SI = ssp. *siamea* and ssp. *burmanica* with Trang, Kanchanaburi and Chanthaburi

Classification Function Coefficients

	n_mopcode		
	MA	SI	Ungrouped cases
Pseudostem height	2.141	-1.199	-.162
Pseudostem appearance	34.699	105.384	81.997
Blotch at the petiole base	5.276	4.784	5.529
Blotch color	-.185	-3.492	-3.463
Petiole canal leaf	4.130	-2.797	-3.916
Wax on leaves	36.309	3.230	-4.580
Peduncle hairiness	1.122	6.625	5.188
Bunch position	6.733	7.267	6.325
Rachis position	13.339	7.691	7.459
Male bud shape	2.383	.667	1.828
Bract imbrication	4.900	1.573	2.591
Color of the bract external face	.995	8.240	11.473
Color of the bract internal face	4.340	5.426	4.454
Color on the bract apex	15.854	22.734	15.191
Color stripes on bract	35.321	35.272	33.329
Wax on the bract	2.403	1.330	4.299
Compound tepal basic color	12.384	11.462	12.820
Lobe color of compound tepal	3.798	13.317	28.055
Fruit apex	75.812	90.033	87.193
Fusion of pedicel	8.446	11.324	10.595
(Constant)	-338.599	-425.850	-430.659

Fisher's linear discriminant functions

In Table 4.8 and the following figures two Classification Functions Coefficients of the two classical taxonomy groups presented in following details:

Classification Function for Group 1: - 338.599 +(2.141) Pseudostem height +(34.699) Pseudostem appearance +(5.276) Blotch at the petiole base +(-0.185) Blotch color +(4.130) Petiole canal leaf +(36.309) Wax on leaves+(1.122) Peduncle hairiness +(6.733) Bunch position +(13.339) Rachis position +(2.383) Male bud shape +(4.900) Bract imbrication +(0.995) Color of the bract external face +(4.340) Color of the bract internal face +(15.854) Color on the bract apex +(35.321) Color stripes on bract +(2.403) Wax on the bract +(12.384) Compound tepal basic color +(3.798) Lobe color of compound tepal +(75.812) Fruit apex +(8.446)Fusion of pedicel

Classification Function for Group 2 : -425.850+(-1.199) Pseudostem height +(105.384) Pseudostem appearance +(4.784) Blotch at the petiole base +(-3.492) Blotch color +(-2.797) Petiole canal leaf +(3.230) Wax on leaves+(6.625) Peduncle hairiness +(7.267) Bunch position +(7.691) Rachis position +(0.667) Male bud shape +(1.573) Bract imbrication +(8.240) Color of the bract external face +(5.426) Color of the bract internal face +(22.734) Color on the bract apex +(35.272) Color stripes on bract +(1.330) Wax on the bract +(11.462) Compound tepal basic color +(13.317) Lobe color of compound tepal +(90.033) Fruit apex +(11.324)Fusion of pedicel**.**

Canonical discriminant function predicted the classification of ssp. *burmanica* with original value and cross-validated only 98.9 % and 98.9%. Ssp. *siamea*, ssp. *burmanica*, Chantaburi and Kanchanaburi were predicted correctly with original value and cross-validated only 99.4%. These confirmed that ssp. *siamea*, ssp. *burmanica*, Chantaburi and Kanchanaburi were numerically classified into the same group, which was not followed the classical taxonomy (Table 4.9 and Figure 4.8) However, ssp. *malaccensis* and Trang were predicted correctly 100 % with both original value and cross-validated. For outgroup of Trang, Chantaburi and Kanchanaburi were predicted correctly as ssp. *malaccensis*, ssp. *siamea* and ssp. *burmanica*, respectively. Outgroup accessions of Trang (ssp. *malaccensis* as Simmonds' description) were numerical classified into the same as ssp. *malaccensis* (samples from numerical taxonomy), after revision of the data, while Chantaburi (ssp. *siamea* as Simmonds' description) and Kanchanaburi (ssp. *burmanica* as Simmonds' description) were numerical classified into the same group of ssp. *siamea* and ssp. *burmanica* (samples from numerical taxonomy). The outlier as ungrouped cases should be the hybrid or mutants, which may required further study. The classification results of all groups by canonical discriminant function can be seen from the Table 4.9 below.

In conclusion, there was a difference within *Musa acuminata* sample population. There are two major groups of variations within this population. They are *(i.)* ssp. *malaccensis* and *(ii.)* the rest of ssp. *siamea* and ssp. *burmanica*, which are classified differently from classical taxonomy classification.

Table 4.9 Classification results of all groups by canonical discriminant functions

Classification Results[b,c]

		n_mopcode	Predicted Group Membership MA	SI	Ungrouped cases	Total
Original	Count	MA	23	0	0	23
		SI	0	316	2	318
		Ungrouped cases	0	2	21	23
	%	MA	100.0	.0	.0	100.0
		SI	.0	99.4	.6	100.0
		Ungrouped cases	.0	8.7	91.3	100.0
Cross-validated[a]	Count	MA	23	0	0	23
		SI	0	316	2	318
		Ungrouped cases	0	2	21	23
	%	MA	100.0	.0	.0	100.0
		SI	.0	99.4	.6	100.0
		Ungrouped cases	.0	8.7	91.3	100.0

a. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

b. 98.9% of original grouped cases correctly classified.

c. 98.9% of cross-validated grouped cases correctly classified.

The list of the accessions in each group which were classified by canonical discriminant functions

ssp. *malaccensis* (Ridl.) Simmonds	**ssp. *siamea* and *burmanica***	**Others**
Up25-Up35	**Up1-Up24, Up37, Up38, Tl1-Tl55, Mw1, Mw3-Mw9, Mw11- Mw48, Mw50, Ph1-Ph61, Ln1-Ln55, Nw1-Nw40, Nw42-Nw48**	**Up36, Up39-Up48, Mw10, Mw49, Mw51-Mw59, Nw41**
11 (3.4%)	**292 (89.5%)**	**23 (7.1%)**

3. Hierarchical Cluster Analysis

Data of twenty morphological characteristics of each sample was analyzed as variable of each case with hierarchical cluster analysis using SPSS for Windows version 10.0 and version 13.0. The results of the cluster analysis are shown in a dendrogram (Figure 4.1.8). The 364 samples were clearly separated into two groups at the 23 of average numerical taxonomic distances respectively (Appendix B). These two groups separated by hierarchical cluster analysis at 23 units of distance were similar to the results of numerical taxonomy using discriminant ananalysis. The statistical classification by canonical discriminant analysis confirmed two major groups separation. They were similar to the results from hierarchical cluster analysis at 23 of average numerical taxonomic distances. The group separation results were *(i.)* ssp. *siamea* and ssp. *burmanica* and *(ii.)* ssp. *malaccensis* (Figure 4.8, Table 4.10 and Appendix B). The average numerical taxonomic distances at 23 of hierarchical cluster analysis reconfirmed the results of statistical classification by canonical discriminant analysis. This hierarchical cluster analysis is suitable for the unknown number of groups in the final separation and nonbiased on factors in the separation criteria. The results indicate all the relationships and cluster levels of all accessions. In contrast, the critical point to apply this technique is the most suitable distance units for group separation. This required the support information and criteria of the taxonomist. Hierarchical cluster analysis was used as crosscheck and to ensure to classified result from discriminant analysis in this study.

In addition, Pearson correlation proved that the classification results by discriminant analysis and hierarchical cluster analysis were similar (Table 4.10). The results of numerical taxonomy were significantly different from the result of classical taxonomy using Simmonds' determination key.

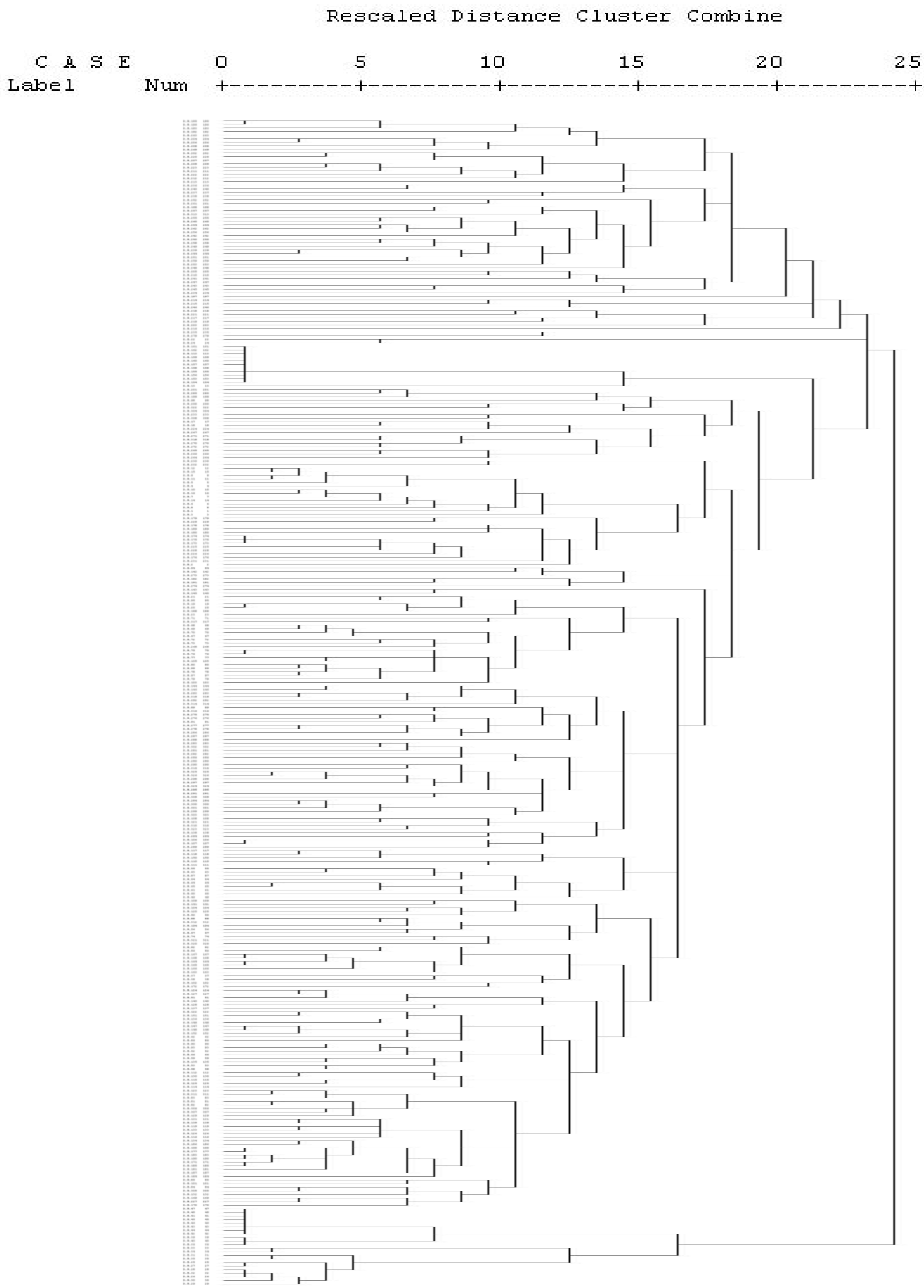


Figure 4.8 Dendrogram show 326 samples of *Musa acuminata* Colla classified by hierarchical cluster analysis

Table 4.10 Pearson Correlation of Hierarchical analysis and Discriminant analysis of 326 accession and 38 accessions of Trang, Kanchanaburi and Chantaburi

		Hierarchical Cluster analysis	Discriminanat analysis
Hierarchical analysis	Pearson Correlation	1	.034**
	Sig. (2-tailed)	-	.515
	N	364	364
Discriminanat analysis	Pearson Correlation	.034**	1
	Sig. (2-tailed)	.515	-
	N	364	364

Classification of two subspecies using numerical taxonomy clustering from three subspecies and hybrid (from classical taxonomy) of wild bananas in lower northern Thailand

ssp. *malaccensis* (Ridl.) Simmonds	**ssp. *siamea* Simmonds**	**Others**
Up25-Up35	**ssp. *siamea* Simmonds: Up1-Up4, Up6-Up9, Up12, Up14, Up19, Up20, Up22-Up24, Up37, Up38, Tl1-Tl3, Tl12, Tl14-Tl18, Tl20-Tl26, Tl28-Tl38, Tl47, Tl53, Tl55, Mw1, Mw3-Mw9, Mw11, Mw13-Mw15, Mw17-Mw30, Mw34, Mw36, Mw37, Mw39, Mw43-Mw46, Mw48, Mw50, Ph1, Ph4, Ph6-Ph17, Ph19-Ph23, Ph26,Ph28, Ph29, Ph37, Ph38, Ph41, Ph49, Ph51-Ph54, Ph61, Ln1, Ln2, Ln4-Ln6, Ln9-Ln20, Ln24-Ln26, Ln28, Ln29, Ln31-Ln42, Ln45, Ln47-Ln55, Nw1, Nw4, Nw5, Nw8, Nw9, Nw12-Nw14, Nw18-Nw20, Nw23, Nw25-Nw28, Nw33-Nw35, Nw37, Nw39, Nw40, Nw42-Nw48** **ssp. *burmanica* Simmonds: Up11, Up13, Up15, Up17, Up18, Up21, Tl4-Tl11, Tl13, Tl19, Tl27, Tl39-Tl46, Tl48-Tl52, Tl54, Mw31, Mw32, Mw40, Mw42, Mw47, Ph3, Ph18, Ph24, Ph25, Ph27, Ph32, Ph35, Ph36, Ph39, Ph40, Ph42, Ph44-Ph46, Ph55-Ph60, Ln3, Ln7, Ln8, Ln43, Ln44, Nw2, Nw3, Nw6, Nw10, Nw11, Nw15-Nw17, Nw21, Nw29-Nw32, Nw36, Nw38** **Hybrid (*siamea x burmanica)* Hybrid: Up5, Up10, Up16, Mw2, Mw12, Mw16, Mw33, Mw35, Mw38, Mw41, Ph2, Ph5, Ph30, Ph31, Ph33, Ph34, Ph43, Ph47, Ph48, Ph50, Ln21- Ln23, Ln27, Ln30, Ln46, Nw7, Nw22, Nw24**	**Others 1: Mw10, Mw49, Mw51-Mw59, Nw41** **Others 2: Up36, Up39-Up48,**
11 (3.4%)	**292 (89.5%)**	**23 (7.1%)**

4. Classical Taxonomy

Classical taxonomy classified all accessions into 3 subspecies and hybrid using classical classification of Simmonds and Shepherd, (1955); Simmonds, (1956); Simmonds and Weatherup (1988) (Table 4.11 – 4.15 and Figure 4.9 - 4.14). These outgroup specimens of Chantaburi and Kanchanaburi and Trang were classified as ssp. *siamea* Simmonds, ssp. *burmanica* Simmonds and ssp. *malaccensis* (Ridl.) Simmonds, respectively.

In contrast, numerical taxonomy detected there is a difference within *Musa acuminata* sample population. There are two major groups of variations within this population. They are *(i.)* ssp. *malaccensis* and *(ii.)* the rest of ssp. *siamea* and ssp. *burmanica*, which are classified differently from classical taxonomy classification. Some following identical characters in classical taxonomy are not relevant in numerical taxonomy. The characters of waxless on sheaths, male bud shape and their color were use to separate ssp. *siamea* from ssp. *burmanica* in classical taxonomy (Table 3.1). Identification characters of ssp. *burmanica* were Sheaths: Waxless except in young suckers and Pseudostems: lightly pigmented; (3 - 5 m high) (male bud shape: advance blooming acute), male bracts crimson red on the internal face, imbricate. Identification characters of ssp. *siamea* were Bract: purplish red on the bract external face, with yellowish tips, often slightly persistent, usually imbricate in the young bud (petiole margin yellowish green; erect) (Simmonds, 1956; Cheesman, 1947a, 1947b, 1948a, 1948b, 1949a, 1949b). But all these characters were less relevant in numerical taxonomy due to their coded as *siamea* and *siamea* x *burmanica* due to the characters variations of accessions in Thailand larger than in identification key (Simmonds, 1956).

Table 4.11 Identification key of wild banana and *M. acuminata* Colla samples of the lower northern Thailand.

1. Pseudostem shiny or no visible sign of wax, petiole canal: erect	**2**
2. Bract external face color: pink purple	**3**
3. Male bud shape: intermediate, bract internal face color: yellow	**Other 1**
3. Male bud shape: like a top (ovate), bract internal face color: orange - red	**Other 2**
2. Bract external face color: purple – deep purple	**4**
4. Male bud shape: like a top or lanceolate, varies in size	**5**
5. Bract external face color: purple, blotch color on petiole base: black - purple	**ssp. *siamea***
5. Bract external face: waxless, deep purple, blotch color on petiole base: brown purple	**ssp. *burmanica***
4. Male bud shape: advanced blooming like a top, more or less acute, petiole canal: erect	**Hybrid** (*siamea x burmanica*)
1. Pseudostem very wax, petiole canal: incurved	**ssp. *malaccensis***

Table 4.12 Classification of three subspecies and hybrid of wild bananas in lower northern Thailand and its members using classical taxonomy

ssp. *malaccensis* (Ridl.) Simmonds	**ssp. *siamea* Simmonds**	***ssp.* burmanica *Simmonds***	*ssp.* siamea x *ssp.* burmanica *Hybrid*	**Others**
Up25-Up35	**Up1-Up4, Up6-Up9, Up12, Up14, Up19, Up20, Up22-Up24, Up37, Up38, Tl1-Tl3, Tl12, Tl14-Tl18, Tl20-Tl26, Tl28-Tl38, Tl47, Tl53, Tl55, Mw1, Mw3-Mw9, Mw11, Mw13-Mw15, Mw17-Mw30, Mw34, Mw36, Mw37, Mw39, Mw43-Mw46, Mw48, Mw50, Ph1, Ph4, Ph6-Ph17, Ph19-Ph23, Ph26,Ph28, Ph29, Ph37, Ph38, Ph41, Ph49, Ph51-Ph54, Ph61, Ln1, Ln2, Ln4-Ln6, Ln9-Ln20, Ln24-Ln26, Ln28, Ln29, Ln31-Ln42, Ln45, Ln47-Ln55, Nw1, Nw4, Nw5, Nw8, Nw9, Nw12-Nw14, Nw18-Nw20, Nw23, Nw25-Nw28, Nw33-Nw35, Nw37, Nw39, Nw40, Nw42-Nw48**	**Up11, Up13, Up15, Up17, Up18, Up21, Tl4-Tl11, Tl13, Tl19, Tl27, Tl39-Tl46, Tl48-Tl52, Tl54, Mw31, Mw32, Mw40, Mw42, Mw47, Ph3, Ph18, Ph24, Ph25, Ph27, Ph32, Ph35, Ph36, Ph39, Ph40, Ph42, Ph44-Ph46, Ph55-Ph60, Ln3, Ln7, Ln8, Ln43, Ln44, Nw2, Nw3, Nw6, Nw10, Nw11, Nw15-Nw17, Nw21, Nw29-Nw32, Nw36, Nw38**	**Up5, Up10, Up16, Mw2, Mw12, Mw16, Mw33, Mw35, Mw38, Mw41, Ph2, Ph5, Ph30, Ph31, Ph33, Ph34, Ph43, Ph47, Ph48, Ph50, Ln21-Ln23, Ln27, Ln30, Ln46, Nw7, Nw22, Nw24**	**(Others 1) Mw10, Mw49, Mw51-Mw59, Nw41** **(Others 2) Up36, Up39-Up48,**
11 (3.4%)	**187 (57.4%)**	**76 (23.3%)**	**29 (8.9%)**	**23 (7.1%)**

The Description of Six Groups

(1.) *M. acuminata* Colla ssp. *malaccensis* (Ridl.) Simmonds, E.E Cheesman in Kew Bull. 26. 1948; N. W. Simmonds in Kew Bull. 466. 1956.

***M. acuminata* Colla ssp. *malaccensis* (Ridl.) Simmonds;** Pseudostem 3.29 – 3.95 m high, 15 - 17 cm in diameter at base olive, green; leaf sheath and petioles glaucous, olive green. Leaf blades oblong, 2.0 - 3.0 m long, 34 - 57 cm wide, truncate at apex, unequal basal lamina, dark green, glaucous, midribs light green and red beneath; petiole 90 - 110 cm long, margin almost curve inward. Inflorescence hanging at 45°, peduncle and rachis slightly hair, peduncle 16 - 50 cm long, 2.5 - 5.0 cm wide; rachis at an angle. Male bud in advanced blooming like a top, more or less acute, the bract non – imbricate and convolute at the tip, color of the bract external face is light red, glabrous; color of the bract internal face is orange red, tined with yellow at tip; male bud ratio about 0.28. Male flower two rows per bract; compound tepal 3.0 - 3.7 cm long, 1.0 - 1.6 cm wide, cream; lobe of compound tepal 0.39 - 1.0 cm long, 0.3 - 0.65 cm wide, yellow; free tepal 1.7 - 2.25 cm long, 0.8 - 1.6 cm wide, tine with yellow; ovary 0.6 - 1.8 cm long, 0.15 - 0.35 cm wide, cream. Fruit bunch very compact, asymmetrical, curve toward stalk, 13 - 26 per hand, an average 20 per hand, 5 - 13.8cm long, 1.05 - 2.20in diameter, pedicel 0.6 - 2.0cm long, 0.2 - 0.8cm wide, partially fused; fruit apex bottle - neck shape; light green at mature, yellow at ripe. Seeds black, angular and wrinkled.

Thailand – NORTHERN: Tak (Umphang)

Distribution – Thailand (Lower northern), uplands

Ecology – Perennial herb in hill evergreen forest at elevation 1037 - 1088 m.

Vernacular. – Kluai Kae (กล้วยเคร่), Kluai Paa (กล้วยป่า) (Uttaradit); Kluai Thuean (กล้วยเถื่อน), Kluai Thuean Namman (กล้วยเถื่อนน้ำมัน) (Peninsular); Pi - Sang Uu - Tan (ปิซังอูตัง) (Malay-Pat-tani).

Specimen examined: R. E. Holltum 244347 (BKF); Up25 - Up35 (Figure 4.1.9).

(2.) *M. acuminata* Colla ssp. *siamea* Simmonds, E. E. Cheesman in Kew Bull. 11. 1948; N. W. Simmonds in Kew Bull. 466. 1956.

***M. acuminata* Colla ssp. *siamea* Simmonds,** pseudostem 1.0 – 6.0 m high, 5 - 19 cm in diameter at base, light green; leaf sheath and petioles glabrous, green. Leaf blades oblong, 1.0 - 4.0 m long, 27 - 86 cm wide, truncate at apex, unequal basal lamina, dark green, glabrous, midribs light green; petiole 26 - 103 cm long, margin almost erect. Inflorescence horizontal, peduncle and rachis hairless, peduncle 10 - 60 cm long, 1.0 - 6.0 cm wide; rachis falling vertically. Male bud in like a topclanceolate or lanceolate, the bract imbricate, colour of the bract external face is purple, glabrous; colour of the bract internal face is red - purple, tined with yellow at tip; male bud ratio about 0.28. Male bud shapes were found in three populations; Annam form 71.1%, Tavoy form 25.9% and Selangor form 3% of the specimens (Cheesman, 1948). Each shapes characters shown in Table 2.1.4. Male flower two rows per bract; compound tepal 2.2 - 4.3 cm long, 0.95 - 1.9 cm wide, cream; lobe of compound tepal 0.2 - 1.5 cm long, 0.1 - 2.0 cm wide, yellow or orange; free tepal 1.1 - 2.75 cm long, 0.75 - 1.85 cm wide, tine with yellow; ovary 0.17 - 1.7 cm long, 0.1 - 2.5 cm wide, cream or yellow. Fruit bunch very compact, asymmetrical, curve toward stalk, 8 - 27 per hand, an average 13 per hand, 5 - 17 cm long, 1.0 - 2.0 in diameter, pedicel 0.3 - 3.0 cm long, 0.35 - 2.0 cm wide, total fused; fruit apex 0.6 - 1.9 cm long, 0.3 - 1.0 cm wide, bottle - neck shape; light green at mature, yellow at ripe. Seeds black, 0.5 - 0.8 high, 0.15 - 0.5 diameter, angular and wrinkled.

Thailand – NORTHERN: Tak (Umphang), Khamphangphet (Mae Wong), Phitsanulok (Phu Hin Rong Kla), Uttaradit (Lumnamnan), Phetchabun (Namnaow), Phitsanulok (Thung Salaeng Luang). Former records: Chiang Mai (Doi Pepo, Doi Chiengdao), Uttaradit (Pangtonpheung), Nan (Banphasing); SOUTHERN: Pattani (Betong).

Distribution – Thailand (Lower northern), uplands; Former record: and perhaps eastern Myanmar - in the west, to Vietnam in the east, to northern Malaysia in the south, and Assam.

Ecology – Perennial herb in hill evergreen forest, dry evergreen forest, mixed deciduous forest, dry dipterocarp forest, moist evergreen forest, grassland, agriculture area within preserved area at elevation 216 - 1611 m.

Vernacular – Kluai Kae (กล้วยเคร่); Kluai Hmon (กล้วยหม่น) (Chiang Mai); Kluai Ling (กล้วยลิง), Kluai Paa (กล้วยป่า) (Uttaradit); Kluai Thuean (กล้วยเถื่อน), Kluai Thuean Namman (กล้วยเถื่อนน้ำมัน) (Peninsular); Pi - Sang Uu - Tan (ปิซังอูตัง) (Malay - Pat - Tani).

Specimen examined: J. F. Maxwell 244333, 244340, A. F. G. Kerr 244335, 244339 (BKF); Up1 - Up4, Up6 - Up9, Up12, Up14, Up19, Up20, Up22 - Up24, Up37, Up38, Tl1 - Tl3, Tl12, Tl14 - Tl18, Tl20 - Tl26, Tl28 - Tl38, Tl47, Tl53, Tl55, Mw1, Mw3 - Mw9, Mw11, Mw13 - Mw15, Mw17 - Mw30, Mw34, Mw36, Mw37, Mw39, Mw43 - Mw46, Mw48, Mw50, Ph1, Ph4, Ph6 - Ph17, Ph19 - Ph23, Ph26, Ph28, Ph29, Ph37, Ph38, Ph41, Ph49, Ph51 - Ph54, Ph61, Ln1, Ln2, Ln4 - Ln6, Ln9 - Ln20, Ln24 - Ln26, Ln28, Ln29, Ln31 - Ln42, Ln45, Ln47 - Ln55, Nw1, Nw4, Nw5, Nw8, Nw9, Nw12 - Nw14, Nw18 - Nw20, Nw23, Nw25 - Nw28, Nw33 - Nw35, Nw37, Nw39, Nw40, Nw42 - Nw48 (Figure 4.1.10).

(3.) *M. acuminata* Colla ssp. *burmanica* Simmonds, E. E. Cheesman in Kew Bull. 22. 1948; N. W. Simmonds in Kew Bull. 468. 1956.

***M. acuminata* Colla ssp. *burmanica* Simmonds;** pseudostem 0.8 – 5.0 m high, 5 - 14 cm in diameter at base, medium green; leaf sheath and petioles glabrous, green. Leaf blades oblong, 1.0 - 2.7 m long, 40 - 82 cm wide, truncate at apex, unequal basal lamina, green or dark green, midrib glabrous, light green; petiole 28 - 103 cm long, margin almost erect. Inflorescence horizontal, peduncle and rachis hairless, peduncle 8 - 70 cm long, 1.5 - 5.0 cm wide; rachis pendulous. Male bud like a top (lanceolate), the bract imbricate, colour of the bract external face is purple, glabrous; color of the bract internal face is red - purple, tined with yellow at tip; male bud ratio about 0.28. Male flower two rows per bract; compound tepal 2.2 - 4.3 cm long, 0.8 - 1.7 cm wide, cream or yellow; lobe of compound tepal 0.2 - 1.5 cm long, 0.1 - 0.6 cm wide, yellow or orange; free tepal 1.15 - 2.90 cm long, 0.6 - 1.8 cm wide, tine with yellow; ovary 0.45 - 1.1 cm long, 0.1 - 0.35 cm wide, cream or yellow. Fruit bunch very compact, asymmetrical, curve toward stalk, 8 - 21 per hand, an average 14 per hand, 5 - 12.0 cm long, 0.5 - 3.0 in diameter, pedicel 0.3 - 2.0 cm long, 0.4 - 1.3 cm wide, total fused; fruit apex 0.5 - 1.3 cm long, 0.4 - 0.8 cm wide, bottle - neck shape; light green at mature, yellow at ripe. Seeds black, 0.5 - 0.75 high, 0.2 - 0.4 diameter, angular and wrinkled.

Thailand – NORTHERN: Tak (Umphang), Khamphangphet (Mae Wong), Phitsanulok (Phu Hin Rong Kla), Uttaradit (Lumnamnan), Phetchabun (Namnaow), Phitsanulok (Thung Salaeng Luang): Former records: SOUTHERN: Peninsular (Kaw Tao), (Mergui archipelag).

Distribution – Thailand (Lower northern), uplands; Former record: Myanmar and extreme S. W. Thailand in east, over east India to Sri Lanka in the south.

Ecology – Perennial herb in hill evergreen forest, dry evergreen forest, mixed deciduous forest, dry dipterocarp forest, moist evergreen forest, grassland, agriculture area within preserved area at elevation 500 - 1200 m.

Vernacular – Kluai Kae (กล้วยเคร่); Kluai Thuean (กล้วยเถื่อน); Kluai Thuean Namman (กล้วยเถื่อนน้ำมัน) (Peninsular).

Specimen examined: A.F.G Kerr 244335 (BKF); Up16, Up13, Up15, Up17, Up18, Up21, Tl4, Tl11, Tl13, Tl19, Tl27, Tl39 - Tl46, Tl48 - Tl52, Tl54, Mw31, Mw32, Mw40, Mw42, Mw47, Ph3, Ph18, Ph24, Ph25, Ph27, Ph32, Ph35, Ph36, Ph39, Ph40, Ph42, Ph44 - Ph46, Ph55 - Ph60, Ln3, Ln7, Ln8, Ln43, Ln44, Nw2, Nw3, Nw6, Nw10, Nw11, Nw15 - Nw17, Nw21, Nw29 - Nw32, Nw36, Nw38 (Figure 4.1.11).

(4.) *M. acuminata* Colla sp., E. E. Cheesman in Kew Bull. 26. 1948; N. W. Simmonds in Kew Bull. 466. 1956.

Hybrid (*siamea* + *burmanica*); pseudostem is 1.5 - 4.8 m high, 5 - 15 cm in diameter at base, light green; leaf sheath and petioles glabrous, green. Leaf blades oblong, 1.0 - 3.2 m long, 35 - 75 cm wide, truncate at apex, unequal basal lamina, green, glabrous, midribs green; petiole 35 - 80 cm long, margin almost erect. Inflorescence horizontal, peduncle and rachis hairless, peduncle 14 - 60 cm long, 1.7 - 5.0 cm wide; rachis falling vertically. Male bud in advanced blooming like a top, more or less acute, the bract imbricate at the apex, color of the bract external face is purple, glabrous; color of the bract internal face is red-purple, tined with yellow at tip; male bud ratio about 0.28. Male flower two rows per bract; compound tepal 2.3 - 4 cm long, 0.9 - 1.8 cm wide, cream; lobe of compound tepal 0.3 - 0.9 cm long, 0.15 - 0.5 cm wide, yellow or orange; free tepal 1.15 - 2.40 cm long, 0.75 - 1.5 cm wide, tine with yellow; ovary 0.4 - 1.0 cm long, 0.1 - 0.3 cm wide, cream. Fruit bunch very compact, asymmetrical, curve toward stalk, 6 - 20 per hand, an average 15 per hand, 5 - 10.8 cm long, 1.6 - 2.8 in diameter, pedicel 0.5 - 1.2 cm long, 0.5 - 1.0 cm wide, total fused; fruit apex 0.6 - 0.9 cm long, 0.5 - 0.8 cm wide, bottle - neck shape; light green at mature, yellow at ripe. Seeds black, 0.6 - 0.7 high, 0.3 - 0.5 diameter, angular, wrinkled.

Thailand – NORTHERN: Tak (Umphang), Khamphangphet (Mae Wong), Phitsanulok (Pu Hin Rong Kla), Uttaradit (Lumnamnan), Phetchabun (Namnaow).

Distribution – Thailand (Lower northern), uplands.

Ecology – Perennial herb in hill evergreen forest, dry evergreen forest, mixed deciduous forest, grassland and moist evergreen forest at elevation 216 – 1,347 m.

Vernacular – Kluai kae (กล้วยเคร่) (Tak); Kluai Paa (กล้วยป่า) (Uttaradit). Kamphangphet, Phitsanulok , Phetchaburn, Tak

Specimens examined. R. E. Holltum 244347 (BKF); Up5, Up10, Up16, Mw2, Mw12, Mw16, Mw33, Mw35, Mw38, Mw41, Ph2, Ph5, Ph30, Ph31, Ph33, Ph34, Ph43, Ph47, Ph48, Ph50, Ln21- Ln23, Ln27, Ln3, Ln46, Nw7, Nw22, Nw24 (Figure 4.1.12).

(5.) *M. acuminata* Colla ssp. E. E. Cheesman in Kew Bull. 26. 1948; N. W. Simmonds in Kew Bull. 466. 1956.

Other 1; pseudostem 3.5 – 6.5 m high, 9 - 20 cm in diameter at base, light green; leaf sheath and petioles glabrous, green. Leaf blades oblong, 2.3 - 3.3 m long, 30 - 70 cm wide, truncate at apex, unequal basal lamina, dark green, glabrous, midribs yellow green; petiole 14 - 58 cm long, margin almost erect. Inflorescence hanging at angle 45°, peduncle and rachis hairless, peduncle 14 - 58 cm long, 2.5 - 5.5 cm wide; rachis falling vertically. Male bud intermediate (ovoid), the bract great imbricate convolute, color of the bract external face is pink purple, glabrous; color of the bract internal face is yellow, tined with light green at tip; male bud ratio > 0.28. Male flower two rows per bract; compound tepal 2.8 - 3.6 cm long, 1.0 - 1.6 cm wide, yellow; lobe of compound tepal 0.2 - 0.95 cm long, 0.2 - 0.5 cm wide, bright yellow; free tepal 1.3 - 2.35 cm long, 0.95 - 1.35 cm wide, translucent white; ovary 0.5 - 0.9 cm long, 0.15 - 0.3 cm wide, yellow. Fruit bunch very compact, asymmetrical, curve toward stalk, 9 - 18 per hand, an average 14 per hand, 4.3 - 8.2 cm long, 1.5 - 2.4 in diameter, pedicel 0.5 - 1.0 cm long, 0.5 - 1.2 cm wide, partially fused; fruit apex 1.0 cm long, 0.5cm wide, bottle - neck shape; light green at mature, yellow at ripe. Seeds black, angular and wrinkled.

Thailand – NORTHERN: Khamphangphet (Mae Wong), Phetchabun (Namnaow).

Distribution – Thailand (Lower northern), uplands

Ecology – Perennial herb in dry evergreen forest at elevation 279 - 461 m.

Vernacular – Kluai Paa (Phetchabun); Kluai Kae (Nakhonsawon).

Specimen examined: Mw10, Mw49, Mw51 - Mw59, Nw41 (Figure 4.1.13).

(6.) *M. acuminata* Colla ssp. E. E. Cheesman in Kew Bull. 1948; N. W. Simmonds in Kew Bull. 1956.

Other 2; pseudostem 2.0 – 3.4 m high, 9 - 16 cm in diameter at base, green yellow; leaf sheath and petioles glabrous, medium green. Leaf blades oblong, 1.75 - 2.0 m long, 46 - 76 cm wide, truncate at apex, unequal basal lamina, dark green, glabrous, midribs green; petiole 34 - 54 cm long, margin almost erect. Inflorescence hanging at angle 45°, peduncle and rachis slightly hair, peduncle 17 - 42 cm long, 1.5 - 6.0 cm wide; rachis falling vertically. Male bud in like a top (ovate), more or less acute, the bract imbricate, color of the bract external face is pink - purple, glabrous; color of the bract internal face is orange red, tined with yellow at tip; male bud ratio about 0.28. Male flower two rows per bract; compound tepal 3.2 - 3.7 cm long, 1.0 - 1.6 cm wide, yellow; lobe of compound tepal 0.39 - 1.0 cm long, 0.15 - 0.5 cm wide, bright yellow; free tepal 1.5 - 2.25 cm long, 0.9 - 1.5 cm wide, tine with yellow; ovary 0.5 - 0.9 cm long, 0.15 - 0.35 cm wide, green yellow. Fruit bunch very compact, asymmetrical, curve toward stalk, 8 - 26 per hand, an average 17 per hand, 5.5 - 13.8 cm long, 1.05 - 2.02 in diameter, pedicel 0.5 - 1.6 cm long, 0.2 - 1.0 cm wide, partially fused; fruit apex bottle-neck shape, light green at mature, yellow at ripe. Seeds black, angular and wrinkled.

Thailand – NORTHERN: Tak (Umphang).

Distribution. – Thailand (Lower northern), uplands.

Ecology – Perennial herb in mixed deciduous forest at elevation 489 - 523 m.

Vernacular – Kluai Kae (กล้วยเคร่); Kluai Ling (กล้วยลิง), Kluai Paa (กล้วยป่า).

Specimens examined. Up36, Up39 - Up48 (Figure 4.1.14).

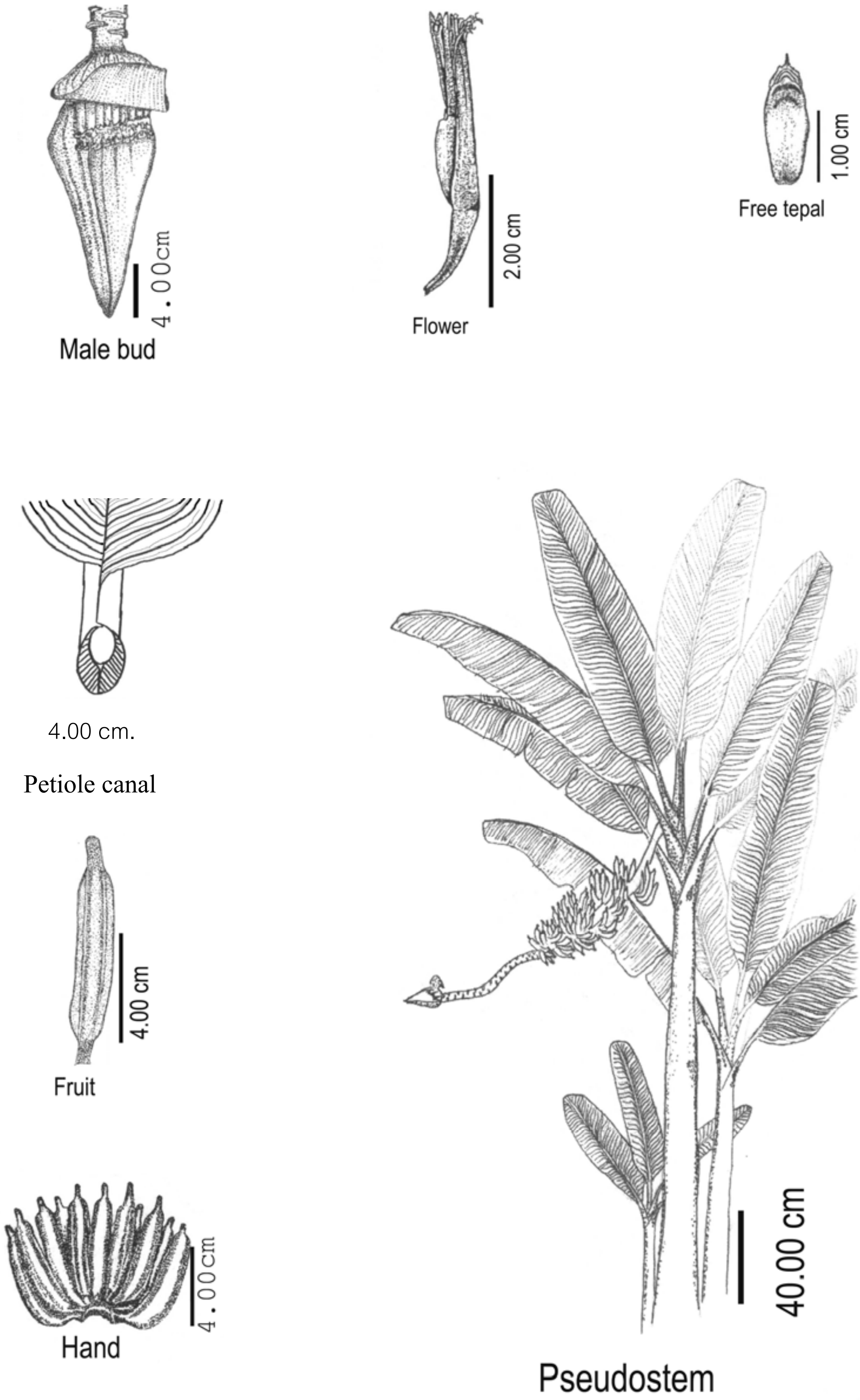


Figure 4.9 Drawn pictures of accession, Up25 of *M. acuminata* Colla ssp. *malaccensis* (Ridl.) Simmonds

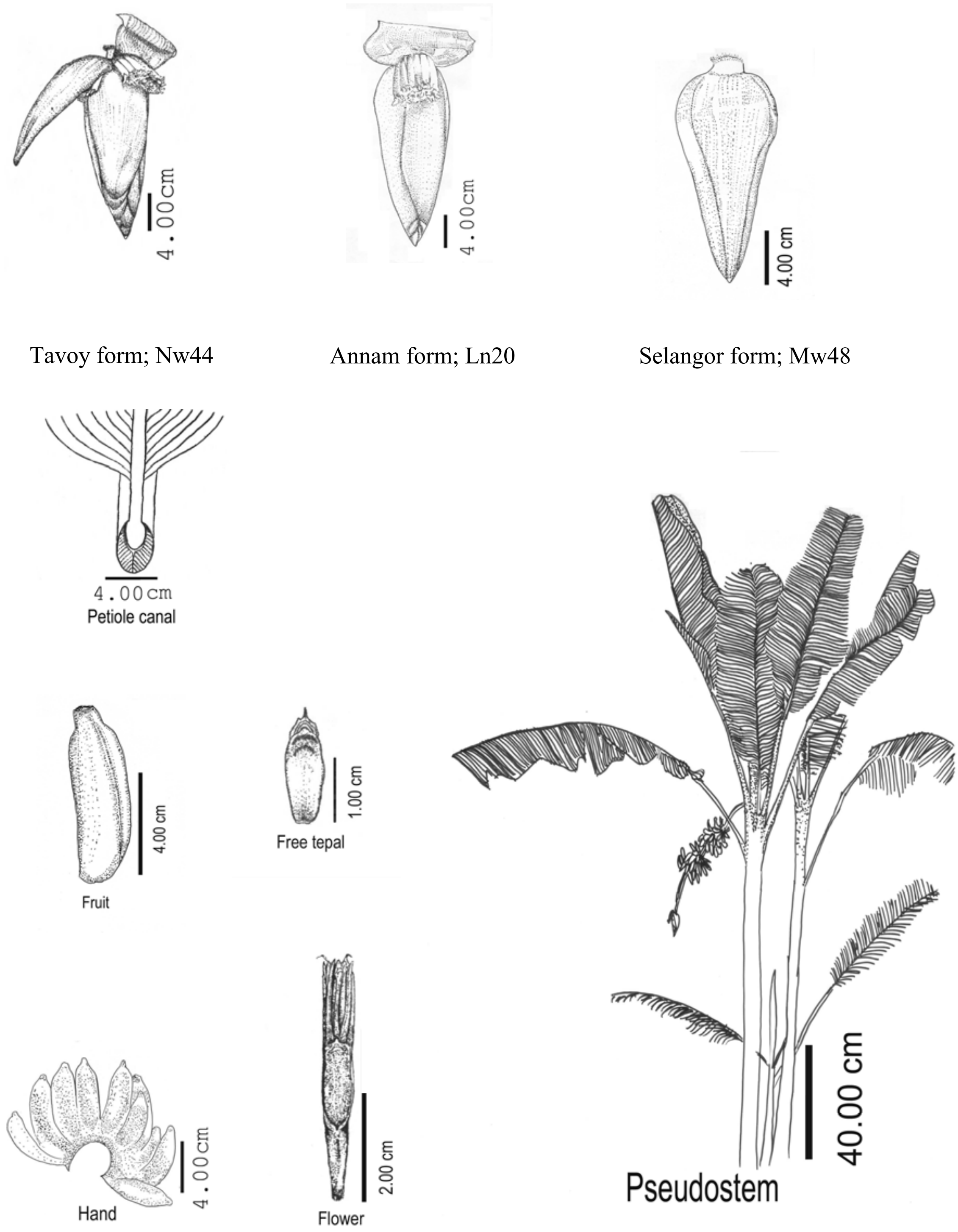


Figure 4.10 Drawn pictures of accession, Ln20 of *M. acuminata* Colla ssp. *siamea* Simmonds; Annam form = Ln20, Tavoy form = Nw44, Selangor form = Mw48

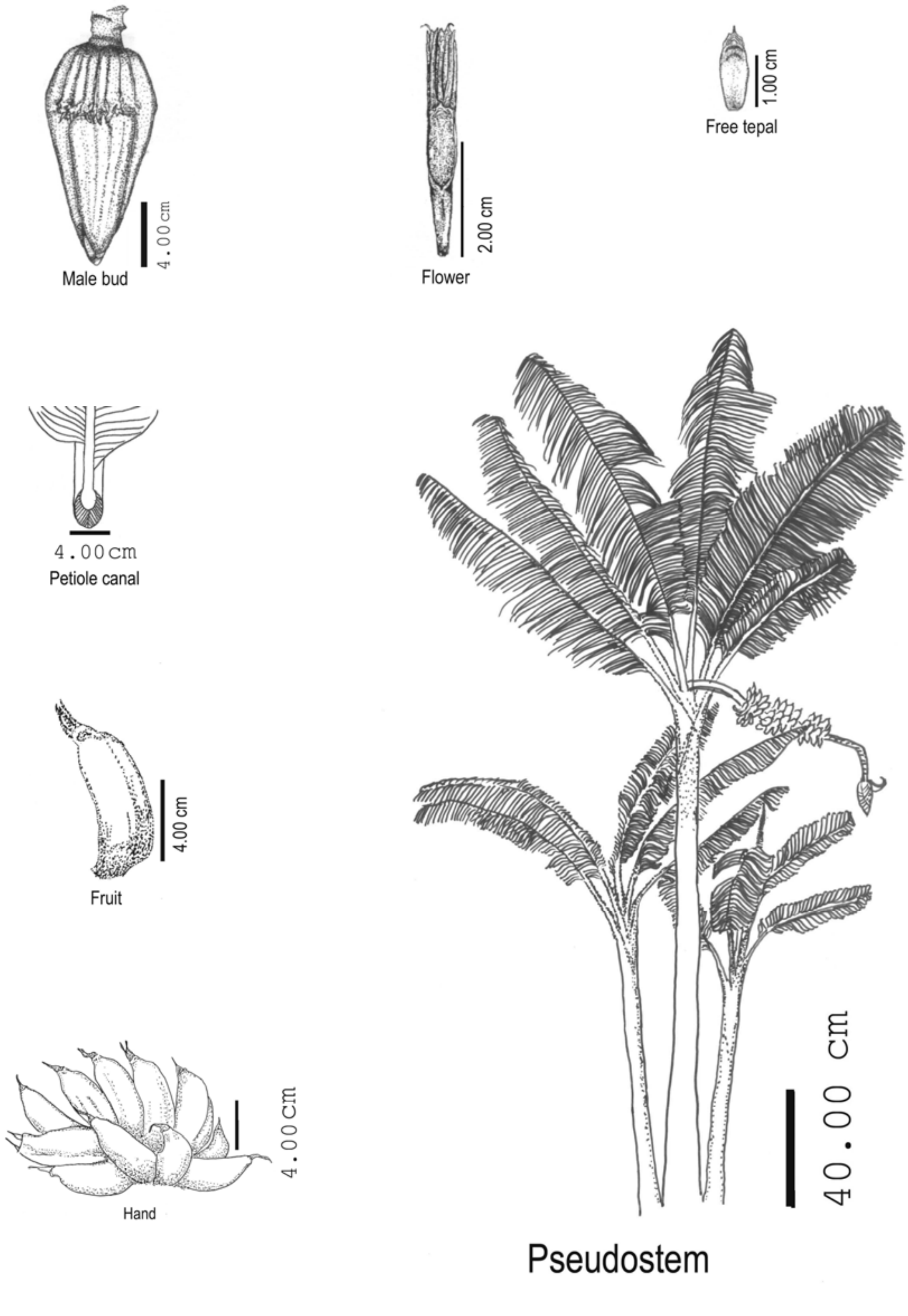


Figure 4.11 Drawn pictures of accession, Up18 of *M. acuminata* Colla ssp. *burmanica* Simmonds

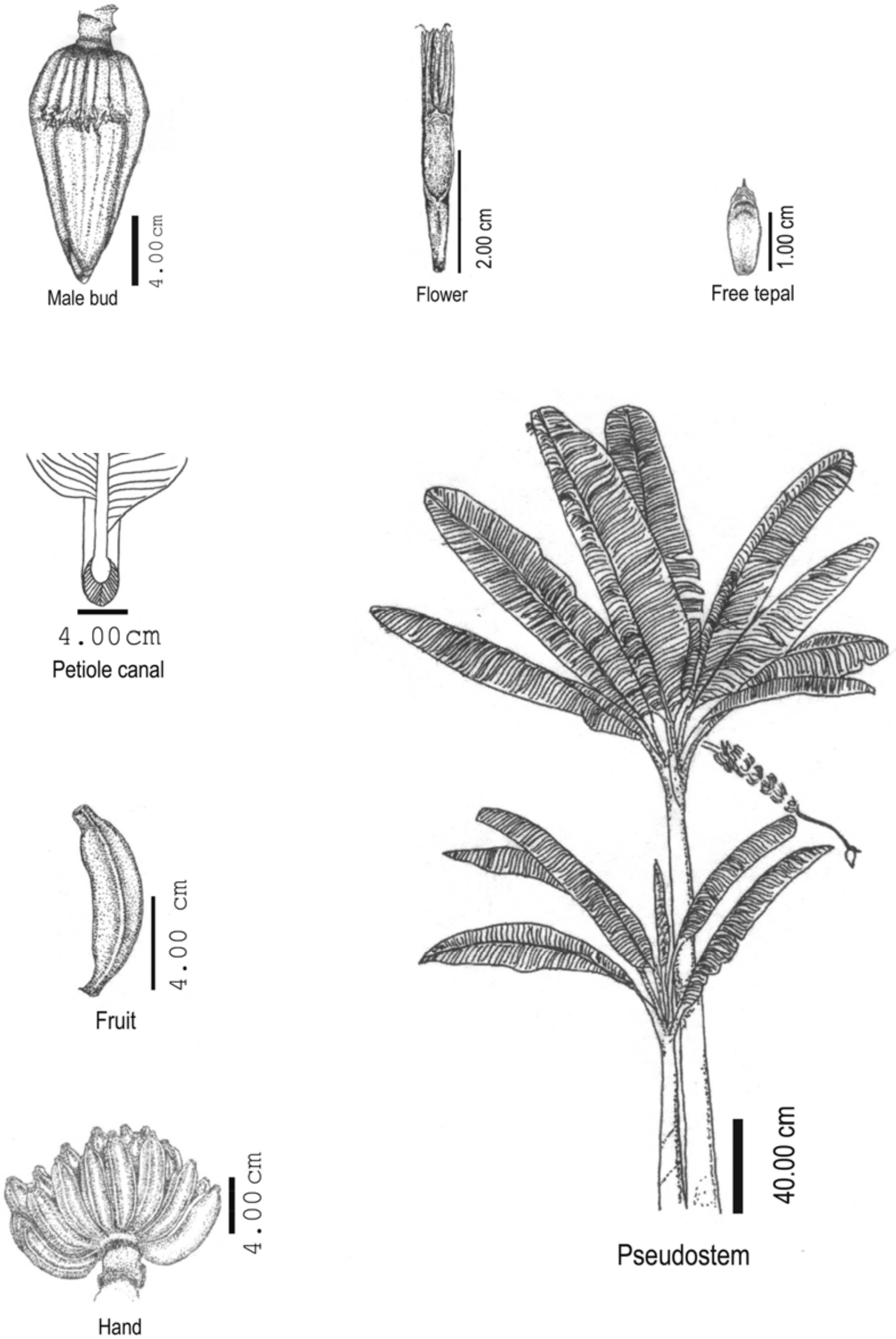


Figure 4.12 Drawn pictures of accession, Mw38 of ssp. *siamea x* ssp. *burmanica*

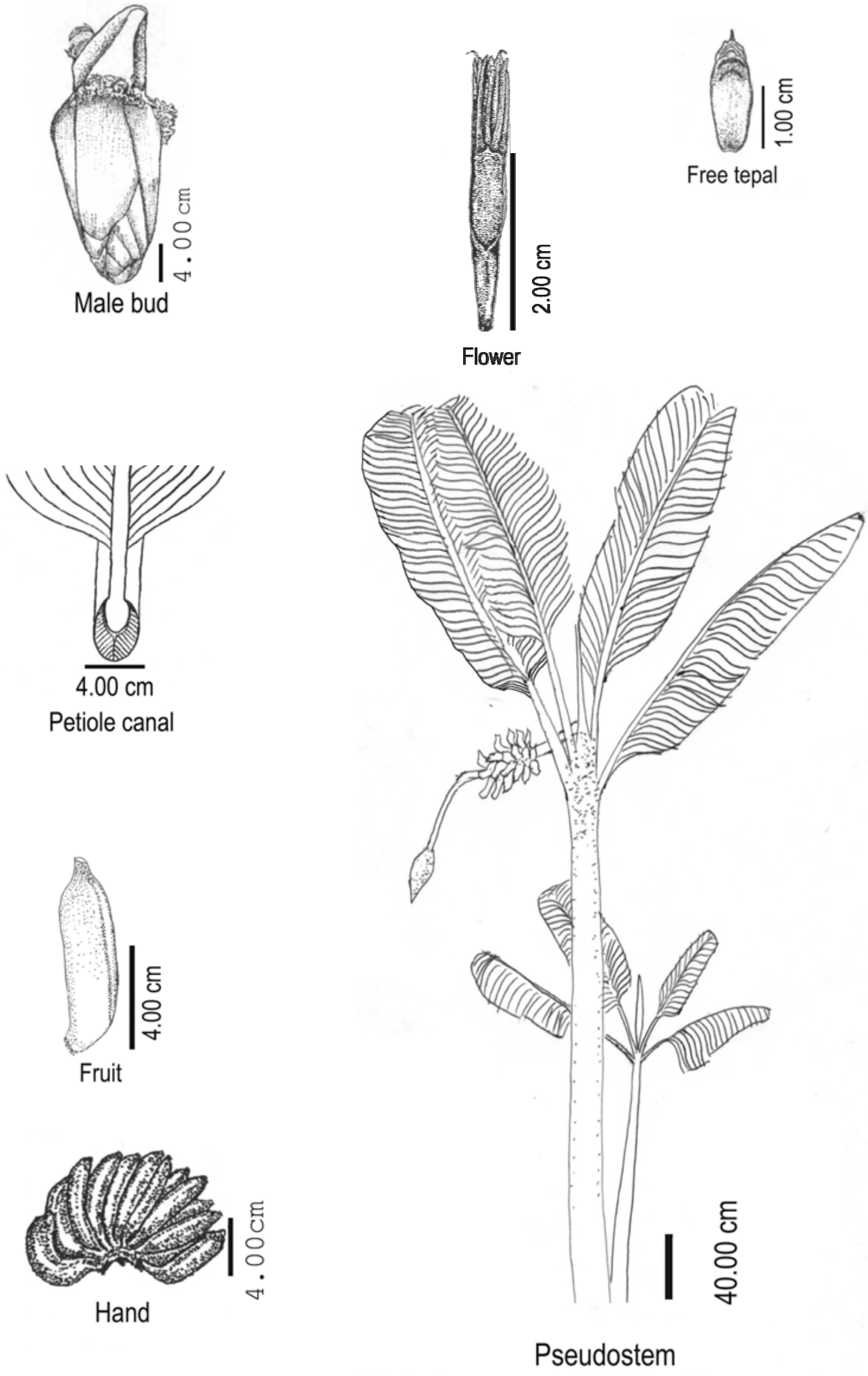


Figure 4.13 Drawn pictures of accession, Mw10 as Others 1

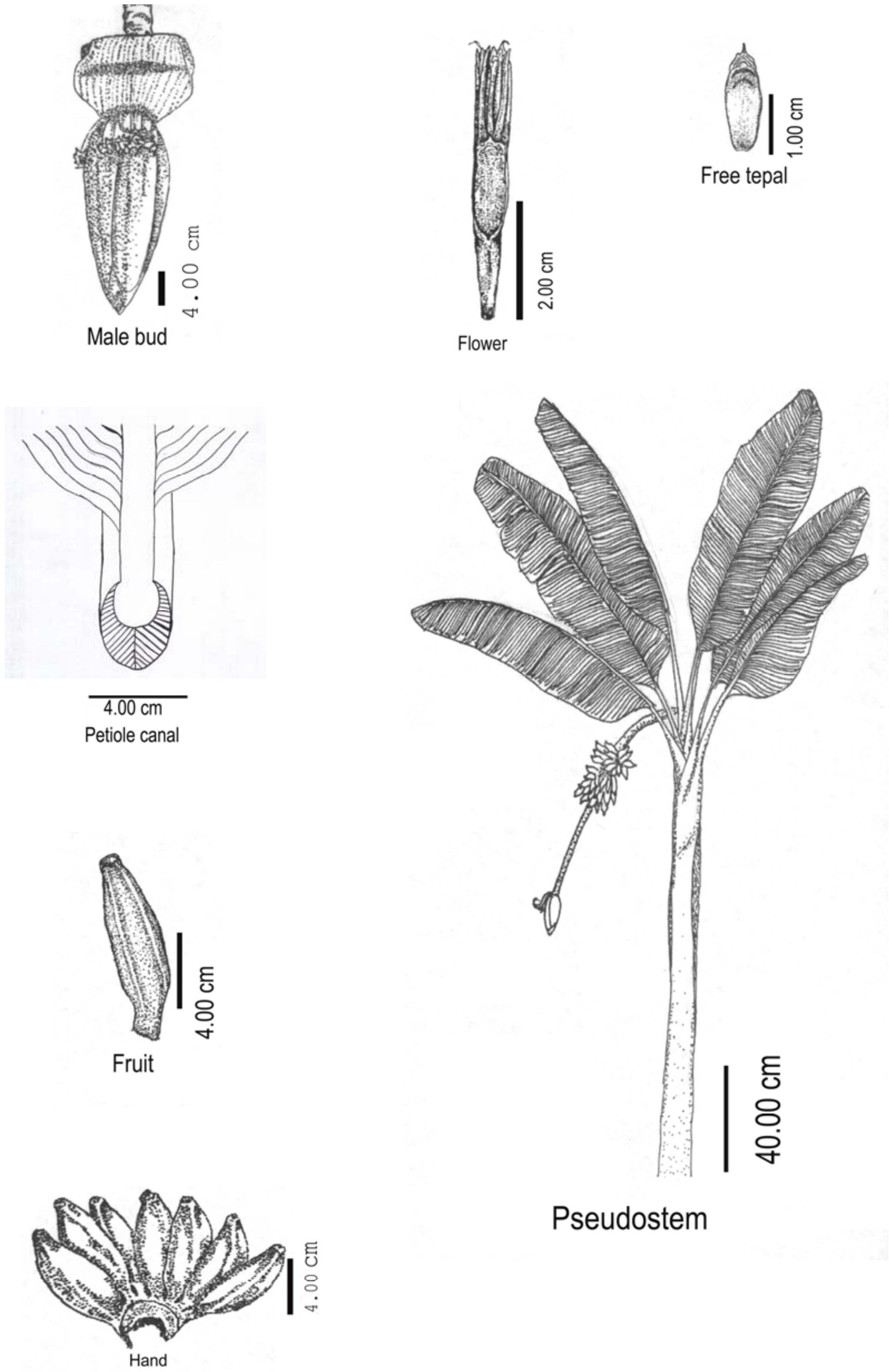


Figure 4.14 Drawn pictures of accession, Up39 as Others 2

Table 4.13 Comparison of observed morphological characters of 3 subspecies, hybrid (*siamea* x *burmanica*) and others from lower northern Thailand.

Remark: The objects in these pictures were not in the same scale (Cheesman, 1948a; Simmonds, 1956; De Langhe *et al.,* 1998).

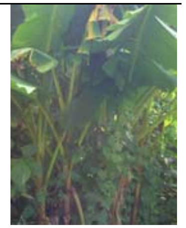
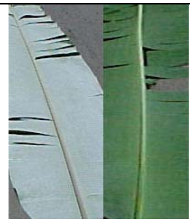
Musa acuminata Colla Character	Hybrid	Other1	*malaccensis* (Ridl.) Simmonds	Other2	*siamea* Simmonds	*burmanica* Simmonds
Pseudostem: more slender than those of most cultivated bananas; 3 - 5m long exceeding 25cm diameter at base, with varying development of brown-black.						
Petiole blade: oblong, 2 - 2.5m long, 40 - 60m wide truncate at apex, usually rounded at base, sometime rounded on one side and acute on the other.						
Midrib: green, greenish yellow, or more or less strongly tinged with red below.						

Table 4.13 Comparison of observed morphological characters of 3 subspecies, hybrid (*siamea* x *burmanica*) and others from lower northern Thailand.

Remark: The objects in these pictures were not in the same scale (Cont.) (Cheesman, 1948a; Simmonds, 1956; De Langhe *et al.,* 1998).

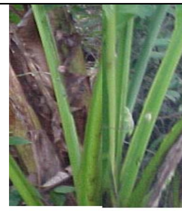
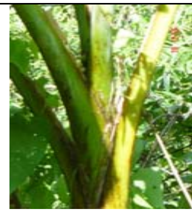
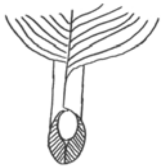
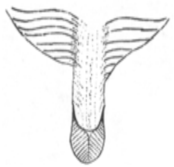
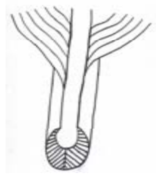
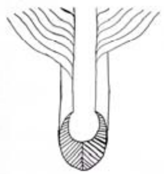
Musa acuminata Colla Character	Hybrid	Other 1	*malaccensis* (Ridl.) Simmonds	Other 2	*siamea* Simmonds	*burmanica* Simmonds
Petiole length and wide: commonly more or less glaucous petioles 60-90cm long, in some forms very slender.						
Petiole canal leaf: sometimes almost erect leaving an open channel, in other forms strongly incurved over the channel and almost covering it.						
Bunch position: sub-horizontal or vertically deflexed, its peduncle and rachis usually more or less thickly pubescent with brown hairs, sometimes glabrous.						

Table 4.13 Comparison of observed morphological characters of 3 subspecies, hybrid (*siamea* x *burmanica*) and others from lower northern Thailand.

Remark: The objects in these pictures were not in the same scale (Cont.) (Cheesman, 1948a; Simmonds, 1956; De Langhe *et al.,* 1998).

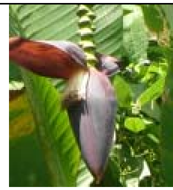
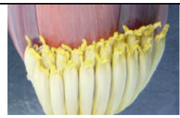
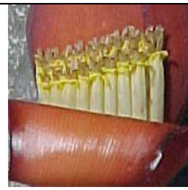
Musa acuminata Colla Character	Hybrid	Other 1	*malaccensis* (Ridl.) Simmonds	Other 2	*siamea* Simmonds	*burmanica* Simmonds
Female flower: about 16 per bract in two rows; compound tepal about 2.5cm long white, yellowish or slightly translucent, about half as long as the compound tepal.						
Male bud: in advanced blooming is ovoid to turbinate, usually acute, the bracts convolute, imbricate at the extreme tip only purple or red, from bright red to dark violet, ovate.						
Male flower: about 20 / bract, in 2 rows; compound tepal 3.5 - 4.5cm long, about 1.2cm wide, white, cream, yellowish, pale orange, sometimes purplish.						

Table 4.13 Comparison of observed morphological characters of 3 subspecies, hybrid (*siamea* x *burmanica*) and others from lower northern Thailand.

Remark: The objects in these pictures were not in the same scale (Cont.) (Cheesman, 1948a; Simmonds, 1956; De Langhe *et al.,* 1998).

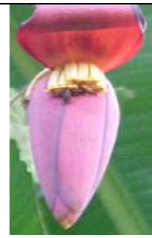
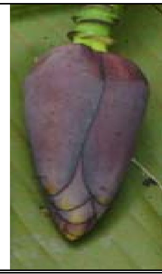
Musa acuminata Colla Character	Hybrid	Other 1	*malaccensis* (Ridl.) Simmonds	Other 2	*siamea* Simmonds	*burmanica* Simmonds
Fruit: individual fruit 8-13cm long, 1.5 - 3cm in diameter, Sub - cylindrical, young fruit almost disappearing at ripeness, bright yellow at full ripeness.						
Bract behaviour: bracts revolute on fading and early deciduous, bract distinctly imbricate at the tip the bracts convolute at the tip.						

Table 4.14 Summary of the morphological characters of 3 subspecies, hybrid (*siamea* x *burmanica*) and others from lower northern Thailand.

Character	Hybrid	Other 1	*malaccensis* (Ridl.) Simmonds	Other 2	*siamea* Simmonds	*burmanica* Simmonds
1. Pseudostem high	2-5 m	3-5 m	3-5 m	3-5 m	2-5 m	2-5 m
2. Pseudostem appearance	Shiny or no visible sign of wax	Shiny or no visible sign of wax	Olive green, Very wax	Few wax	Shiny or no visible sign of wax or slightly waxy, Dull yellowish green	Shiny or no visible sign of wax, Bright green
3. Blotch at petiole base	Large blotch	Large blotch	Large blotch	Large blotch	Large blotch	Large blotch
4. Blotch color	Black purple	Black purple	Black purple	Brown	Black purple	Brown-black
5. Petiole canal leaf	Erect	Erect	Curve inward, Midribs are red beneath	Erect Open	Erect Open	Erect, Open Pale green or Yellowish
6. Wax on leaf	Absent or no visible sign of wax	Absent or no visible sign of wax	Very wax	Absent or no visible sign of wax	Absent or no visible sign of wax	Absent or no visible sign of wax

Table 4.14 Summary of the morphological characters of 3 subspecies, hybrid (*siamea* x *burmanica*) and others from lower northern Thailand. (Cont.)

Character	Hybrid	Other 1	*malaccensis* (Ridl.) Simmonds	Other 2	*siamea* Simmonds	*burmanica* Simmonds
7. Peduncle hairiness	Hairless	Hairless	Slightly hair	Slightly hair	Hairless	Hairless
8. Bunch position	Horizontal	Hanging at angle 45^0	Hanging at angle 45^0	Hanging at angle 45^0	Horizontal	Horizontal
9. Rachis position	Pendulous	Pendulous	At an angle	Pendulous	Pendulous	Pendulous
10. Male bud shape	Advance blooming like a top, more or less acute	Intermediate (ovoid)	Advance blooming like a top, more or less acute	Like a top (ovate), more or less acute	Like a top and lanceolate, varies in size, three shapes	Like a top and lanceolate, varies in size.
11. Bract imbrication	Imbrication at apex	Strong Imbrication	Imbrication at apex	Imbrication at apex	Imbrication at apex	Imbrication at apex
12. Color on the bract external face	Purple	Pink - purple	Red-purple (Reddish purple)	Pink - purple	Purple	Purple

Table 4.14 Summary of the morphological characters of 3 subspecies, hybrid (*siamea* x *burmanica*) and others from lower northern Thailand. (Cont.)

13. Color on the bract internal face	Red - purple	Yellow	Orange - red (Light red)	Orange - red	Red - purple	Red - purple
14. Color on the bract apex	Tine with yellow	Large bright green	Tine with yellow	Tine with yellow	Tine with yellow	Tine with yellow
15. Color stripe on the bract	Without discolor	Without discolor	Without discolor	Without discolor	Without discolor	Without discolor
16. Wax on the bract	Very little or no visible sign of wax	Very little or no visible sign of wax	Very little or no visible sign of wax	Very little or no visible sign of wax	Varies waxy	Varies waxy
17. Compound tepal basic color	Cream	Yellow	Cream	Yellow	Cream	Cream
18. Lobe color of compound tepal	Yellow or orange	Bright yellow	Yellow	Bright yellow	Yellow	Yellow
19. Fruit apex	Bottle - neck	Bottle - neck	Bottle - neck	Bottle - neck	Bottle - neck	Bottle - neck
20. Fusion of pedicel	Partially or totally fuse	Partially fuse	Partially or totally fuse	Partially fuse	Partially or totally fuse	Partially or totally fuse

Table 4.15 Comparison of identical and co–characters of Annam form, Tavoy form, Selangor form (Cheesman, 1948) and Other 1.

Character	**Annam form** or ssp. *siamea* Simmonds	**Tavoy form** or ssp. *burmanica* Simmonds	**Selangor form** or ssp. *malaccensis* (Ridl.) Simmonds	**Other 1**
Upper parts of leaf - sheath	Dull yellowish green	Bright green	Olive green with a purplish tinge	Green (Viridescent)
Blotch	Moderately heavy brown blotch, slightly wax	Heavy reddish brown blotch, not at all waxy	Moderately heavy black blotching	Large Blotch, not at all waxy
Leaf blades	Not glaucous beneath		Heavily waxy beneath	Not glaucous beneath
Petiole canal	Erect		Narrow incurved	Erect
Midrib	Yellowish-green, moderately waxy lower side	Pale green or yellowish	Red beneath and often purplish above also	Green (Viridescent)
Male bud	Annam form	Tavoy form	Selangor form	- Annam form - Tavoy form - Selangor form
Bract imbricate	Distinctly imbricate at the tip		Convolute at the tip	Imbricate at the tip
Compound tepal	Whitish		Cream	Cream, White
Lobe of compound tepal	Bright yellow	Yellow	Bright yellow	Yellow
Bunch position	Nearly horizontal	Pendent and compact (Exception)	Nearly horizontal	Horizontal
Peduncle	Rarely seen glabrous	Densely pubescent	Densely pubescent	Hairless (glabrous)
Fusion of pedicel	Partially fused	Partially fused	Very partially fused	Partially fused

Photographs indicating the prominent characters of each wild banana group were shown in Table 4.11 -4.13. The morphological characters of each group and identification were presented in the Table 4.14 and Figure 4.9 to 4.14. There was similarity identification in morphological characters comparison between three subspecies of classical taxonomy with the outgroup accessions. There were two and three male bud shape variations in Kanchanaburi (ssp. *burmanica*) and Chantaburi (ssp. *siamea*), respectively (Appendix B). However, there were some variations in outgroup. Subspecies *siamea* have little or no visible sign of wax on pseudostem appearance (Simmonds, 1956; Cheesman, 1948). Besides, variations of male bud shapes were found in three sub-populations. The typical male bud shape of ssp. *siamea* was easily recognized as 71.1% of Annam form (Cheesman, 1948). It is found that two male bud shapes that differ from the typical characters are 25.9% of Tavoy form and 3% of Selangor form. Both bud characters are similar to the identical characters of ssp. *burmanica* Simmonds and ssp. *malaccensis* (Ridl.) Simmonds. This is new adding recognition data to this subspecies information (Figure 4.10). It is interesting to note that this has never been reported before (Cheesman, 1948; Simmonds, 1956). Investigation on the morphological classification of previous works of Simmonds (1956) and Cheesman (1948) presented the classical taxonomy development of the form to subspecies (Appendix B). In addition, comparison of identical and co–characters of Annam form, Tavoy form, Selangor form (Cheesman, 1948) and Other 1 is shown in Table 4.15

5. Comparisons between Numerical Taxonomy and Classical Taxonomy

The sample population classification results of classical taxonomy, into three subspecies (ssp. *malaccensis*, ssp. *siamea* and ssp. *burmanica*), hybrid (*siamea* x *burmanica*) and others (Table 4.12), which are different from the results of numerical taxonomy. The accessions are mathematically classified into two subspecies and outliers (Table 4.9). The numerical taxonomy is more reliable due to its mathematic and statistic methods. There is a difference within sample population. An interesting question is “what are these two groups”? The hypothesis was accepted and indicated that there were two major groups of variations within this population, which were classified differently from previous classical taxonomy classification. They were *(i.)* ssp. *malaccensis* and *(ii.)* the rest of ssp. *siamea* and ssp. *burmanica* (Figure 4.5). However, there are some outliers in numerical taxonomy, which were the others in classical taxonomy. They should be hybrids of others species or mutant. This point is needed to do further research. These results ensure that there are only two subspecies of *M. acuminata* in the lower northern Thailand. They were *(i.)* ssp. *malaccensis* and *(ii.)* ssp. *siamea*. In addition, ssp. *burmanica* and the hybrid of *siamea* x *burmanica* (in classical taxonomy) are in the group of ssp. *siamea*.

Some identical characters in classical taxonomy are not relevant in numerical taxonomy. Classical taxonomy classify *M. acuminata* Colla accession from the lower northern Thailand into three subspecies using identification key of Simmonds (1956) and Cheesman (1947a, 1947b, 1948a, 1948b,1949a, 1949b) (Table 3.1). The major identity characters to separate ssp. *burmanica* are the sheaths is waxless except in young suckers**.** Pseudostems are lightly pigmented and male bud shape is advance blooming acute. Male bracts are crimson red on the internal face and imbricate.

Sheaths of ssp. *siamea* are also waxless, which are similar to ssp. *burmanica.* Bract of ssp. *siamea* is purplish red on the bract external face with yellowish tips. Bract is often slightly persistent and usually imbricate in the young bud. Petiole margin is yellowish green and erect.

While, sheaths of ssp. *malaccensis* are waxless or little wax. Bracts are bright red on the bract external face, quickly deciduous and non-imbricate (red beneath and often purplish above). Moreover, petiole margin is induplicate).

CONCLUSION AND DISCUSSION

Numerical Taxonomy

Cluster analyses of twenty morphological characters of 326 accessions from lower northern Thailand with 38 accessions of outgroup presented the separation of two major groups *(i.)* ssp. *siamea*, ssp. *burmanica*, Chantaburi and Kanchanaburi *(ii.)* ssp. *malaccensis* and Trang with some intermediate individuals (Figure 4.5) Discriminant analysis indicated that there was no different to separate ssp. *burmanica* from ssp. *siamea*. They were in the same group. Which were different from classical taxonomy. Canonical discriminant and hierarchical cluster analyses are the methods base on statistic to ensure the classification. In contrast, classical taxonomy provided interesting information of morphological variations by observed of those characteristics. The results may variously depend upon the decision of taxonomists based on the limited materials in hand. The accessions of Chantaburi and Kanchanaburi which were judged to represent the *siamea* and *burmanica* subspecies respectively, which were also in the same group (Figure 4.5, 4.7) This may due to the waxiness character which is not the major character to separate both subspecies in classical taxonomy. Besides, it is not following the key of Simmonds (1956). In conclusion, the result of Canonical discriminant and hierarchical cluster analyses were realizable due to their standard and uniformity system. Moreover, the scattering outliers should due to their cross and hybridizations.

It can be stated that the unbalanced and vast different in the number of accessions in each group or cluster occur naturally in the forest created non - uniform in sample size and variances. Future survey on those low number accessions and outlier of classical taxonomy should be collected and investigated in order to understand their variations and identifications as new germplasm. However, the classical taxonomy is still important method for a fundamental classification of *M. acuminata* in the field study and survey. The integration of numerical taxonomy with classical taxonomy will review and develop the suitable classification covering the variation.

Simmonds (1956) mentioned that ssp. *siamea* is the closest ssp. to ssp. *malaccensis* and different from ssp. *burmanica*. The separation of three subspecies were conducted follow the classical taxonomy. In contrast, this is not correct due to cluster analyses. While, there were only two subspecies. This should be reclassified again with molecular analyses to indicate their relationship within *Musa* complex. Further study has to focus on the current key and banana classifications of Simmonds (1956), which may not cover the new characters of new specimens and has to be reviewed.

Classical Taxonomy

In conclusion, there is a large group of ssp. *siamea* including former ssp. *siamea*, ssp. *burmanica* and Hybrid (*siamea x burmanica*). The group shares characters and pool into one group which support by the numerical taxonomy and cluster analyses. This is different from the previous classical taxonomy works (Simmonds & Shepherd, 1955; Simmonds, 1956; Simmonds & Weatherup, 1988). The character of wax and no wax may not be the major criteria to separate ssp. *siamea* from ssp. *burmanica*. On the other hand, ssp. *malaccensis*, Other 1 and Other 2 are clearly separated. This outlier status of Other 1 and Other 2 only indicates the hybrid or mutant characters. However, these results show that the diversity of this species especially ssp. *siamea* in Thailand is larger than previous reports which were described and collected from a few specimens. These 20 morphological characteristics criteria are still practically used for primary identification on these specimens from lower northern Thailand. Subspecies or forms identification were possibly required for more new characters from other advance molecular techniques to explain the whole picture of these variations.

There are some discussions on classical taxonomy of accessions into 3 subspecies, hybrid and others.

Hybrid (*siamea x burmanica*) pronounced characters of *M. acuminata* Colla ssp. *siamea* and ssp. *burmanica*. The identical subspecies characteristic was creamy compound tepal which was basic color of the selangor form. Moreover, lobe of compound tepal was yellow or orange and male bud was advanced blooming like a top and more or less acute (Cheesman, 1948a). This form looks like *M. terminiflora* hybrid (Jaeson). In conclusion, Hybrid was statistically classified in the same group with ssp. *siamea* (Table 4.9; Figure 4.15)This indicated highly diversified in the group of ssp. *siamea.* This is needed to reconfirm in cp-DNA analysis in the next chapter.

Other 1 presented some characters similar to *M. acuminata* and *M. flaviflora* N. W. Simmonds (Cheesman, 1948b). However, male bud form of this group was similar to *M. zebrina* Van Houtte ex Planch (Cheesman, 1948). Moreover, various characters were very different from the description subspecies of *M. acuminata* and *M. flaviflora* N. W. Simmonds (Cheesman, 1948b; Simmonds , 1956; De Langhe *et al*., 1998) such as pink - purple of the bract external face, strongly imbricate bract, prominent 1 / 3 bright light green or viridescent color on the tip of male bud. These characters indicate this form and were separated from the former 5 subspecies of *M. acuminata*. However, overall characters of this form were visually close to ssp. *siamea* Simmonds, due to its scar of rachis, fruits and hands in bunch, as well as pseudostem characters. Some characteristics were similar to *M. flaviflora* N. W. Simmonds (Cheesman, 1948b), such as slightly horizontal bunch position, yellow or lutescent color on the internal face of bract (Cheesman, 1948a). Other 1 was statistically classified into the outlier groups (Table 4.9; Figure 4.15). However, this outlier information indicated that Other 1 may possibly be the hybrid of *M. acuminata* with other *Musa* or the mutant. The further work should be focused on the integration of numerical taxonomy with molecular study to explain at the subspecies level (Jong and Argent, 2001).

Subspecies *malaccensis* (Ridl.) Simmonds (1956) Simmond identified by Cheesman (1948). Distinctive characters were the incurve petiole canal, heavy wax on the leaf, creamy compound tepal and male bud form. Ssp. ***malaccensis*** was classified in the same group at 100% of original value by canonical discriminant analysis (Table 4.9; Figure 4.15). This strongly confirmed the separation from ssp. *siamea* and ssp. *burmanica*

Other 2 presented some characters which were similar to ssp. *malaccensis* (Ridl.) Simmonds, It was composed of more large brown blotch on petiole base also in ssp. *siamea* and ssp. *burmanica* but ssp. *malaccensis* is more blotch. Compound tepal was creamy. Lobe of compound tepal was bright yellow and apex shape of fruit was bottle - neck with partially fused pedicel (Cheesman, 1948). This accession was slightly horizontal bunch position and slightly hair on peduncle (Simmonds, 1956). Few characteristics were closed to typical *M. flaviflora* N. W. Simmonds, such as petiole margin was erect and leaf blades were not glaucous beneath. Lobe of compound tepal is bright yellow. However, some characters were significantly different from ssp. *malaccensis* (Ridl.) Simmonds and *M. flaviflora*. These characters have never been recorded before, such as glossy pink - purple color of the bract external face and orange - red color of the bract internal face. These findings may be induced by hybridization of both species. However, this accession appearance looked like *M. laterita* but the different characters were without running suckers and the upright male flower then curve down at fully mature. Other 2 was classified as outlier by canonical discriminant analysis (Table 4.9; Figure 4.15). This strongly confirmed the separation from the other accessions in cluster analysis. This outlier information indicated that Other 2 may possibly be the hybrid of *M. acuminata* with other *Musa* or the mutant.

Subspecies *siamea* Simmonds had little or no visible sign of wax on pseudostem appearance (Simmonds, 1956; Cheesman, 1948). However, variations of male bud shapes are found in three populations. The typical male bud shape of ssp. *siamea* is easily recognized as 71.1% of Annam form (Cheesman, 1948). Two male bud shapes that differ from the typical characters are 25.9% of Tavoy form and 3% of Selangor form. Both bud characters are similar to the identical characters of ssp. *burmanica* Simmonds and ssp. *malaccensis* (Ridl.) Simmonds. These are new adding recognition data to this subspecies information (Table 4.13; Figure 4.10). That has never been reported before (Cheesman, 1948; Simmonds, 1956). The result of canonical discriminant analysis was classified ssp. *siamea* coverd ssp. *siamea*, ssp. *burmanica* and Hybrid (*siamea x burmanica*) (Table 4.9; Figure 4.15). This strongly confirmed that ssp. *siamea* was in the same group with ssp. *burmanica* and Hybrid. This was also reconfirmed with the outgroup classification of Kanchanaburi (ssp. *burmanica*) and Chantaburi (ssp. *siamea*) which were in the same group (Figure 4.7)

Subspecies *burmanica* Simmonds presented identical characters of reddish - brown large blotch on pseudostem and blotch at petiole base with light red beneath leaf and midrib. However,The result of canonical discriminant analysis was reclassified ssp. *burmanica* into ssp. *siamea* (Table 4.9; Figure 4.15). This strongly confirmed that ssp. *burmanica* was in the same group with ssp. *siamea* and Hybrid (*siamea x burmanica*). This was also confirmed with the outgroup reclassification of Kanchanaburi (ssp. *burmanica*) and Chantaburi (ssp. *siamea*) Figure 4.7)

The classical classification or morphological taxonomy was properly and suitably identify wild bananas in the subspecies level of *M. acuminata* when compared with other techniques (Argent, 2001). However, these are required to be revised. Due to uncertain status of outliers, Others 1 and Others 2 were unclear to recognize as new forms, subspecies, species, new hybrids, or mutant. These should be further investigations using molecular techniques. However, the results of this study indicated that after explorations with higher numbers of accessions from various locations in Thailand, which introduced morphological variations and reflex the complexity of wild banana diversity larger than the previous taxonomy reports.

The *Musa* identification in this study using classical taxonomy did not represent any samples of ssp. *microcarpa* (Becc.) Simmonds and ssp. *banksii* F. V. Simmonds. However, the sample of Nw39 was 6 m high which was only the identical character of ssp. *microcarpa*. This should be due to the highly competitive growth of an isolated sample of Nw39 within the dense population of *M. itinerans* Cheesman. In addition, ssp. *banksii* was not found in this study. This may be due to its center of distribution was in Indonesia islands (Simmonds, 1960). In addition, samples of *M. flaviflora* or Mariani form and *M. zebrina* Van Houtte ex Planch or Buitenzorg form were not found in this study. Its distributions were previously recorded only in Assam and Java (Cheesman, 1948).

It can be remarked that this morphological or classification techniques acquire highly understanding in banana taxonomy with large number of specimens represents actual variations. Well knowledge with practical skills on the family *Musaceae* will be informative and useful for the accuracy identification. Morphological data collection is very important for banana classical taxonomy especially in the vegetative and reproductive stages. Perfect information should consist of taxonomy detail, picture, drawing and specimen. These kinds of research should be paralleling developed and improved the methods with numerical taxonomy and modern molecular techniques. Germplasm should be preserved in the long-term by other advance technology.

HABITAT ENVIRONMENT OF WILD BANANA (*Musa acuminata* Colla) GROUPS

SUMMARY

This study aimed to investigate the primary relationships data between different groups of the wild banana and their habitat environment. Three hundred and twenty six samples were found and collected from six natural forests of the lower northern Thailand, during 2001-2007. They were identified using classical taxonomy into 3 subspecies of *M. acuminata* Colla ssp. *malaccensis* (Ridl.), ssp. *siamea* Simmonds and ssp. *burmanica* Simmonds, 1 hybrid of ssp. *siamea x* ssp. *burmanica* and others.

Wild bananas were found mostly in the open area, along water ways and creeks of various forest types, except in pines and bamboo forests. Most of wild bananas were found in the area of light intensity between 0.68 – 98.40 Klx, air temperature between 17 -45 °C, soil water holding capacity (%WHC) between 10 - 90%, soil pH from 4 - 9, relative humidity (%RH) between 20 -100% and elevation from 200 - 1700 m. However, results from multivariate analyses indicated that different groups were significantly preferred different environmental conditions. Hybrid, ssp. *siamea* and ssp. *burmanica* were significantly presented strong correlations to altitude, soil pH, %WHC, temperature, %RH, light intensity, and open space. Other1, 2 and ssp. *malaccensis* were specifically found in unique environmental conditions of Umphang Wildlife Sanctuary. The relationships of habitat environment and different groups of wild bananas were essential information for further study on the germplasm utilization and conservation. This habitat information was very important due to banana morphology and physiology respond variously to various habitat environment and genetic component. Morphological variations were variously different, even ssp. *siamea*, ssp. *burmanica* and hybrid which were classified into the same group by numerical taxonomy.

Keywords: *Musa acuminata* Colla, Habitat Environment, Wild Banana

INTRODUCTION

This work is aim to understand the habitats environment of wild banana which are classified by classical taxonomy to gain better picture with their morphological characters.

Edible bananas are derived from *M. acuminata* Colla (Stover & Simmonds, 1987). Thailand and nearby countries in Southeast Asia are in the wild banana distribution center. Morphological variations and taxonomy of them in northern Thailand have been called for more information since the works of Cheesman (1948), Simmonds (1956), and De Langhe *et al.* (1998). The variations of geographical and environmental conditions in lower northern Thailand created ecological diversity, which possibly introduced morphological variations of this species. This region was the important destination of *M. acuminata* diversity explorations because of no previous systematic surveys records. In addition, this area has been proposed as the interception of *M. acuminata* subspecies' distribution and high priority study area in Thailand (De Langhe *et al.*, 1998).

Morphological variations and environmental factors play major roles in the struggle, survival, adaptation and loss of plant species (Hansson *et al.*, 1995). Environmental factors functions as natural selection pressures that affect morphological variations, diversities and distributions. Geographical features such as elevation of land and latitude changes are associated with changes in climate and environment that result in major changes on life forms (Jones, 1992; Morin, 1999). However, the influences of environmental factors on the diversity of bananas in this sub - regions are usually overlooked and not clearly investigate.

In addition, the wild bananas in lower northern Thailand are in danger due to the rapid expansion of agricultural lands and forest devastations. Some isolated wild banana populations may be well adapted under unique environmental conditions and may develop beneficial genetic materials / morphological characters. The study on environmental factors in relation to variations of wild banana groups in lower northern Thailand will be an interesting model and will provide useful information for further utilization of germplasm resources as well as conservation. According to the main constraints of commercial variety improvements and breeding programs Edible bananas are derived from *M. acuminata* Colla (Stover & Simmonds, 1987). Thailand and nearby countries in Southeast Asia are in the wild banana distribution center. Morphological variations and taxonomy of them in northern Thailand have been called for more information since the works of Cheesman (1948), Simmonds (1956), De Langhe *et al.* (1998). The variations of geographical and environmental conditions in lower northern Thailand created ecological diversity, which possibly introduced morphological variations of this species. This region also was the important destination of *M. acuminata* diversity explorations because of no previous systematic surveys records. In addition, this area has been proposed as the interception of *M. acuminata* subspecies' distribution and high priority study area in Thailand (De Langhe *et al.*, 1998).

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MATERIALS AND METHODS

Habitat Environment of Wild Banana (*Musa acuminata* Colla) Groups were analyzed following the methods of Ludwig and Reynolds (1988), ASEAN (1990), Jones (1992), Griffiths (1994), Petersen (1994), Jorgensen *et al.* (1996), Kaosa – ard (1989), Kimmins (1997), Morin (1999), and Gliessman (2000). The aims are to gain the baseline information of the habitat and understand the primary environmental conditions. They were altitude, relative humidity (%RH), air temperature, light intensity, elevation, soil texture, soil pH, and soil Water Holding Capacity (%WHC). Plant community profiles were recorded and were redrawn on profile diagram using the method derived from Elliott *et al.* (1989). The survey lines, sample locations and zoning of the different forest types were analyzed on GIS framework using ARCVIEW 3.2 (Haines-Young *et al*., 1993; Frohn, 1998).

RESULTS

Habitat of Wild Banana (*Musa acuminata* Colla)

1) Forest Conditions of the Study Sites

Umphang Wildlife Sanctuary area is about 2,519 km^2 consists of mountainous range of 100-2,152 m. The main forests are hill evergreen forest, dry evergreen forest and mixed deciduous forests. Thung Salaeng Luang National Park area is 1,262.55 km^2 consists of hill evergreen, dry evergreen, deciduous and pine forests. Mae Wong National Park is about 894 km^2. The major forest is deciduous forest. Phu Hin Rong Kra National Park is consists of dry dipterocarp, hill evergreen and pine forests. Lamnamnan National Park is about 999.15 km^2 consists of mix deciduous, dipterocarp, bamboo, grassland, dry evergreen and hill evergreen forests. Namnaow National Park is about 966 km^2 consists of dipterocarp, mix evergreen, evergreen, pine and grassland. The environmental conditions of six study sites were varied. Summary of site's information on geographical features, climatic conditions, plants and wildlife was presented in Appendix C

2) Wild Banana Groups in Different Forest Types

Difference morphological groups of wild banana were found in difference forest types within 6 study sites of lower northern Thailand (Table 4.16; Figure 4.15) Their positions were recorded on the GIS map in Figure 4.1 Ssp. *siamea*, ssp. *burmanica* and ssp. *siamea x* ssp. *burmanica* hybrid distributed widely in various forest types through out this sub - region while ssp. *malaccensis* and other groups located in specific areas of the western forests (Table 4.16) Moreover, the environmental factors of wild bananas in the habitats were presented in Table 4.16– 4.22 and forest profiles were shown in Figure 4.15 It is interesting that all samples were found in the open space of the forests, where taller trees were absent and the banana canopies could receive optimum sunlight.

In addition, they were always found in the higher moisture areas than in the drier areas within the same forest types. Most of the time, they were found close to the waterways and creeks (Figure 4.15)

Table 4.16 Number of samples in parenthesis distributed in various forest types of six wild banana

groups within 6 study sites.

Forest Type	ssp. *siamea x* ssp. *burmanica* hybrid	ssp. *malaccensis*	other 1	other 2	ssp. *siamea*	ssp. *burmanica*
HEF	(3) Up, (4) Mw, (9) Ph, (4) Ln	(11) Up	(11) Mw	-	(11) Up, (16) Mw, (9) Ph, (25) Ln	(2) Up, (4) Mw, (11) Ph, (1) Ln
DEF	(1) Ln	-	(1) Nw	(1) Nw	(7) Ln	(2) Ln
MDF	(2) Mw, (2) Ph, (5) Ln	-	-	(11) Up	(7) Up, (18) Tl, (20) Mw, (21) Ph, (10) Ln	(3) Up, (8) Tl, (1) Mw, (6) Ph, (2) Ln
GL	(4) Ph	-	-	-	(2) Tl	(5) Ph
AG	-	-	-	-	(13) Tl	(8) Tl
DD	-	-	-	-	(2) Ln, (1) Nw	(1) Ln
MEF	(3) Nw	-	-	-	(26) Nw	(15) Nw

Remark: Up = Umphang Wildlife Sanctuary, Tl = Thung Salaeng Luang National Park, Mw = Mae Wong National Park, Ph = Phu Hin Rong Kra National Park, Ln = Lumnamnan National Park; Nw = Namnaow National Park, HEF= Hill Evergreen Forest, DEF= Dry Evergreen Forest, MDF= Mixed Deciduous Forest, DD = Dry Dipterocarp Forest, MEF = Moist Evergreen Forest, Gl = Grassland, AG= New Agriculture area.

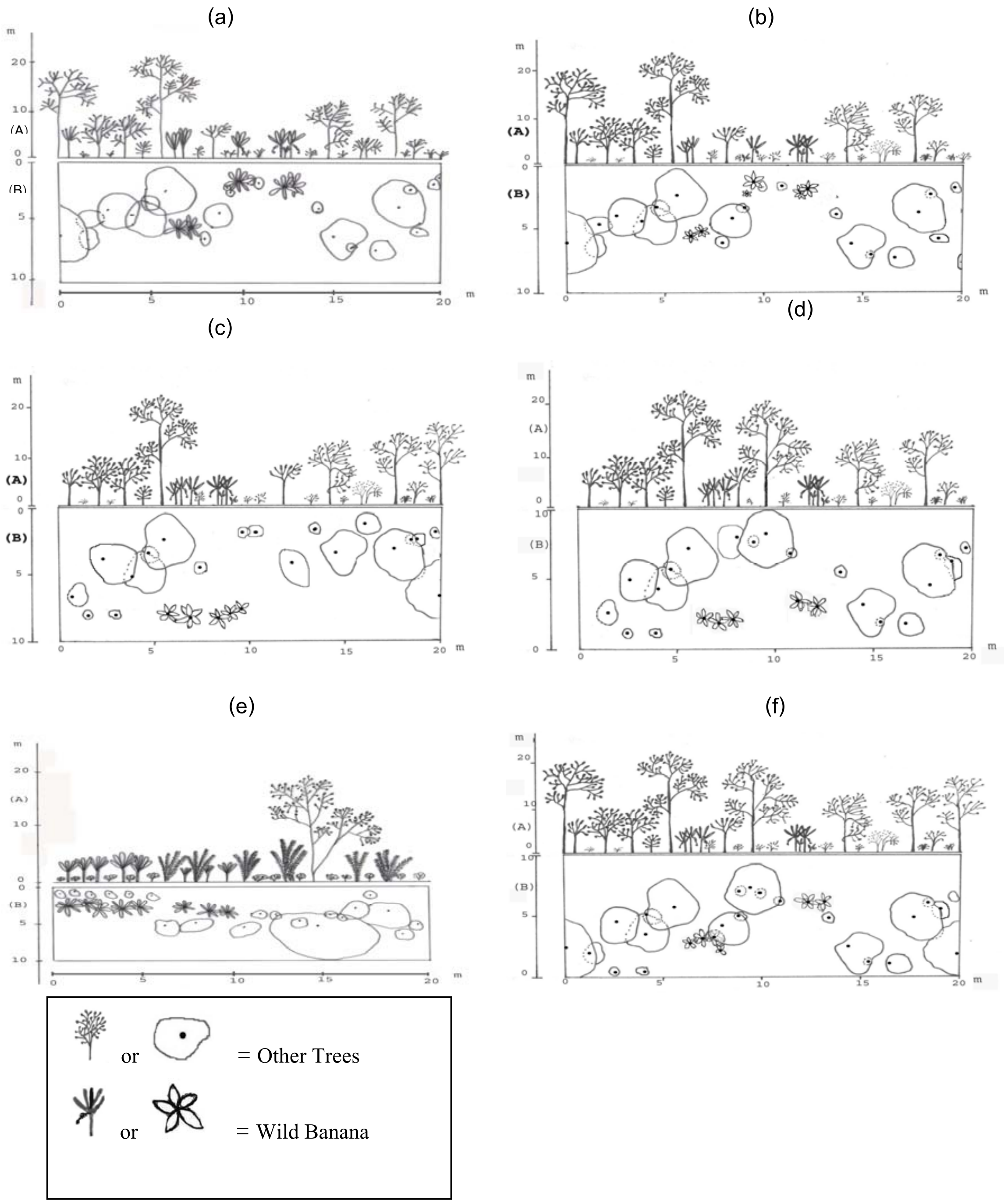


Figure 4.15 Forest profiles **(A)** and top view **(B)** of the banana populations along the transect Lines of **(a)** Up16 (ssp. *siamea x* ssp. *burmanica* hybrid**), (b)** Mw10 (Other 1), **(c)** Up25 (ssp. *malaccensis* (Ridl.)), **(d)** Up36 (Other 2), **(e)** Mw11 (ssp. *siamea* Simmonds), and **(f)** Up17 (ssp. *burmanica* Simmonds)

Environmental conditions of wild banana habitats are shown in the Table 4.17 – 4.22

Table 4.17 Minimum, maximum and means with standard errors of environmental conditions of ssp. *siamea x* ssp. *burmanica* hybrid

Factor	Minimum	Maximum	Mean, ± S.E
Altitude (m)	216.00	1347.00	952.24 ± 65.60
pH	5.09	7.45	5.90 ± 0.11
Water Holding capacity (%)	12.44	53.50	34.14 ± 1.03
Slope (%)	5.00	65.00	34.14 ± 4.17
Temperature under the canopy (^{0}C)	16.57	39.90	28.50 ± 1.03
Temperature outside the habitat (^{0}C)	21.40	40.90	31.08 ± 0.92
Moisture under the canopy (%RH)	24.80	85.30	56.90 ± 3.00
Moisture outside the habitat (%RH)	37.00	85.90	54.92 ± 2.41
Light intensity under the canopy (Klx)	0.15	26.60	5.36 ± 1.27
Light intensity at the top of canopy (Klx)	1.29	85.50	17.26 ± 3.29
Light intensity outside the habitat (Klx)	6.29	131.50	51.63 ± 6.68
Space under the canopy (%)	10.00	85.00	30.86 ± 3.35
Space at the canopy (%)	5.00	70.00	38.79 ± 3.24
Space above the canopy (%)	5.00	70.00	30.34 ± 2.99
Soil Type : Silt loam,	Soil is narrow to deep, well to very well drainage. Soil was found on steep slope such hill or mountainous areas		
Loam	Soil it is allocated on almost flat or steep slope areas, bedrock and laterite were found in 50 cm depth from soil surface		

Table 4.18 Minimum, maximum and means with standard errors of environmental conditions of Other 1

Factor	Minimum	Maximum	Mean, ± S.E
Altitude (m)	279.00	461.00	304.00 ± 14.31
pH	4.77	8.00	6.63±0.31
Water Holding Capacity (%)	12.65	84.80	51.72±5.80
Slope (%)	5.00	50.00	16.25 ± 4.31
Temperature under the canopy (^{0}C)	25.00	37.50	33.20 ± 1.18
Temperature outside the habitat (^{0}C)	31.60	37.30	35.50 ± 0.61
Moisture under the canopy (%RH)	36.70	69.70	50.40 ± 3.73
Moisture outside the habitat (%RH)	37.40	67.70	42.98 ± 2.89
Light intensity under the canopy (Klx)	1.30	3.51	2.67 ± 0.20
Light intensity at top of canopy (Klx)	6.98	22.00	13.33 ± 1.52
Light intensity outside the habitat (Klx)	21.80	41.10	28.94 ± 1.72
Space under the canopy (%)	10.00	30.00	18.33 ± 2.97
Space at canopy (%)	40.00	60.00	46.67± 2.84
Space above the canopy (%)	10.00	50.00	35.00 ± 5.57
Soil Type : Silt loam,	Soil is narrow to deep, well to very well drainage. Soil was found on steep slope such hill or mountainous areas		
Loam	Soil it is allocated on almost flat or steep slope areas, bedrock and laterite were found in 50 cm depth from soil surface		

Table 4.19 Minimum, maximum and means with standard errors of environmental conditions of *M. acuminata* Colla ssp. *malaccensis* (Ridl.)

Factor	Minimum	Maximum	Mean, ± S.E
Altitude (m)	1037.00	1088.00	1067.18 ± 4.15
pH	5.99	8.20	6.94 ± 0.19
Water Holding Capacity (%)	6.29	19.70	9.31 ± 1.41
Slope (%)	10.00	60.00	45.45 ± 6.62
Temperature under the canopy (^{0}C)	30.40	36.70	32.09 ± 0.87
Temperature outside the habitat (^{0}C)	33.00	38.50	34.50 ± 0.77
Moisture under the canopy (%RH)	43.60	49.00	47.75 ± 0.67
Moisture outside the habitat (%RH)	36.40	46.50	43.74 ± 1.42
Light intensity under the canopy (Klx)	1.90	11.77	9.44 ± 0.79
Light intensity at top of canopy (Klx)	5.96	95.30	71.00 ± 12.57
Light intensity outside the habitat (Klx)	86.00	121.40	95.65 ± 4.98
Space under the canopy (%)	20.00	30.00	27.27 ± 1.41
Space at canopy (%)	20.00	50.00	28.18 ± 4.23
Space above the canopy (%)	30.00	50.00	44.55 ± 2.82
Soil Type : Silt loam	Soil is narrow to deep, well to very well drainage. Soil was found on steep slope such hill or mountainous areas		

Table 4.20 Minimum, maximum and means with standard errors of environmental conditions of Other 2

Factor	Minimum	Maximum	Mean, $\pm$ S.E
Altitude (m)	489.00	523.00	498.27 $\pm$ 4.79
pH	5.74	8.08	7.12$\pm$0.27
Water Holding Capacity (%)	9.33	67.74	27.44$\pm$6.29
Slope (%)	10.00	40.00	25.45 $\pm$ 3.12
Temperature under the canopy (^{0}C)	28.70	34.05	31.27 $\pm$ 0.64
Temperature outside the habitat (^{0}C)	35.05	37.70	36.57 $\pm$ 0.29
Moisture under the canopy (%RH)	44.35	55.70	50.65 $\pm$ 1.30
Moisture outside the habitat (%RH)	36.20	47.20	43.19 $\pm$ 1.67
Light intensity under the canopy (Klx)	1.86	12.15	4.33 $\pm$ 1.18
Light intensity at top of canopy (Klx)	12.65	49.67	26.47 $\pm$ 3.74
Light intensity outside the habitat (Klx)	18.60	108.75	48.09 $\pm$ 11.89
Space under the canopy (%)	30.00	50.00	42.73 $\pm$ 3.04
Space at canopy (%)	10.00	40.00	31.82 $\pm$ 4.23
Space above the canopy (%)	10.00	40.00	25.45 $\pm$ 3.90
Soil type : Silt loam	Soil is narrow to deep, well to very well drainage. Soil was found on steep slope such hill or mountainous areas		

Table 4.21 Minimum, maximum and means with standard errors of environmental conditions of *M. acuminata* Colla ssp. *siamea* Simmonds.

Factor	Minimum	Maximum	Mean, $\pm$ S.E
Altitude (m)	216.00	1611.00	720.24 $\pm$ 23.22
pH	4.23	8.33	6.24 $\pm$ 0.06
Water Holding Capacity (%)	8.27	48.32	24.63 $\pm$ 0.75
Slope (%)	5.00	75.00	35.03 $\pm$ 1.75
Temperature under the canopy (^{0}C)	2.92	45.30	29.58 $\pm$ 0.37
Temperature outside the habitat (^{0}C)	3.50	49.00	31.49 $\pm$ 0.32
Moisture under the canopy (%RH)	29.60	95.70	66.27 $\pm$ 0.85
Moisture outside the habitat (%RH)	31.00	93.90	63.15 $\pm$ 0.91
Light intensity under the canopy (Klx)	0.09	10.35	6.74 $\pm$ 0.79
Light intensity at top of canopy (Klx)	0.68	95.60	21.02 $\pm$ 1.43
Light intensity outside the habitat (Klx)	5.22	131.50	50.11 $\pm$ 2.42
Space under the canopy (%)	0.00	90.00	38.38 $\pm$ 1.27
Space at canopy (%)	5.00	80.00	35.48 $\pm$ 1.08
Space above the canopy (%)	0.00	70.00	26.28 $\pm$ 1.24
Soil type : Silt loam	Soil is narrow to deep, well to very well drainage. Soil was found on steep slope such hill or mountainous areas		
Loam	Soil it is allocated on almost flat or steep slope areas, bedrock and laterite were found in 50 cm depth from soil surface		
Loamy sand	Soil is deep, moderate to well drainage, medium-coarse textured soil and low in soil fertility		

Table 4.22 Minimum, maximum and means with standard errors of environmental conditions of *M. acuminata* Colla ssp. *burmanica* Simmonds.

Factor	Minimum	Maximum	Mean, ± S.E
Altitude (m)	296.00	1611.00	846.39 ± 37.94
pH	4.96	8.80	6.52 ± 0.08
Water Holding Capacity (%)	7.42	58.20	25.33 ± 1.34
Slope (%)	5.00	80.00	24.08 ± 2.38
Temperature under the canopy (^{0}C)	19.67	38.70	30.33 ± 0.44
Temperature outside the habitat (^{0}C)	23.80	45.10	31.83 ± 0.46
Moisture under the canopy (%RH)	35.50	89.30	63.83 ± 1.55
Moisture outside the habitat (%RH)	31.40	92.20	59.95 ± 1.70
Light intensity under the canopy (Klx)	0.23	22.30	5.94 ± 0.67
Light intensity at the top of canopy (Klx)	0.68	98.40	24.67 ± 2.71
Light intensity outside the habitat (Klx)	5.81	136.00	52.98 ± 4.49
Space under the canopy (%)	0.00	90.00	6.38 ± 2.41
Space at canopy (%)	10.00	60.00	34.41 ± 1.69
Space above the canopy (%)	0.00	70.00	29.08 ± 2.35
Soil type : Silt loam	Soil is narrow to deep, well to very well drainage. Soil was found on steep slope such hill or mountainous areas		
Loam	Soil it is allocated on almost flat or steep slope areas, bedrock and laterite were found in 50 cm depth from soil surface		
Loamy sand	Soil is deep, moderate to well drainage, medium-coarse textured soil and low in soil fertility		

3) Multivariate Analysis of Variance between Habitat Environment and Groups of Wild Banana

Multivariate analysis of variance was used to investigate environmental factors relation to groups of wild banana (Appendix C) Bartlett's test of sphericity was used to detect the relationships between environmental factors and groups. The significant value shown in the Table 4.23 indicated that the relationships were significant different among them at $p = 0.05$. Each Group of wild bananas responded differently to environmental factors.

The variances of environmental factors were significantly different among six groups at $p = 0.05$ (Table 4.24). There were altitude, %WHC, slope, temperature under wild banana canopy and temperature ratio, moisture under banana canopy and moisture ratio, light intensity at top of wild banana canopy and light intensity ratio, population space at top and under of wild banana canopy. These indicated that each group of wild bananas required different environmental conditions. However, pH and the open space of population at the forest canopy (population canopy) were not significant different among groups.

Table 4.23 Hypothesis testing on the residual covariance matrix.

Intercept = environmental factors, and Group = Group of wild banana

Bartlett's Test of Sphericity [a]

Likelihood Ratio	.000
Approx. Chi-Square	18386.026
df	90
Sig.	.000

Tests the null hypothesis that the residual covariance matrix is proportional to an identity matrix.

a. Design: Intercept+group

Table 4.24 Levene's test of equality of error variance's

Levene's Test of Equality of Error Variances[a]

	F	df1	df2	Sig.
Altitude (m)	11.741	5	320	.000
pH	2.069	5	320	.069
Water Holding Capacity (%)	6.539	5	320	.000
Slope (%)	7.129	5	320	.000
Temperature under canopy (Celsius)	2.543	5	320	.028
Temperature out side (Celsius)	4.130	5	320	.001
Moisture under canopy (%)	5.722	5	320	.000
Moisture out side (%)	5.653	5	320	.000
Light intensity under canopy (Klx)	4.953	5	320	.000
Light intensity top canopy (Klx)	8.436	5	320	.000
Population under canopy (%)	4.115	5	320	.001
Population canopy (%)	.898	5	320	.482
Population top canopy (%)	2.977	5	320	.012

Tests the null hypothesis that the error variance of the dependent variable is equal across groups.

a. Design: Intercept+group

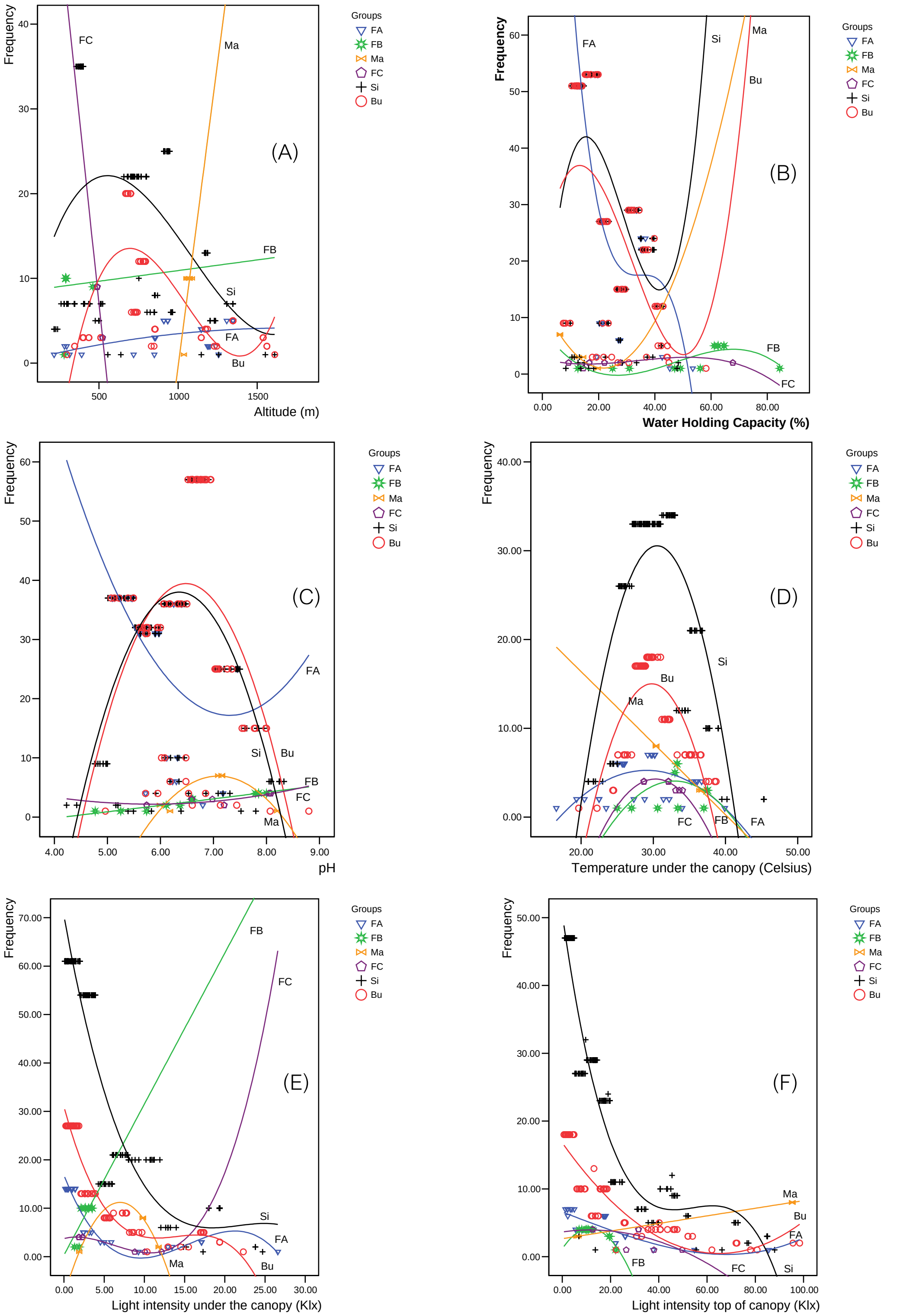


Figure 4.16 Relationships of **(A)** various altitudes **(B)** water holding capacity percentage (%WHC) of the soils, **(C)** soil pH, **(D)** temperatures under their canopies, **(E)** light intensity (Klx) under banana canopy within habitats, **(F)** light intensity (Klx) at the top of wild banana canopy within the habitats and distribution of 3 subspecies and 3 forms of wild banana in lower northern Thailand. Ma = ssp. *malaccensis* (Ridl.) Simmonds; Si = ssp. *siamea* Simmonds; Bu = ssp. *burmanica* Simmonds; FA = ssp. *siamea x* ssp. *burmanica* hybrid; FB = Other1; FC = Other2

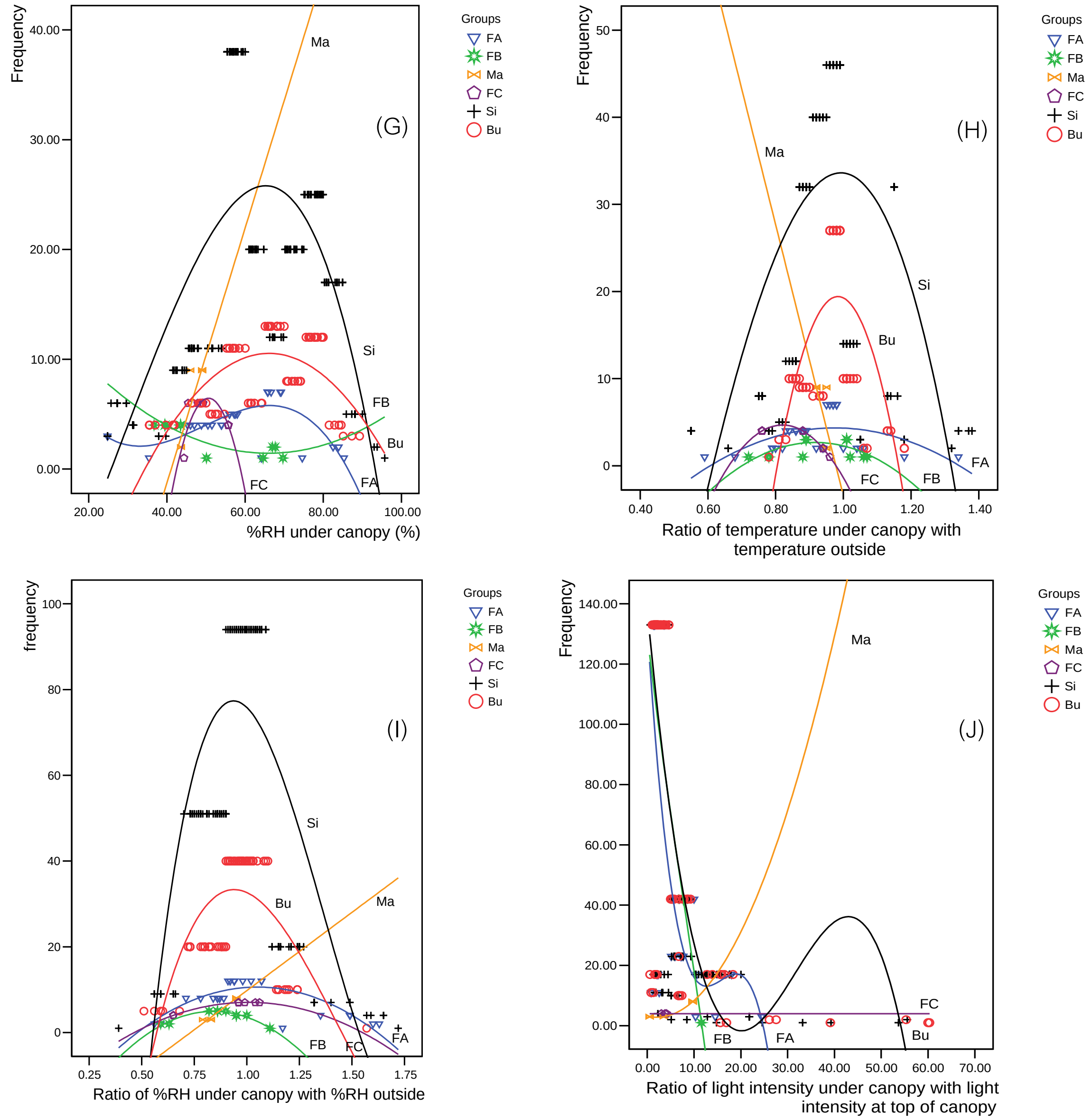


Figure 4.16 Relationships of **(G)** relative humidity conditions under canopy within the habitats, **(H)** ratio between temperatures under canopy and at the open space outside the sampling area, **(I)** relative humidity percentage ratio at the ground surface under the sample canopy and at the open space outside the sampling area, **(J)** light intensity ratio between at ground surface under banana canopy and at the open space outside the sampling area and distribution of 3 subspecies and 3 forms of wild banana in lower northern Thailand, Ma = ssp. *malaccensis* (Ridl.) Simmonds; Si = ssp. *siamea* Simmonds; Bu = ssp. *burmanica* Simmonds; FA = ssp. *siamea x* ssp. *burmanica* hybrid; FB = Other 1; FC = Other 2 (Cont.)

4) Groups of Wild Bananas and their Environmental Factors

Environmental factors of wild bananas in relevance to the morphological groups were demonstrated in Figure 4.16 and were summarized as follows:

A. Altitude

Morphological groups of wild bananas in lower northern Thailand were distributed in differential elevation between 200 – 1,700 m above mean sea level (Figure 4.16, A). Ssp. *siamea x* ssp. *burmanica* hybrid was a small group but showed broad distribution ranges. 29 samples were spreading in 5 sites between 216 – 1,347 m and intensively distributed at 800 – 1,200 m (Table 4.18, A). Other1, 2 and ssp. *malaccensis* were rare and were found only within narrow areas of some forest communities. Their low population sizes limited them within isolated habitats with clumped distribution pattern in each forest. Other1, with low number of 12 samples, was found only in two national parks. They were particularly established at 279 and 461 m within the rain forests of Mw and Nw. Eleven samples of ssp. *malaccensis* showed clumped distribution within a specific area of Up at the elevation of 1,037 – 1,088 m. Other2 also indicated specific distribution range in small area of Up at the elevation of 489 - 523 m.

Subspecies *siamea* had wide distribution in all study sites, establishing at 216 - 1611 m. It indicated that this group can distribute in the low lands. Other 2 populations was found only in flat lands of mixed deciduous forests at altitude between 477 - 523 m of Up, where the areas were very dry in dry season. This indicated an ecological difference to *M. acuminata* Colla's habitat. Subspecies *burmanica* distributed widely in 6 study sites between altitude of 500 - 1200 m. Different Groups distributed differently according to its altitudes (Figure 4.16, A).

B. Soil Water Holding Capacity

Samples of wild bananas found in lower northern Thailand were distributed in various levels of the soil water holding capacity of the habitats (Figure 4.16, B). The %WHC of *ssp. malaccensis* was short due to their low population sizes with clumped distribution in specific habitats. They were found only at the soil with %WHC of 9.31 $\pm$ 1.41%.

Ssp. *siamea* x ssp. *burmanica* hybrid was well established between 15-50 %WHC, while the number of samples decreased with the higher %WHC, indicating poor establishment in wet soil. On the other hand, Other1 distributed in broader %WHC range of 10 - 90%. However, this form was found only in the rainforests of Mw and Nw, where the water was available to the root zone throughout the year. Therefore, %WHC may not be the limiting factor of this form.

Subspecies *malaccensis* was well established within a narrow %WHC between 5 - 20%. The limited %WHC was the result of rare status. Other 2 distributed in wider range of %WHC between 10 - 70%. This indicated that Other 2 could establish in wider area as they were commonly found along the survey trails of the Up study site.

Large samples of ssp. *siamea* were distributed intensively between 8 - 50 %WHC of six study sites. The population size was reduced as %WHC increase. This indicated that when %WHC was higher than 50%, it would limit the distribution of this subspecies.

Subspecies *burmanica* was distributed intensively between 15 - 45% WHC and decreased rapidly outside this range. This indicated that this subspecies preferred the well drainage soil with low to medium %WHC. Samples of this subspecies were found in most forest types with high rainfall and high relative humidity. They were not found in pine forests, grasslands and bamboo forests due to the long dry periods and forest fires. In addition, the response of them to %WHC showed significantly different form others (Figure 4.16, B).

C. Soil pH

Wild bananas responded to soil pH in various patterns. However, all samples were found between pH 5 - 8.5 (Figure 4.16, C). Most of them were reduced in numbers when the pH was lower or higher than 6.5 or 7.5. Ssp. *siamea x* ssp. *burmanica* hybrid was well established between pH 5 – 6.5. Then the numbers were reduced rapidly when the soil pH was higher than 6.5. Other 1 spread out uniformly between pH 5 - 8. This phenomenon reflected that pH was not a strong influence on Other 1 distribution pattern. Subspecies *malaccensis* and Other 2 were well grown in the pH conditions similar to those of Other 1.

Eleven samples of ssp. *malaccensis* were grown in clumped in a specific habitat at Up and established in pH between 6 - 8.

Subspecies *siamea* was well established and well grown in pH between 4 - 8, in which the optimum pH was between 6.5 - 7.5. Subspecies *burmanica* was well established between pH 5 - 9. The frequency curve behaved quite similar to those of the ssp. *siamea*. These may be due to both groups distributed in similar locations and grew in the same habitats in all 6 study sites. The means and standard errors of pH were significantly different among groups (Figure 4.16, C), whereas the relationships of pH and groups were not significant.

D. Temperature under Canopy

Temperature data were collected under canopy of wild bananas in its habitats. Banana of different groups grew and distributed in various temperatures under the canopies, ranging between 17 - 45^{0}C (Figure 4.16, D). Ssp. *siamea x* ssp. *burmanica* hybrid, Other 1, Other 2, ssp. *siamea* and ssp. *burmanica* responded to the temperature under their canopies in similar patterns. But, there were differences with high or low frequencies accordance to their upper or lower limitation of temperatures. Ssp. *siamea x* ssp. *burmanica* hybrid was well established between 16.6 - 39.9^{0}C. Other 1 was established between 25.0 - 37.5^{0}C. The range of optimum temperature of Other 2 was between 28.7 - 34.1^{0}C. Subspecies *siamea* grew well in wider range of temperature between 20.9 – 45.3^{0}C. The optimum conditions of ssp. *burmanica* was between 19.6 – 38.7^{0}C. This curve is similar to ssp. *siamea*, but the range of temperature was narrow than ssp. *siamea*. This means that ssp. *siamea* grew and survived in wider temperature conditions in various habitats. The response curves indicated that the lowest temperature for wild bananas was about 15 ^{0}C.

Distribution patterns of ssp. *malaccensis* were different from the rest. They were found between 30.4 - 36.7 $^{\circ}$C, probably because they were the isolation population from the central distribution areas in the south of Thailand. These numbers of samples were low and its distribution was limited in only one habitat. In addition, means and standard errors of temperature under banana canopy were significantly different among groups (Figure 4.17, D).

E. Light Intensity under Canopy

Light intensity data were collected under canopy of wild bananas in their habitats. Three subspecies and three forms were distributed with similar patterns of the light intensity under the canopy between 0.09 – 27.76 Klx (Figure 4.17, E). General observations were that wild bananas were never found in thick and dense forests, where the sunlight could not penetrate through the forest ground.

Ssp. *siamea x* ssp. *burmanica* hybrid was well established at the light intensity under the canopy between 0.15 - 26.60 Klx. This pattern was similar to Other 2, ssp. *siamea*, and ssp. *burmanica*. However, there were different in the lowest limited of light intensity. These were associated with the low numbers with clumped distribution patterns in the specific habitats. Other 2, ssp. *siamea*, and ssp. *burmanica* were found between 1.86 – 12.15, 0.09 – 10.35, and 0.23 – 22.30 Klx, respectively. On the other hand, the light intensity conditions under the canopy of Other 1 and ssp. *malaccensis* were between 1.30 – 3.51 Klx and 1.90 – 11.7 Klx, respectively. Moreover, means and standard errors of light intensity under the banana canopies were significantly different (Figure 4.17, E).

F. Light Intensity at the Top of Canopy

Light intensity data were collected at the top of the canopy in the wild bananas. They were distributed generally between the ranges of 0.68 – 98.40 Klx. All wild bananas were not found under the light intensity lower than 0.09 Klx. This is probably due to the high competition among plants to receive enough solar energy. Favorable light intensity conditions were between 0.09 – 27.76 Klx. Their responded patterns were quite similar to the light intensity conditions under the canopy (Figure 4.16, F).

Ssp. *siamea x* ssp. *burmanica* hybrid, Other 1, ssp. *malaccensis*, Other 2, ssp. *siamea* and ssp. *burmanica* were well established between 1.29 – 85.50, 6.98 – 22.00, 5.96 – 95.30, 12.65 – 49.67, 0.68 – 95.60 and 0.68 – 98.40 Klx, respectively. Furthermore, the light intensity at the top of banana canopies was significantly different among groups at $p = 0.05$ (Figure 4.17, F).

G. Relative Humidity under Canopy

Air moisture or relative humidity (%RH) data were collected under the canopy of wild bananas within the forest habitats (Figure 4.16, G). Most of them responded to %RH between 20 - 100% and grew well at 40 - 90%RH.

Ssp. *siamea x* ssp. *burmanica* hybrid was distributed between 24.8 – 85.3%RH in all 5 study sites. Other 1 established at %RH between 36.70 – 69.70. This form was quite interesting due to its isolated distribution in Mw and Nw. The distributions of spp. *malaccensis* and Other 2 indicated such narrow ranges between 43.60 – 49.00%RH and 44.35 – 55.70%RH, respectively. This situation may be due to their low population numbers and clumped distribution within a specific habitat of Up. Subspecies *siamea* established the widest range between 29.60 – 95.72%RH. This was also meaningful to explain their capacity to grow in larger areas and in various habitats. Subspecies *burmanica* responded in the similar directions as ssp. *siamea* but with narrower range of %RH between 35.50 – 89.30. Moreover, means and standard errors of %RH were significantly different among groups (Figure 4.17, G).

H. Temperature Ratio

The temperature ratio values were the temperature under the canopy of wild bananas divided by the temperature of adjacent open area where this wild banana tree was not found (Figure 4.16, H). The distributions of all wild banana groups responded positively to the cooler temperatures within the forest habitats, where the temperature ratios were between 0.70 – 1.90. There were two subsets. Firstly, Other 1, Other 2 and ssp. *malaccensis* were found between the ratios of 0.70 - 1.07. Other 1, Other 2 and ssp. *malaccensis* were distributed between ratios of 0.72 – 1.07, 0.76 – 0.9 and 0.92 – 0.95, respectively. Narrow ranges of the ratio values were possibly due to their small samples of Other 1, Other 2 and ssp. *malaccensis*, and their specific habitats with clumped distribution pattern. To understand these situations, its required more information and more studies. Secondly, ssp. *siamea x* ssp. *burmanica* hybrid, ssp. *siamea* and ssp. *burmanica* were found in the wider range of the ratio between 0.70 - 1.90. This second subset was ssp. *siamea x* ssp. *burmanica* hybrid, ssp. *siamea* and ssp. *burmanica*, which distributed in the wider range. Ssp. *siamea x* ssp. *burmanica* hybrid established well in the widest range of the temperature ratios between 0.59 - 1.34. Subspecies *siamea* and ssp. *burmanica* were established in narrower ranges, 0.55 – 1.38 and 0.78 – 1.18. In addition, there were significant differences between means and standard errors of these temperature ratios.

I. Relative Humidity Ratios

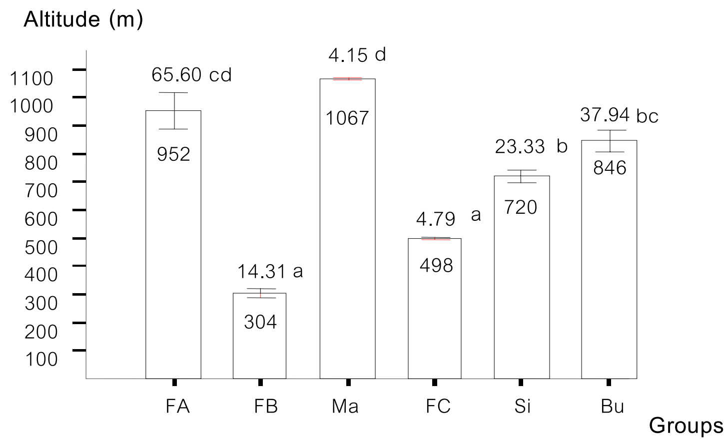
The ratios of %RH values were %RH under the canopy of wild bananas in the habitats divided by %RH of the adjacent open space where the other banana tree was absent. All wild banana groups grew under high %RH (Figure 4.16, I) within the forest habitats, where the range of ratios between %RH under the canopy and %RH in the open space were between 0.4 – 2.0. There were two subsets. Ssp. *siamea x* ssp. *burmanica* hybrid, ssp. *siamea* and ssp. *burmanica* were in the first subset. The ratios of them were between 0.56 – 1.63, 0.39 – 1.72 and 0.51 – 1.34, respectively. Its were very interesting that the average means of these three groups were close to the ratios value of 1.1 while the highest peak of the curves depended upon larger size of samples. The second subsets of %RH ratios were Other 1, Other 2 and ssp.

malaccensis, which were in various patterns. However, most of them were distributed within the ratio of %RH between 0.50 - 1.10. Other 1 samples established wider within the ratio of %RH between 0.59 – 1.11 whereas ssp. *malaccensis* and Other 2 were distributed between the ratios of 079 – 0.95 and 0.65 – 1.06, respectively. In addition, there were significant differences between means and standard errors of %RH ratios.

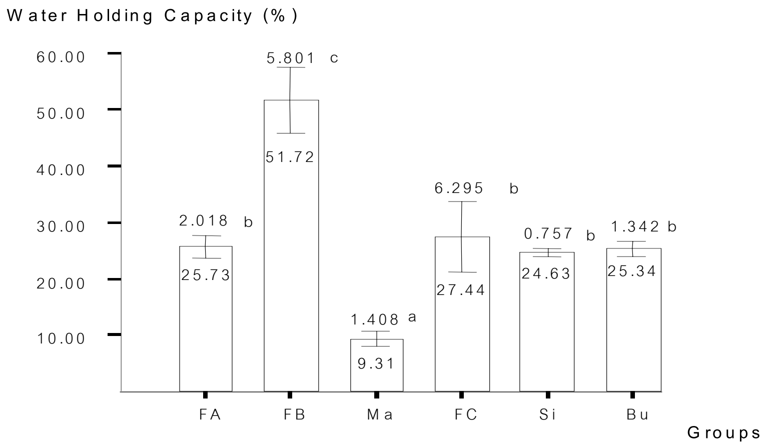
J. Light Intensity Ratios

Light intensity ratio data were calculated from the light intensity under the canopy of wild bananas divided by the light intensity of adjacent open space (Figure 4.16, J). All groups grew where the range of the ratios were between 0.02 - 0.98 (Figure 4.16, E - F). It was very interesting that all wild bananas were intensively distributed under the low light intensity ratios between 0.02 - 0.50. There was no banana found when the ratios were lower than 0.02 or higher than 1.0.

The relationships between different morphological groups and the light intensity ratio conditions can be explained by two subsets. First subset was ssp. *siamea x* ssp. *burmanica* hybrid, ssp. *siamea* and ssp. *burmanica*, where the ratios were between 0.001 – 0.40, 0.01 – 0.96 and 0.01 – 0.66, respectively. Second subsets of Other 1, Other 2 and ssp. *malaccensis* were partially vary in ratios and showed various patterns of which the ratios were in such narrow and specific ranges of 0.03 – 0.41, 0.07 – 0.12 and 0.02 – 0.33, respectively. In addition, there were significant differences between means and standard errors of light Intensity ratios.



(A)



(B)

Figure 4.17 Thirteen environmental factors demonstrate on the relations to six morphological groups of wild banana within the habitats of lower northern, Thailand. There were **(A)** altitude (m), **(B)** Water Holding Capacity (%), **(C)** pH, **(D)** temperature under the canopy (^{o}C), **(E)** light intensity under the canopy (Klx), **(F)** light intensity at top of canopy (Klx), **(G)** moisture under the canopy (%RH), **(H)** temperature outside the habitat (^{o}C), **(I)** moisture outside the habitat (%RH), **(J)** light intensity outside the habitat (Klx), **(K)** slope (%), **(L)** population space under the canopy (%), **(M)** population space at canopy (%), **(N)** population space above the canopy (%), Ma = ssp. *malaccensis* (Ridl.) Simmonds; Si = ssp. *siamea* Simmonds; Bu = ssp. *burmanica* Simmonds; FA = ssp. *siamea x* ssp. *burmanica* hybrid; FB = Other 1; FC = Other 2

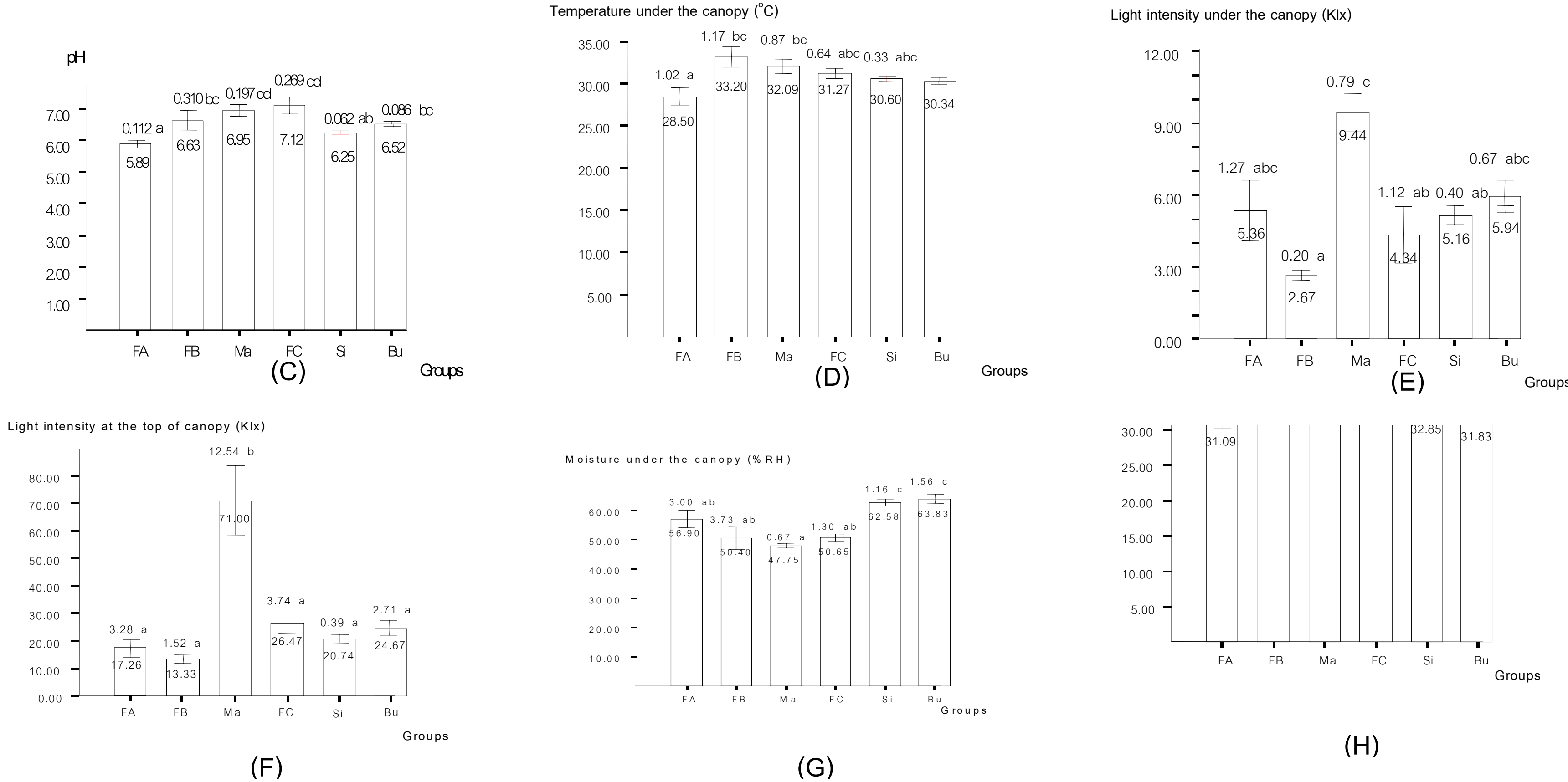


Figure 4.17 Thirteen environmental factors demonstrate on the relations to six morphological groups of wild banana within the habitats of lower northern, Thailand. (Cont.)Ma = ssp. *malaccensis* (Ridl.) Simmonds; Si = ssp. *siamea* Simmonds; Bu = ssp. *burmanica* Simmonds; FA = ssp. *siamea x* ssp. *burmanica* hybrid; FB = Other 1; FC = Other 2

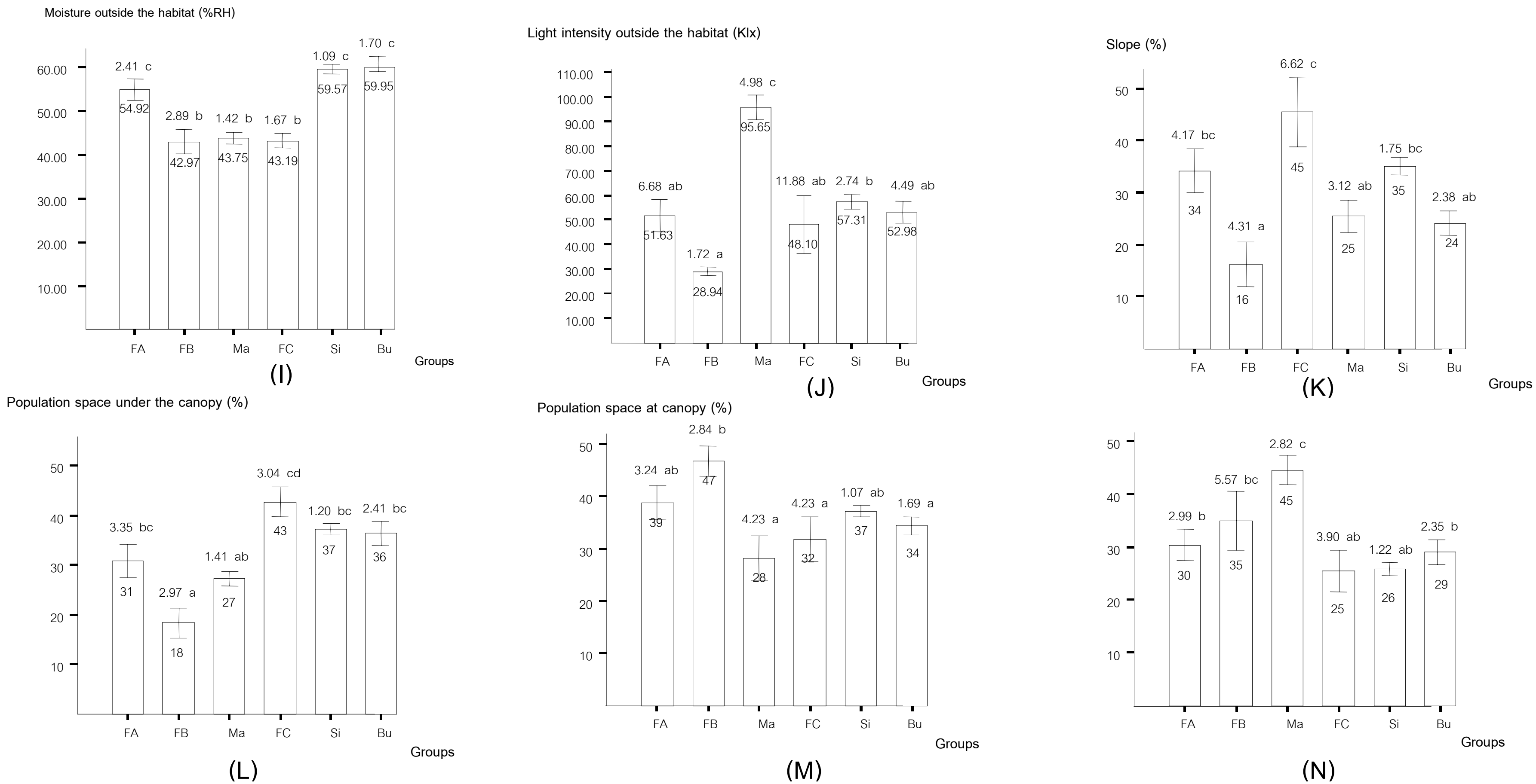


Figure 4.17 Thirteen environmental factors demonstrate on the relations to six morphological groups of wild banana within the habitats of lower northern, Thailand. (Cont.))Ma = ssp. *malaccensis* (Ridl.) Simmonds; Si = ssp. *siamea* Simmonds; Bu = ssp. *burmanica* Simmonds; FA = ssp. *siamea x* ssp. *burmanica* hybrid; FB = Other 1; FC = Other 2

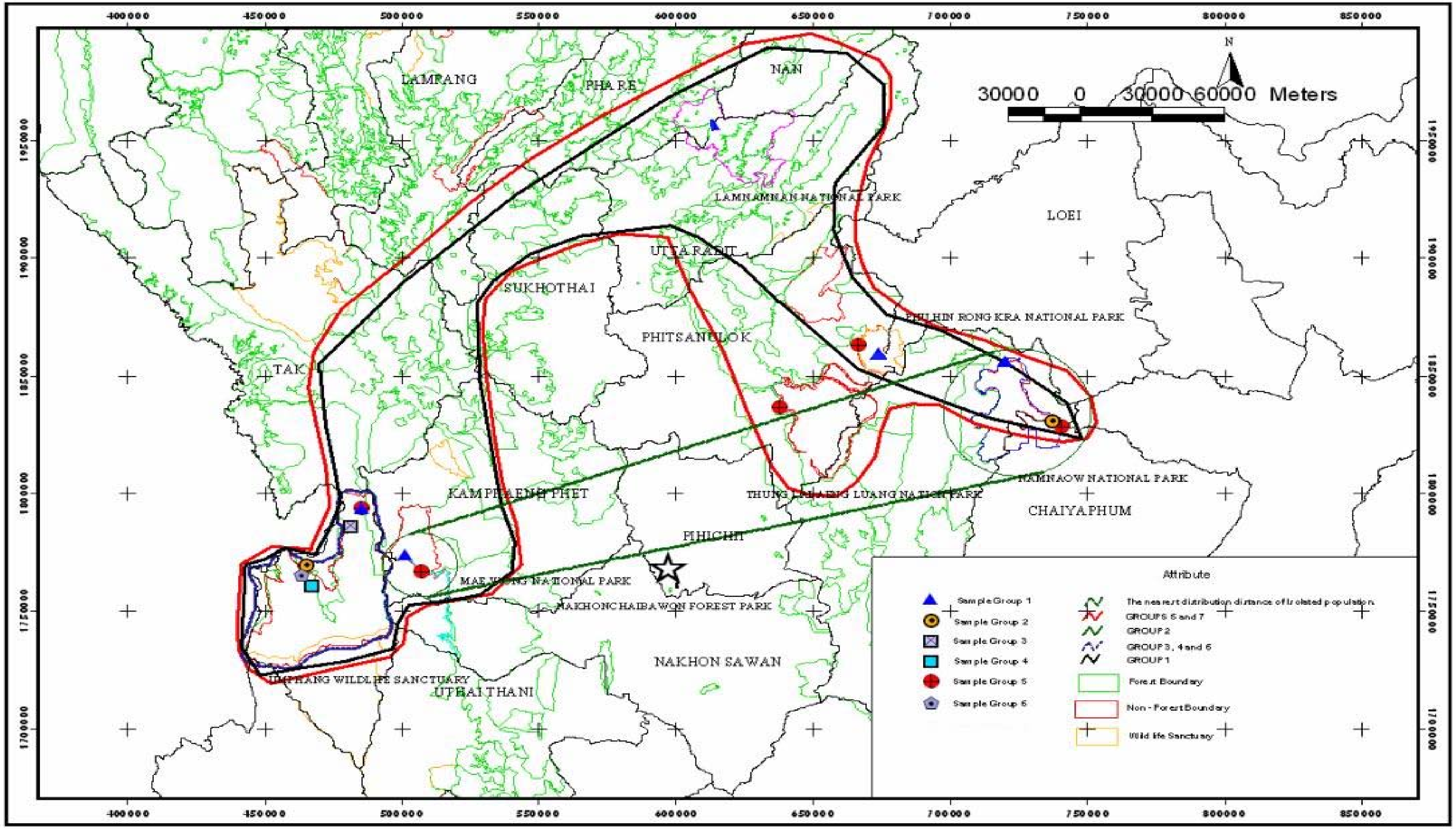


Figure 4.18 Distribution map of six morphological groups of wild bananas in lower northern, Thailand

CONCLUSION AND DISCUSSION

The baseline information of the accessions' habitat are primary reflect the primary environmental conditions of habitat relation to different group from classical taxonomy. These results indicated that altitude, soil Water Holding Capacity (%WHC) and soil pH of ssp. *siamea x* ssp. *burmanica* hybrid, ssp. *siamea* and ssp. *burmanica* habitat are quite similar in pattern and intercepted in the same range. While the other information are not indicated any relation to the accession distribution such as humidity (%RH), air temperature, light intensity and soil texture. Moreover, the habitat conditions of ssp. *malaccensis*, Other 1 and Other 2 were different from each other. It is very interesting that these results are synchronized with the group separation from numerical taxonomy. Ssp. *siamea x* ssp. *burmanica* hybrid, ssp. *siamea* and ssp. *burmanica* are in one group, while ssp. *malaccensis* is isolated in other group. Other 1 and Other 2 are classified as outliers of mutant or other hybrids. However, further research should be conducted on the different group distribution and respond to different habitat condition.

The results in this study are primary information of the accessions' habitat. Six morphological groups of wild bananas distributed in various forest types (Table 4.16; Figure 4.15) The distributions and their morphological variations among groups may be due to the genetic variations of the populations, dispersal process and adaptations to the habitats (Table 4.17 – 4.23) Different wild banana groups showed different responses to 13 environmental factors (Table 4.23 – 4.24; Figure 4.16 – 4.17) Their adaptations to these environmental factors can be demonstrated by various graphs (Figure 4.16 – 4.17) Ssp. *siamea x* ssp. *burmanica* hybrid, ssp. *siamea* and ssp. *burmanica* distributed with large number of samples in many locations which showed wider and broader areas. On the other hand, Other 1, Other 2 and ssp. *malaccensis* were found in the specific environmental conditions with low number of samples. These may due to their narrow and specific optimum environmental conditions. Future researches should be focused on the intensive explorations of these low population groups and investigation on the environmental conditions of each group. Moreover, the establishments of *in situ* experiments with continuous environmental monitoring systems are necessary. These *in situ* experiments should cover all variations of wild bananas which are found in lower northern Thailand, such as in Thung Salaeng Luang National Park and / or Umphang Wildlife Sanctuary or Mae Wong

National Park. These will provide further information and understanding on groups' performances.

This study indicated that water is the most important limiting factor in banana life cycle. Low rainfalls with long dry period in lower northern Thailand (Appendix C) increase higher amount of water evaporation from soil and reduce soil water content (Appendix C) Low %RH for a long time induces vapor pressure deficit. If the air temperature, evaporation and light intensity are also too high during summer with poor %WHC, it will cause severe effects to wild bananas. It was found that all wild bananas did not established in soil with %WHC lower than 10. The effects of too high and too low with rapid changing of these factors can cause seriously impacts on the rates of various processes such as respiration, transpiration, growth and *etc.* Most of wild bananas are dried out and become wilting with serious damages, and do not survive in these conditions. Forest fires would generally destroy and change those suitable habitats and community conditions. However, forest fires also provide optimum space and environmental conditions for young banana seedlings after rainy season. Changes of both unsuitable and suitable environmental conditions have been driving the balances and successions of those wild banana groups.

The observations on wild bananas showed that they were always located in the open space of the forest canopy where taller trees were absent (Table 4.17 – 4.23) The optimum open space will allow enough light intensity to pass through the top of the banana canopy. In addition, when the forest or plant community is changing through the succession stages, the seeds of wild bananas will germinate under the suitable temperature, %WHC, and low light intensity. That is why wild bananas have been called a pioneer species due to its rapidly growth after the forests have been destroyed. However, the high number of wild banana populations will dominate in those areas until the trees take over the habitats. Then, the wild bananas will face less suitable environmental conditions because the light intensity ratio required by bananas are about half of the solar energy and less than this ratio of growth and productivity will be reduced (Figure 4.16 J). Most of cultivated bananas grow well in soil with well drainage and pH is between 4 to 8.5. In addition, suitable slope will provide better runoff with no flooding and water logging. These conditions are observed in these wild banana habitats.

The results from the ratios of environmental factors, such as temperature, light intensity and relative humidity, indicated the balance of ecological conditions that secure or reduce the environmental factor fluctuation of all non- and rhythmic changes. Treatable and harmful conditions are reduced by the intact, primary, secondary and/or multi-stories forest profiles. Forests types or plant communities have functioned like boundary layers to protect wild bananas from unfavorable conditions. These microclimate environments with optimum conditions will ensure and fulfill the banana requirements, which introduce growth after seeds disposal and then germinated, which considerably reduce the negative environmental impacts or further damages.

All banana samples were always located in the higher moisture conditions than those dryer areas within the same forest type and/or most of the time closed to the waterways that are similar to the observations of Cheesman (1948) and De Langhe *et al.* (1998). Moreover, this study indicate ranges of environmental conditions of habitats such as light intensity above canopy (0.68 - 98.40 Klx), air temperatures (17 - 45°C), %WHC (10 - 90%), pH (4-9), %RH (20 - 100%), and elevation (200 - 1700m) (Figure 4.16 – 4.17) These environmental conditions are provided more details and similar to the reports of Howes (1928), Simmonds (1956), and De Langhe *et al.* (1998).

Ssp. *siamea x* ssp. *burmanica* hybrid was widely distributed in five study sites, except in the southeast of lower northern Thailand (Table 4.17) Other1 was distributed within small isolated areas and in unique environmental conditions of Mae Wong and Namnaow National Parks, where the former large forests between Kamphang Phet, Phichit and south of Phetchabun were changed to agricultural areas long times ago. Promising character is low temperature tolerance, which should be useful for future breeding program. The interesting point is that other1 had similar male bud form characters of *M. flaviflora* N. W. Simmonds, which is never found in Thailand, while, *M. flaviflora* central distribution is in Malaysia and north of Australia (Simmonds, 1956). Further advanced taxonomic and molecular genetic works are required on this promising group.

M. acuminata Colla ssp. *malaccensis* (Ridl.) Simmonds, which is a new record in lower northern Thailand, has its intensively distribution center in the southern region of Thailand (Simmonds, 1956; Howes, 1928).

Other 2 presents mixed characters of ssp. *malaccensis* and *M. flaviflora*, which has never been recognized because ssp. *malaccensis* is always found crossing with ssp. *siamea* within upper northern region of Thailand (De Langhe *et al.*, 1998). However, ssp. *malaccensis*, ssp. *siamea* and ssp. *burmanica* were commonly distributed in six study sites. The distributions of ssp. *burmanica* is found along the Thai - Burma border and reconfirmed its distributions as mentioned by Simmonds (1956). In addition, these results are also filled up the central distribution gaps of *M. acuminata* Colla within lower northern Thailand and linked up with the distributions in the upper northern survey of De Langhe *et al.* (1998).

In conclusion, ssp. *siamea x* ssp. *burmanica* hybrid, ssp. *siamea* and ssp. *burmanica* are low fidelity due to their wider distributions in six study sites. This means that they are highly adaptive to broader environmental conditions. In contrast, Other 1, Other 2 and ssp. *malaccensis* are high fidelity, which distribute in the narrower environmental conditions. This may be the reason why they are found in unique habitats with low population density. Further comparison studies on the morphology and environmental factors should be expanded to the northeastern and western regions of Thailand, where morphological variations among groups should be focused and investigated along the geographical ranges. The understanding on environmental factors and further R&D will provide future utilization of these valuable genetic materials for the world banana industry and food security. The relationships of habitat environment and different groups of wild bananas were essential information for further study on the germplasm utilization and conservation. This habitat information was very important due to banana morphology and physiology respond variously to various habitat environment and genetic component. Morphological variations were variously different, even ssp. *siamea*, ssp. *burmanica* and ssp. *siamea x* ssp. *burmanica* hybrid which were classified into the same group by cluster analyses.

CHAPTER 5

PHYLOGENY OF *(Musa acuminata* Colla) FROM LOWER NORTHERN THAILAND AND ITS RELATED CULTIVARS ON DNA ANALYSIS

ABSTARCT

Phylogentic study focused on 36 accessions of *Musa acuminata* Colla (AA) and reference accessions. There were 16 accessions from the Lower Northern Thailand and the outgroup taxa were 20 accessions from other regions in Thailand. The complex of banana was determined by polymorphisms in chloroplast non - coding loci. Four cp - marker loci (*rpl* 16, *ndh* A introns, *psa* A - *ycf* 3 and *pet* A - *psb* J – *psb*L - *psb*F intergenic spacers) with PCR - RF - SSCP (Polymerase Chain Reaction-Restriction Fragment - Single Strand Conformation Polymorphism or PRS) analyses were employed to understand its relations within wild bananas. The clusters of accessions were also recognized by the polymorphic bands by each cp - marker. PRS techniques presented primary useful information on diversity within *M. acuminata*. In addition, better distinguish and cluster among all accessions were clearer with 4 cp - markers. Polymorphism within each of the genomes included single different nucleotide substitutions and insertions / deletions (indels). In DNA sequence data indicated a distinct population on phylogenetic analyses using the program MrBayes 3.1.2. These indicated the different within population from the same location and also presented the network or close relationships within all accessions from different areas. The mutation points in the network analyses were very important information to understand the relationships and evolution of all banana accessions. These indicated that various kind relations of different locations may strongly introduced with their parental genetic materials. Moreover, these techniques provided clearer understanding on *M. acuminata* diversity and reconfirmed the classical and numerical taxonomy. However, intensive researches with various

and vast number of cp - markers and large number sample of world accessions are required to explain the complete banana taxonomy and evolution.

Keywords: Phylogeny, *Musa acuminata*, Bananas, DNA Analysis.

INTRODUCTION

The phylogeny of wild banana (*M. acuminata* Colla: AA) in Thailand with DNA information is urgently required to investigate due to very confusing in its classical taxonomy and classification. Most of DNA research works focused on only the domesticated cultivars and the existing accessions in the world collection. However, there was an interesting work which focused on *M. balbisiana* Colla or BB and its related cultivars. The Southeast Asia ABB / BBA complex of bananas were determined by polymorphisms in chloroplasts with non - coding loci. Four cp - marker loci (*rpl* 16, *ndh* A introns, *psa* A - *ycf* 3 and *pet* A - *psb* J - *psb*L - *psb*F intergenic spacers) with PCR - RF - SSCP (Polymerase Chain Reaction-Restriction Fragment - Single Strand Conformation Polymorphism or PRS) analysis were employed to understand its diversity (Swangpol, 2003; Swangpol *et al.,* 2007). Polymorphism within each of the genomes included single nucleotide substitutions and insertions / deletions (indels). DNA sequence data with different treatments of indels indicated a distinct population of wild *M. balbisiana* in northern Thailand based on phylogenetic analyses (Swangpol, 2003; Swangpol *et al.,* 2007). These techniques are also applied in this research.

The objective of this study was to investigate cpDNA diversity to of *M. acuminata* Colla from Lower Northern Thailand and its related accessions.

MATERIALS AND METHODS

DNA sequences were obtained from thirty - six accessions of *M. acuminata* (Musa section Eumusa, 11 chromosomes) representing different locations in Thailand (Table 5.1). These DNA sequences were analysed as phylogentic trees and network.

1. DNA Sequences Analyses

DNA of the 36 accessions was extracted from banana buds using DNeasy Plant Minikit. Sixteen accessions of *M. acuminata* from the lower northern Thailand were selected representing different groups identified by classical and numerical taxonomy. They were AAw_LN20, AAw_MW10, AAw_MW20, AAw_MW31, AAw_NW22, AAw_NW33, AAw_NW38, AAw_NW41, AAw_PH04, AAw_PH05, AAw_TL18, AAw_UP16, AAw_UP18, AAw_UP25, AAw_UP36 and AAw_UP37. 10 more accessions of *M. acuminata* from different parts of Thailand were selected from other 3 regions of Thailand. They were AAw_Chanthaburi1, AAw_Chanthaburi2, AAw_Chanthaburi3 and AAw_Chanthaburi4 as representating ssp. *siamea,* AAw_Kanchanaburi1, AAw_Kanchanaburi2 and AAw_Kanchanaburi3 representating ssp. *burmanica, and* AAw_Trang1, AAw_Trang2 and AAw_Trang3 representating of ssp. *malaccensis*. In addition, nine individual accessions of wild *M. acuminata* were also introduced from different parts of Thailand, which were AAw_MaeYom, AAw_Ranong, AAw_Salaween, AAw_Chanthaburi, AAw_Yala, AAw_Prachuabkhirikhan, AAw_Rayong, AAw_Mukdahan, AAw_Trang. M. schizocarpa was used as an outgroup accession.

Four primer sets were chosen from chloroplast DNA sequences of NCBI Genebank for amplifications of the non-coding region (Appendix D). Comparison of the chloroplast of rice, tobacco and other species indicated that these regions contained mononucleotide repeats. PCR amplification primers were designed in the flanking conserved regions (Sawangpol *et al.,* 2007). The locations of the selected fragment on rice cp - genome were in Appendix D. PRS analyses protocols (Orita *et al*., 1989; Jordan *et al*., 1998; Sato & Nishio 2002) modified were based on previous techniques of Swangpol (2003) and Swangpol *et al.,* (2007). PCR was conducted in a total reaction mixture of 10 microL. Restriction enzyme was added and the digestion let to proceed. Formamide loading dye was added to the digested products and the reactions were denatured for 10 min at 95°C and cooled down to stabilize single strands. Then 3.5 ml aliquots were loaded on non - denaturing polyacrylamide gel and electrophoresis was performed with standard procedure of silver straining. Accessions showing polymorphic bands were grouped as haplotypes and were selected for cloning and sequences or sequenced directly.

For cloning and sequencing, undigested PCR fragments were purified by using MinElute PCR Purification Kit (Qiagen), ligated into either TOPO TA Cloning kit (Invitrogen) or pGEM-T Vector System (Promega) and transformed into *E. coli* 'DH10B' using electroporation. Plasmids were extracted using the Wizard® *Plus* SV miniprep DNA Purification System (Promega) and sent for sequencing (Macrogen, Inc, Seoul, South Korea) (Appendix D).

The selected haplotypic fragments and nucleotide sequences were aligned with the GeneDoc program version 2.6.002 (Nicholas & Nicholas, 1997; Swangpol, 2003; Swangpol; *et al.,* 2007). Then the base compositions were determined by analysis of the aligned matrix using the DnaSP program version 4 (Rozas *et al.,* 2003; Swangpol, 2003; Swangpol *et al*., 2007). Then all cpDNA sequences were analyses and compared.

2. Phylogenetic and Network Analyses

Phylogenetic analyses on the relationships among *Musa* cpDNA were inferred with the out group accessions using the program MrBayes 3.1.2 on DNA comparison and analyses. These extracted DNA samples were kindly collaborated by Dr. Hugo Volkaert, Center of Agricultural Biotechnology (CAB), Kasetsart University Kamphaengsaen Campus. M_schizocarpa_ITC was included as an out group in both phylogenetic and network analyses.

The Bayesian trees were created equally weighted of 36 accessions with all characters for phylogenetic analyses. General time reversible model of nucleotide substitutions was used with gamma distribution of rates of substitution and a proportion of invariants. The Markov Chains were run for 1,000,000 generations. The 50% majority consensus tree was then calculated for all saved trees. Bayesian posterior probabilities are indicated.

Gene genealogies were estimated on these accessions by parsimony haplotype network reconstruction using statistical parsimony algorithm (Templeton *et al*., 1992) and generated by the program TCS 1.13 (Clement *et al*., 2000) with unrooted cladograms of a high probability (>95%). Insertion deletions were counted as one mutational event irrespective of their length and analyzed as fifth stage. Nucleotide substitutions with indels were treated as additional events (Swangpol, 2003; Swangpol *et al.,* 2007). The signal mutations could code from indels.

Table 5.1 List of *Musa* accessions, origins and sources of accessions.

No.	**Code**	**Origin** [a]	**Source** [b]	**Species/Cultivar**
1	AAw_LN20 *	Lumnamnam, Uttaradit, Thailand	DW	Wild *M. acuminata* Colla
2	AAw_MW10 *	Mae Wong, Khamphagphet, Thailand	DW	Wild *M. acuminata* Colla
3	AAw_MW20 *	Mae Wong, Khamphagphet, Thailand	DW	Wild *M. acuminata* Colla
4	AAw_MW31 *	Mae Wong, Khamphagphet, Thailand	DW	Wild *M. acuminata* Colla
5	AAw_NW22 *	Namnaow, Phetchabun, Thailand	DW	Wild *M. acuminata* Colla
6	AAw_NW33 *	Namnaow, Phetchabun, Thailand	DW	Wild *M. acuminata* Colla
7	AAw_NW38 *	Namnaow, Phetchabun, Thailand	DW	Wild *M. acuminata* Colla
8	AAw_NW41 *	Namnaow, Phetchabun, Thailand	DW	Wild *M. acuminata* Colla
9	AAw_PH04 *	Phu Hin Rong Kla, Phitsanulok, Thailand	DW	Wild *M. acuminata* Colla

Table 5.1 List of *Musa* accessions, origins and sources of accessions. (Cont.)

No.	Code	Origin [a]	Source [b]	Species/Cultivar
10	AAw_PH05 *	Phu Hin Rong Kla, Phitsanulok, Thailand	DW	Wild *M. acuminata* Colla
11	AAw_TL18 *	Thung Salaeng Luang, Phitsanulok, Thailand	DW	Wild *M. acuminata* Colla
12	AAw_UP16 *	Umphang, Tak, Thailand	DW	Wild *M. acuminata* Colla
13	AAw_UP18 *	Umphang, Tak, Thailand	DW	Wild *M. acuminata* Colla
14	AAw_UP25 *	Umphang, Tak, Thailand	DW	Wild *M. acuminata* Colla
15	AAw_UP36 *	Umphang, Tak, Thailand	DW	Wild *M. acuminata* Colla
16	AAw_UP37 *	Umphang, Tak, Thailand	DW	Wild *M. acuminata* Colla
17	AAw_Chanthaburi1 *	Chanthaburi, Thailand	DW	Wild ssp. *siamea*
18	AAw_Chanthaburi2 *	Chanthaburi, Thailand	DW	Wild ssp. *siamea*
19	AAw_Chanthaburi3 *	Chanthaburi, Thailand	DW	Wild ssp. *siamea*
20	AAw_Chanthaburi4 *	Chanthaburi, Thailand	DW	Wild ssp. *siamea*
21	AAw_Kanchanaburi1 *	Kanchanaburi, Thailand	DW	Wild ssp. *burmanica*
22	AAw_Kanchanaburi2 *	Kanchanaburi, Thailand	DW	Wild ssp. *burmanica*
23	AAw_ Kanchanaburi3 *	Kanchanaburi , Thailand	DW	Wild ssp. *burmanica*
24	AAw_Trang1 *	Trang, Thailand	DW	Wild ssp. *malaccensis*
25	AAw_Trang2 *	Trang , Thailand	DW	Wild ssp. *malaccensis*

Table 5.1 List of *Musa* accessions, origins and sources of accessions. (Cont.)

No.	Code	Origin [a]	Source [b]	Species/Cultivar
26	AAw_Trang3 *	Trang, Thailand	DW	Wild ssp. *malaccensis*
27	AAw_MaeYom**	LomDong, MaeYom, Phrae, Thailand	CAB, KU	Wild ssp. *siamea*
28	AAw_Ranong **	Ranong, Thailand	CAB, KU	Wild ssp. *malaccensis*
29	AAw_Chanthaburi **	Chanthaburi, Thailand	CAB, KU	Wild ssp. *siamea*
30	AAw_Yala **	Betong, Yala, Thailand	CAB, KU	Wild ssp. *malaccensis*
31	AAw_Prachuabkhirikhan **	Prachuabkhirikhan, Thailand	CAB, KU	Wild ssp. *burmanica*
32	AAw_Rayong **	Rayong, Thailand	CAB, KU	Wild ssp. *siamea*
33	AAw_Mukdahan **	Mukdahan, Thailand	CAB, KU	Wild ssp. *siamea*
34	AAw_Trang **	Trang, Thailand	CAB, KU	Wild ssp. *malaccensis*
35	AAw_Salaween **	Salaween, MaeHongSon, Thailand	CAB, KU	Wild ssp. *malaccensis*
36	M_schizocarpa_ITC **	?	ITC	*M. schizocarpa*

* = accessions from the field survey and DNA sequencing; ** = The out group accessions for Phylogenetic and Network analyses, **a** = Indicates known origins; **b =** indicates sources of accessions; **DW** = Field Collection by Det Wattanachaiyingcharoen; **CAB, KU** = Center of Agricultural Biotechnology, Kasetsart University Kamphaengsaen Campus; **ITC** = International Transit Center, International Network for the Improvement of Banana and Plantain (INIBAP), Leuven, Belgium.

RESULTS

1. Chloroplast Haplotype Analysis by PRS

Eighteen haplotypes of 35 accessions from Thailand were distinguished by PRS analyses of the four cp - regions (Table 5.2). The polymorphic bands indicated the different among these accessions (Figure 5.1).

Table 5.2 Chloroplast haplotypes of 35 accessions from PCR - RF - SSCP (PRS) analyses of *Musa* with R - IN/*Hfl*, PY - S, N - IN/*Hfl* and AF - S/*Tql*.

Cp Haplotypes[a]	Accession Code [b]
AAw1?	AAw_Ranong
AAw2?	AAw_Yala
AAw3?	AAw_Prachuabkhirikhan, AAw_Chanthaburi3
AAw	AAw_Mukdahan, AAw_Chanthaburi4
AAw	AAw_Trang
AAw	AAw_Rayong
AAw	AAw_Chanthaburi
AAw	AAw_MaeYom, AAw_LN20
AAw	AAw_MW10, AAw_MW20,AAw_MW31, AAw_UP16, AAw_UP18
AAw	AAw_Salaween, AAw_UP25, AAw_UP37
AAw	Aw_NW22, AAw_NW33, AAw_NW38, AAw_NW41, AAw_PH04, Aw_PH05, AAw_TL18, AAw_Kanchanaburi1, AAw_Kanchanaburi3,
AAw	AAw_UP36
AAw	AAw_Chanthaburi1
AAw	AAw_Chanthaburi2
AAw	AAw_Kanchanaburi2

Table 5.2 Chloroplast haplotypes of 35 accessions from PCR - RF - SSCP (PRS) analyses of *Musa* with R - IN/*Hfl*, PY - S, N - IN/*Hfl* and AF - S/*Tql*. (Cont.)

Cp Haplotypes[a]	Accession Code [b]
AAw	AAw_Trang1, AAw_Trang2
AAw	AAw_Trang3

[a] Chlorplast haplotypes of four regions; R - IN/*HfI* = *rpl16* intron digested with *HinfI* restriction enzyme, PY - S = undigested *psa*A - *ycf3* intergenic spacer, N - IN/*HfI* = *ndh*A intron digested with *HinfI* restriction enzyme, and AF - S/*TqI* = *pet*A – *psb*J – *psb*L - *psb*F intergenic spacers digested with *TaqI* restriction enzymes; [b] Accession code appears according to Table 5.1.

Remark: Only accessions from Thailand; *M. schizocarpa* is not included.

2. Cp DNA Sequence Analyses

The 35 accessions were representatively selected on their haplotypes and geographical distribution in Thailand for DNA sequencing. The objectives were to focus on distinguishes and to understand the relations mainly within Thailand and related accessions. The complete cp-sequences are presented in Appendix D. The sequence of the four cpDNA regions consisted for 73% of non-coding regions (Appendix D). The sequences length ranged from 5,461 - 5,506 bp (Appendix D) and was summarized in Table 5.3 – 5.6.

For the *rpl*16 sequences, six subgroups within two major groups could be differentiated (Table 5.3) according to the changes at the 5 positions of single nucleotide substitutions and insertions/deletions (indels) (Appendix D). Various indels of base positions were in AAw_Trang, AAw_Yala, AAw_Ranong, AAw_Chanthaburi1 and AAw_Chanthaburi2 at 44, 232, 693, 450 and 450, respectively. In contrast, the deletions of base positions were in group 2 at 0 - 387. Again six subgroups within two major groups were distinguished using *psa*A sequences (Table 5.4) according to the changes and different in the 3 areas of single nucleotide substations and insertions/deletions (indels) (Appendix D). Two major groups were separated by the indels at 0 - 192, 246 and 481 - 505, respectively.

Figure 5.1 Example of polymorphic bands in *psa*A gel, which indicated some different between 35 accessions.

Remark: Only accessions from Thailand; *M. schizocarpa* is not included.

Table 5.3 Groups of 35 *Musa* accessions patterns with *rpl*16 .

GROUP	***rpl*16 Accessions**
1	AAw_Prachuabkhirikhan, AAw_MW10, AAw_MW20, AAw_MW31, AAw_UP16, AAw_UP18, AAw_Rayong, AAw_Chanthaburi, AAw_Mukdahan, AAw_UP25, AAw_UP37, AAw_LN20, AAw_MaeYom, AAw_NW22, AAw_NW33, AAw_NW38, AAw_NW41, AAw_PH04, AAw_PH05, AAw_TL18, AAw_UP36
1.1	AAw_Trang
1.2	AAw_Yala
1.3	AAw_Ranong
2	AAw_Chanthaburi3, AAw_Chanthaburi4, AAw_Kanchanaburi1, AAw_Kanchanaburi2, AAw_ Kanchanaburi3, AAw_Trang1, AAw_Trang2, AAw_Trang3
2.1	AAw_Chanthaburi1, AAw_Chanthaburi2

Table 5.4 Groups of 35 *Musa* accessions patterns with *psa*A.

GROUP	***psa*A Accessions**
1	AAw_Ranong, AAw_Yala, AAw_Trang, AAw_Prachuabkhirikhan, AAw_Rayong, AAw_Chanthaburi, AAw_Mukdahan, AAw_Salaween
1.1	AAw_MaeYom
2	AAw_MW10, AAw_MW20, AAw_MW31, AAw_UP16, AAw_UP18, AAw_UP25, AAw_UP37, AAw_Chanthaburi1, AAw_Chanthaburi2, AAw_Chanthaburi3, AAw_Chanthaburi4, AAw_Trang3
2.1	AAw_LN20, AAw_NW22, AAw_NW33, AAw_NW38, AAw_NW41, AAw_PH04, AAw_PH05, AAw_TL18, AAw_UP36, AAw_Kanchanaburi1, AAw_Kanchanaburi2, AAw_ Kanchanaburi3
2.2	AAw_Trang1, AAw_Trang2

There were 11 subgroups within 5 major groups under ndhA sequences (Table 5.5) according to the changes and different in the 3 areas of single nucleotide substations and insertions/deletions (indels) (Appendix D). Five major groups were separated by the indels at 597, 640, 705 - 730, 738, 797, 859 and 1135 -1160, respectively.

There were 10 subgroups within 2 major groups under *pet*A sequences (Table 5.6) according to the changes and different in the 7 areas of single nucleotide substations and insertions / deletions (indels) (Appendix D). Five major groups were separated by the indels at 749 - 751, 933 - 934, 1420 - 1440, 1769 - 1780, 1790 - 1803, 2179 and 2232, respectively.

Table 5.5 Groups of 35 *Musa* accessions patterns with *ndh*A.

GROUP	***ndh*A Accessions**
1	AAw_Prachuabkhirikhan, AAw_Chanthaburi2, AAw_Chanthaburi3,
	AAw_Trang1, AAw_Trang2 AAw_Trang3, AAw_MW10, AAw_MW20,
1.1	AAw_MW31, AAw_UP16, AAw_UP18
	AAw_Kanchanaburi1, AAw_Kanchanaburi3, AAw_NW22, AAw_NW33,
1.2	AAw_NW38, AAw_NW41, AAw_PH04, AAw_PH05, AAw_TL18, AAw_UP36
1.3	AAw_Kanchanaburi2
1.4	AAw_Ranong
	AAw_Chanthaburi1
2	AAw_Rayong, AAw_Mukdahan, AAw_Chanthaburi4
3	AAw_MaeYom, AAw_Chanthaburi, AAw_LN20
3.1	AAw_Yala
3.2	AAw_Trang
4	AAw_Salaween, AAw_UP25, AAw_UP37,

Table 5.6 Groups of 35 *Musa* accessions patterns with *pet*A.

GROUP	***pet*A Accessions**
1	AAw_Yala, AAw_ Prachuabkhirikhan, AAw_Ranong
1.1	AAw_Trang
2	AAw_Chanthaburi, AAw_Mukdahan, AAw_UP25, AAw_UP37, AAw_Salaween, AAw_Chanthaburi1, AAw_Chanthaburi2, AAw_Chanthaburi3, AAw_Chanthaburi4, AAw_Trang1, AAw_Trang2
2.1	AAw_NW22, AAw_NW33, AAw_NW41
2.2	AAw_NW38, AAw_PH04, AAw_PH05, AAw_TL18, AAw_Kanchanaburi2,
2.2.1	AAw_ Kanchanaburi3
	AAw_Kanchanaburi1
2.3	AAw_UP36
2.4	AAw_LN20
2.5	AAw_MaeYom
2.6	AAw_Trang3
2.7	AAw_MW10, AAw_MW20, AAw_MW31, AAw_UP16, AAw_UP18, AAw_Rayong

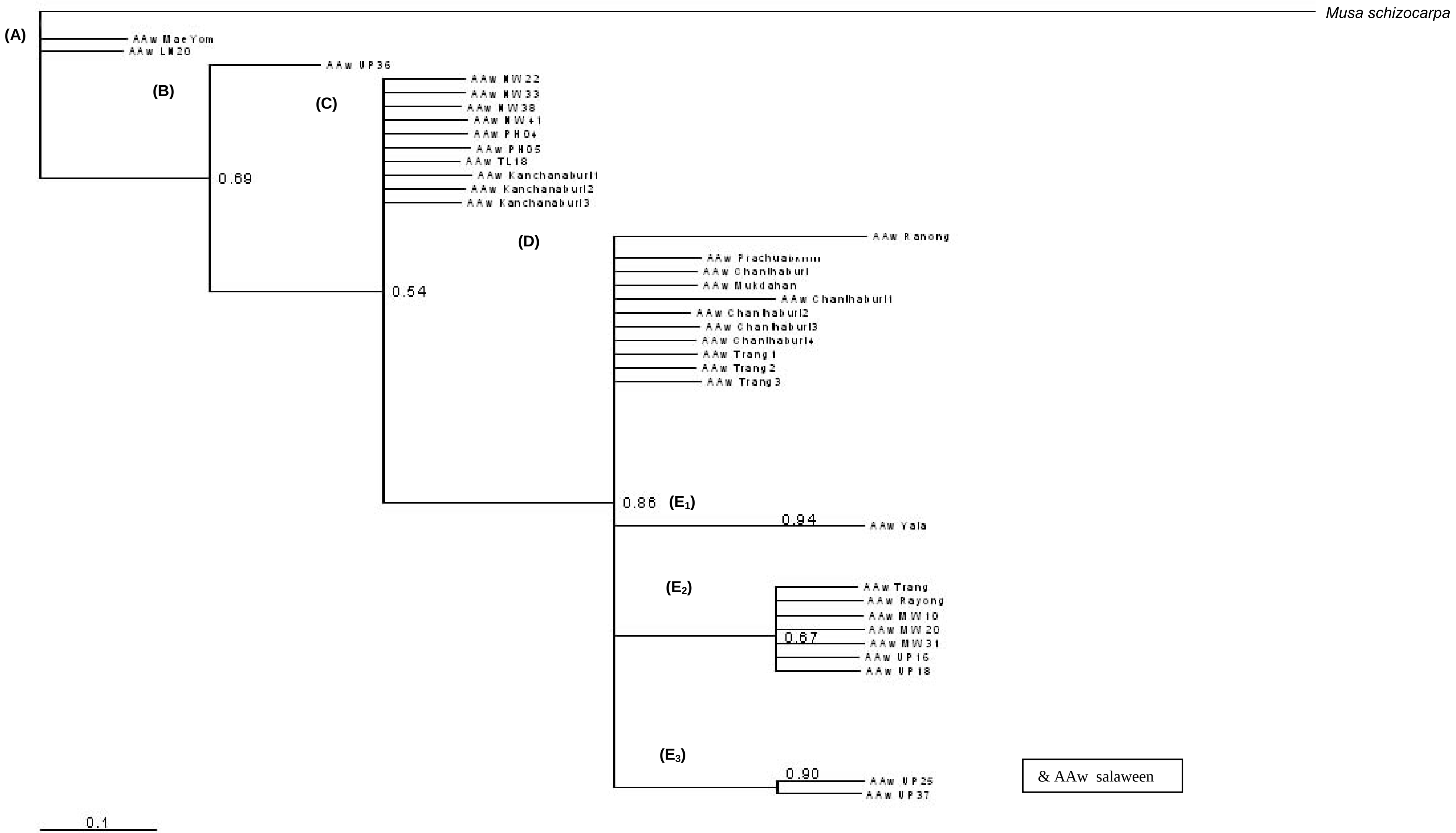


Figure 5.2 Phylogenetic tree reconstructed with the program MrBayes 3.1.2. General time reversible model of nucleotide substitutions and gamma distribution of rates of substitution with proportion of invariants. The Markov Chains were run for 1.000.000 generations. The 50% majority consensus tree was calculated for all most-parsimomious. Bayesian posterior probabilities are indicated for 36 accessions.

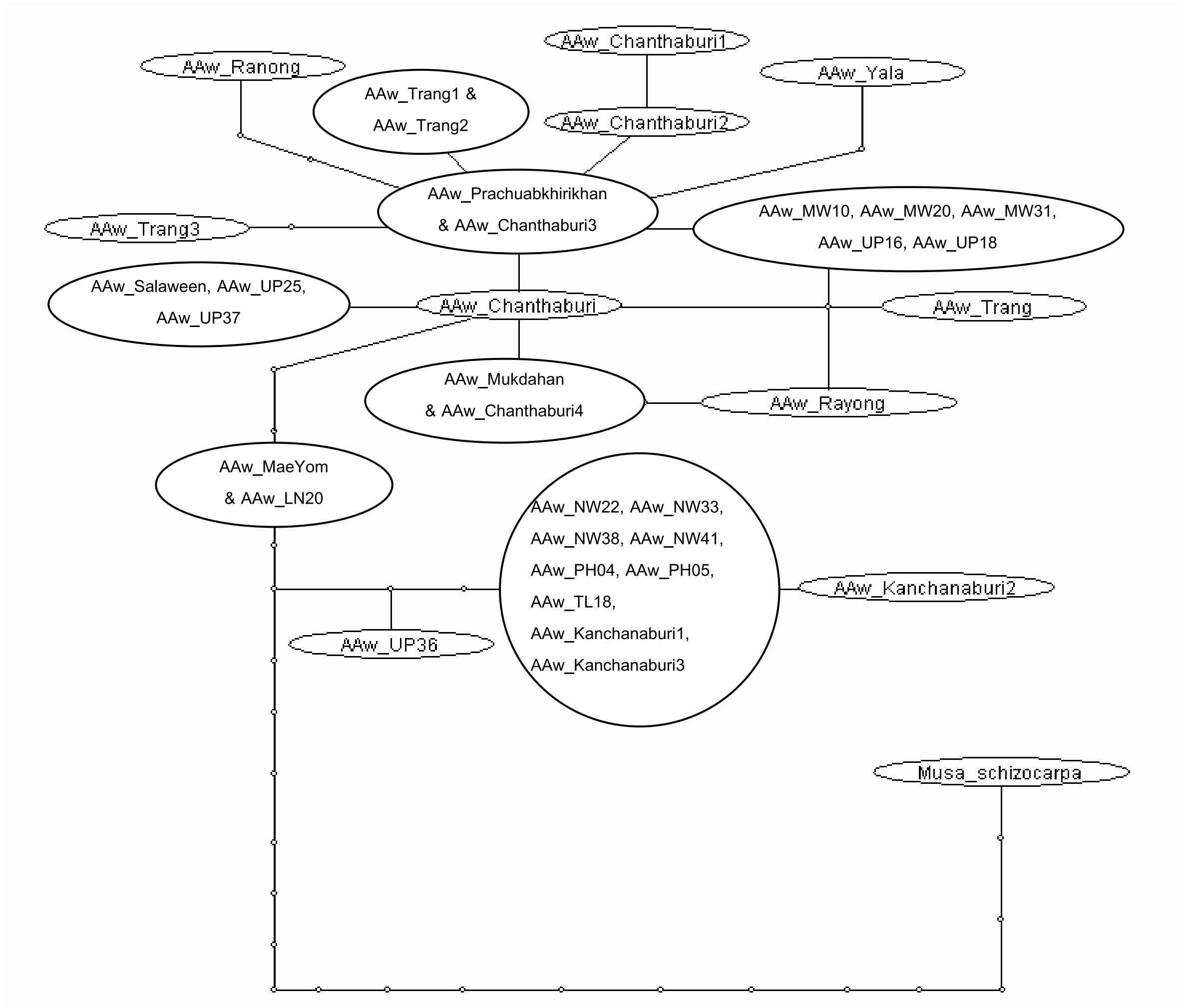


Figure 5.3 Statistical parsimony haplotype network of 36 cpDNA sequences. o = Indication of mutation point within the network analysis with Musa_schizocarpa.

3. Phylogenetic and Network Analyses

PRS analyses of the 4 cp - regions indicated 18 haplotypes of the 36 accessions from the field surveys in Thailand and M_schizocarpa as an out group. The haplotypes were clearly grouped the *M. accuminata* accessions with one loci (Table 5.7). All data were analysed with the program MrBayes 3.1.2. Phylogenetic tree was reconstructed with general time reversible model of nucleotide substitutions, gamma distribution of rates of substitution with a proportion of invariants. The Markov Chains were run for 1,000,000 generations. The 50% majority consensus tree was then calculated for all saved trees. Bayesian posterior probabilities are indicated (Figure 5.2 and Table 5.7).

The analyses presented multistate lineages of different branches among the 7 clades (Figure 5.2). M_schizocarpa was very isolated from all accessions. The closest accessions were the AAw_MaeYom and AAw_Ln20 in clade A the AAw_UP36 in clade B, which was isolated from the other. There were 10 accessions from lower northern and western of Thailand in the clade C. This was an interesting point on the relations to the accessions of AAw_Kanchanaburi 1, 2 and 3, which were *M. acuminata* ssp. *burmanica.* There were 11 accessions within clade D. The accessions of AAw_Ranong and AAw_Chanthaburi 1 were indicated little isolation from the clade D. There were 3 subclades within the clade E. AAw_Yala was in the subclade E1. There were 7 accessions in the subclade E2. The accessions of AAw_MW10, 20, 31, UP16 and 18 were clustered with AAw_Trang (ssp. *malaccensis*), AAw_Rayong (ssp. *siamea*). The accessions of AAw_UP25 and 37 were clustered with AAw_Salaween in the subclade E3 (Figure 5.2).

Table 5.7 Chloroplast haplotypes of 36 accessions with *Musa schizocarpa* from PCR-RF-SSCP (PRS) analyses by R-IN/*Hfl*, PY-S, N-IN/*Hfl* and AF-S/*Tql.*

Cp Haplotypes [a]	**Within Accession Code** [b]
S1	M_schizocarpa_ITC
AAw1	AAw_Ranong
AAw2	AAw_Yala
AAw3	AAw_Prachuabkhirikhan, AAw_Chanthaburi3,
AAw4	AAw_Trang
AAw5	AAw_Chanthaburi
AAw6	AAw_Rayong
AAw7	AAw_Mukdahan, AAw_Chanthaburi4
AAw8	AAw_MaeYom, AAw_LN20
AAw9	AAw_Salaween, AAw_UP25, AAw_UP37
AAw10	AAw_MW10, AAw_MW20, AAw_MW31, AAw_UP16, AAw_UP18
AAw11	AAw_NW22, AAw_NW33, AAw_NW38, AAw_NW41, AAw_PH04, AAw_PH05, AAw_TL18, AAw_Kanchanaburi1, AAw_Kanchanaburi3
AAw12	AAw_UP36
AAw13	AAw_Chanthaburi1
AAw14	AAw_Chanthaburi2
AAw15	AAw_Kanchanaburi2
AAw16	AAw_Trang1, AAw_Trang2
AAw17	AAw_Trang3

[a]Chlorplast haplotypes of four regions; R - IN/*HfI* = *rpl16* intron digested with *HinfI* restriction enzyme, PY - S = undigested *psa*A - *ycf3* intergenic spacer, N - IN/*HfI* = *ndh*A intron digested with *HinfI* restriction enzyme, and AF - S/*TqI* = *pet*A – *psb*J – *psb*L - *psb*F intergenic spacers digested with *TaqI* restriction enzymes; [b] Accession code appears according to Table 5.1.

4. Statistical Parsimony Haplotypes Network of cpDNA Sequences

The relationships among 36 accessions were graphically presented in Figure 5.3. *M. acuminata* network analysis indicated the related parsimony haplotypes were synchronized with the results of phylogenetic tree. The length of sequences were 4,330 nucleotides with 30 steps of parsimony probability, which was P (95%) = 0.947139. The number of haplotypes was 18, which was employed in the network distant matrix and out group weights analyses. The total positive difference matrix is 126.0. The total negative difference matrix is 0.0. The biggest out group probability is AAw_Prachubkhirikhan (0.1981981981981982).

The multi - dimensions of statistical parsimony haplotype network of cpDNA sequences presented the linkages of different branches of the 9 clades include Musa_schizocarpa (Figure 5.3). M_schizocarpa was very isolated from all accessions due to 19 mutation points from AAw_LN20 of clade A, where AAw_UP36 of the clade B was connected to the clade A and C of AAw_Kanchanaburi_1, 2 and 3 (ssp. *burmanica*). The AAw_Chanthaburi 3 (ssp. *siamea*) was the closest accession from AAw_Prachubkhirikhan. This accession was the most central connection in the network via clades A, B, C, D and E. There were two interesting clusters which should be intermediate types. These are the clusters of AAw_MW10 and AAw_NW22. After re-examination with the results of numerical classification, the cluster of AAw_MW10 was Form B and indicated the strong characters similar to ssp *burmanica* with *M. rubra*. While, cluster of AAw_NW22 was Form A and indicated the strong characters similar to ssp. *burmanica* and some characters of ssp. *malaccensis* x ssp. *siamea* and *M. rubra*. However, there were other three small clusters of *(1)* AAw_Salaween, AAw_UP25 and UP27, *(2)* AAw_MaeYom and AAw_LN20, *(3)* AAw_UP36. They indicated the characters of ssp. *malaccensis,* ssp. *siamea* and ssp. *malaccensis*, respectively.

The AAw_Chanthaburi 1, 2, 3, Prachuabkhirikhan, Mukdahan and Rayong (ssp. *siamea*) were closed and interlinked to the Southern accessions of AAw_Trang, Yala, Ranong (ssp. *malaccensis*). The clusters of AAw_MW10 were in the middle links. On the other hand the clusters of AAw_NW22, 33, 38, 41, PH04, 05, TL18, and Kanchanaburi group (ssp. *burmanica*) were isolated away from both previous clusters via AAw_MaeYom and LN20, and AAw_UP36 (Figure 5.3).

CONCLUSION AND DISCUSSION

M. acuminata accessions were separated into 9 clades from the result of chloroplast haplotypic analysis by PRS (Table 5.2, 5.3 – 5.6), phylogenetic tree (Figure 5.2) and parsimony haplotype network of cpDNA sequences (Figure 5.3). The primary clusters of accessions were also recognized by the polymorphic bands (Figure 5.1). PRS techniques presented useful information on diversity within the Eumusa section, which is able to distinguish all accessions among AA, BB and their hybrids similar to the works of Jordan *et al.,* (1998), Sato and Nishio (2002)**,** and Swangpol, 2003; Swangpol *et al.,* (2007).

The cpDNA sequence analyses focused precisely on the different among accessions with four primers. In the sequences information indicated visually repeation, insertions and deletions combinations of A, T, C, G, which caused length variations in non - coding cp - sequences (Levinson and Gutman, 1987; Morton, 1995; Swangpol, 2003; Swangpol *et al.,* 2007). Under *rpl*16 sequences identified six subgroups within two major groups as in Table 5.5 according to the changes and different in the 5 positions of single nucleotide substations and insertions/deletions (indels) (Appendix D). Various indels of base positions were inserted base A composition in AAw_Trang and AAw_Yala, and inserted base C composition in AAw_Ranong, and inserted bases TATAACA composition in AAw_Chanthaburi1 and AAw_Chanthaburi2 at 44, 232, 693, 450 and 450, respectively. The group 1 was separated from the group 2 by the deletions of base positions at 0 - 387. In addition, AAw_Trang, AAw_Ranong and AAw_Yala were identified as *M. acuminata* Colla ssp. *malaccensis* with characteristics of mixed two flower forms, the bunch curved bend down then curved upward of male flower within the sea shore habitat, while AAw_Yala was light white on the leaves of young seedlings. The interesting characters of AAw_Ranong within the sea short habitat were curved bunch bend down follow geotropic force, but the male flower was up right at the end.

On the other hand, *psa*A sequences clearly presented the cluster of five subgroups within two major groups according to the 3 areas of indels (Table 5.4 and Appendix D). Two major groups were separated by the deletions at 0-192, by base insertions of C at 246 such as AAw_LN20, by deletions of ATACCTATATGAATCTACTTCCA at 481 - 505 such as AAw_MaeYom and AAw_Kanchanaburi 1, and by insertions of the double of the same bases composition of ATACCTATATGAATCTACTTCCA at 504 - 529 in AAw_Trang 1 and 2, respectively.

In addition, *ndh*A sequences were sensitively separated all accessions into 10 subgroups within 4 major groups due to 7 indels (Table 5.5 and Appendix D). Five major groups were separated by the insertion of T at 597, which indicated some relationships within AAw_Salaween, AAw_UP25 and AAw_UP37. The insertions and deletetions of T, TT and TTT at 640 provided various different combinations of DNA sequences. The indels of TAATAATG and TCGAATTAATAA at 705 – 730 were the identical of AAw_Ranong. The deletion of A at 738 was the identical point of AAw_Kanchanaburi 2. The indels of G at 797 were the characters of AAw_Kanchanaburi 1-3, AAw_NW22, 33, 38, 41, AAw_PH04, 05 and AAw_UP36. AAw_Chacthaburi1 was isolated from the other by insertion of A at 859. In addition, AAw_Kanchanaburi 1 - 3 showed the good agronomic characteristic of well - from bunch a liked Calcutta 4, which may be the best in breeding program.

There were 10 subgroups within 2 major groups under *pet*A sequences according to the 7 indels (Table 5.6 and Appendix D). Five major groups were separated by the indels at 1 to 749 - 751 such as AAw_Ranong, AAw-Yala, AAw_Trang and AAw_Prachuabkirikhan. The indels of T and TT at 933 - 934 indicated the relations in the group of AAw_NW, PH, TL, Kanchanaburi 1 - 3 and UP36. The insertion of G at 1419 presented the relation among AAw_LN20, MaeYom and UP36. The deletions of AT at 1417 - 1418 and insertion of T at 1438 were the identical of AAw_Trang3. The relations of the group of AAw_NW, PH, TL and Kanchanaburi1 - 3 were indicated by the insertions of GTA…….TGA at 1420 - 1440 and close relation to AAw_Trang3. The insertions of CCCTCC, TTG and GCGA indicated the strong relations within the cluster of AAw_Trang, AAw_MW10, 20, 31, UP16 and 18 at 1769 - 1780 and at 1790 - 1803, respectively. The isolation of AAw_Ranong and AAw_Kanchanaburi1 were confirmed again with indels of A and C at 2179 and 2232, respectively. In the cp - sequences of *rpl*16 and *psa*A distinguished the accessions in BB gemone and hybrids better than the sequences of *ndh*A and *pet*A, which were clearly distinguished the AA genome and hybrids accessions. These were supported the separation of chloroplast haplotypes from PRS analyses of *Musa* with the four primers in four regions of R - IN/*Hf*I, PY - S, N - IN/*Hf*I and AF - S/*Tq*I (Swangpol, 2003; Swangpol *et al.,* 2007). However, more studied with other primers and more accessions of other species within

Musa were seriously examined to distinguish the whole diversity complex. According to the results in the Figure 5.2 and 5.3 clearly indicated the different lengths and the large number of mutation points of AAw_M_schizocarpa in the phylogenetic and the network of cpDNA sequences analyses.

However, the haplotypes (Table 5.7) were clearly grouped into 18 clades but indicated the different within subclades such as AAw_M_Schizocarpa in the clade A, and AAw_Ranong, AAw_Chanthaburi 1 in the clade D (Figure 5.2).

The combined chloroplast sequences with four primers results were also reconfirmed in the parsimony haplotypes network by the program TCS 1.13 (Figure 5.3). The advantage of this technique is the indication of the number of mutation points (Signal of Mutations) which presented in the branching lines within the network. There were some interesting points in the network analysis (Figure 5.3). The out group taxa of Chanthaburi 1 - 4 and Kanchanaburi 1 - 3 were separated to be 5 and 2 groups, respectively. In contrast, these accessions were identified into three and two forms of male flowers by classical taxonomy, respectively (Appendix 4.5). This indicated the mutation points of each subgroup which were occurred during the evolution of each accession and subclade. These were the important information to discuss on the accessions identification with the classical taxonomy and scoring techniques of the previous works, which were less sensitive than the molecular techniques (Figure 5.3). (Simmonds, 1962; Shepherd, 1990; Cheesman, 1997; Ude *et al.,* 2002) However, these were required further study on the mutation points which refer to the different on cpDNA sequences and higher number of different accessions. In addition, these results provide adequate information to ensure the different within subgroups, which were distinguished by classical and numerical taxonomy of the lower northern Thailand collection in previous chapters. The other benefits were the better understanding on the relations and different among accessions at the base compositions in the DNA sequences (Table 5.3 – 5.6). These techniques and results could apply to explain the unsolved and difficulties inquiries in *Musa* researches such as genetics, hybridization, classification and breeding (Table 5.8 and Figure 5.4).

In conclusion, three major ssp. Clusters studied were *(1)* ssp. *malaccensis (2)* ssp. *siamea* and *(3)* ssp. *burmanica* in Phylogenetic and Network Analyses (Figure 5.4). These indicated that ssp. *malaccensis* and ssp. *siamea* were developed parallel, while ssp. *burmanica* were developed with ssp *siamea*. However, the characters of accessions in ssp. *burmanica* were more diversified. These were well accepted due to their DNA sequencings and the comparisons within outgroup with classical and numerical taxonomy. For example, AAw_UP25, UP27 and UP36 were ssp. *malaccensis*, in numerical taxonomy. All of them were classified as ssp. *malaccensis* in Phylogenetic and Network Analyses. AAw_LN20 was ssp. *siamea* in both techniques. However, there were some interesting points in AAw_MW10 and AAw_NW22 sub-clusters. Both were classified as ssp. *burmanica* in Phylogenetic and Network Analyses. AAw_MW10, and 20, 31, and UP16, 18 were classified as ssp. *burmanica* and ssp. *siamea* characters in numerical taxonomy. While, AAw_NW22, 33, 38, 41, AAw_PH4, 5, and TL18 were previously classified into ssp. *siamea* and ssp. *burmanica*. They were indicated some characters of ssp. *burmanica* and ssp. *siamea* in classical and numerical taxonomy.

Table 5.8 List of *Musa* accessions, origins and sources of accessions.

No.	Code	Classical [a]	Numerical [b]	Cp Haplotypes [c]	Remark
1	AAw_LN20 *	Si	Si	AAw 8	ssp. *siamea*
2	AAw_MW10 *	Bu + Other 1	Bu	AAw 10	ssp. *burmanica* + *siamea* + *malaccensis*
3	AAw_MW20 *	Si + Bu	Bu	AAw 10	ssp. *burmanica* + *siamea* + *malaccensis*
4	AAw_MW31 *	Si + Bu	Bu	AAw 10	ssp. *burmanica* + *siamea* + *malaccensis*
5	AAw_NW22 *	Hy + Ml	Bu	AAw 11	ssp. *burmanica* + *siamea*
6	AAw_NW33 *	Si + Bu	Bu	AAw 11	ssp. *burmanica* + *siamea*
7	AAw_NW38 *	Bu	Bu	AAw 11	ssp. *burmanica* + *siamea*
8	AAw_NW41 *	Si + Bu + Other 1	Bu	AAw 11	ssp. *burmanica* + *siamea*
9	AAw_PH04 *	Si + Bu	Bu	AAw 11	ssp. *burmanica* + *siamea*
10	AAw_PH05 *	Hy	Bu	AAw 11	ssp. *burmanica* + *siamea*
11	AAw_TL18 *	Si	Bu	AAw 11	ssp. *burmanica* + *siamea*
12	AAw_UP16 *	Bu	Bu	AAw 10	ssp. *burmanica* + *siamea* + *malaccensis*

Table 5.8 List of *Musa* accessions, origins and sources of accessions. (Cont.)

No.	Code	Classical [a]	Numerical [b]	Cp Haplotypes [c]	Remark
13	AAw_UP18 *	Bu	Bu	AAw 10	ssp. *burmanica* + *siamea* + *malaccensis*
14	AAw_UP25 *	Ml	Ml	AAw 9	ssp. *malaccensis*
15	AAw_UP36 *	Other 2	Ml	AAw 12	ssp. *malaccensis* x *burmanica*
16	AAw_UP37 *	Ml	Ml	AAw 9	ssp. *malaccensis*
17	AAw_Chanthaburi1 *	Si	Si	AAw 13	ssp. *siamea*
18	AAw_Chanthaburi2 *	Si	Si	AAw 14	ssp. *siamea*
19	AAw_Chanthaburi3 *	Si	Si	AAw 3	ssp. *siamea*
20	AAw_Chanthaburi4 *	Si	Si	AAw 7	ssp. *siamea*
21	AAw_Kanchanaburi1 *	Bu	Bu	AAw 11	ssp. *burmanica* + *siamea*
22	AAw_Kanchanaburi2 *	Bu	Bu	AAw 15	ssp. *burmanica*
23	AAw_ Kanchanaburi3 *	Bu	Bu	AAw 11	ssp. *burmanica* + *siamea*
24	AAw_Trang1 *	Ml	Ml	AAw 16	ssp. *malaccensis*
25	AAw_Trang2 *	Ml	Ml	AAw 16	ssp. *malaccensis*
26	AAw_Trang3 *	Ml	Ml	AAw 17	ssp. *malaccensis*
27	AAw_MaeYom**	-	-	AAw 8	ssp. *siamea*
28	AAw_Ranong **	-	-	AAw 1	ssp. *malaccensis*
29	AAw_Chanthaburi **	-	-	AAw 5	ssp. *siamea*
30	AAw_Yala **	-	-	AAw 2	ssp. *malaccensis*
31	AAw_Prachuabkhirikhan **	-	-	AAw 3	ssp. *burmanica* + ssp. *siamea*

Table 5.8 List of *Musa* accessions, origins and sources of accessions. (Cont.)

No.	Code	Classical [a]	Numerical [b]	Cp Haplotypes [c]	Remark
32	AAw_Rayong **	-	-	AAw 6	ssp. *siamea*
33	AAw_Mukdahan **	-	-	AAw 7	ssp. *siamea*
34	AAw_Trang **	-	-	AAw 4	ssp. *malaccensis*
35	AAw_Salaween **	-	-	AAw 9	ssp. *malaccensis*
36	M_schizocarpa_ITC**	*M. schizocarpa*	*M. schizocarpa*	*S1*	*M. schizocarpa*

* = accessions from the field survey and DNA sequencing; ** = The outgroup accessions for Phylogenetic and Network analyses, **a** = Indicates known origins; **b** = indicates sources of accessions; **DW** = Field Collection by Det Wattanachaiyingcharoen; **CAB, KU** = Center of Agricultural Biotechnology, Kasetsart University Kamphaengsaen Campus; **ITC** = International Transit Center, International Network for the Improvement of Banana and Plantain (INIBAP), Leuven, Belgium; **Si** = ssp. *siamea*; **Bu** = ssp. *burmanica*; **Ml** = ssp. *malaccensis*; **Hy** = Hybrid (ssp. *siamea x* ssp. *burmanica*).

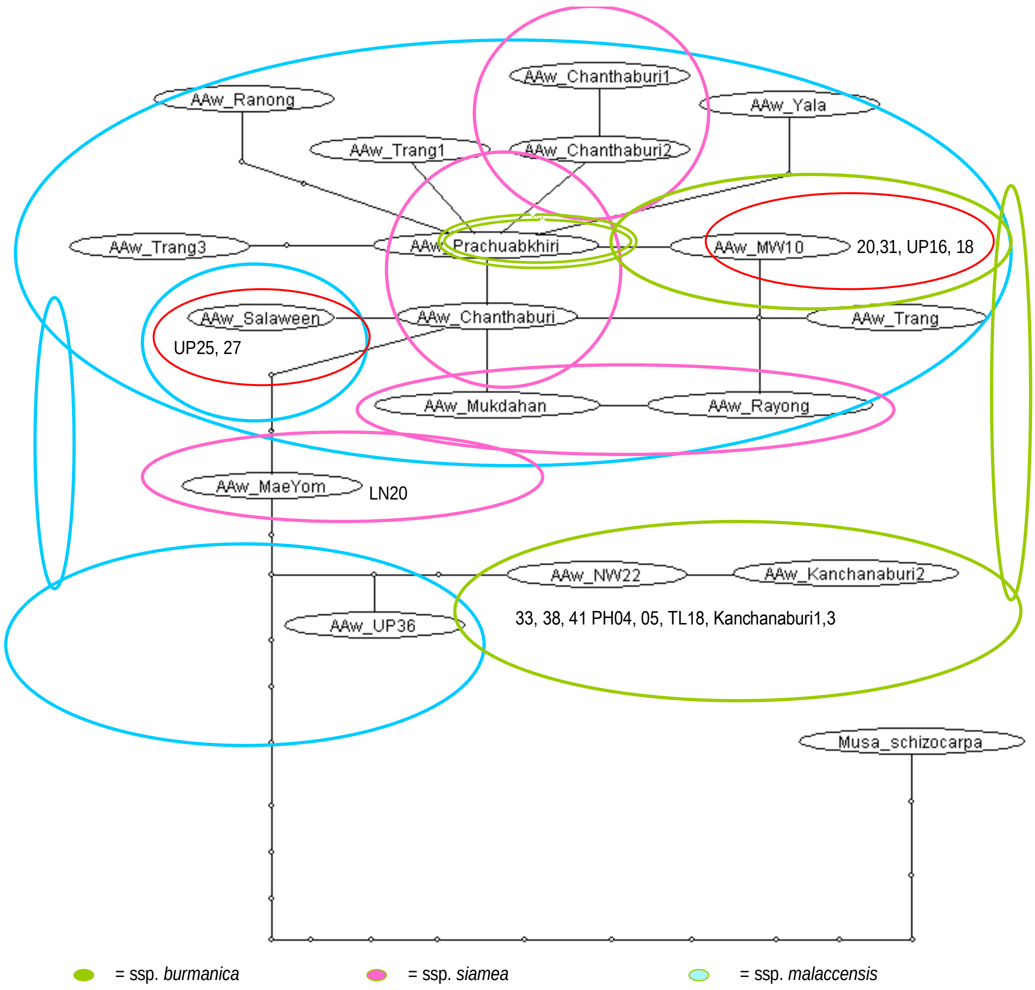


Figure 5.4 Subspecies identification and inter-linked under Parsimony haplotype network of 36 cpDNA sequences.

CHAPTER 6

CONCLUSIONS AND RECOMMENDATIONS

6.1 Conclusions

This research aimed to provide a better understanding on morphological and genetic variations of wild banana populations in lower northern Thailand and to examine their taxonomic status, as well as their environmental factors relationships.

6.1.1 Morphological and Genetic Variations among Populations of *M. acuminata* Colla

Morphological variations of wild bananas in this region can be classified by classical taxonomy into 3 subspecies and hybrids (Chapter 4). The morphological variations of all samples were identified into *M. acuminata* ssp. *malaccensis* (Ridl.), *M. acuminata* ssp. *siamea* Simmonds and *M. acuminata* ssp. *burmanica* Simmonds. However, Numerical taxonomy identified them into two groups of *(i.)* ssp. *malaccensis* and *(ii.)* ssp. *siamea* and ssp. *burmanica* (Chapter 4). Moreover, hierarchical cluster analyses indicated *M. acuminata* ssp. *siamea* and ssp. *burmanica* were clearly in the same group. Some outliers presented character of like green at the tip of male flower, while some outliers presented characters of *M. acuminata* ssp. *malaccensis* (Ridl.) and *M. flaviflora* N. W. Simmonds. They should be hybrid or mutant. Both ssp. *microcarpa* (Becc.) Simmonds, and ssp. *banksii* (F.v. Muell.) Simmonds within *M. acuminata* Colla did not found in this study. In addition, classical taxonomy with 20 major qualitative characteristics was suitable and primary effective to classified wild bananas (*M. acuminata* Colla) found naturally in this region (Chapter 4). However, the identification key is needed to be revised following the numerical taxonomy result. The demands for more specimens of outlier from each site in previous classical taxonomy were to understand their variations and taxonomic status. However, 4cp - markers of DNA and phylogeny analyses were clearly detected the different and relations among accessions. These confirmed the high demand on intensive study of additional characteristics within classical taxonomy or other techniques. The taxonomy and evolution understanding on phenotypic and genotypic characters of these accessions from both molecular and taxonomy were seriously acquired more information in both morphological and genetic variations cover their diversity complex.

Table 6.1 Morphological Characteristics of *(M. acuminata* Colla) Subspecies and outliers in Lower Northern Thailand.

Subspecies	Noticeable Characters	Remarks
ssp. *malaccensis* (Ridl.) Simmonds	Induplicate and incurve petiole canal, heavy wax on the leaf, and creamy compound tepal	Typical characters
ssp. *siamea* Simmonds	Advance blooming acute, Distinctly imbricate at the tip (ssp. *siamea* Simmonds in classical taxonomy)	New record on variations of three male buds forms: Annam, Tavoy and Selangor
	Reddish brown large blotch on pseudostem, and reddish brown blotch at petiole base, beneath leaf and midrib (ssp. *burmanica* Simmonds in classical taxonomy)	Typical characters in classical taxonomy
Other 1 or Outlier 1 (ssp. *siamea* Simmonds and *M. rubra*	Bright light green on the bract external face and strongly convolute	Promising new subspecies or form? Isolated and clumped distribution in cooler environment
Other 2 or Outlier 2	Bract external: glossy pink purple, Bract internal: bright orange red Upright male flower in early state and then curved down in final state	With some similar characters of ssp. *malaccensis* (Ridl.) Simmonds and *M. flaviflora* N. W. Simmonds similar to *M. laterita* but without running sucker

Remark: ssp. *siamea* Simmonds and ssp. *burmanica* Simmonds from classical taxonomy were in the same group after numerical taxonomy.

Genetic variations of the *M. acuminata* accessions and it related hybrids were separated into 9 clades from the results of chloroplast haplotypic analysis by PRS (Table 5.3, 5.5 – 5.8), phylogenetic tree (Figure 5.3) and Parsimony haplotype network of cpDNA sequences (Figure 5.4). The combined chloroplast sequences with four primers results were also reconfirmed in the parsimony haplotypes network. These provided better and clear separation and sensitive relation with mutation points of all samples synchronizes with the results from classical taxonomy. These indicated that various kind relations of different genomes may strongly introduced by their parental genetic materials. However, these were required further study on the mutation points which refer to the different on cpDNA sequences and higher number of different accessions. In addition, more cp - markers and genetic variation researches at molecular levels are important in the future work for biodiversity utilization.

6.1.2 Phylogeny of *Musa acuminata* Colla and Its Related Cultivars on DNA Analysis

Accessions were separated into 9 clades from the result of chloroplast haplotypic analysis by PRS, phylogenetic tree and parsimony haplotype network of cpDNA sequences. All techniques presented useful information on diversity within the Eumusa section, which is able to distinguish all accessions among AA, BB and their hybrids. The cpDNA sequence analyses focused precisely on the different among accessions with four primers. In the sequences information indicated visually repeation, insertions and deletions combinations.

The parsimony haplotypes network of the combined chloroplast sequences with four primers and the number of mutation points (Signal of Mutations) were required further study on the mutation points. In conclusion, Phylogenetic and Network Analyses (Figure 5.4) indicated that ssp. *malaccensis* and ssp. *siamea* were developed separately, while ssp. *burmanica* were developed with ssp *siamea*. The characters of accessions in ssp. *siamea*, *burmanica* and hybrid (ssp *siamea x* ssp. *burmanica*) were more diversified within the same group. However, the outliers of other forms were influence by hybridization or mutation.

6.2 Recommendations

(i.) These accessions of wild bananas may be used as new promising genetic materials for breeding program for global utilization due to their vigorous and agronomic characters. These may requires the establishment of *in situ* experimentations with continuous environmental factors monitoring systems, and field tests to compare with previous international germplasm collections.

(ii.) Other numerical taxonomy and molecular systematic is needed to be conducted on these new promising genetic materials to ensure their status. The use of their variability and inheritance of traits should be study on the number of gene involved with molecular mapping of the important traits for breeding programs.

(iii) Higher number of specimens of *Musa acuminata* Colla subspecies and forms may by required to review after intensive surveys in Thailand and Southeast Asia. The further explorations should be done in the western forest complex of Thailand due to their unique ecology and richness in biodiversity.

(iv.) Information on morphological and genetic variations, taxonomic status and their habitat preference were fundamentally benefits to future conservation, preservation, utilization and breeding programs. The field collection in common garden experiments should intensively focus on agronomic traits such as bunch size, growth rate, plant size, and diseases resistance.

(v.) The vast biodiversity material with localize, intermediate and distinct regional forms such as Up 36, Kanchanaburi and ssp. *burmanica* should be urgently introduced to Thai and global banana breeding program due to their variant with potential breeding values, the monoculture of narrow genetic cultivar, slow progress relies on limited germplasm of breeding programs.

(vi.) The cpDNA sequence analyses provide the results with adequate information to identify the differences within *Musa acuminata* Colla subgroups. These techniques and results could apply to explain the unsolved and difficulties inquiries in *Musa* researches such as genetics, hybridization, classification and breeding.

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APPENDIXES

APPENDIX A

MORPHOLOGICAL DATA

1. COLLECTING FORM

Date:

Expedition:

Collectors:

Sample n^{o}:

Photo n^{o}:

Genus:

Section:

Species/group:

Subspecies/subgroup:

Local name:

Local people:

Source- Wild / Farm / Market

- description:

Site, Province:

Location km: from:

Lat: Long:

Elevation:

Landform:

Soil pH: fertility: Low / M / H

Soil type:

Water source:

Rainfall -Annual mean (mm):

Mean J F M A M J J A S O N D

(mm)

(^{o}C)

Plant density: Low / M / H

Shaded / Sunny

Sample type: Sucker / seed / bud / other:

N^{o} of plants sampled:

Status: Wild / Weedy / Primitive / Breeders / Advanced

Parts used:

Uses:

Prevailing stresses:

Treatment and storage:

Pseudostem (m) (to peduncle):

Size: Normal / Dwarf (leaves overlap, leaf r <2.5)

Color (chart A):

Predominant underlying color:

Other pigment: Pi-Pu / Re / Pu / Other:

Wax on leaf sheaths: 1 (none) / 2 / 3 / 4 (very)

At 100cm: Slender / Normal / Robust

Waxy(dull) / Not waxy(shiny)

Sap color (chart A): watery / milky

Peduncle -length (leaf crown to first hand)(cm):

- N^{o} of empty nodes:
- Width:
- Color:
- Hairy: no / slight / much, short / much, long (>2mm)

Bunch -position: 1(vertical) 2 3 4(Horizontal) 5(Erect)

- Shape: cylindrical / cone / asymmetric / curve / spiral
- Between hands: Lax / compact / very compact
- Flowers: female / hermaphrodite (pollen present)
- Fruits: uniseriate / biseriate / biseriate and fused

Leaves: Erect / intermediate / drooping / other:

N^{o} of leaves (living):

3rd most recent unfolded -Petiole base blotches: sparse / small / large / extensive / no pigment

Blotch color: Br / DBr / Br-Black / Black-Pu / Other:

Canal leaf III Margins: spreading / wide / straight / inward / overlapping

Margin at pseudostem: Winged: Yes / No

Dry winged: Yes / No

Clasping: Yes / No

Margin color: Gr / Re / Pu to Blue / Other:

Edge of petiole margin: colorless / colored

Petiole margin width: <1cm / >1cm / can't define

Blade length (cm):

Blade width (cm):

Petiole length (cm):

Upper surface:

- Gr-Ye / Gr / DGr / DGr+Re-Pu / Blue / Other:
- Dull / Shiny

Lower surface:

- Gr-Ye / Gr / DGr / DGr+Re-Pu / Blue / Other:
- Dull / Shiny

Wax on leaves: 1 (none) / 2 / 3 / 4 (very)

Blade on petiole: Symmetric / Asymmetric

Blade base: sides rounded / sides pointed / one r, one p

Corrugation: Smooth / few stripes / very corrugated

Color midrib dorsal (chart A):

Color midrib ventral (chart A):

Color cigar leaf (chart A):

Blotches on leaf of water suckers: no / little / large

Suckers: >50cm from parent / vertical / angle

- Tallest vs. parent: taller , > ¾ , ¼-¾ , inhibited
- N^{o} of suckers

Fruit -Number of fruits (mid-hand):

N^{o} of hands:

Rel' to stalk: curved toward / parallel / 45^{o} / 90^{o} / pendant

Length (internal arc, not pedicel) cm:

Shape: Straight / straight distally / curved / S curve / other

Transverse section: Pronounced ridges / Slight / Rounded

Apex: Point / lengthy / blunt / bottle-neck / rounded

Flower relics: None / persistent style / base of style

Pedicel - Length (mm):

- Width (mm):
- Surface: hairless / hairy

Fusion: not / partial / totally

Peel color - immature (chart B):

- mature (chart B):

Mature - peel thickness (mm):

- peeling: peels easily / not easy
- cracks: present / not present
- Pulp: present / absent

Pulp color - immature (chart B):

- mature (chart B):

Persistence: persistent / deciduous

Flesh texture: Firm / Soft

Taste: astringent / mild / sweet / sugary / sweet + acidic

Apex: 1 (pointed) / 2 / 3 / 4 (obtuse) / 5 (obtuse and split)

Overlap: Old bracts / young bracts, slight / Y. bracts great

External color (chart A):

Internal color (chart A):

External apex color: Yellow tint / Uniform

External color stripes: Discolored lines or stripes / None

Scars on rachis: Very prominent / Not

Inside color: Fading toward base / Uniform

Shape (x/y): <0.28 / 0.28-0.3 / >0.3 (Ovate)

Bract lifting: Persistent / One at a time / Two or more

Behavior: Revolute / Not revolute

Wax: 1 (none) / 2 / 3 / 4 (very)

Grooves external: smooth / moderate / strong

Male bud: present / degenerate before maturity / absent

- Shape: like a top/ lanceolate/ intermediate/ ovoid/ round

Rachis: truncated + no bract scar / present

- Position: vertical / angle / curve / horizontal / erect
- Appearance: bare

neutral flowers (few hands, bare below)

male flowers, bracts above male bud

withered bracts

flowers whole stalk, bracts not persist' small bunch just above male bud

other:

Male flower falling: before / with / after bract / persistent

Compound tepal basic color (chart B):

Pigmentation: none / rust colored / pinkish

Lobe color (chart B):

Free tepal color: translucent / opaque / yellowish/ pinkish

- shape: rectangular / oval / rounded / fan-shaped
- appearance: smooth / simple fold / several folds
- apex: little development / developed / very dev'

- apex shape: thread-like / triangular / obtuse

Anther exsertion: exserted / level / inserted

Filament: white / cream / yellow

Anther color, dorsal (chart B):

Pollen sac color (chart B):

Number of seeds:

Seed surface: smooth / wrinkle

Seed shape: Flat / angular / spherical / rounded

Bract (1st external) - shoulder: small / medium / large

Pollen vitality (% normal grains):

Style -basic color (chart B):

- Pigmentation: Purple / None

- Exsertion: exserted / level / inserted

- Curves: Under stigma / at base / both / straight

Stigma color (chart B):

Ovary -shape: Straight / Arched

- Basic color (chart B)

- Pigmentation: little or none / red-purple

Basic color of male flower (chart B):

Irregular flowers (nº per cluster):

Arrangement of ovules: two / four-rowed

Notes

2. The morphological characteristic details.

Twenty characteristics and criteria were used to identify the samples (IPGRI/INIBAP/CIRAD, 1997).

(1.) pseudostem height is measured from the base of the stem to the neck of the banana tree.

(2.) pseudostem appearance

(3.) present of blotches at petiole base

(4.) blotch color

(5.) petiole cannel

(6.) wax on leaf

(7.) peduncle hairiness

(8.) bunch position

(9.) rachis position

(10.) male bud shape

(11.) bract imbrication

(12.) color of the bract external face

(13.) color of the bract internal face

(14.) wax on the bract

(15.) compound tepal basic color

(16.) lobe color of compound tepal

(17.) color on the bract apex

(18.) color stripe on the bract

(19.) fruit apex

(20.) fusion of pedicel.

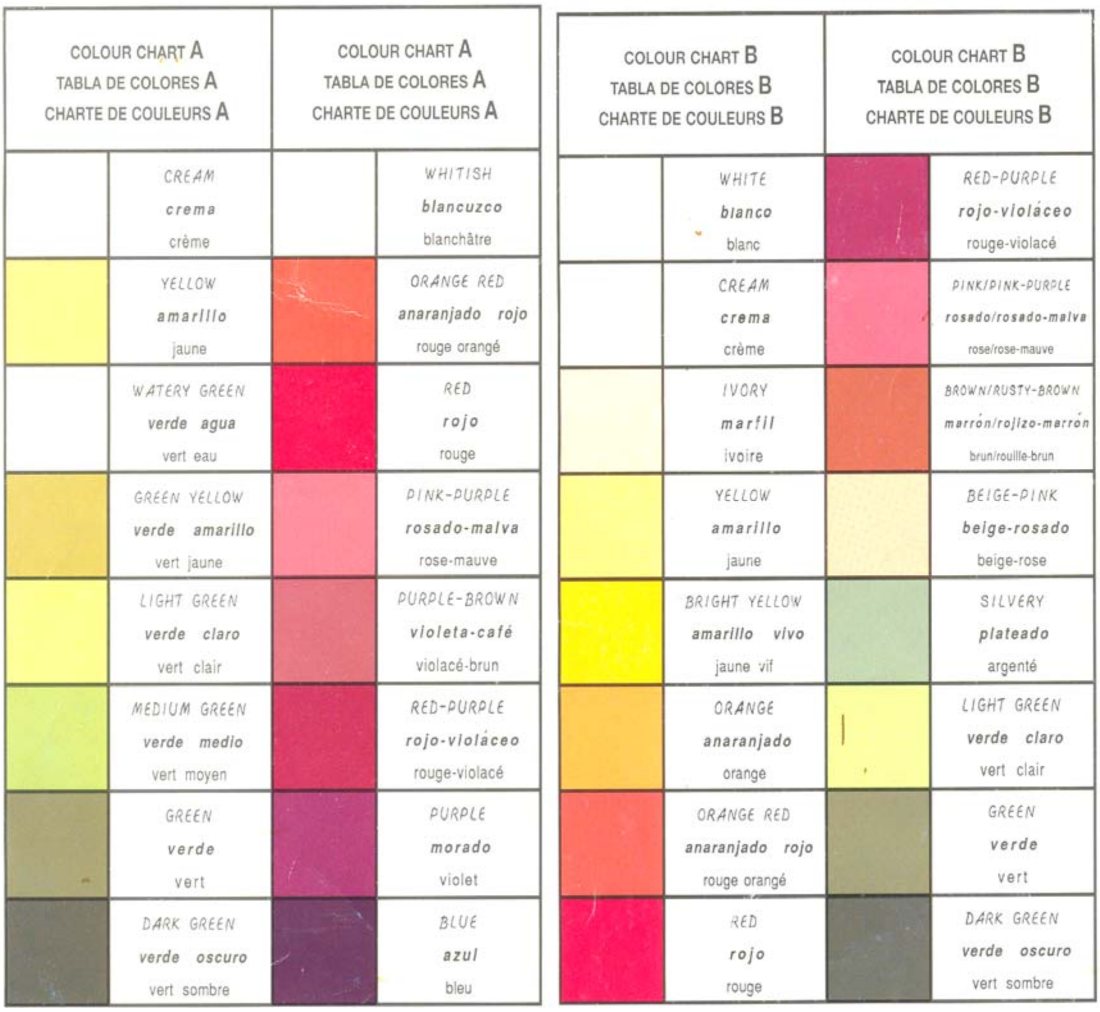


Figure 1 Color charts (A) and (B) for characterizations and classifications of *Musa acuminata* Colla. (IPGRI/INIBAP/CIRAD, 1996)

APPENDIX B

TAXONOMY

1. Summary description of wild banana (*Musa acuminata* Colla.)

1.1 Summary on the description of wild banana (*Musa acuminata* Colla.)

The morphological characteristic of this species are reviewed and summarized as following; Plant character is stooling sparsely (1-2 stems) or freely (4-30 stems). The pseudostems are more slender than those of most cultivated bananas and usually 3-5 metres high (up to 7 m.). The pseudostem is rarely exceeding 25 cm in diameter at base. There is various developments of brown-black markings from almost green to almost entirely black, or sometimes reddish brown in lower parts. Leaf-sheaths and petioles are commonly more or less glaucous or pruinose, but extremely in various development of wax.

Leaf blades character is oblong, 2-2.5 m. long, 40-60 cm. wide and truncate at apex usually rounded at base and sometimes rounded on one side and acute on the other side. Its colour is various from green or green tinged with purple to wholly purple on the lower surface, and green above with or without flecks or bars of purplish brown pigmentation. There are some variable characters such as heavily to slightly waxy beneath or none. Midribs are green, greenish yellow, and more or less strongly tinged with red below. Petioles are 60-90 cm. long. Sometimes they are very slender in some forms, but stouter in others. Their margins are sometimes almost erect and leaving an open adaxial channel. In other forms, they characteristics are strongly incurved over the channel and almost covered it which are usually definitely developed. Where the petiole passes into the leaf-sheath, and here usually closely appressed to the pseudostem. Which are occasionally slightly bent outward away from it, early becoming scarious in this region, when young often bordered with a red line.

Inflorescence is sub-horizontal or vertically deflexed, its peduncle and rachis are usually more or less thickly pubescent with brown hairs and sometimes glabrous. Basal flowers are female and the number of female “hands” is vary up to about 10, which are commonly fewer, but occasionally more where the upper hands is male flower.

Female flowers are about 16 per bract in binary rows. Compound tepal is about 2.5 cm. long to 4.2 cm. It is white, yellowish or slightly purple, with white or yellow tip and lobes. Free tepal is translucent and about half as long as the compound tepal. Ovary is pale green, yellowish green, or purplish, glabrous or with a few fine hairs near the base. But sometimes, the ovary is yellowish green, or purplish, glabrous or with a few fine hairs near the base, or more or less thickly covered with soft hairs.

Male bud character in advanced blooming is ovoid to turbinate, usually acute, the bracts are convolute, imbricate at the extreme tip only, or rather strongly imbricate. Bracts are in the various shades of purple or red, from bright red to dark violet, ovate, usually acute at apex, sometimes yellow at the extreme tip. The outer surface is more or less glaucous, and faintly ribbed longitudinally. The inner surface is paler, light red or yellowish, and always paling towards the base. Only one bract lifted at a time and some bracts revolute on fading and early deciduous, often a little before the flowers they subtend.

Male flowers are also about 20 per bract and in two rows. Compound tepal is 3.5-4.5 cm. long and about 1.2 cm. wide. Its color are white, cream, yellowish or pale orange, and sometimes purplish. The upper part of tepal includes the yellow teeth are varied from pale lemon yellow to bright orange. The two outer teeth are varied from 2 to 7 mm. long, with a dorsal appendage 1-2 mm. long. The centre lobe is usually slightly shorter and broader. Free tepal is about half as long as the compound tepal, and is translucent with boat-shaped. Its apex is variable but usually transversed and corrugated just below the apicula. Stamens are at first as long as the perianth or slightly shorter, and later exserted. Their anthers are usually pink before dehiscence.

Fruit bunch is asymmetrical, if it borne sub-horizontally. If the position is vertically, the bunch is compact. The fruits exhibiting marked geotropic curvature in either case. Individual fruit is 8-13 cm. long, 1.5-3 cm. in diameter, which is sub-cylindrical. The angles of the young fruit are almost disappearing at ripeness in most forms. The fruit is rather abruptly narrowed at base into a pedicel of about 1 cm. and sometimes pubescent, and at apex into a prominent acumen 0.6-1.5 cm. long. Pericarp is about 2 mm. thick, with bright yellow at full ripeness, while the pulp is whitish or cream to yellow.

Mature seeds are dull black and smooth or more commonly minute tuberculate, and irregularly angulate–depressed. Seeds size is about 6-7 mm. across and about 3 mm. long (De Langhe *et. al.,* 1998; Silayoi, 1983; Simmonds, 1956; Cheesman, 1948).

1.2 The summary on characteristic of the five subspecies belonged to *M. acuminata* Colla.

1.2.1 *Musa acuminata* Colla spp. *microcarpa* (Becc.) Simmonds

The first work on clone Buitenzorg by Cheesman (1948a) was the identification
at Buitenzorg (the I.C.T.A collection from Java comes only from the Botanic Garden). The description of Clone Buitenzorg or Buitenzorg form was the pseudostem at upper parts of leaf-sheaths. Its colours are olive green and purple brown at pseudostem with moderately heavy black blotching or marking, and not waxy. Upper and lower surface of leaf blades is green. Green midribs is lightly glaucous beneath. Petioles are slender with narrow erect margins. Male bud in advanced blooming is blunt. The bracts are dull purple, lightly glaucous outside and shining, lightly red inside, and slightly imbricate at the tip. Colour on the bract external face is deep violet (Cheesman, 1948a).

Male flowers are whitish, tinged purple at base. The yellow teeth or the compound tepal are only about 2 mm. long. Fruit bunch is nearly horizontal. Its peduncle is densely pubescent (Cheesman, 1948a). Fruit is about 8-12.5 cm. long, and 2 cm. in diameter, and minutely pubescent towards the base. The pedicel is very short and not very distinct, and acumen at least 1 cm. long This subspecies is a big banana with 20 ft. tall. Other character was a purple-brown pseudostem.

Cheesman, 1947b referred that Beccari described character of *M.microcarpa* (Becc.) Simmonds in 1902, that the fruit was smaller than *M. microcarpa* Beccari (Nelle Foreste di Borneo, 623/1902) (Cheesman,1947b). In 1956, Simmonds was mentioned that this subspecies is characterized by the yellowish tinge and virtual waxlessness of the foliage. The intense chocolate brown pigmentation is on the sheaths and often on the midrib. The fading purple flush is on the peduncle. Bract is purple on the external face, and pule red on the bract internal face, also weakly rolled at the time of falling.

The fruits are variable in sizes. The bunch position is usually horizontal, but sometimes oblique (De Langhe *et. al.,* 1998; Simmonds, 1956; Silayoi, 1983; Simmonds, 1956; Cheesman, 1948b).

1.2.2 *Musa acuminata* Colla spp. *malaccensis* (Ridl.) Simmonds

The sample from Kajang, Selangor, F.M.S., Malaysia in 1928 was collected by F. N. Howes, authentically found *M. malaccensis* Ridley. which Cheesman recorded and described as the Selangor form.

The pseudostem characteristics were olive green on the upper parts of leaf-sheaths with a purplish tinge, moderately heavy black blotching, and rather heavily waxy.

Leaf-blades are rather heavily waxy beneath. Midribs are red beneath and often purplish above. Young leaves on suckers are often with blotches or bars of purplish brown. Petioles are very slender, with narrow incurved margins.

Male bud in advanced blooming is acute. The bracts are convolute at the tip and reddish purple and lightly glaucous on the bract external face, light red and shining on the bract internal face.

Male flowers or compound tepal are cream with no purple tinge. The bright yellow lobe of the compound tepal are nearly 5 mm. long. Fruit bunch is nearly horizontal. Its peduncle is densely pubescent. Fruit is about 12 cm. long, and greatest diameter is about 2.5 cm. including about 1.5 cm. very distinct pedicel, and at least 1 cm. acumen (Cheesman, 1948a).

However, Simmonds (1956) described in more detail on this form. This subspecies was a slender plant usually strongly waxy. Midribs are commonly bright red beneath (but not always), with a horizontal bunch. Bract is bright red on the bract external face and non-imbricate on the bract apex.

1.2.3 *Musa acuminata* Colla spp. *burmannica* Simmonds

The Tavoy form has been mention in Cheesman (1948a) described form I.R. 124 (clone Calcutta 4), received from the "Royal Botanic Garden, Calcutta in 1931; and I.R. 187 (clone Tavoy and Long Tavoy) received in 1938 from C.W.D.Kermode, Esq., Sylviculturist, Maymyo, "Burma". The pseudostem character was bright green on the upper parts of leaf-sheaths with heavy reddish brown blotching, and none waxy.

Leaf blades are not glaucous beneath. Mid ribs are pale green or yellowish. Petioles are relatively stout, with well developed of erect margins, and becoming scarious very early where appressed to pseudostem.

Male bud is acute in advanced blooming. Bracts are usually distinctly imbricate at the tip, with dark violet-purple and glaucous on the bract external face, and shining light red on the internal face. Male flowers are whitish and the bright yellow teeth of the compound tepal. Lobe of compound tepal is bright yellow and up to 7 mm. long. Fruit bunch is pendent and compact. Its peduncle is densely pubescent. Fruits are 8-12 cm. long. Pedicel is very short and not very distinct. Acumen is about 0.5 cm. long, persistent style at fruit apex.

Simmonds (1956) made distinguished additional description by its yellowish and waxlessness foliage, and light brown markings on the pseudostem. Bunch is pendulous compact. Male bud is strongly imbricate bract at the apex and purple on the bract external face. Simmonds (1956) also made addition description and finally called spp. *burmannica* Simmonds.

1.2.4 *Musa acuminata* Colla spp. *siamea* Simmonds

Clone Annam was collected form Kew botanical garden. Cheesman used the material form Siam. It has these characters: upper part of pseudostem and leaf-sheaths is dull yellowish green, with moderately heavy brown blotching, and slightly waxy.

Leaf blades were not glaucous underneath. Midribs are yellowish-green, and moderately waxy on the lower side. Petioles are rather slender with well-developed erect margins. Petiole is early becoming scarious where appressed to pseudostem.

Male bud in advanced blooming is acute. The bract is distinctly imbrication at the tip, and none distinguishable in all respects from the bud of the Tavoy form. Male flowers or compound tepal is whitish. The Lobe of compound tepal is bright yellow about 5 mm long. Fruit bunch is nearly horizontal. Its peduncle and rachis are glabrous. Fruit is about 10 cm. long, 3 cm. in diameter. Pedicel is short about 0.5 cm. but quite distinct and well-marked. Acumen is 0.5 cm. long.

Simmonds (1956) concluded that the difference is that the plants are commonly (but not always) of shorter stature. There is less black and brown smudging on the fruits. Fruits are commonly smaller when compare to most forms. The male buds are imbricate and have paler bracts, more purple in tone on the bract external face, often slightly yellow streaked with pale yellowish tips. This subspecies *siamea* Simmonds has been recognized since then.

1.2.5 *Musa acuminata* Colla spp. *banksii* (F.v. Muell.) Simmonds

Cheesman (1948) described the characters of "the Mariani form" as the original information of this subspecies. Pseudostem and upper parts of leaf-sheaths are dull pale green, with light to moderate black blotching, and rather heavily waxy.

Leaf blades is not glaucous underneath. Midribs are green like the lamina, and only waxed near the base beneath. Petiole is relatively stout, with well developed erect margins and is not as closely appressed to the pseudostem at base as in most forms, that is not soon to become scarious.

Male flowers or compound tepal is pale orange-yellow, the lobe of compound tepal is deep orange and is about 5 mm. long.

Fruit bunch has carried slightly below the horizontal. Its peduncle is glabrous. Fruit is about 10-12 cm. long, 2.5-3 cm. in diameter. Pedicel is about 1 cm.. Acumen is 0.5 cm. and less pronounced than in the other forms.

Simmonds (1956) added description on this subspecies character that there is the predominantly brown pseudostem. Wax slightly developed on the leaf blade. Male is fertility of the female flowers. Bract is non-imbricate with often yellow on the bract internal face. The bunch is large and sometimes more or less ageotropic. Fruit is long-pedicellate and obtuse or very shortly acuminate.

Table 1 Shown the comparison and similarity of the *Musa acuminata* Colla forms and subspecies

Forms (Cheesman,1948)	**Annam**	**Tavoy**	**Selangor**	***Buitenzorg***	***Mariani***
Subspecies (Simmonds, 1956)	*siamea* Simmonds	*Burmannica* Simmonds	*Malaccensis* (Ridl.) Simmonds	*M. zebrina* Van Houtte ex Planch	*M. flaviflora* N. W. Simmonds

2. Discriminant of 326 accessions, Trung, Chantaburi and Kanchaanaburi

Table 2 Analysis Case Processing Summary.

Unweighted Cases		N	Percent
Valid		326	89.6
Excluded	Missing or out-of-range group codes	38	10.4
	At least one missing discriminating variable	0	.0
	Both missing or out-of-range group codes and at least one missing discriminating variable	0	.0
	Total	38	10.4
Total		364	100.0

Table 3 Group Statistics.

	Morphological characters	Mean	Std. Deviation	Valid N (listwise)	
				Unweighted	Weighted
FA	Pseudostem height	2.38	.728	29	29.000
	Pseudostem appearance	2.00	.000	29	29.000
	Blotch at the petiole base	2.55	.948	29	29.000
	Blotch color	3.52	1.153	29	29.000
	Petiole canal leaf	2.79	.559	29	29.000
	Wax on leaves	1.31	.471	29	29.000
	Peduncle hairiness	1.55	.783	29	29.000
	Bunch position	3.28	.960	29	29.000
	Rachis position	1.07	.258	29	29.000
	Male bud shape	1.41	.682	29	29.000
	Bract imbrication	1.62	.677	29	29.000
	Color of the bract external face	6.21	.620	29	29.000
	Color of the bract internal face	7.28	1.386	29	29.000
	Color on the bract apex	1.17	.384	29	29.000
	Color stripes on bract	1.14	.351	29	29.000
	Wax on the bract	1.41	.628	29	29.000
	Compound tepal basic color	2.28	.455	29	29.000
	Lobe color of compound tepal	2.48	.509	29	29.000
	Fruit apex	4.00	.000	29	29.000
	Fusion of pedicel	2.34	.721	29	29.000

Table 3 Group Statistics. (Cont.)

	Morphological characters	Mean	Std. Deviation	Valid N (listwise)	
				Unweighted	Weighted
FB	Pseudostem height	3.00	.000	12	12.000
	Pseudostem appearance	2.00	.000	12	12.000
	Blotch at the petiole base	2.92	.669	12	12.000
	Blotch color	3.83	.389	12	12.000
	Petiole canal leaf	2.17	.389	12	12.000
	Wax on leaves	1.00	.000	12	12.000
	Peduncle hairiness	1.08	.289	12	12.000
	Bunch position	3.08	.289	12	12.000
	Rachis position	1.00	.000	12	12.000
	Male bud shape	2.67	.778	12	12.000
	Bract imbrication	2.00	.000	12	12.000
	Color of the bract external face	7.83	.577	12	12.000
	Color of the bract internal face	3.00	2.335	12	12.000
	Color on the bract apex	1.00	.000	12	12.000
	Color stripes on bract	1.00	.000	12	12.000
	Wax on the bract	2.00	.000	12	12.000
	Compound tepal basic color	2.92	.289	12	12.000
	Lobe color of compound tepal	4.50	1.168	12	12.000
	Fruit apex	4.00	.000	12	12.000
	Fusion of pedicel	2.08	.289	12	12.000

Table 3 Group Statistics. (Cont.)

	Morphological characters	Mean	Std. Deviation	Valid N (listwise)	
				Unweighted	Weighted
MA	Pseudostem height	3.00	.000	11	11.000
	Pseudostem appearance	1.00	.000	11	11.000
	Blotch at the petiole base	3.00	.000	11	11.000
	Blotch color	4.00	.000	11	11.000
	Petiole canal leaf	4.82	.603	11	11.000
	Wax on leaves	4.00	.000	11	11.000
	Peduncle hairiness	2.00	.000	11	11.000
	Bunch position	2.82	.405	11	11.000
	Rachis position	2.00	.000	11	11.000
	Male bud shape	1.18	.405	11	11.000
	Bract imbrication	1.00	.000	11	11.000
	Color of the bract external face	3.82	.405	11	11.000
	Color of the bract internal face	4.18	2.040	11	11.000
	Color on the bract apex	1.09	.302	11	11.000
	Color stripes on bract	1.00	.000	11	11.000
	Wax on the bract	1.00	.000	11	11.000
	Compound tepal basic color	2.18	.405	11	11.000
	Lobe color of compound tepal	2.09	.302	11	11.000
	Fruit apex	3.64	.809	11	11.000
	Fusion of pedicel	3.00	.000	11	11.000

Table 3 Group Statistics. (Cont.)

	Morphological characters	Mean	Std. Deviation	Valid N (listwise)	
				Unweighted	Weighted
FC	Pseudostem height	1.73	.467	11	11.000
	Pseudostem appearance	1.00	.000	11	11.000
	Blotch at the petiole base	3.00	.000	11	11.000
	Blotch color	1.82	1.401	11	11.000
	Petiole canal leaf	2.00	.000	11	11.000
	Wax on leaves	1.00	.000	11	11.000
	Peduncle hairiness	2.00	.000	11	11.000
	Bunch position	3.00	.000	11	11.000
	Rachis position	1.00	.000	11	11.000
	Male bud shape	1.00	.000	11	11.000
	Bract imbrication	1.00	.000	11	11.000
	Color of the bract external face	8.00	.000	11	11.000
	Color of the bract internal face	3.00	.000	11	11.000
	Color on the bract apex	1.00	.000	11	11.000
	Color stripes on bract	1.00	.000	11	11.000
	Wax on the bract	1.00	.000	11	11.000
	Compound tepal basic color	3.00	.000	11	11.000
	Lobe color of compound tepal	5.00	.000	11	11.000
	Fruit apex	4.00	.000	11	11.000
	Fusion of pedicel	1.73	.467	11	11.000

Table 3 Group Statistics. (Cont.)

	Morphological characters	Mean	Std. Deviation	Valid N (listwise)	
				Unweighted	Weighted
SI	Pseudostem height	2.07	.776	187	187.000
	Pseudostem appearance	1.99	.103	187	187.000
	Blotch at the petiole base	2.41	1.029	187	187.000
	Blotch color	3.32	.991	187	187.000
	Petiole canal leaf	2.69	.622	187	187.000
	Wax on leaves	1.22	.418	187	187.000
	Peduncle hairiness	1.68	.777	187	187.000
	Bunch position	3.44	.849	187	187.000
	Rachis position	1.19	.466	187	187.000
	Male bud shape	1.36	.524	187	187.000
	Bract imbrication	2.03	.517	187	187.000
	Color of the bract external face	6.26	.655	187	187.000
	Color of the bract internal face	7.29	1.539	187	187.000
	Color on the bract apex	1.04	.203	187	187.000
	Color stripes on bract	1.07	.264	187	187.000
	Wax on the bract	1.63	.687	187	187.000
	Compound tepal basic color	2.34	.567	187	187.000
	Lobe color of compound tepal	2.21	.480	187	187.000
	Fruit apex	3.97	.218	187	187.000
	Fusion of pedicel	2.24	.756	187	187.000

Table 3 Group Statistics. (Cont.)

	Morphological characters	Mean	Std. Deviation	Valid N (listwise)	
				Unweighted	Weighted
BU	Pseudostem height	2.11	.741	76	76.000
	Pseudostem appearance	2.00	.000	76	76.000
	Blotch at the petiole base	2.51	.872	76	76.000
	Blotch color	3.54	1.038	76	76.000
	Petiole canal leaf	2.68	.616	76	76.000
	Wax on leaves	1.14	.354	76	76.000
	Peduncle hairiness	1.50	.622	76	76.000
	Bunch position	3.54	.791	76	76.000
	Rachis position	1.42	.659	76	76.000
	Male bud shape	1.34	.776	76	76.000
	Bract imbrication	1.88	.692	76	76.000
	Color of the bract external face	6.30	.693	76	76.000
	Color of the bract internal face	7.33	1.464	76	76.000
	Color on the bract apex	1.14	.354	76	76.000
	Color stripes on bract	1.08	.271	76	76.000
	Wax on the bract	1.62	.673	76	76.000
	Compound tepal basic color	2.43	.499	76	76.000
	Lobe color of compound tepal	2.17	.379	76	76.000
	Fruit apex	3.99	.115	76	76.000
	Fusion of pedicel	2.26	.755	76	76.000

Table 3 Group Statistics. (Cont.)

	Morphological characters	Mean	Std. Deviation	Valid N (listwise)	
				Unweighted	Weighted
Total	Pseudostem height	2.16	.768	326	326.000
	Pseudostem appearance	1.93	.262	326	326.000
	Blotch at the petiole base	2.50	.950	326	326.000
	Blotch color	3.38	1.051	326	326.000
	Petiole canal leaf	2.73	.729	326	326.000
	Wax on leaves	1.29	.640	326	326.000
	Peduncle hairiness	1.63	.719	326	326.000
	Bunch position	3.40	.819	326	326.000
	Rachis position	1.25	.516	326	326.000
	Male bud shape	1.39	.655	326	326.000
	Bract imbrication	1.89	.613	326	326.000
	Color of the bract external face	6.30	.895	326	326.000
	Color of the bract internal face	6.89	1.949	326	326.000
	Color on the bract apex	1.08	.267	326	326.000
	Color stripes on bract	1.07	.262	326	326.000
	Wax on the bract	1.58	.665	326	326.000
	Compound tepal basic color	2.39	.543	326	326.000
	Lobe color of compound tepal	2.40	.816	326	326.000
	Fruit apex	3.97	.233	326	326.000
	Fusion of pedicel	2.20	.754	326	326.000

Table 4 Tests of Equality of Group Means.

	Wilks' Lambda	F	df1	df2	Sig.
Pseudostem height	.888	8.060	5	320	.000
Pseudostem appearance	.089	655.152	5	320	.000
Blotch at the petiole base	**.968**	**2.096**	**5**	**320**	**.066**
Blotch color	.898	7.282	5	320	.000
Petiole canal leaf	.663	32.538	5	320	.000
Wax on leaves	.361	113.084	5	320	.000
Peduncle hairiness	.949	3.457	5	320	.005
Bunch position	.959	2.718	5	320	.020
Rachis position	.866	9.861	5	320	.000
Male bud shape	.842	12.037	5	320	.000
Bract imbrication	.808	15.229	5	320	.000
Color of the bract external face	.507	62.338	5	320	.000
Color of the bract internal face	.613	40.383	5	320	.000
Color on the bract apex	.958	2.808	5	320	.017
Color stripes on bract	**.986**	**.895**	**5**	**320**	**.485**
Wax on the bract	.925	5.215	5	320	.000
Compound tepal basic color	.907	6.599	5	320	.000
Lobe color of compound tepal	.355	116.149	5	320	.000
Fruit apex	.927	5.053	5	320	.000
Fusion of pedicel	.938	4.265	5	320	.001

Table 5 Pooled Within-Groups Matrices[a].

		pheh	psap	bpb	bc	pcl	wol	peh	bp	rp	mbus	bri	cbxf	cbri	cobra	csob	wob	ctbc	lcoct	fa	fop
Covariance	pheh	**.532**	.000	.045	.107	.043	-.014	.031	-.047	-.021	-.009	-.007	.000	-.248	.020	.015	.045	.013	.005	.005	.007
	psap	.000	.006	-.004	-.004	-.002	.001	-.002	-.004	.001	-.001	.000	-.002	-.004	.000	.000	.004	.005	.001	.000	-.005
	bpb	.045	-.004	.888	.129	.048	-.074	-.048	-.087	-.005	-.017	.016	-.018	.078	-.036	.019	.002	.028	-.074	-.005	.038
	bc	.107	-.004	.129	1.007	-.059	.003	-.024	-.032	.005	-.042	-.107	-.001	-.075	.087	.023	-.072	.018	.057	.000	-.012
	pcl	.043	-.002	.048	-.059	.358	.011	.009	.017	-.018	-.005	.040	.057	.058	-.024	-.009	.077	.025	-.049	.023	.081
	wol	-.014	.001	-.074	.003	.011	.151	.090	.007	-.007	.042	-.055	.025	-.104	.022	-.001	-.053	-.033	.091	.001	-.035
	peh	.031	-.002	-.048	-.024	.009	.090	.498	.043	-.003	-.010	-.011	.023	-.062	-.024	-.012	-.048	-.084	.058	.012	-.020
	bp	-.047	-.004	-.087	-.032	.017	.007	.043	.654	.065	.006	-.027	.005	.119	.001	-.051	.056	-.019	.024	1.47E-005	.042
	rp	-.021	.001	-.005	.005	-.018	-.007	-.003	.065	.234	.015	-.027	-.041	.065	.008	-.008	.033	.009	.001	.001	.020
	mbus	-.009	-.001	-.017	-.042	-.005	.042	-.010	.006	.015	.367	-.048	.004	-.083	.013	.004	.016	-.015	.086	-.019	-.020
	bri	-.007	.000	.016	-.107	.040	-.055	-.011	-.027	-.027	-.048	.308	.051	.057	-.047	.015	.082	.000	-.089	.019	-.020
	cbxf	.000	-.002	-.018	-.001	.057	.025	.023	.005	-.041	.004	.051	.412	-.008	.024	.024	.001	-.030	.067	.021	.001
	cbri	-.248	-.004	.078	-.075	.058	-.104	-.062	.119	.065	-.083	.057	-.008	2.364	-.008	-.069	.070	.007	-.224	-.036	.122
	cobra	.020	.000	-.036	.087	-.024	.022	-.024	.001	.008	.013	-.047	.024	-.008	.069	.009	-.040	-.006	.047	-.010	-.034
	csob	.015	.000	.019	.023	-.009	-.001	-.012	-.051	-.008	.004	.015	.024	-.069	.009	.069	-.022	.002	-.006	.001	-.039

Table 5 Pooled Within-Groups Matrices[a]. (Cont.)

		pheh	psap	bpb	bc	pcl	wol	peh	bp	rp	mbus	bri	cbxf	cbri	cobra	csob	wob	ctbc	lcoct	fa	fop
	wob	.045	.004	.002	-.072	.077	-.053	-.048	.056	.033	.016	.082	.001	.070	-.040	-.022	.415	-.047	-.085	-.001	.151
	ctbc	.013	.005	.028	.018	.025	-.033	-.084	-.019	.009	-.015	.000	-.030	.007	-.006	.002	-.047	.271	.002	.009	-.007
	lcoct	.005	.001	-.074	.057	-.049	.091	.058	.024	.001	.086	-.089	.067	-.224	.047	-.006	-.085	.002	.240	-.001	-.048
	fa	.005	.000	-.005	.000	.023	.001	.012	1.47E-005	.001	-.019	.019	.021	-.036	-.010	.001	-.001	.009	-.001	.051	-.028
	fop	.007	-.005	.038	-.012	.081	-.035	-.020	.042	.020	-.020	-.020	.001	.122	-.034	-.039	.151	-.007	-.048	-.028	.541
Correlation	pheh	1.000	.008	.066	.146	.099	-.050	.061	-.080	-.058	-.021	-.018	.000	-.221	.104	.080	.096	.034	.014	.027	.013
	psap	.008	1.000	-.050	-.054	-.041	.046	-.036	-.055	.031	-.019	.005	-.030	-.037	.013	.023	.077	.128	.034	-.009	-.082
	bpb	.066	-.050	1.000	.136	.085	-.202	-.072	-.114	-.012	-.030	.031	-.030	.054	-.147	.076	.004	.057	-.161	-.021	.054
	bc	.146	-.054	.136	1.000	-.099	.008	-.034	-.040	.009	-.069	-.193	-.001	-.049	.331	.086	-.112	.034	.116	.002	-.016
	pcl	.099	-.041	.085	-.099	1.000	.045	.021	.036	-.061	-.013	.120	.149	.063	-.156	-.059	.200	.082	-.168	.171	.184
	wol	-.050	.046	-.202	.008	.045	1.000	.328	.022	-.035	.179	-.256	.101	-.174	.216	-.008	-.210	-.161	.477	.010	-.122
	peh	.061	-.036	-.072	-.034	.021	.328	1.000	.076	-.010	-.023	-.028	.052	-.057	-.130	-.064	-.105	-.229	.168	.077	-.039
	bp	-.080	-.055	-.114	-.040	.036	.022	.076	1.000	.167	.013	-.061	.010	.095	.005	-.243	.108	-.046	.061	.000	.070
	rp	-.058	.031	-.012	.009	-.061	-.035	-.010	.167	1.000	.050	-.100	-.132	.087	.062	-.060	.105	.034	.003	.010	.057
	mbus	-.021	-.019	-.030	-.069	-.013	.179	-.023	.013	.050	1.000	-.144	.009	-.089	.081	.025	.040	-.048	.291	-.140	-.046

Table 5 Pooled Within-Groups Matrices[a]. (Cont.)

		pheh	psap	bpb	bc	pcl	wol	peh	bp	rp	mbus	bri	cbxf	cbri	cobra	csob	wob	ctbc	lcoct	fa	fop
Correlation	bri	-.018	.005	.031	-.193	.120	-.256	-.028	-.061	-.100	-.144	1.000	.144	.067	-.323	.103	.230	-.001	-.326	.150	-.048
	cbxf	.000	-.030	-.030	-.001	.149	.101	.052	.010	-.132	.009	.144	1.000	-.009	.144	.144	.002	-.090	.212	.148	.001
	cbri	-.221	-.037	.054	-.049	.063	-.174	-.057	.095	.087	-.089	.067	-.009	1.000	-.019	-.172	.071	.009	-.297	-.103	.108
	cobra	.104	.013	-.147	.331	-.156	.216	-.130	.005	.062	.081	-.323	.144	-.019	1.000	.129	-.238	-.046	.363	-.172	-.176
	csob	.080	.023	.076	.086	-.059	-.008	-.064	-.243	-.060	.025	.103	.144	-.172	.129	1.000	-.132	.013	-.046	.024	-.200
	wob	.096	.077	.004	-.112	.200	-.210	-.105	.108	.105	.040	.230	.002	.071	-.238	-.132	1.000	-.141	-.270	-.005	.319
	ctbc	.034	.128	.057	.034	.082	-.161	-.229	-.046	.034	-.048	-.001	-.090	.009	-.046	.013	-.141	1.000	.008	.075	-.018
	lcoct	.014	.034	-.161	.116	-.168	.477	.168	.061	.003	.291	-.326	.212	-.297	.363	-.046	-.270	.008	1.000	-.012	-.134
	fa	.027	-.009	-.021	.002	.171	.010	.077	.000	.010	-.140	.150	.148	-.103	-.172	.024	-.005	.075	-.012	1.000	-.170
	fop	.013	-.082	.054	-.016	.184	-.122	-.039	.070	.057	-.046	-.048	.001	.108	-.176	-.200	.319	-.018	-.134	-.170	1.000

a. The covariance matrix has 320 degrees of freedom.

Table 6 Covariance Matrices[(a)].

Morphological Characters		pheh	psap	bpb	bc	pcl	wol	peh	bp	rp	mbus	bri	cbxf	cbri	cobra	csob	wob	ctbc	lcoct	fa	fop
FA	pheh	.530	.000	.176	.154	.081	-.086	-.324	-.251	-.099	-.055	.006	-.046	-.180	.004	.017	.052	-.037	-.083	.000	-.028
	psap	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	bpb	.176	.000	.899	-.224	.011	-.142	-.244	-.086	-.039	-.094	.217	-.083	.128	-.206	-.007	.192	.021	-.169	.000	.160
	bc	.154	.000	-.224	1.330	-.139	-.131	-.474	-.219	-.108	-.115	-.190	.032	-.576	.229	.105	-.079	-.005	.027	.000	-.113
	pcl	.081	.000	.011	-.139	.313	.031	.047	.059	-.021	.017	.062	.009	-.084	-.034	-.042	.053	.059	-.039	.000	.002
	wol	-.086	.000	-.142	-.131	.031	.222	.180	.054	.049	.153	.015	.005	.018	.052	-.044	-.062	-.053	.131	.000	-.075
	peh	-.324	.000	-.244	-.474	.047	.180	.613	.271	.103	.156	.038	.096	-.050	-.063	-.043	-.165	-.015	.153	.000	-.090
	bp	-.251	.000	-.086	-.219	.059	.054	.271	.921	.052	.203	-.070	.262	.385	-.049	-.111	-.011	.100	.148	.000	.151
	rp	-.099	.000	-.039	-.108	-.021	.049	.103	.052	.067	.042	-.009	-.015	.052	-.012	-.010	-.030	.016	.037	.000	-.025
	mbus	-.055	.000	-.094	-.115	.017	.153	.156	.203	.042	.466	-.123	.018	.096	.069	-.023	.037	-.083	.115	.000	-.041
	bri	.006	.000	.217	-.190	.062	.015	.038	-.070	-.009	-.123	.458	.046	-.213	-.111	.054	.091	.037	-.167	.000	-.115
	cbxf	-.046	.000	-.083	.032	.009	.005	.096	.262	-.015	.018	.046	.384	-.131	-.001	.042	-.053	-.059	.039	.000	-.074
	cbri	-.180	.000	.128	-.576	-.084	.018	-.050	.385	.052	.096	-.213	-.131	1.921	.094	-.182	.132	.064	.076	.000	.366
	cobra	.004	.000	-.206	.229	-.034	.052	-.063	-.049	-.012	.069	-.111	-.001	.094	.148	.011	-.038	-.049	.057	.000	-.026
	csob	.017	.000	-.007	.105	-.042	-.044	-.043	-.111	-.010	-.023	.054	.042	-.182	.011	.123	-.059	-.039	-.033	.000	-.156

Table 6 Covariance Matrices[(a)] (Cont.)

Morphological Characters		pheh	psap	bpb	bc	pcl	wol	peh	bp	rp	mbus	bri	cbxf	cbri	cobra	csob	wob	ctbc	lcoct	fa	fop
	wob	.052	.000	.192	-.079	.053	-.062	-.165	-.011	-.030	.037	.091	-.053	.132	-.038	-.059	.394	-.011	-.207	.000	.209
	ctbc	-.037	.000	.021	-.005	.059	-.053	-.015	.100	.016	-.083	.037	-.059	.064	-.049	-.039	-.011	.207	-.031	.000	.044
	lcoct	-.083	.000	-.169	.027	-.039	.131	.153	.148	.037	.115	-.167	.039	.076	.057	-.033	-.207	-.031	.259	.000	-.030
	fa	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	fop	-.028	.000	.160	-.113	.002	-.075	-.090	.151	-.025	-.041	-.115	-.074	.366	-.026	-.156	.209	.044	-.030	.000	.520
FB	pheh	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	psap	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	bpb	.000	.000	.447	.076	-.076	.000	.098	-.174	.000	.152	.000	.348	-.455	.000	.000	.000	-.098	.227	.000	.098
	bc	.000	.000	.076	.152	-.152	.000	-.076	-.076	.000	.303	.000	.152	-.909	.000	.000	.000	.076	.455	.000	-.076
	pcl	.000	.000	-.076	-.152	.152	.000	.076	.076	.000	-.303	.000	-.152	.909	.000	.000	.000	-.076	-.455	.000	.076
	wol	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	peh	.000	.000	.098	-.076	.076	.000	.083	-.008	.000	-.152	.000	.015	.455	.000	.000	.000	-.083	-.227	.000	.083
	bp	.000	.000	-.174	-.076	.076	.000	-.008	.083	.000	-.152	.000	-.167	.455	.000	.000	.000	.008	-.227	.000	-.008
	rp	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	mbus	.000	.000	.152	.303	-.303	.000	-.152	-.152	.000	.606	.000	.303	-1.818	.000	.000	.000	.152	.909	.000	-.152

Table 6 Covariance Matrices[(a)] . (Cont.)

Morphological Characters		pheh	psap	bpb	bc	pcl	wol	peh	bp	rp	mbus	bri	cbxf	cbri	cobra	csob	wob	ctbc	lcoct	fa	fop
FB	bri	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	cbxf	.000	.000	.348	.152	-.152	.000	.015	-.167	.000	.303	.000	.333	-.909	.000	.000	.000	-.015	.455	.000	.015
	cbri	.000	.000	-.455	-.909	.909	.000	.455	.455	.000	-1.818	.000	-.909	5.455	.000	.000	.000	-.455	-2.727	.000	.455
	cobra	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	csob	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	wob	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	ctbc	.000	.000	-.098	.076	-.076	.000	-.083	.008	.000	.152	.000	-.015	-.455	.000	.000	.000	.083	.227	.000	-.083
	lcoct	.000	.000	.227	.455	-.455	.000	-.227	-.227	.000	.909	.000	.455	-2.727	.000	.000	.000	.227	1.364	.000	-.227
	fa	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	fop	.000	.000	.098	-.076	.076	.000	.083	-.008	.000	-.152	.000	.015	.455	.000	.000	.000	-.083	-.227	.000	.083
MA	pheh	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	psap	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	bpb	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	bc	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000

Table 6 Covariance Matrices[(a)]. (Cont.)

Morphological Characters		pheh	psap	bpb	bc	pcl	wol	peh	bp	rp	mbus	bri	cbxf	cbri	cobra	csob	wob	ctbc	lcoct	fa	fop
MA	pcl	.000	.000	.000	.000	.364	.000	.000	-.036	.000	.036	.000	-.036	.236	.018	.000	.000	-.164	.018	-.073	.073
	wol	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	peh	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	bp	.000	.000	.000	.000	-.036	.000	.000	.164	.000	-.164	.000	-.036	-.564	-.082	.000	.000	.036	.018	.327	-.327
	rp	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	mbus	.000	.000	.000	.000	.036	.000	.000	-.164	.000	.164	.000	.036	.564	.082	.000	.000	-.036	-.018	-.327	.327
	bri	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	cbxf	.000	.000	.000	.000	-.036	.000	.000	-.036	.000	.036	.000	.164	.236	.018	.000	.000	.036	.018	-.073	.073
	cbri	.000	.000	.000	.000	.236	.000	.000	-.564	.000	.564	.000	.236	4.164	.282	.000	.000	-.236	-.118	-1.127	1.127
	cobra	.000	.000	.000	.000	.018	.000	.000	-.082	.000	.082	.000	.018	.282	.091	.000	.000	-.018	-.009	-.164	.164
	csob	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	wob	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	ctbc	.000	.000	.000	.000	-.164	.000	.000	.036	.000	-.036	.000	.036	-.236	-.018	.000	.000	.164	-.018	.073	-.073
	lcoct	.000	.000	.000	.000	.018	.000	.000	.018	.000	-.018	.000	.018	-.118	-.009	.000	.000	-.018	.091	.036	-.036

Table 6 Covariance Matrices[(a)]. (Cont.)

Morphological Characters		pheh	psap	bpb	bc	pcl	wol	peh	bp	rp	mbus	bri	cbxf	cbri	cobra	csob	wob	ctbc	lcoct	fa	fop
MA	fa	.000	.000	.000	.000	-.073	.000	.000	.327	.000	-.327	.000	-.073	-1.127	-.164	.000	.000	.073	.036	.655	-.655
	fop	.000	.000	.000	.000	.073	.000	.000	-.327	.000	.327	.000	.073	1.127	.164	.000	.000	-.073	-.036	-.655	.655
FC	pheh	.218	.000	.000	-.655	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.218
	psap	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	bpb	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	bc	-.655	.000	.000	1.964	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	-.655
	pcl	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	wol	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	peh	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	bp	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	rp	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	mbus	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	bri	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	cbxf	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000

Table 6 Covariance Matrices[(a)] . (Cont.)

Morphological Characters		pheh	psap	bpb	bc	pcl	wol	peh	bp	rp	mbus	bri	cbxf	cbri	cobra	csob	wob	ctbc	lcoct	fa	fop
FC	cbri	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	cobra	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	csob	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	wob	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	ctbc	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	lcoct	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	fa	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	fop	.218	.000	.000	-.655	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.218
SI	pheh	.603	.001	.052	.090	.049	-.005	.097	-.020	-.035	-.041	.025	.020	-.251	.002	.006	.075	.025	-.004	.007	-.006
	psap	.001	.011	-.006	-.007	-.003	.002	-.003	-.006	.002	-.002	.000	-.003	-.008	.000	.001	.007	.009	.002	.000	-.008
	bpb	.052	-.006	1.060	.251	.057	-.097	-.075	-.099	-.001	-.028	.008	-.078	.049	-.012	.023	-.019	.056	-.101	-.011	.025
	bc																				
	pcl	.049	-.003	.057	-.002	.387	.006	.004	.013	-.012	-.028	.058	.096	.063	-.014	-.009	.061	.051	-.037	.035	.075
	wol	-.005	.002	-.097	-.003	.006	.175	.141	.009	.001	.048	-.072	.039	-.173	.017	.005	-.066	-.038	.114	.001	-.049

Table 6 Covariance Matrices[(a)] (Cont.)

Morphological Characters		pheh	psap	bpb	bc	pcl	wol	peh	bp	rp	mbus	bri	cbxf	cbri	cobra	csob	wob	ctbc	lcoct	fa	fop
SI	peh	.097	-.003	-.075	.032	.004	.141	.604	.053	-.011	-.032	-.033	.012	-.059	-.024	-.035	-.060	-.119	.104	.018	-.047
	bp	-.020	-.006	-.099	-.045	.013	.009	.053	.721	.073	-.002	-.014	-.011	.055	.003	-.033	.074	-.030	.026	-.015	.028
	rp	-.035	.002	-.001	.010	-.012	.001	-.011	.073	.217	.024	-.033	-.027	.085	.019	.002	.044	-.004	.004	.000	.008
	mbus	-.041	-.002	-.028	-.067	-.028	.048	-.032	-.002	.024	.274	-.049	.015	-.013	.017	-.005	-.032	.013	.092	-.017	-.038
	bri	.025	.000	.008	-.075	.058	-.072	-.033	-.014	-.033	-.049	.268	.088	.039	-.012	.003	.098	-.011	-.071	.028	-.013
	cbxf	.020	-.003	-.078	.025	.096	.039	.012	-.011	-.027	.015	.088	.428	-.042	.021	.024	.021	-.033	.054	.045	.024
	cbri	-.251	-.008	.049	.111	.063	-.173	-.059	.055	.085	-.013	.039	-.042	2.368	-.039	-.038	.087	.090	-.227	.002	.129
	cobra	.002	.000	-.012	.029	-.014	.017	-.024	.003	.019	.017	-.012	.021	-.039	.041	.018	-.027	.002	.023	-.004	-.037
	csob	.006	.001	.023	.013	-.009	.005	-.035	-.033	.002	-.005	.003	.024	-.038	.018	.070	-.026	.012	.000	.002	-.040
	wob	.075	.007	-.019	-.046	.061	-.066	-.060	.074	.044	-.032	.098	.021	.087	-.027	-.026	.472	-.035	-.072	-.005	.166
	ctbc	.025	.009	.056	.036	.051	-.038	-.119	-.030	-.004	.013	-.011	-.033	.090	.002	.012	-.035	.321	-.006	.009	-.001
	lcoct	-.004	.002	-.101	-.008	-.037	.114	.104	.026	.004	.092	-.071	.054	-.227	.023	.000	-.072	-.006	.230	.000	-.040
	fa	.007	.000	-.011	.009	.035	.001	.018	-.015	.000	-.017	.028	.045	.002	-.004	.002	-.005	.009	.000	.048	-.015
	fop	-.006	-.008	.025	.051	.075	-.049	-.047	.028	.008	-.038	-.013	.024	.129	-.037	-.040	.166	-.001	-.040	-.015	.571

Table 6 Covariance Matrices[(a)]. (Cont.)

Morphological Characters		pheh	psap	bpb	bc	pcl	wol	peh	bp	rp	mbus	bri	cbxf	cbri	cobra	csob	wob	ctbc	lcoct	fa	fop
BU	pheh	.549	.000	-.001	.262	.034	-.015	.013	-.058	.035	.084	-.094	-.032	-.368	.078	.045	-.013	.007	.062	.001	.025
	psap	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
	bpb	-.001	.000	.760	-.001	.071	-.022	.060	-.067	-.006	.009	-.032	.096	.229	-.049	.026	-.015	-.012	-.036	.007	.023
	bc	.262	.000	-.001	1.078	-.174	.068	.007	.065	.036	-.014	-.202	-.099	-.246	.214	.024	-.165	-.024	.186	-.019	-.037
	pcl	.034	.000	.071	-.174	.379	.020	.000	.013	-.039	.083	.002	.030	-.041	-.060	-.001	.158	-.008	-.039	.022	.138
	wol	-.015	.000	-.022	.068	.020	.125	-.033	-.012	-.048	.003	-.063	.009	-.022	.032	.002	-.037	-.024	.055	.002	.001
	peh	.013	.000	.060	.007	.000	-.033	.387	-.047	-.027	.000	.020	.033	-.167	-.020	.053	.007	-.047	-.033	.007	.053
	bp	-.058	.000	-.067	.065	.013	-.012	-.047	.625	.076	.000	-.055	-.019	.234	.028	-.096	.062	-.051	.013	-.006	.096
	rp	.035	.000	-.006	.036	-.039	-.048	-.027	.076	.434	-.013	-.029	-.102	.046	-.008	-.034	.043	.041	-.020	.006	.074
	mbus	.084	.000	.009	-.014	.083	.003	.000	.000	-.013	.601	-.039	-.078	-.167	-.024	.039	.132	-.084	-.033	.005	.002
	bri	-.094	.000	-.032	-.202	.002	-.063	.020	-.055	-.029	-.039	.479	-.017	.226	-.129	.036	.074	.012	-.139	.012	-.008
	cbxf	-.032	.000	.096	-.099	.030	.009	.033	-.019	-.102	-.078	-.017	.481	.219	.049	.029	-.030	-.026	.068	-.009	-.041
	cbri	-.368	.000	.229	-.246	-.041	-.022	-.167	.234	.046	-.167	.226	.219	2.144	-.008	-.133	.034	-.118	-.004	-.009	-.154
	cobra	.078	.000	-.049	.214	-.060	.032	-.020	.028	-.008	-.024	-.129	.049	-.008	.125	-.012	-.091	-.010	.122	-.011	-.065

Table 6 Covariance Matrices[(a)] (Cont.)

Morphological Characters		pheh	psap	bpb	bc	pcl	wol	peh	bp	rp	mbus	bri	cbxf	cbri	cobra	csob	wob	ctbc	lcoct	fa	fop
BU	csob	.045	.000	.026	.024	-.001	.002	.053	-.096	-.034	.039	.036	.029	-.133	-.012	.074	-.009	-.008	-.014	.001	-.008
	wob	-.013	.000	-.015	-.165	.158	-.037	.007	.062	.043	.132	.074	-.030	.034	-.091	-.009	.452	-.112	-.107	.008	.155
	ctbc	.007	.000	-.012	-.024	-.008	-.024	-.047	-.051	.041	-.084	.012	-.026	-.118	-.010	-.008	-.112	.249	.005	.006	-.022
	lcoct	.062	.000	-.036	.186	-.039	.055	-.033	.013	-.020	-.033	-.139	.068	-.004	.122	-.014	-.107	.005	.144	-.011	-.059
	fa	.001	.000	.007	-.019	.022	.002	.007	-.006	.006	.005	.012	-.009	-.009	-.011	.001	.008	.006	-.011	.013	.004
	fop	.025	.000	.023	-.037	.138	.001	.053	.096	.074	.002	-.008	-.041	-.154	-.065	-.008	.155	-.022	-.059	.004	.570
Total	pheh	.590	-.013	.070	.164	.099	.064	.016	-.073	-.005	.033	-.028	-.048	-.404	.022	.013	.043	.014	.038	-.004	-.014
	psap	-.013	.068	-.037	.028	-.048	-.080	-.027	.029	-.016	.020	.060	.025	.216	.003	.005	.043	-.008	-.075	.010	.040
	bpb	.070	-.037	.903	.122	.064	-.033	-.047	-.109	.002	-.006	-.021	-.006	-.114	-.036	.015	-.014	.045	.008	-.009	.012
	bc	.164	.028	.122	1.104	.015	.067	-.052	-.026	.036	-.004	-.084	-.117	.018	.094	.024	-.048	-.008	-.054	-.007	-.003
	pcl	.099	-.048	.064	.015	.531	.218	.037	-.011	.046	-.035	-.009	-.192	.031	-.019	-.011	.038	-.016	-.171	-.002	.034
	wol	.064	-.080	-.033	.067	.218	.410	.127	-.046	.064	.015	-.134	-.235	-.300	.024	-.006	-.107	-.062	.028	-.031	-.108
	peh	.016	-.027	-.047	-.052	.037	.127	.517	.035	.002	-.043	-.029	-.018	-.069	-.027	-.013	-.068	-.091	.044	.007	-.035
	bp	-.073	.029	-.109	-.026	-.011	-.046	.035	.671	.062	-.002	.007	.013	.287	.003	-.048	.074	-.028	-.043	.006	.067

Table 6 Covariance Matrices[(a)] . (Cont.)

Morphological Characters		pheh	psap	bpb	bc	pcl	wol	peh	bp	rp	mbus	bri	cbxf	cbri	cobra	csob	wob	ctbc	lcoct	fa	fop
Total	rp	-.005	-.016	.002	.036	.046	.064	.002	.062	.266	-.001	-.044	-.129	.061	.012	-.009	.021	-.001	-.052	-.008	.002
	mbus	.033	.020	-.006	-.004	-.035	.015	-.043	-.002	-.001	.429	-.028	.071	-.206	.010	.002	.045	.003	.158	-.016	-.014
	bri	-.028	.060	-.021	-.084	-.009	-.134	-.029	.007	-.044	-.028	.375	.079	.262	-.050	.017	.125	-.012	-.165	.027	.019
	cbxf	-.048	.025	-.006	-.117	-.192	-.235	-.018	.013	-.129	.071	.079	.800	-.238	.014	.021	.040	.055	.364	.052	.035
	cbri	-.404	.216	-.114	.018	.031	-.300	-.069	.287	.061	-.206	.262	-.238	3.797	.015	-.038	.147	-.141	-.900	-.010	.296
	cobra	.022	.003	-.036	.094	-.019	.024	-.027	.003	.012	.010	-.050	.014	.015	.071	.010	-.041	-.009	.034	-.010	-.031
	csob	.013	.005	.015	.024	-.011	-.006	-.013	-.048	-.009	.002	.017	.021	-.038	.010	.068	-.021	-.001	-.017	.002	-.033
	wob	.043	.043	-.014	-.048	.038	-.107	-.068	.074	.021	.045	.125	.040	.147	-.041	-.021	.442	-.046	-.105	.005	.172
	ctbc	.014	-.008	.045	-.008	-.016	-.062	-.091	-.028	-.001	.003	-.012	.055	-.141	-.009	-.001	-.046	.295	.101	.012	-.015
	lcoct	.038	-.075	.008	-.054	-.171	.028	.044	-.043	-.052	.158	-.165	.364	-.900	.034	-.017	-.105	.101	.665	.006	-.096
	fa	-.004	.010	-.009	-.007	-.002	-.031	.007	.006	-.008	-.016	.027	.052	-.010	-.010	.002	.005	.012	.006	.054	-.018
	fop	-.014	.040	.012	-.003	.034	-.108	-.035	.067	.002	-.014	.019	.035	.296	-.031	-.033	.172	-.015	-.096	-.018	.568

a. The total covariance matrix has 325 degrees of freedom.

Analysis : Box's Test of Equality of Covariance Matrices

Table 7 Log Determinants

Morphological characters	Rank	Log Determinant
FA	18	.[a]
FB	.[b]	.[c]
MA	.[d]	.[c]
FC	.[d]	.[c]
SI	20	-28.883
BU	19	.[a]
Pooled within-groups	20	-28.837

The ranks and natural logarithms of determinants printed are those of the group covariance matrices.

a Singular, b Rank < 12, c Too few cases to be non-singular, d Rank < 11

Test Results(a)

Box's M	

Tests null hypothesis of equal population covariance matrices.

a No test can be performed with fewer than two nonsingular group covariance matrices.

Summary of Canonical Discriminant Functions

Table 8 Eigenvalues

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	13.821[a]	68.9	68.9	.966
2	5.252[a]	26.2	95.1	.917
3	.747[a]	3.7	98.9	.654
4	.131[a]	.7	99.5	.340
5	.098[a]	.5	100.0	.299

a. First 5 canonical discriminant functions were used in the analysis.

Table 9 Wilks' Lambda

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1 through 5	.005	1654.665	100	.000
2 through 5	.074	813.496	76	.000
3 through 5	.461	241.609	54	.000
4 through 5	.805	67.594	34	.001
5	.911	29.163	16	.023

Table 10 Standardized Canonical Discriminant Function Coefficients

	Function				
	1	2	3	4	5
Pseudostem height	-.013	.080	.329	.282	.078
Pseudostem appearance	**.953**	.107	.215	.087	.011
Blotch at the petiole base	-.054	-.029	.095	.068	.190
Blotch color	.099	.172	.351	-.183	.051
Petiole canal leaf	-.090	.220	.145	.254	.100
Wax on leaves	-.328	**.785**	.390	-.028	-.159
Peduncle hairiness	.083	-.087	-.378	-.165	-.218
Bunch position	.114	.056	-.065	-.105	.064
Rachis position	-.106	.119	.097	-.418	**.540**
Male bud shape	.207	.054	.313	-.131	-.002
Bract imbrication	.074	.106	.272	-.409	-.390
Color of the bract external face	.084	-.368	-.006	-.396	.177
Color of the bract internal face	.128	.052	-.241	.400	-.144
Color on the bract apex	.096	.140	-.381	.063	.490
Color stripes on bract	.008	.002	-.151	.345	-.027
Wax on the bract	-.183	-.151	.103	-.210	-.032
Compound tepal basic color	-.175	-.092	.013	-.364	.143
Lobe color of compound tepal	-.158	-.832	**.405**	**.533**	-.178
Fruit apex	.155	-.051	-.178	.268	.167
Fusion of pedicel	.206	-.003	-.093	.270	.041

Table 11 Structure Matrix

	Function				
	1	2	3	4	5
Pseudostem appearance	**.857***	.090	.255	.020	.017
Lobe color of compound tepal	-.158	**-.496***	.465	.331	.064
Color of the bract external face	.061	-.418*	.039	-.140	.073
Wax on leaves	-.250	.388*	.370	.226	-.142
Petiole canal leaf	-.096	.263*	.130	.142	.043
Fruit apex	.054	-.080*	-.078	.075	.073
Male bud shape	.032	-.062	**.453***	-.007	.014
Color of the bract internal face	.157	.161	-.449*	.083	-.047
Pseudostem height	-.027	.040	.360*	.251	.159
Bract imbrication	.116	.011	.040	**-.477***	-.465
Wax on the bract	.064	-.016	.131	-.278*	-.061
Color stripes on bract	.021	.014	-.050	.193*	.043
Bunch position	.046	.011	-.099	-.188*	.110
Fusion of pedicel	.067	-.009	-.059	.109*	.037
Rachis position	-.043	.120	.017	-.375	**.586***
Color on the bract apex	.009	.030	-.034	.241	.550*
Peduncle hairiness	-.038	.025	-.157	-.012	-.361*
Blotch color	.027	.098	.241	.032	.316*
Compound tepal basic color	-.024	-.123	.086	-.195	.234*
Blotch at the petiole base	-.039	-.023	.086	.057	.181*

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions .

Variables ordered by absolute size of correlation within function.

* Largest absolute correlation between each variable and any discriminant function

Table 12 Canonical Discriminant Function Coefficients.

	Function				
	1	2	3	4	5
Pseudostem height	-.017	.109	.451	.386	.107
Pseudostem appearance	12.118	1.356	2.736	1.112	.134
Blotch at the petiole base	-.058	-.030	.101	.073	.202
Blotch color	.099	.171	.350	-.182	.051
Petiole canal leaf	-.151	.368	.243	.424	.167
Wax on leaves	-.847	2.023	1.005	-.072	-.411
Peduncle hairiness	.117	-.123	-.535	-.234	-.308
Bunch position	.141	.069	-.080	-.130	.079
Rachis position	-.219	.247	.202	-.865	1.116
Male bud shape	.342	.089	.516	-.216	-.004
Bract imbrication	.133	.191	.491	-.736	-.704
Color of the bract external face	.131	-.573	-.009	-.617	.276
Color of the bract internal face	.083	.034	-.157	.260	-.094
Color on the bract apex	.365	.533	-1.448	.241	1.864
Color stripes on bract	.029	.007	-.577	1.316	-.104
Wax on the bract	-.284	-.235	.160	-.327	-.049
Compound tepal basic color	-.336	-.176	.025	-.699	.275
Lobe color of compound tepal	-.323	-1.698	.827	1.089	-.363
Fruit apex	.686	-.224	-.788	1.183	.737
Fusion of pedicel	.280	-.004	-.126	.368	.055
(Constant)	-26.247	.756	-5.968	-5.521	-6.657

Unstandardized coefficients

5 canonical equations

(1) -26.247+(-.017) Pseudostem height +(12.118) Pseudostem appearance +(-.058) Blotch at the petiole base +(.099) Blotch color +(-.151) Petiole canal leaf +(-.847) Wax on leaves+(.117) Peduncle hairiness +(.141) Bunch position + (-.219) Rachis position +(.342) Male bud shape +(.133) Bract imbrication +(.131) Color of the bract external face +(.083) Color of the bract internal face +(.365) Color on the bract apex +(.029) Color stripes on bract +(-.284) Wax on the bract +(-.336) Compound tepal basic color +(-.323) Lobe color of compound tepal +(.686) Fruit apex +(.280)Fusion of pedicel

(2) .756+(.109) Pseudostem height +(1.356) Pseudostem appearance +(-.030) Blotch at the petiole base +(.171) Blotch color +(.368) Petiole canal leaf +(2.023) Wax on leaves+(-.123) Peduncle hairiness +(.069) Bunch position +(.247) Rachis position +(.089) Male bud shape +(.191) Bract imbrication +(-.573) Color of the bract external face +(.034) Color of the bract internal face +(.533) Color on the bract apex +(.007) Color stripes on bract +(-.235) Wax on the bract +(-.176) Compound tepal basic color +(-1.698) Lobe color of compound tepal +(-.224) Fruit apex +(-.004)Fusion of pedicel

(3) -5.968+(.451) Pseudostem height +(2.736) Pseudostem appearance +(.101) Blotch at the petiole base +(.350) Blotch color +(.243) Petiole canal leaf +(1.005) Wax on leaves+(-.535) Peduncle hairiness +(-.080) Bunch position +(.202) Rachis position +(.516) Male bud shape +(.491) Bract imbrication +(-.009) Color of the bract external face +(-.157) Color of the bract internal face +(-1.448) Color on the bract apex +(-.577) Color stripes on bract +(.160) Wax on the bract +(.025) Compound tepal basic color +(.827) Lobe color of compound tepal +(-.788) Fruit apex +(-.126)Fusion of pedicel

(4) -5.521+(.386) Pseudostem height +(1.112) Pseudostem appearance +(.073) Blotch at the petiole base +(-.182) Blotch color +(.424) Petiole canal leaf +(-.072) Wax on leaves+(-.234) Peduncle hairiness +(-.130) Bunch position +(-.865) Rachis position +(-.216) Male bud shape +(-.736) Bract imbrication +(-.617) Color of the bract external face +(.260) Color of the bract internal face +(.241) Color on the bract apex +(1.316) Color stripes on bract +(-.327) Wax on the bract +(-.699) Compound tepal basic color +(1.089) Lobe color of compound tepal +(1.183) Fruit apex +(.368)Fusion of pedicel

(5) -6.657+(.107) Pseudostem height +(.134) Pseudostem appearance +(.202) Blotch at the petiole base +(.051) Blotch color +(.167) Petiole canal leaf +(-.411) Wax on leaves+(-.308) Peduncle hairiness +(.079) Bunch position +(1.116) Rachis position +(-.004) Male bud shape +(-.704) Bract imbrication +(.276) Color of the bract external face +(-.094) Color of the bract internal face +(1.864) Color on the bract apex +(-.104) Color stripes on bract +(-.049) Wax on the bract +(.275) Compound tepal basic color +(-.363) Lobe color of compound tepal +(-.363) Fruit apex +(.055)Fusion of pedicel

Table 13 Functions at Group Centroids.

Morphological characters	Function				
	1	2	3	4	5
FA	1.034	.142	.048	1.131	.146
FB	.488	-5.238	3.891	-.139	.047
MA	-14.886	7.196	1.281	-.023	.038
FC	-12.376	-8.324	-1.691	.032	.001
SI	.954	.264	-.139	-.081	-.237
BU	1.127	.285	-.232	-.212	.515

Unstandardized canonical discriminant functions evaluated at group means

Classification Statistics

Table 14 Classification Processing Summary.

	Processed	**364**
Excluded	Missing or out-of-range group codes	0
	At least one missing discriminating variable	0
	Used in Output	364

Table 15 Prior Probabilities for Groups.

Morphological characters	Prior	Specified Prior	Effective Prior	Cases Used in Analysis	
				Unweighted	Weighted
FA	.167			29	29.000
FB	.167			12	12.000
MA	.167			11	11.000
FC	.167			11	11.000
SI	.167			187	187.000
BU	.167			76	76.000
Total	1.000			326	326.000

P(FA) = P(FB) = P(MA) = P(FC) = P (SI) = P(BU) = 0.167

Table 16 Classification Function Coefficients.

	Morphological Characters					
	FA	FB	MA	FC	SI	BU
Pseudostem height	4.394	5.047	5.540	2.478	3.816	3.803
Pseudostem appearance	351.938	347.112	170.673	171.960	349.224	351.042
Blotch at the petiole base	5.754	6.226	6.477	6.498	5.571	5.693
Blotch color	2.303	2.897	2.581	-.886	2.452	2.502
Petiole canal leaf	-.103	-1.619	4.686	-2.101	-.668	-.639
Wax on leaves	2.806	-3.622	31.923	-4.579	3.179	2.681
Peduncle hairiness	3.821	2.691	.734	4.526	4.298	4.165
Bunch position	7.612	7.011	5.904	5.411	7.751	7.861
Rachis position	-.909	-.357	5.449	.377	-.279	.623
Male bud shape	10.435	12.026	6.505	4.432	10.586	10.624
Bract imbrication	8.022	9.810	8.786	4.679	9.105	8.653
Color of the bract external face	5.918	9.651	.460	9.662	6.481	6.781
Color of the bract internal face	6.336	5.186	4.765	4.934	6.084	6.009
Color on the bract apex	29.236	20.114	24.921	21.809	28.535	30.115
Color stripes on bract	22.002	18.068	19.368	21.116	20.553	20.362
Wax on the bract	-3.174	-.721	.276	2.718	-2.795	-2.858
Compound tepal basic color	1.042	3.125	5.952	7.715	1.783	2.018
Lobe color of compound tepal	7.765	18.908	.727	23.886	6.249	5.665
Fruit apex	95.425	91.651	80.516	88.085	93.774	94.361
Fusion of pedicel	16.060	14.971	10.999	12.148	15.594	15.648
(Constant)	-690.201	-715.417	-403.595	-438.669	-676.987	-685.552

Fisher's linear discriminant functions

Territorial Map

(Assuming all functions but the first two are zero)

Canonical Discriminant Function 2

```
   -15.0    -10.0     -5.0       .0       5.0      10.0      15.0
     □□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□
 15.0 □                     35  56                       □
     □                   35   56                       □
     □                   35   56                       □
     □      M           35    56                       □
     □                  35     56                      □
     □                  35     56                      □
 10.0 □        □        □ 35      □56       □        □         □
     □                35       56                      □
     □               35        56                      □
     □*               35         56                     □
     □               35         56                     □
     □              35          56                     □
  5.0 □        □    35 □       □ 56      □        □         □
     □              35           56                    □
     □             35           56      FA                      
     □            35            56                  BU     
     □            35            56                     □
     □           35             56                     □
   .0 □     333333335      □         □ * 56      □        □         □     SI
     □3333334444444445                56                   □
     □444444        45               56                    □
     □             45              56                      □
     □              4555555555555    56                       □
     □              422222222222225555556666666666              □
 -5.0 □        □      42□         2*22222222222222266666666666666 □
     □               42                     222222222222226□   FB
     □     FC                                   2□
     □                                        □
     □   *            42                         □
     □                 42                         □
-10.0 □        □         42        □        □        □        □
     □                 42                         □
     □                 42                         □
     □                  42                         □
     □                  42                         □
     □                  42                         □
-15.0 □                   42                         □
     □□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□
   -15.0    -10.0     -5.0       .0       5.0      10.0      15.0
```

Canonical Discriminant Function 1

□

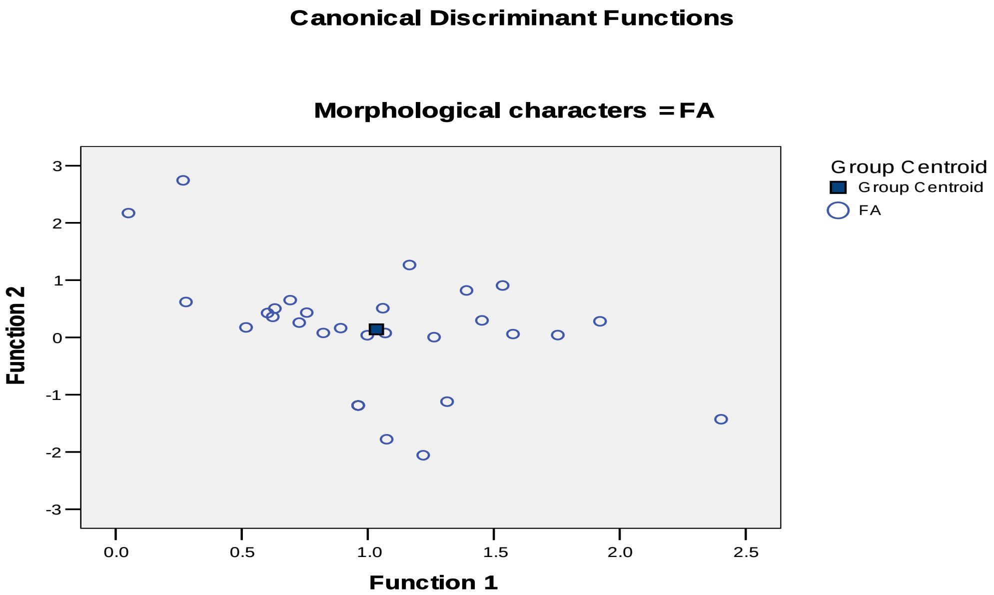
Symbols used in territorial map

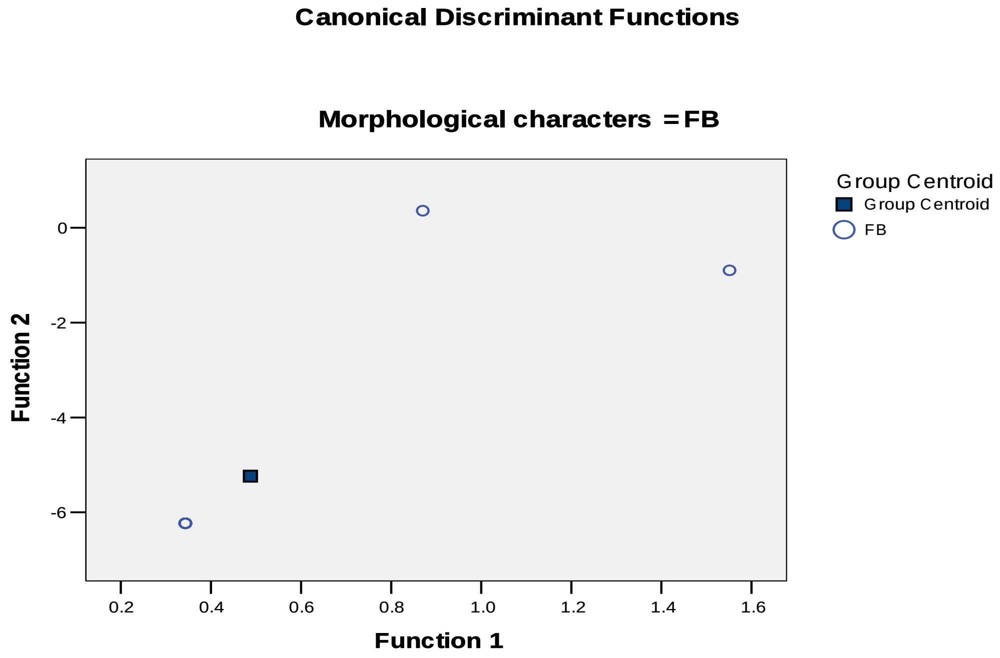
Symbol Group Label

------ ----- --------------------

1	1 FA
2	2 FB
3	3 MA
4	4 FC
5	5 SI
6	6 BU
*	Indicates a group centroid

Separate-Groups Graphs

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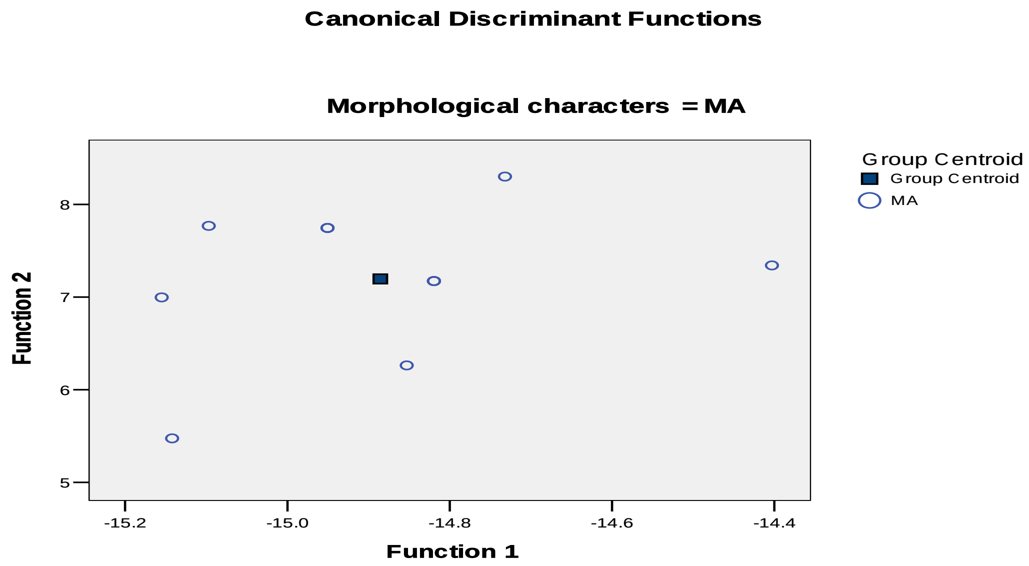
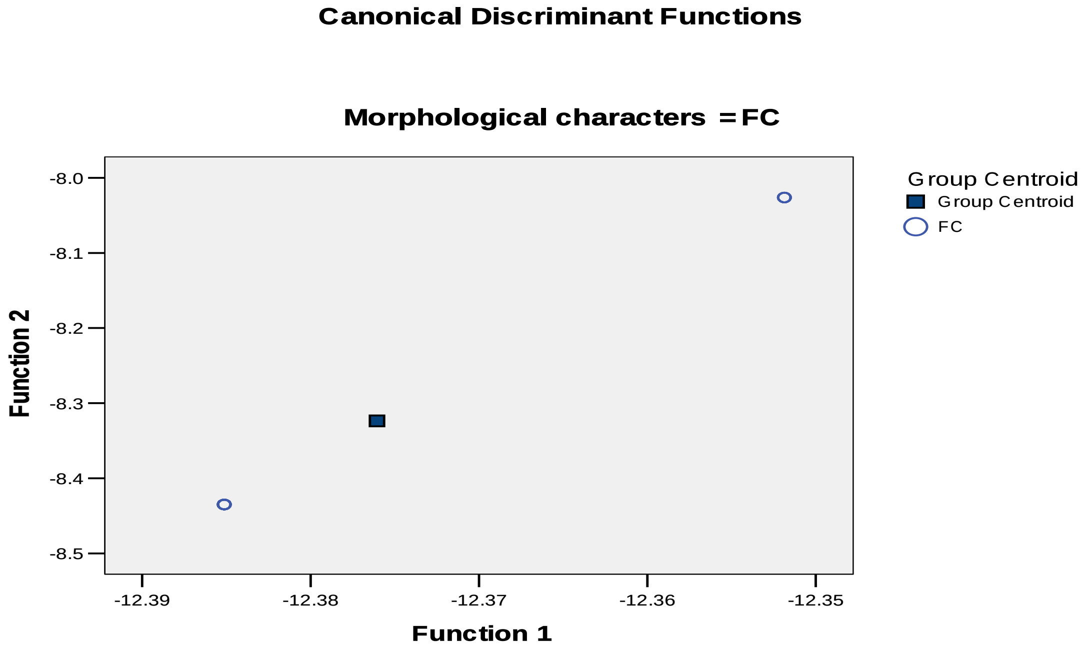
Morphological characters = FB
Function 2
Function 1
0
-2
-4
-6
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
Group Centroid
Group Centroid
FB


Canonical Discriminant Functions
Morphological characters = MA
Function 2
Function 1
8
7
6
5
-15.2
-15.0
-14.8
-14.6
-14.4
Group Centroid
Group Centroid
MA


Canonical Discriminant Functions
Morphological characters = FC
Function 2
-8.0
-8.1
-8.2
-8.3
-8.4
-8.5
-12.39
-12.38
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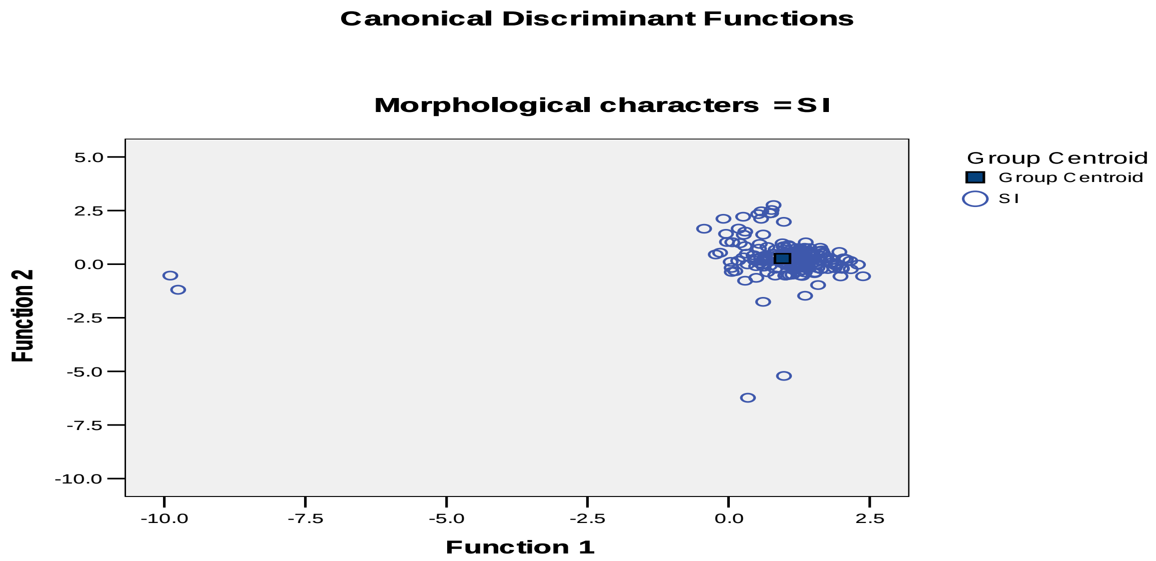
-12.35
Function 1
Group Centroid
Group Centroid
FC


Canonical Discriminant Functions
Morphological characters = SI
Function 2
5.0
2.5
0.0
-2.5
-5.0
-7.5
-10.0
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-7.5
-5.0
-2.5
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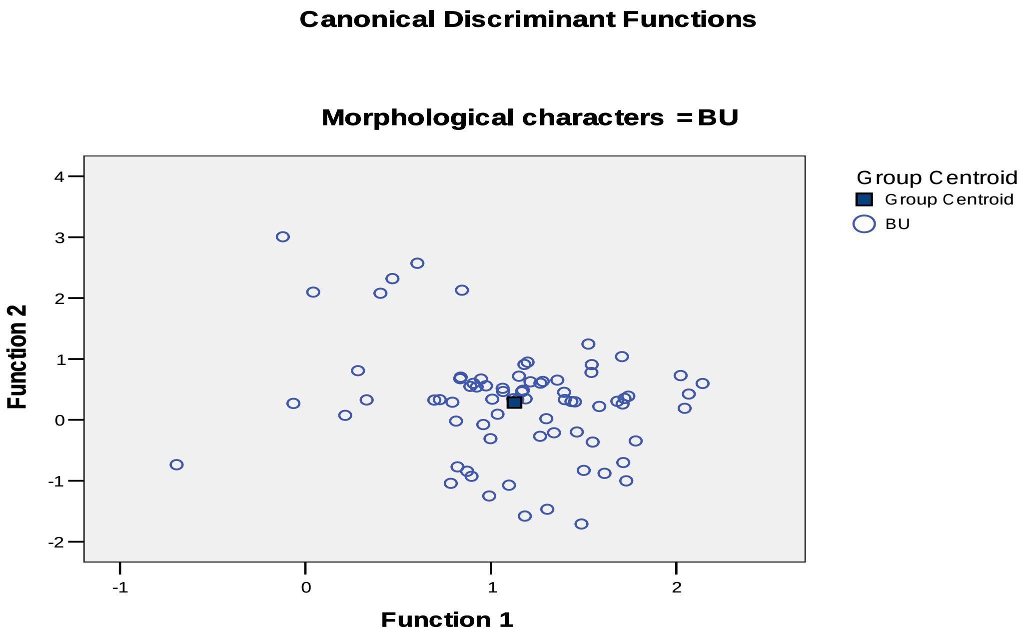
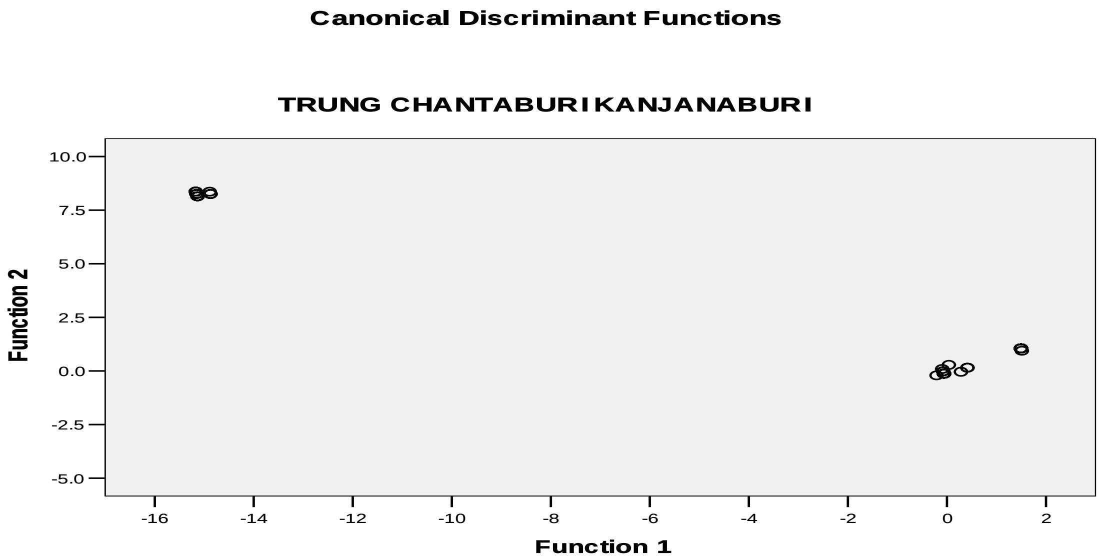
2.5
Function 1
Group Centroid
Group Centroid
SI


Canonical Discriminant Functions
Morphological characters = BU
Group Centroid
Group Centroid
BU
Function 2
Function 1
4
3
2
1
0
-1
-2
-1
0
1
2


Canonical Discriminant Functions
TRUNG CHANTABURI KANJANABURI
Function 2
Function 1
10.0
7.5
5.0
2.5
0.0
-2.5
-5.0
-16
-14
-12
-10
-8
-6
-4
-2
0
2

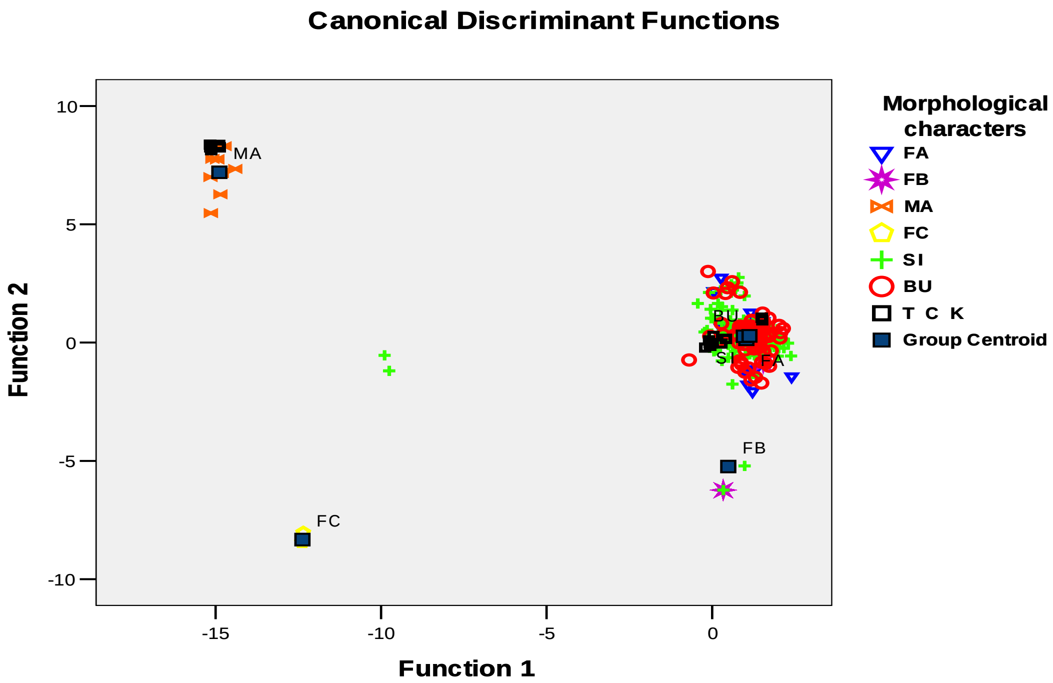

Canonical Discriminant Functions
Function 2
Function 1
10
5
0
-5
-10
-15
-10
-5
0
MA
FC
FB
BU
SI
FA
Morphological characters
FA
FB
MA
FC
SI
BU
T C K
Group Centroid

Table 17 Classification Results[b,c].

			Predicted Group Membership						
			FA	FB	MA	FC	SI	BU	Total
Original	Count	FA	17	0	0	0	10	2	29
		FB	0	10	0	0	1	1	12
		MA	0	0	11	0	0	0	11
		FC	0	0	0	11	0	0	11
		SI	30	2	0	2	103	50	187
		BU	13	0	0	0	27	36	76
		T C K	0	0	12	0	0	26	38
	%	FA	58.6	.0	.0	.0	34.5	6.9	100.0
		FB	.0	83.3	.0	.0	8.3	8.3	100.0
		MA	.0	.0	100.0	.0	.0	.0	100.0
		FC	.0	.0	.0	100.0	.0	.0	100.0
		SI	16.0	1.1	.0	1.1	55.1	26.7	100.0
		BU	17.1	.0	.0	.0	35.5	47.4	100.0
		T C K	.0	.0	31.6	.0	.0	68.4	100.0
Cross-validated[a]	Count	FA	12	0	0	0	12	5	29
		FB	0	10	0	0	1	1	12
		MA	0	0	11	0	0	0	11
		FC	0	0	0	11	0	0	11
		SI	34	2	0	2	94	55	187
		BU	14	0	0	0	31	31	76
		T C K							
	%	FA	41.4	.0	.0	.0	41.4	17.2	100.0
		FB	.0	83.3	.0	.0	8.3	8.3	100.0
		MA	.0	.0	100.0	.0	.0	.0	100.0
		FC	.0	.0	.0	100.0	.0	.0	100.0
		SI	18.2	1.1	.0	1.1	50.3	29.4	100.0
		BU	18.4	.0	.0	.0	40.8	40.8	100.0
		T C K							

a. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

b. 57.7% of original grouped cases correctly classified.

c. 51.8% of cross-validated grouped cases correctly classified. Morphological characters

Hierarchical Cluster Analysis of Trung Kanjanaburi and Chantaburi

Table 18 Case Processing Summary(a).

Cases					
Valid		Missing		Total	
N	Percent	N	Percent	N	Percent
364	100.0	0	.0	364	100.0

a Average Linkage (Between Groups)

Table 19 Agglomeration Schedule

Stage	Cluster Combined		Coefficients	Stage Cluster First Appears		Next Stage
	Cluster 1	Cluster 2		Cluster 1	Cluster 2	
1	363	364	.000	0	0	2
2	352	363	.000	0	1	4
3	361	362	.000	0	0	4
4	352	361	.000	2	3	6
5	359	360	.000	0	0	6
6	352	359	.000	4	5	8
7	357	358	.000	0	0	8
8	352	357	.000	6	7	10
9	355	356	.000	0	0	10
10	352	355	.000	8	9	11
11-360	…	…	…	…	…	…
361	13	216	37.066	359	349	362
362	1	13	45.250	358	361	363
363	1	25	59.145	362	360	0

Table 20 Cluster Membership

Case	Label	363 Clusters
1:D.W.1		1
2:D.W.2		2
3:D.W.3		3
4:D.W.4		4
5:D.W.5		5
6:D.W.6		6
7:D.W.7		7
8:D.W.8		8
9:D.W.9		9
10-360		…
361:D.W.361		361
362:D.W.362		362
363:D.W.363		363
364:D.W.364		363

* * * * * * H I E R A R C H I C A L C L U S T E R A N A L Y S I S * * * * * *

Dendrogram using Average Linkage (Between Groups)

```
                    Rescaled Distance Cluster Combine

  C A S E      0        5        10       15       20       25
 Label    Num  +---------+---------+---------+---------+---------+

 D.W.363   363   □□
 D.W.364   364   □□
 D.W.352   352   □□
 D.W.361   361   □□
 D.W.362   362   □□
 D.W.359   359   □□
 D.W.360   360   □□
 D.W.357   357   □□
 D.W.358   358   □□
 D.W.355   355   □□
 D.W.356   356   □□□□□□□□□□□□□
 D.W.354   354   □□     □
 D.W.353   353   □□     □
 D.W.347   347   □□□□    □□□□□□□□
 D.W.349   349   □□ □    □  □
 D.W.345   345   □□ □    □  □
 D.W.346   346   □□ □□□□□□□□□□  □
 D.W.341   341   □□ □      □
 D.W.350   350   □□ □      □
 D.W.351   351   □□□□      □□□□□□□□□□□□□□□□□
 D.W.343   343   □□       □     □
 D.W.344   344   □□       □     □
 D.W.339   339   □□       □     □
 D.W.340   340   □□       □     □
 D.W.342   342   □□       □     □
 D.W.348   348   □□       □     □
 D.W.216   216   □□□□□□□□□□□□□□□□□□□□      □
 D.W.161   161   □□            □
 D.W.162   162   □□            □
 D.W.113   113   □□            □
 D.W.159   159   □□            □
 D.W.160   160   □□            □
 D.W.157   157   □□            □□□□□□□□□□
 D.W.158   158   □□            □   □
 D.W.155   155   □□□□□□□□□□□□□□□□□□       □   □
 D.W.156   156   □□      □      □   □
 D.W.153   153   □□      □      □   □
 D.W.154   154   □□      □      □   □
```

```
D.W.47    47
D.W.48    48
D.W.41    41
D.W.45    45
```

******HIERARCHICAL CLUSTER ANALYSIS******

```
  C A S E    0      5      10      15      20      25

 Label    Num  +---------+---------+---------+---------+---------+

D.W.46    46
D.W.43    43
D.W.44    44
D.W.42    42
D.W.39    39
D.W.40    40
D.W.36    36
D.W.13    13
D.W.314   314
D.W.217   217
D.W.223   223
D.W.222   222
D.W.287   287
D.W.291   291
D.W.112   112
D.W.130   130
D.W.115   115
D.W.322   322
D.W.132   132
D.W.110   110
D.W.235   235
D.W.143   143
D.W.145   145
D.W.114   114
D.W.326   326
D.W.54    54
D.W.248   248
D.W.252   252
D.W.263   263
D.W.267   267
D.W.71    71
D.W.247   247
D.W.239   239
D.W.244   244
D.W.242   242
```

D.W.256 256

D.W.260 260

D.W.241 241

D.W.178 178

D.W.197 197

D.W.22 22

D.W.24 24

D.W.240 240

D.W.294 294

D.W.300 300

* * * * * * H I E R A R C H I C A L C L U S T E R A N A L Y S I S * * * * * *

C A S E 0 5 10 15 20 25

Label Num +---------+---------+---------+---------+---------+

D.W.289 289

D.W.299 299

D.W.111 111

D.W.188 188

D.W.192 192

D.W.232 232

D.W.238 238

D.W.213 213

D.W.219 219

D.W.250 250

D.W.253 253

D.W.261 261

D.W.262 262

D.W.243 243

D.W.245 245

D.W.246 246

D.W.255 255

D.W.234 234

D.W.280 280

D.W.275 275

D.W.324 324

D.W.310 310

D.W.323 323

D.W.121 121

D.W.292 292

D.W.279 279

D.W.117 117

D.W.118 118

D.W.116 116

D.W.174 174
D.W.175 175
D.W.173 173
D.W.228 228
D.W.231 231
D.W.180 180
D.W.150 150
D.W.230 230
D.W.215 215
D.W.2 2
D.W.75 75
D.W.76 76
D.W.86 86
D.W.92 92
D.W.265 265
D.W.270 270

* * * * * * H I E R A R C H I C A L C L U S T E R A N A L Y S I S * * * * * *

C A S E 0 5 10 15 20 25

Label Num +---------+---------+---------+---------+---------+

D.W.266 266
D.W.249 249
D.W.258 258
D.W.251 251
D.W.236 236
D.W.204 204
D.W.206 206
D.W.221 221
D.W.218 218
D.W.208 208
D.W.269 269
D.W.207 207
D.W.209 209
D.W.210 210
D.W.211 211
D.W.205 205
D.W.202 202
D.W.220 220
D.W.214 214
D.W.203 203
D.W.67 67
D.W.68 68
D.W.317 317

```
D.W.23    23
D.W.304   304
D.W.316   316
D.W.274   274
D.W.293   293
D.W.319   319
D.W.286   286
D.W.290   290
D.W.302   302
D.W.281   281
D.W.283   283
D.W.282   282
D.W.184   184
D.W.225   225
D.W.226   226
D.W.17    17
D.W.18    18
D.W.224   224
D.W.273   273
D.W.264   264
D.W.19    19
D.W.20    20
```

******HIERARCHICAL CLUSTER ANALYSIS******

```
  C A S E    0       5      10      15      20      25

Label     Num  +---------+---------+---------+---------+---------+

D.W.60    60
D.W.21    21
D.W.179   179
D.W.229   229
D.W.254   254
D.W.257   257
D.W.259   259
D.W.237   237
D.W.147   147
D.W.148   148
D.W.169   169
D.W.227   227
D.W.170   170
D.W.313   313
D.W.315   315
D.W.277   277
D.W.278   278
```

D.W.66 66
D.W.276 276
D.W.288 288
D.W.296 296
D.W.52 52
D.W.53 53
D.W.90 90
D.W.93 93
D.W.101 101
D.W.79 79
D.W.97 97
D.W.80 80
D.W.99 99
D.W.77 77
D.W.78 78
D.W.103 103
D.W.89 89
D.W.49 49
D.W.191 191
D.W.128 128
D.W.137 137
D.W.182 182
D.W.122 122
D.W.151 151
D.W.136 136
D.W.149 149
D.W.58 58
D.W.189 189

* * * * * * H I E R A R C H I C A L C L U S T E R A N A L Y S I S * * * * * *

C A S E 0 5 10 15 20 25

Label Num +---------+---------+---------+---------+---------+

D.W.98 98
D.W.298 298
D.W.325 325
D.W.309 309
D.W.50 50
D.W.104 104
D.W.62 62
D.W.152 152
D.W.55 55
D.W.63 63
D.W.64 64

D.W.65	65
D.W.61	61
D.W.144	144
D.W.146	146
D.W.129	129
D.W.108	108
D.W.91	91
D.W.141	141
D.W.297	297
D.W.284	284
D.W.295	295
D.W.106	106
D.W.107	107
D.W.138	138
D.W.271	271
D.W.318	318
D.W.272	272
D.W.37	37
D.W.38	38
D.W.70	70
D.W.105	105
D.W.102	102
D.W.69	69
D.W.164	164
D.W.165	165
D.W.163	163
D.W.96	96
D.W.95	95
D.W.195	195
D.W.196	196
D.W.193	193
D.W.172	172
D.W.134	134
D.W.198	198

```
******HIERARCHICAL CLUSTER ANALYSIS******

 CASE    0     5     10     15     20     25

Label    Num  +---------+---------+---------+---------+---------+

D.W.100   100  □□ □ □ □  □    □              □
D.W.177   177  □□ □ □ □  □    □              □
D.W.171   171  □□□□ □ □  □    □              □
D.W.185   185  □□ □□□ □  □    □              □
D.W.186   186  □□ □ □ □  □    □              □
D.W.181   181  □□ □ □ □  □    □              □
D.W.183   183  □□ □ □ □  □    □              □
D.W.190   190  □□ □ □ □  □    □              □
D.W.131   131  □□ □ □ □  □    □              □
D.W.139   139  □□□□ □ □  □    □              □
D.W.194   194  □□ □ □ □  □    □              □
D.W.187   187  □□□□ □ □  □    □              □
D.W.119   119  □□□□ □ □  □    □              □
D.W.133   133  □□ □□□ □  □    □              □
D.W.120   120  □□□□ □□□  □    □              □
D.W.124   124  □□  □ □  □    □              □
D.W.127   127  □□□□ □ □  □    □              □
D.W.51    51  □□ □□□ □  □    □              □
D.W.140   140  □□□□ □ □  □    □              □
D.W.56    56  □□□□□□ □  □    □              □
D.W.125   125  □□□□□□ □  □    □              □
D.W.57    57  □□□□□□ □  □    □              □
D.W.301   301  □□□□ □□□  □    □              □
D.W.312   312  □□□□□□ □  □    □              □
D.W.74    74  □□□□□□ □  □    □              □
D.W.321   321  □□□□ □ □  □    □              □
D.W.123   123  □□  □ □  □    □              □
D.W.311   311  □□□□ □ □  □    □              □
D.W.83    83  □□ □ □□□  □    □              □
D.W.87    87  □□□□□□   □    □              □
D.W.84    84  □□□□ □   □    □              □
D.W.88    88  □□ □ □   □    □              □
D.W.85    85  □□□□ □   □    □              □
D.W.81    81  □□□□ □   □    □              □
D.W.82    82  □□ □ □   □    □              □
D.W.307   307  □□□□ □   □    □              □
D.W.305   305  □□□□□□   □    □              □
D.W.109   109  □□□□    □    □              □
D.W.306   306  □□□□□□□□□□ □    □              □
D.W.320   320  □□□□□□  □□□    □              □
D.W.308   308  □□□□□□□□□□ □    □              □
```

```
D.W.142   142
D.W.176   176
D.W.285   285
D.W.303   303
```

******HIERARCHICAL CLUSTER ANALYSIS******

```
  C A S E    0      5      10      15      20      25
 Label    Num  +---------+---------+---------+---------+---------+

 D.W.199   199
 D.W.201   201
 D.W.200   200
 D.W.72    72
 D.W.73    73
 D.W.268   268
 D.W.126   126
 D.W.135   135
 D.W.59    59
 D.W.94    94
 D.W.167   167
 D.W.168   168
 D.W.166   166
 D.W.233   233
 D.W.10    10
 D.W.16    16
 D.W.7     7
 D.W.14    14
 D.W.9     9
 D.W.11    11
 D.W.12    12
 D.W.15    15
 D.W.5     5
 D.W.4     4
 D.W.8     8
 D.W.6     6
 D.W.1     1
 D.W.3     3
 D.W.212   212
 D.W.33    33
 D.W.34    34
 D.W.30    30
 D.W.333   333
 D.W.334   334
 D.W.330   330
```

```
D.W.328   328
D.W.329   329
D.W.336   336
D.W.337   337
D.W.331   331
D.W.335   335
D.W.338   338
D.W.327   327
D.W.332   332
D.W.25    25
```

```
* * * * * * H I E R A R C H I C A L  C L U S T E R   A N A L Y S I S * * * * * *

 C A S E     0       5      10      15      20      25

Label     Num  +---------+---------+---------+---------+

D.W.27     27
D.W.28     28
D.W.32     32
D.W.26     26
D.W.35     35
D.W.29     29
D.W.31     31
```

Table 21 Correlations of Trung Kanjanaburi and Chantaburi

		Hierarchical Cluster analysis	**Classical Taxonomy**
Hierarchical Cluster analysis	Pearson Correlation	1	.034
	Sig. (2-tailed)		.515
	N	364	364
Classical Taxonomy	Pearson Correlation	.034	1
	Sig. (2-tailed)	.515	
	N	364	364

3. Hierarchical Cluster Analysis

Table 21 Agglomeration Schedule form hierarchical cluster analysis.

Agglomeration Schedule

Stage	Cluster Combined		Coefficients	Stage Cluster First Appears		Next Stage
	Cluster 1	Cluster 2		Cluster 1	Cluster 2	
1	195	196	1.000	0	0	107
2	183	190	1.000	0	0	37
3	171	185	1.000	0	0	37
4	100	177	1.000	0	0	70
5	174	175	1.000	0	0	6
6	173	174	1.000	0	5	106
7	167	168	1.000	0	0	75
8	164	165	1.000	0	0	75
9	161	162	1.000	0	0	10
10	113	161	1.000	0	9	12
11	159	160	1.000	0	0	12
12	113	159	1.000	10	11	14
13	157	158	1.000	0	0	14
14	113	157	1.000	12	13	16
15	155	156	1.000	0	0	16
16	113	155	1.000	14	15	18
17	153	154	1.000	0	0	18
18	113	153	1.000	16	17	286
19	147	148	1.000	0	0	54
20	106	107	1.000	0	0	203
21	75	76	1.000	0	0	155
22	47	48	1.000	0	0	23
23	41	47	1.000	0	22	25
24	45	46	1.000	0	0	25
25	41	45	1.000	23	24	27
26	43	44	1.000	0	0	27
27	41	43	1.000	25	26	28
28	41	42	1.000	27	0	174
29	39	40	1.000	0	0	30
30	36	39	1.000	0	29	174
31	28	32	1.000	0	0	32
32	26	28	1.000	0	31	42
33	25	27	1.000	0	0	69
34	19	20	1.000	0	0	135
35	325	326	.968	0	0	66
36	123	311	.968	0	0	68
37	171	183	.968	3	2	67
38	81	82	.968	0	0	89
39	64	65	.968	0	0	121

Table 21 Agglomeration Schedule form hierarchical cluster analysis. (Cont.)

Stage	Cluster Combined		Coefficients	Stage Cluster First Appears		Next Stage
	Cluster 1	Cluster 2		Cluster 1	Cluster 2	
40	31	35	.968	0	0	92
41	33	34	.968	0	0	263
42	26	30	.968	32	0	65
43	12	15	.968	0	0	45
44	9	11	.968	0	0	45
45	9	12	.935	44	43	87
46	293	319	.935	0	0	129
47	84	305	.935	0	0	137
48	284	300	.935	0	0	72
49	277	278	.935	0	0	141
50	239	244	.935	0	0	188
51	169	227	.935	0	0	143
52	204	206	.935	0	0	166
53	134	186	.935	0	0	93
54	147	152	.935	19	0	136
55	122	151	.935	0	0	144
56	131	139	.935	0	0	110
57	119	133	.935	0	0	110
58	112	130	.935	0	0	152
59	124	127	.935	0	0	79
60	117	118	.935	0	0	108
61	80	99	.935	0	0	82
62	78	97	.935	0	0	82
63	68	69	.935	0	0	83
64	10	16	.935	0	0	86
65	26	29	.927	42	0	69
66	298	325	.919	0	35	124
67	171	181	.919	37	0	70
68	83	123	.919	0	36	126
69	25	26	.916	33	65	92
70	100	171	.910	4	67	93
71	306	307	.903	0	0	89
72	284	301	.903	48	0	97
73	209	223	.903	0	0	119
74	202	220	.903	0	0	151
75	164	167	.903	8	7	90
76	144	146	.903	0	0	185
77	59	135	.903	0	0	172
78	115	125	.903	0	0	152
79	51	124	.903	0	59	147
80	77	105	.903	0	0	154
81	90	93	.903	0	0	120
82	78	80	.903	62	61	117

Table 21 Agglomeration Schedule form hierarchical cluster analysis. (Cont.)

Stage	Cluster Combined		Coefficients	Stage Cluster First Appears		Next Stage
	Cluster 1	Cluster 2		Cluster 1	Cluster 2	
83	68	70	.903	63	0	88
84	55	63	.903	0	0	153
85	53	58	.903	0	0	172
86	7	10	.903	0	64	118
87	5	9	.903	0	45	145
88	67	68	.892	0	83	214
89	81	306	.887	38	71	91
90	164	166	.887	75	0	168
91	81	129	.887	89	0	126
92	25	31	.887	69	40	263
93	100	134	.885	70	53	125
94	271	318	.871	0	0	187
95	88	312	.871	0	0	134
96	283	302	.871	0	0	130
97	284	299	.871	72	0	228
98	201	285	.871	0	0	142
99	275	276	.871	0	0	160
100	270	272	.871	0	0	187
101	265	266	.871	0	0	204
102	254	262	.871	0	0	132
103	255	260	.871	0	0	191
104	250	258	.871	0	0	163
105	225	228	.871	0	0	106
106	173	225	.871	6	105	149
107	193	195	.871	0	1	231
108	117	150	.871	60	0	244
109	136	149	.871	0	0	144
110	119	131	.871	57	56	122
111	108	121	.871	0	0	220
112	92	96	.871	0	0	197
113	21	95	.871	0	0	183
114	72	73	.871	0	0	161
115	22	24	.871	0	0	323
116	17	18	.871	0	0	207
117	78	79	.871	82	0	154
118	7	14	.860	86	0	146
119	209	211	.855	73	0	181
120	52	90	.855	0	81	148
121	61	64	.855	0	39	192
122	119	126	.855	110	0	123
123	116	119	.852	0	122	184
124	297	298	.849	0	66	150
125	100	187	.846	93	0	175

Table 21 Agglomeration Schedule form hierarchical cluster analysis. (Cont.)

Stage	Cluster Combined		Coefficients	Stage Cluster First Appears		Next Stage
	Cluster 1	Cluster 2		Cluster 1	Cluster 2	
126	81	83	.841	91	68	235
127	310	323	.839	0	0	220
128	290	315	.839	0	0	178
129	292	293	.839	0	46	185
130	281	283	.839	0	96	179
131	251	259	.839	0	0	188
132	254	256	.839	102	0	191
133	236	240	.839	0	0	285
134	88	194	.839	95	0	190
135	19	188	.839	34	0	183
136	62	147	.839	0	54	177
137	84	132	.839	47	0	176
138	104	120	.839	0	0	189
139	85	101	.839	0	0	219
140	56	57	.839	0	0	190
141	277	286	.839	49	0	180
142	199	201	.839	0	98	277
143	169	170	.839	51	0	176
144	122	136	.839	55	109	193
145	4	5	.832	0	87	234
146	6	7	.831	0	118	156
147	51	140	.828	79	0	238
148	52	66	.828	120	0	196
149	173	226	.826	106	0	186
150	297	324	.823	124	0	178
151	202	207	.823	74	0	254
152	112	115	.823	58	78	195
153	55	87	.823	84	0	182
154	77	78	.823	80	117	155
155	75	77	.820	21	154	217
156	6	8	.813	146	0	216
157	74	321	.806	0	0	199
158	89	316	.806	0	0	240
159	291	309	.806	0	0	241
160	91	275	.806	0	99	218
161	72	268	.806	114	0	214
162	198	257	.806	0	0	248
163	249	250	.806	0	104	215
164	243	245	.806	0	0	284
165	179	229	.806	0	0	278
166	204	208	.806	52	0	213
167	182	191	.806	0	0	271
168	163	164	.806	0	90	197

Table 21 Agglomeration Schedule form hierarchical cluster analysis. (Cont.)

Stage	Cluster Combined		Coefficients	Stage Cluster First Appears		Next Stage
	Cluster 1	Cluster 2		Cluster 1	Cluster 2	
169	143	145	.806	0	0	310
170	109	141	.806	0	0	236
171	128	137	.806	0	0	238
172	53	59	.806	85	77	196
173	37	38	.806	0	0	239
174	36	41	.806	30	28	301
175	100	184	.803	125	0	184
176	84	169	.799	137	143	219
177	62	86	.798	136	0	193
178	290	297	.797	128	150	222
179	281	282	.796	130	0	194
180	277	287	.796	141	0	218
181	209	222	.796	119	0	223
182	54	55	.796	0	153	224
183	19	21	.796	135	113	225
184	100	116	.793	175	123	227
185	144	292	.790	76	129	233
186	173	176	.790	149	0	242
187	270	271	.790	100	94	273
188	239	251	.790	50	131	215
190	56	88	.790	140	134	258
191	254	255	.785	132	103	237
192	60	61	.785	0	121	224
193	62	122	.784	177	144	246
194	281	296	.782	179	0	232
195	112	114	.782	152	0	256
196	52	53	.782	148	172	246
197	92	163	.780	112	168	266
198	200	322	.774	0	0	293
199	74	320	.774	157	0	258
200	71	317	.774	0	0	262
201	233	308	.774	0	0	308
202	138	294	.774	0	0	255
203	106	289	.774	20	0	255
204	264	265	.774	0	101	273
205	252	261	.774	0	0	295
206	230	232	.774	0	0	309
207	17	224	.774	116	0	257
208	214	215	.774	0	0	259
209	205	210	.774	0	0	260
210	178	189	.774	0	0	221
211	102	172	.774	0	0	239
212	110	111	.774	0	0	244

Table 21 Agglomeration Schedule form hierarchical cluster analysis. (Cont.)

Stage	Cluster Combined		Coefficients	Stage Cluster First Appears		Next Stage
	Cluster 1	Cluster 2		Cluster 1	Cluster 2	
213	204	269	.774	166	0	272
214	67	72	.774	88	161	226
215	239	249	.772	188	163	251
216	1	6	.769	0	156	234
217	75	103	.767	155	0	226
218	91	277	.766	160	180	240
219	84	85	.763	176	139	227
220	108	310	.758	111	127	282
221	178	180	.758	210	0	243
222	290	295	.756	178	0	247
223	209	212	.750	181	0	254
224	54	60	.750	182	192	265
225	19	23	.748	183	0	292
226	67	75	.747	214	217	262
227	84	100	.746	219	184	235
228	284	303	.742	97	0	241
229	218	221	.742	0	0	280
230	94	142	.742	0	0	250
231	192	193	.742	0	107	261
232	280	281	.735	0	194	270
233	144	314	.735	185	0	274
234	1	4	.733	216	145	245
235	81	84	.732	126	227	256
236	50	109	.731	189	170	279
237	242	254	.729	0	191	264
238	51	128	.726	147	171	281
239	37	102	.726	173	211	266
240	89	91	.724	158	218	267
241	284	291	.723	228	159	247
242	173	231	.719	186	0	243
243	173	178	.716	242	221	268
244	110	117	.715	212	108	288
245	1	3	.715	234	0	300
246	52	62	.714	196	193	269
247	284	290	.714	241	222	270
248	198	313	.710	162	0	275
249	235	279	.710	0	0	322
250	94	273	.710	230	0	290
251	239	253	.710	215	0	264
252	237	238	.710	0	0	285
253	217	219	.710	0	0	280
254	202	209	.705	151	223	291
255	106	138	.704	203	202	282

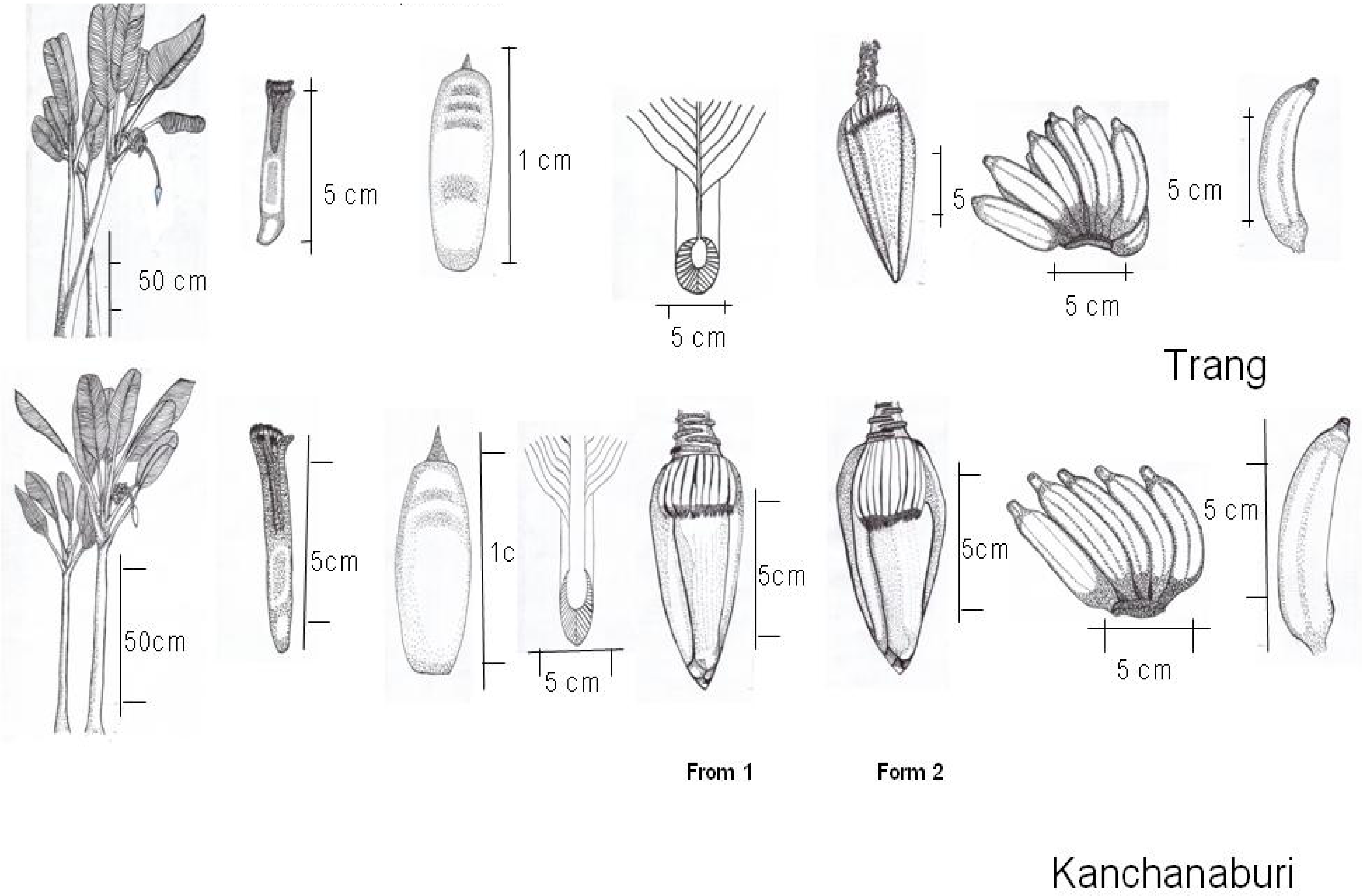
Table 21 Agglomeration Schedule form hierarchical cluster analysis. (Cont.)

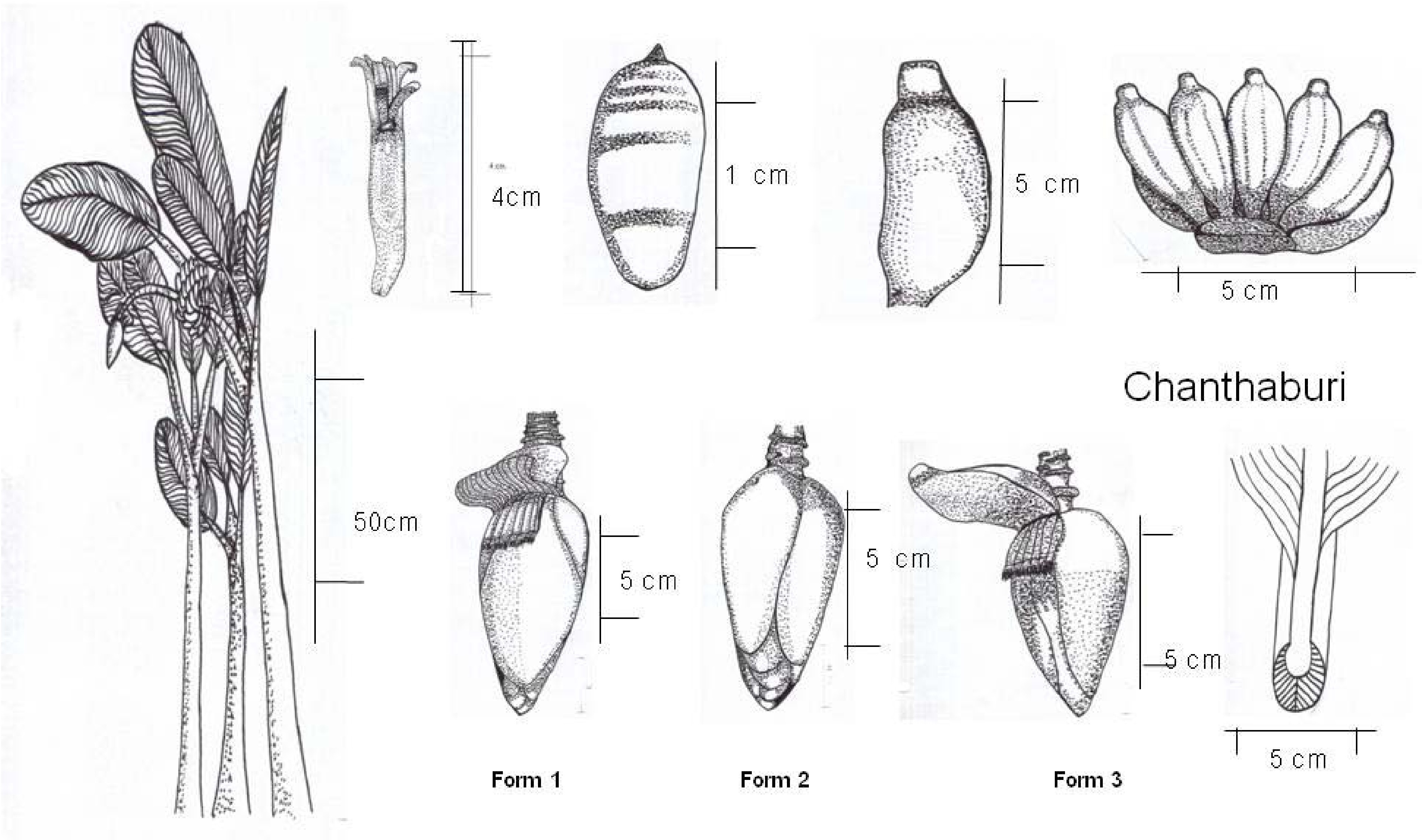
Stage	Cluster Combined		Coefficients	Stage Cluster First Appears		Next Stage
	Cluster 1	Cluster 2		Cluster 1	Cluster 2	
256	81	112	.700	235	195	269
257	17	267	.699	207	0	296
258	56	74	.695	190	199	279
259	214	246	.694	208	0	318
260	205	241	.694	209	0	276
261	192	263	.694	231	0	272
262	67	71	.694	226	200	292
263	25	33	.690	92	41	301
264	239	242	.690	251	237	275
265	49	54	.690	0	224	288
266	37	92	.688	239	197	287
267	89	288	.685	240	0	274
268	2	173	.683	0	243	278
269	52	81	.683	246	256	281
270	280	284	.682	232	247	283
271	182	274	.677	167	0	290
272	192	204	.673	261	213	305
273	264	270	.672	204	187	296
274	89	144	.672	267	233	289
275	198	239	.671	248	264	294
276	205	247	.667	260	0	304
277	98	199	.667	0	142	298
278	2	179	.664	268	165	300
279	50	56	.663	236	258	297
280	217	218	.661	253	229	306
281	51	52	.661	238	269	287
282	106	108	.653	255	220	283
283	106	280	.649	282	270	289
284	234	243	.645	0	164	304
285	236	237	.645	133	252	307
286	13	113	.645	0	18	319
287	37	51	.644	266	281	297
288	49	110	.641	265	244	299
289	89	106	.638	274	283	302
290	94	182	.634	250	271	313
291	202	213	.633	254	0	305
292	19	67	.632	225	262	303
293	200	304	.629	198	0	298
294	198	248	.628	275	0	295
295	198	252	.625	294	205	307
296	17	264	.624	257	273	308
297	37	50	.624	287	279	299
298	98	200	.605	277	293	312

Table 21 Agglomeration Schedule form hierarchical cluster analysis. (Cont.)

Stage	Cluster Combined		Coefficients	Stage Cluster First Appears		Next Stage
	Cluster 1	Cluster 2		Cluster 1	Cluster 2	
299	37	49	.600	297	288	302
300	1	2	.598	245	278	309
301	25	36	.595	263	174	325
302	37	89	.586	299	289	303
303	19	37	.579	292	302	310
304	205	234	.578	276	284	314
305	192	202	.574	272	291	311
306	203	217	.573	0	280	320
307	198	236	.571	295	285	311
308	17	233	.565	296	201	312
309	1	230	.563	300	206	315
310	19	143	.563	303	169	313
311	192	198	.549	305	307	314
312	17	98	.548	308	298	316
313	19	94	.538	310	290	315
314	192	205	.531	311	304	317
315	1	19	.529	309	313	316
316	1	17	.521	315	312	319
317	192	197	.493	314	0	318
318	192	214	.475	317	259	320
319	1	13	.466	316	286	323
320	192	203	.462	318	306	321
321	192	216	.436	320	0	322
322	192	235	.428	321	249	324
323	1	22	.426	319	115	324
324	1	192	.408	323	322	325
325	1	25	.380	324	301	0

4. Outgroup Taxa Accessions: Trang as ssp. *malaccensis*; **Kanchanaburi as ssp.** *burmanica*; **Chanthaburi as ssp.** *siamea*




4cm
1 cm
5 cm
5 cm
Chanthaburi
50cm
5 cm
5 cm
5 cm
5 cm
Form 1
Form 2
Form 3

APPENDIX C

ENVIRONMENT

Table 22 Information of seven studies sites.

Site	Location	Area	Geographic Feature	Temperature	Rainfall	Forest Type	Plant wild life	Remark
Up	In the North and Western part of Thailand. The area covers from Tak province which is in Umphang District	The total area is about 1,619,280 rais or 2,519 km^2	Consists of mountainous range of 100-2,152 m. height. The middle area is low land	3.9 – 39 Celsius	The highest amount of rain is 299.2 mm a day	The main forests are hill evergreen forest, dry evergreen forest, mixed deciduous forests	-	357 species that can be divided into 4 categories;
Tl	covers the area of Wongthong and Nakhonthai Districts of Phitsanulok province, and Lomsak, City, and Chon Dan Districts of Phetchabun province	The area of park is 1,262.55 km^2 or 789,000 rais	. The highest peak is at Care Mountain with 1,028 meter above the sea level	About 39 ^{0}C during March to June	about 1,700 mm	The forest consists of hill evergreen, dry evergreen, deciduous and pine forests	*Pinus merkusii* Jungh. & de Vriese (สนสองใบ), *Lithocarpus* (ไม้ก่อ), *Dipterocarpus tuberculatus* Roxb. Var. tomentosus Kerr (ยาง) *etc.*	-

Table 22 Information of seven studies sites. (Cont.)

Site	Location	Area	Geographic Feature	Temperature	Rainfall	Forest Type	Plant wild life	Remark
Mw	Covers the area of Pang Sila Thong District, Khamphaengphet province, and Mae Wong and Mae Pern Districts, Nakhon Sawan province	About 894 km^2 or 558.750 rais. Most of area are the mountainous rolling land	This national park is in the Thanon Thong Chai mountain range of 40-50 mountains to the low land of vast plain area.	Average 20-30^{0}C throughout the year	The rainy season was start in May but there were some rains during March and April	There are deciduous forests located in the riverbanks and the hills	*Tectona grandis* Linn.(ไม้สัก), *Shorea floribunda* G. Don (พะยอม), *Dalbergia oliveri* Gamble (ชิงชัน) *etc.*	-
Ph	-	-	These mountain ranges fall down from east to west	Annual average temperature is about 18-25 ^{0}C	Heavy rain in rainy season	Dry dipterocarp, hill evergreen and pine forests	*Shorea obtusa* Wall. ex Blume, *Shorea siamensis* Miq. *ect./* *Panthera tigris* (Tiger), *Cervus unicolor* (Sambar deer), mouse deer, beer, and birds.	Hill evergreen forest can be found many plants such as rattan and palm. There is also wild orchid in the rock yard including ferns and lichens.

Table 22 Information of seven studies sites. (Cont.)

Site	Location	Area	Geographic Feature	Temperature	Rainfall	Forest Type	Plant wild life	Remark
Ln	Covers the area in City District of Phrae province, and Tha Pa and Nam Pad Districts of Uttaradit. The forest area covers the high mountain range and low land	About 999.15 km^2 or 624,468 rais.	Many fertile and secondary forests in this national park area	The climate is hot and warm.	Average rainfall is 1,440 mm./year	Mix Deciduous, Dipterocarp, Bamboo, Grassland, Dry Evergreen and Hill Evergreen forests at various altitudes	*Tectona grandis* Linn., *etc./* , *Prionodon*, *Macaca*, porcupine, *Felis viverrinus* (Fishing Cat) *etc.*	-
Nw	In Muang and Lom Sak Districts; Phetchabun, and Konsan District; Chaiyaphum.	About 966 km^2 or 603,750 rais.	Surrounding mountain range is composed to be the mainwatershade of streams such as Phasak River, Namphong River etc.	Average 20-30^{0}C the year	There were rainfalls in very months throughout the year in Namnaow National Park and higher than the other study sites	Dipterocarp, Mix Evergreen, Evergreen, Pine and Grassland	*Pterocarpus macrocarpu* Kurz. (ประดู่), *Afzelia* sp. (มะค่า), *Dalbergia oliveri* Gamble (ชิงชัน) *etc./* barking deer, asiatic black bear, malayan bear	-

Up = Umphang Wildlife Sanctuary; ***Tl*** = Thung Salaeng Luang National Park; ***Mw*** = Mae Wong National Park;

Ph = Phu Hin Rong Kra National Park; ***Ln*** = Lumnamnan National park; ***Nw*** = Namnaow National Park.

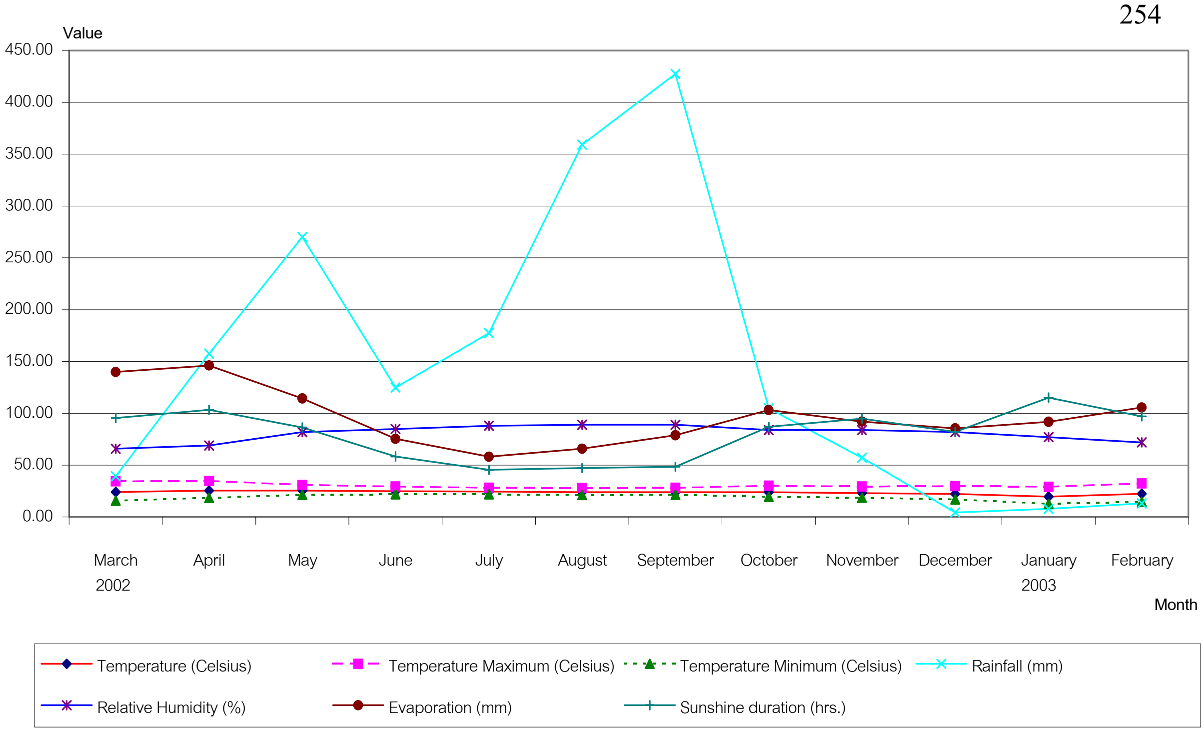


Figure 1 The average monthly environmental factors: rainfall, relative humidity, evaporation, temperature and sunshine in Umphang Wildlife Sanctuary.

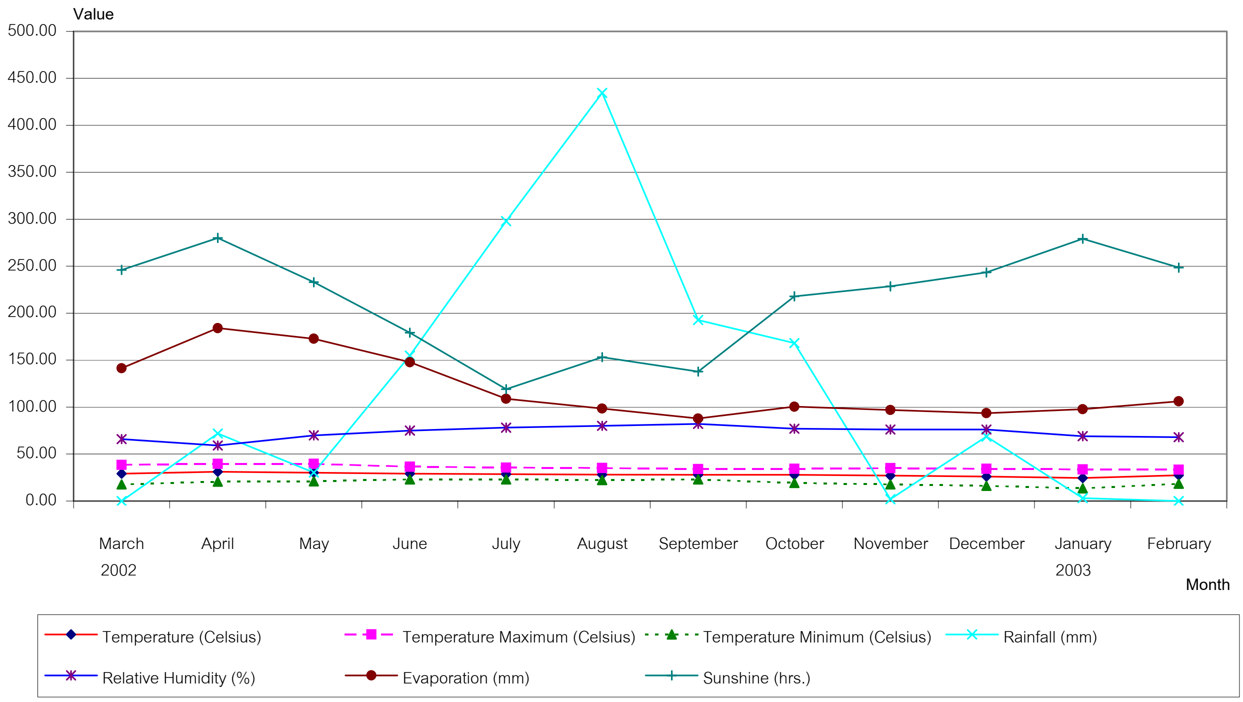


Figure 2 The average monthly environmental factors: rainfall, relative humidity, evaporation, temperature and sunshine in Thung Salaeng Luang National Park.

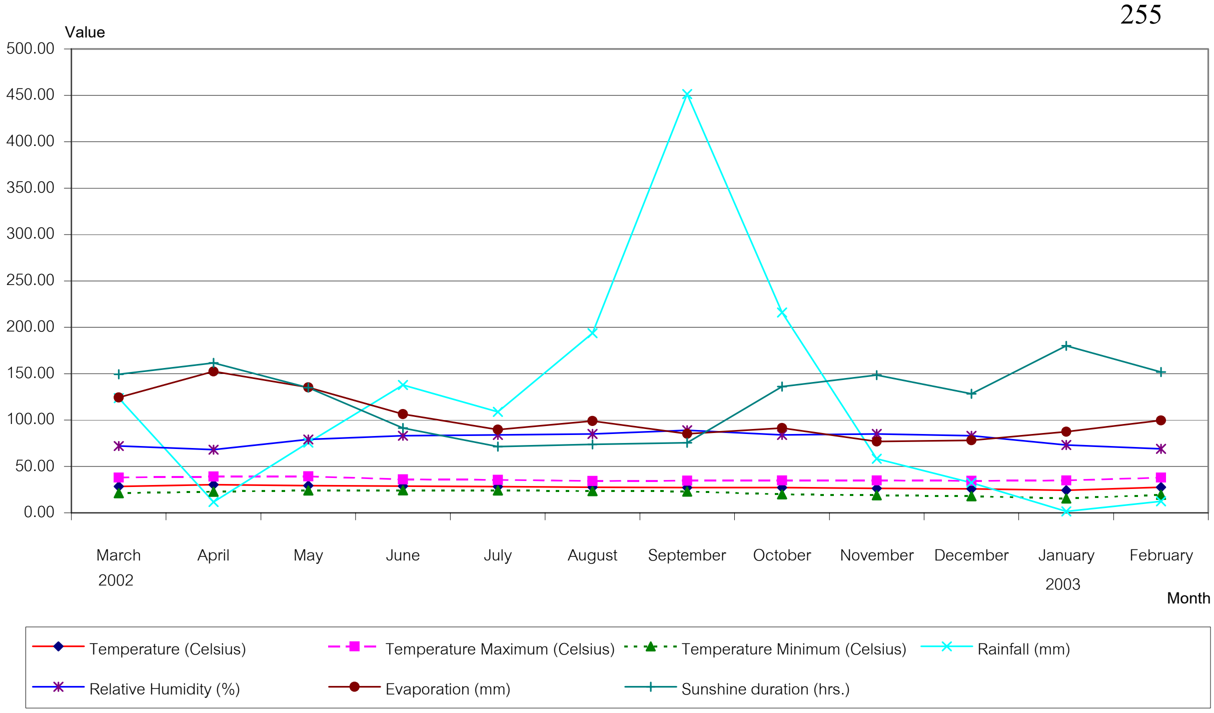


Figure 3 The average monthly environmental factors: rainfall, relative humidity, evaporation, temperature and sunshine in Mae Wong National Park.

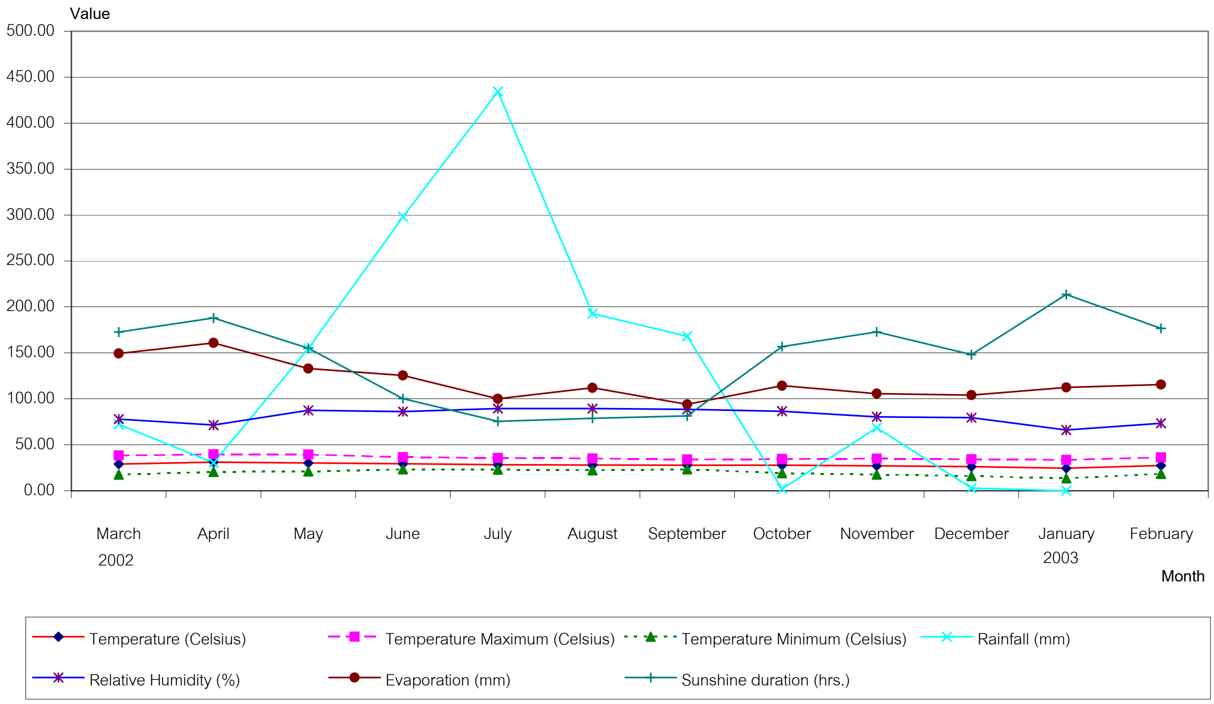


Figure 4 The average monthly environmental factor: rainfall, relative humidity, evaporation, temperature and sunshine in Phu Hin Rong Kra National Park.

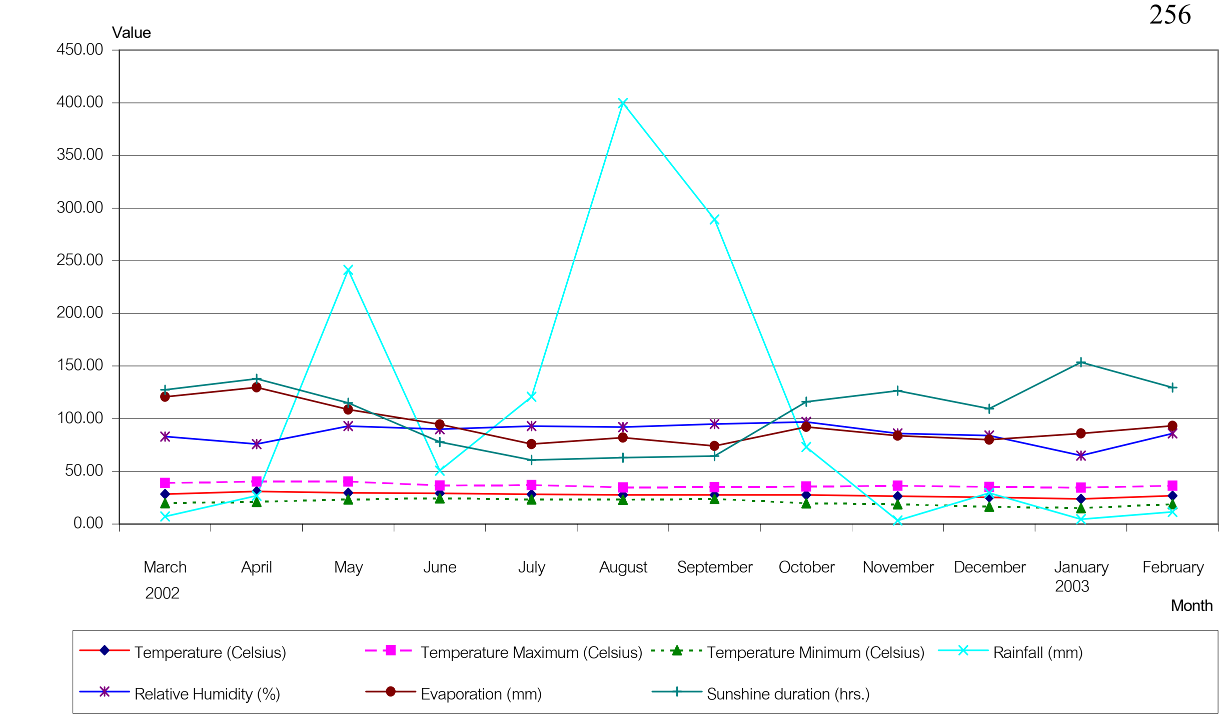


Figure 5 The average monthly environmental factors: rainfall, relative humidity, evaporation, temperature and sunshine in Lumnamnan National Park.

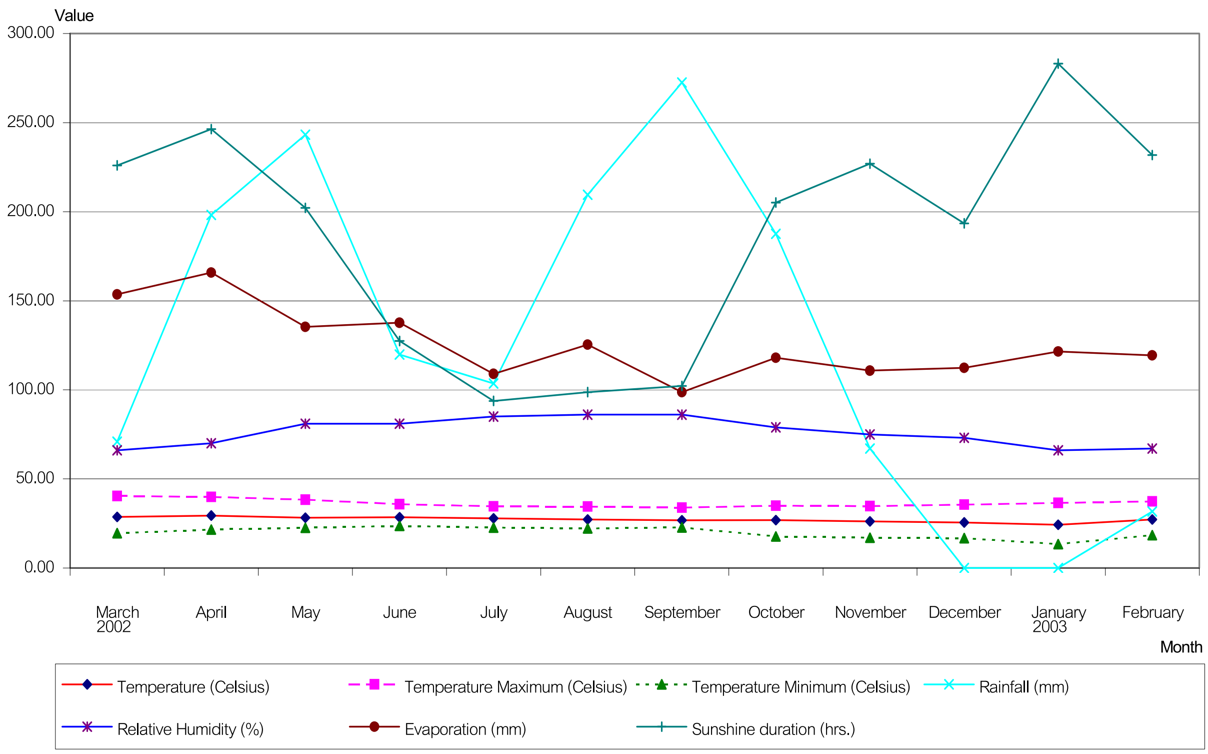


Figure 6 The average monthly environmental factors: rainfall, relative humidity, evaporation, temperature and sunshine in Namnaow National Park.

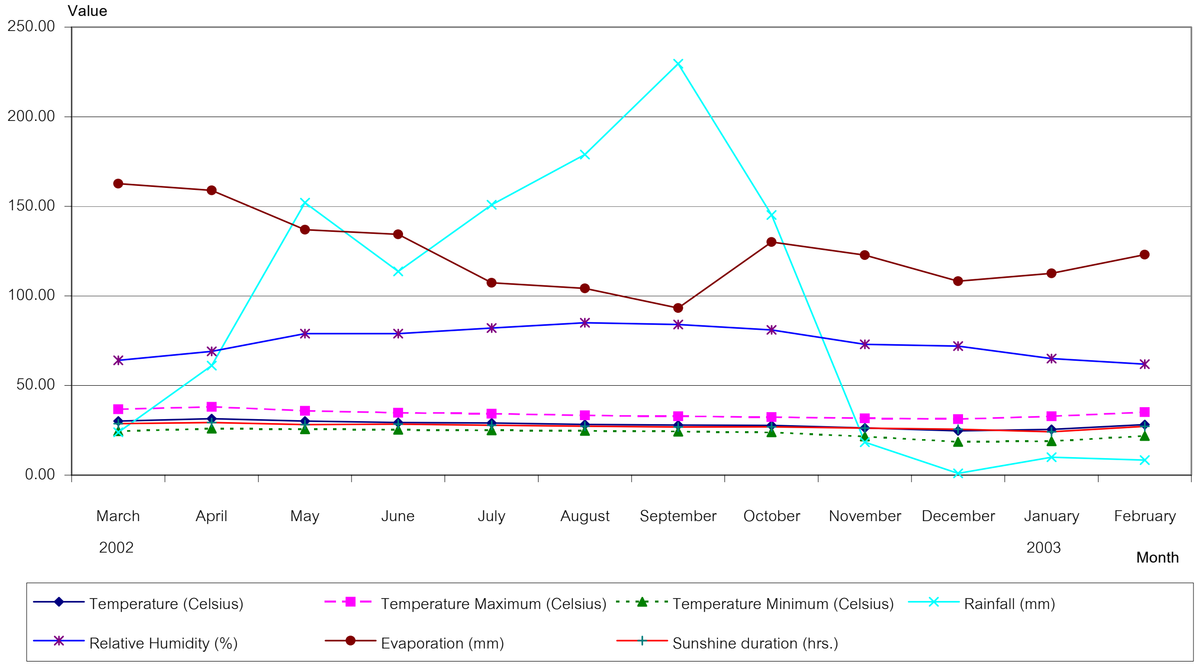


Figure 7 The average monthly environmental factors: rainfall, relative humidity, evaporation, temperature and sunshine in Nakhonchaibawon Forest Park.

Test of homogeneity of variances and ANOVA of Altitude, pH, %WHC and slope

Test of Homogeneity of Variances

Altitude (m)

Levene Statistic	df1	df2	Sig.
12.868	6	329	.000

ANOVA

Altitude (m)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	6914265	6	1152377.499	12.438	.000
Within Groups	3.0E+07	329	92646.457		
Total	3.7E+07	335			

Altitude (m)

Duncan[a,b]

Groups	N	Subset for alpha = .05			
		1	2	3	4
2	12	304.00			
6	10	491.90			
4	11	498.27			
5	187		720.24		
7	76		846.39	846.39	
1	29			952.24	952.24
3	11				1067.18
Sig.		.081	.230	.314	.275

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 16.741.

b. The group sizes are unequal. The harmonic mean of the group sizes is used. Type I error levels are not guaranteed.

Test of Homogeneity of Variances

pH

Levene Statistic	df1	df2	Sig.
1.833	6	329	.092

ANOVA

pH

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	31.810	6	5.302	8.037	.000
Within Groups	217.021	329	.660		
Total	248.831	335			

pH

Duncan[a,b]

Groups	N	Subset for alpha = .05			
		1	2	3	4
1	29	5.8866			
5	187	6.2452	6.2452		
7	76		6.5218	6.5218	
2	12		6.6267	6.6267	
3	11			6.9473	6.9473
4	11			7.1182	7.1182
6	10				7.3580
Sig.		.201	.202	.051	.169

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 16.741.

b. The group sizes are unequal. The harmonic mean of the group sizes is used. Type I error levels are not guaranteed.

Test of Homogeneity of Variances

Water Holding Capacity (%)

Levene Statistic	df1	df2	Sig.
6.057	6	329	.000

ANOVA

Water Holding Capacity (%)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	12249.40	6	2041.567	15.584	.000
Within Groups	43101.64	329	131.008		
Total	55351.04	335			

Water Holding Capacity (%)

Duncan[a,b]

Groups	N	Subset for alpha = .05		
		1	2	3
3	11	9.3100		
6	10	15.6620		
5	187		24.6329	
7	76		25.3365	
1	29		25.7317	
4	11		27.4373	
2	12			51.7167
Sig.		.108	.526	1.000

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 16.741.

b. The group sizes are unequal. The harmonic mean of the group sizes is used. Type I error levels are not guaranteed.

Test of Homogeneity of Variances

Slope (%)

Levene Statistic	df1	df2	Sig.
9.007	6	329	.000

ANOVA

Slope (%)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	12030.76	6	2005.127	4.067	.001
Within Groups	162218.0	329	493.064		
Total	174248.8	335			

Slope (%)

Duncan[a,b]

Groups	N	Subset for alpha = .05		
		1	2	3
2	12	16.25		
7	76	24.08	24.08	
4	11	25.45	25.45	
6	10	31.50	31.50	31.50
1	29		34.14	34.14
5	187		35.03	35.03
3	11			45.45
Sig.		.069	.210	.097

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 16.741.

b. The group sizes are unequal. The harmonic mean of the group sizes is used. Type I error levels are not guaranteed.

Test of homogeneity of variances and ANOVA of temperatures and %RHs

Test of Homogeneity of Variances

Temperature under the canopy (C)

Levene Statistic	df1	df2	Sig.
2.470	6	329	.024

ANOVA

Temperature under the canopy (C)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	334.499	6	55.750	3.068	.006
Within Groups	5978.064	329	18.170		
Total	6312.564	335			

Temperature under the canopy (C)

Duncan [a,b]

		Subset for alpha = .05		
Groups	N	1	2	3
1	29	28.5028		
7	76	30.3354	30.3354	
5	187	30.6020	30.6020	30.6020
4	11	31.2682	31.2682	31.2682
3	11		32.0909	32.0909
2	12		33.2000	33.2000
6	10			33.6200
Sig.		.087	.083	.067

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 16.741.

b. The group sizes are unequal. The harmonic mean of the group sizes is used. Type I error levels are not guaranteed.

Test of Homogeneity of Variances

Temperature outside the habitat (C)

Levene Statistic	df1	df2	Sig.
6.112	6	329	.000

ANOVA

Temperature outside the habitat (C)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	550.517	6	91.753	5.001	.000
Within Groups	6036.311	329	18.347		
Total	6586.828	335			

Temperature outside the habitat (C)

Duncan [a,b]

		Subset for alpha = .05			
Groups	N	1	2	3	4
1	29	31.0879			
7	76	31.8311	31.8311		
5	187	32.8479	32.8479	32.8479	
3	11		34.5000	34.5000	34.5000
2	12			35.5000	35.5000
6	10				36.2350
4	11				36.5773
Sig.		.265	.088	.090	.205

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 16.741.

b. The group sizes are unequal. The harmonic mean of the group sizes is used. Type I error levels are not guaranteed.

of the group sizes is used. Type I error levels are not guaranteed.

b. The group sizes are unequal. The harmonic mean of the group sizes is used. Type I error levels are not guaranteed.

Test of Homogeneity of Variances

Moisture under the canopy (%RH)

Levene Statistic	df1	df2	Sig.
6.955	6	329	.000

ANOVA

Moisture under the canopy (%RH)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	6021.384	6	1003.564	4.695	.000
Within Groups	70320.73	329	213.741		
Total	76342.12	335			

Moisture under the canopy (%RH)

Duncan [a,b]

		Subset for alpha = .05		
Groups	N	1	2	3
3	11	47.7455		
2	12	50.4000	50.4000	
4	11	50.6545	50.6545	
1	29	56.8966	56.8966	56.8966
6	10		61.1300	61.1300
5	187			62.5773
7	76			63.8322
Sig.		.099	.051	.215

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 16.741.

b. The group sizes are unequal. The harmonic mean of the group sizes is used. Type I error levels are not guaranteed.

Test of Homogeneity of Variances

Moisture outside the habitat (%RH)

Levene Statistic	df1	df2	Sig.
6.994	6	329	.000

ANOVA

Moisture outside the habitat (%RH)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	14323.30	6	2387.216	12.146	.000
Within Groups	64663.20	329	196.545		
Total	78986.49	335			

Moisture outside the habitat (%RH)

Duncan [a,b]

		Subset for alpha = .05		
Groups	N	1	2	3
6	10	32.6750		
2	12		42.9750	
4	11		43.1864	
3	11		43.7455	
1	29			54.9207
5	187			59.5745
7	76			59.9505
Sig.		1.000	.882	.331

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 16.741.

b. The group sizes are unequal. The harmonic mean of the group sizes is used. Type I error levels are not guaranteed.

Test of homogeneity of variances and ANOVA of light intensities and %population spaces

Test of Homogeneity of Variances

Light intensity under the canopy (Klx)

Levene Statistic	df1	df2	Sig.
3.959	6	329	.001

ANOVA

Light intensity under the canopy (Klx)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	369.591	6	61.599	2.003	.065
Within Groups	10118.15	329	30.754		
Total	10487.74	335			

Light intensity under the canopy (Klx)

Duncan [a,b]

Groups	N	Subset for alpha = .05		
		1	2	3
2	12	2.6725		
4	11	4.3382	4.3382	
5	187	5.1630	5.1630	
1	29	5.3629	5.3629	5.3629
7	76	5.9397	5.9397	5.9397
6	10		7.7840	7.7840
3	11			9.4400
Sig.		.132	.111	.051

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 16.741.

b. The group sizes are unequal. The harmonic mean of the group sizes is used. Type I error levels are not guaranteed.

Test of Homogeneity of Variances

Light intensity at the top of canopy (Klx)

Levene Statistic	df1	df2	Sig.
8.285	6	329	.000

ANOVA

Light intensity at the top of canopy (Klx)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	29015.37	6	4835.895	10.497	.000
Within Groups	151574.3	329	460.712		
Total	180589.7	335			

Light intensity at the top of canopy (Klx)

Duncan [a,b]

Groups	N	Subset for alpha = .05	
		1	2
2	12	13.3317	
1	29	17.2567	
6	10	17.5200	
5	187	20.7352	
7	76	24.6728	
4	11	26.4718	
3	11		71.0018
Sig.		.124	1.000

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 16.741.

b. The group sizes are unequal. The harmonic mean of the group sizes is used. Type I error levels are not guaranteed.

Test of Homogeneity of Variances

Light intensity outside the habitat (Klx)

Levene Statistic	df1	df2	Sig.
5.088	6	329	.000

ANOVA

Light intensity outside the habitat (Klx)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	35964.04	6	5994.006	4.494	.000
Within Groups	438845.2	329	1333.876		
Total	474809.3	335			

Light intensity outside the habitat (Klx)

Duncan [a,b]

Groups	N	Subset for alpha = .05		
		1	2	3
6	10	27.6600		
2	12	28.9417		
4	11	48.0955	48.0955	
1	29	51.6328	51.6328	
7	76	52.9825	52.9825	
5	187		57.3135	
3	11			95.6545
Sig.		.073	.514	1.000

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 16.741.

b. The group sizes are unequal. The harmonic mean of the group sizes is used. Type I error levels are not guaranteed.

Test of Homogeneity of Variances

Population space under the canopy (%)

Levene Statistic	df1	df2	Sig.
3.785	6	329	.001

ANOVA

Population space under the canopy (%)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	8372.443	6	1395.407	4.801	.000
Within Groups	95627.48	329	290.661		
Total	103999.9	335			

Population space under the canopy (%)

Duncan [a,b]

Groups	N	Subset for alpha = .05			
		1	2	3	4
2	12	18.33			
3	11	27.27	27.27		
1	29		30.86	30.86	
7	76		36.38	36.38	
5	187		37.19	37.19	
4	11			42.73	42.73
6	10				51.00
Sig.		.129	.126	.065	.160

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 16.741.

b. The group sizes are unequal. The harmonic mean of the group sizes is used. Type I error levels are not guaranteed.

Test of homogeneity of variances and ANOVA of %population spaces

Test of Homogeneity of Variances

Population space at canopy (%)

Levene Statistic	df1	df2	Sig.
1.875	6	329	.085

ANOVA

Population space at canopy (%)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	2806.202	6	467.700	2.188	.044
Within Groups	70329.44	329	213.767		
Total	73135.64	335			

Population space at canopy (%)

Duncan [a,b]

Groups	N	Subset for alpha = .05	
		1	2
3	11	28.18	
4	11	31.82	
7	76	34.41	
6	10	37.00	37.00
5	187	37.14	37.14
1	29	38.79	38.79
2	12		46.67
Sig.		.065	.080

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 16.741.

b. The group sizes are unequal. The harmonic mean of the group sizes is used. Type I error levels are not guaranteed.

Test of Homogeneity of Variances

Population space above the canopy (%)

Levene Statistic	df1	df2	Sig.
2.619	6	329	.017

ANOVA

Population space above the canopy (%)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	6183.265	6	1030.544	3.387	.003
Within Groups	100114.1	329	304.298		
Total	106297.3	335			

Population space above the canopy (%)

Duncan [a,b]

Groups	N	Subset for alpha = .05		
		1	2	3
6	10	16.00		
4	11	25.45	25.45	
5	187	25.83	25.83	
7	76		29.08	
1	29		30.34	
2	12		35.00	35.00
3	11			44.55
Sig.		.124	.163	.113

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 16.741.

b. The group sizes are unequal. The harmonic mean of the group sizes is used. Type I error levels are not guaranteed.

APPENDIX D

DNA

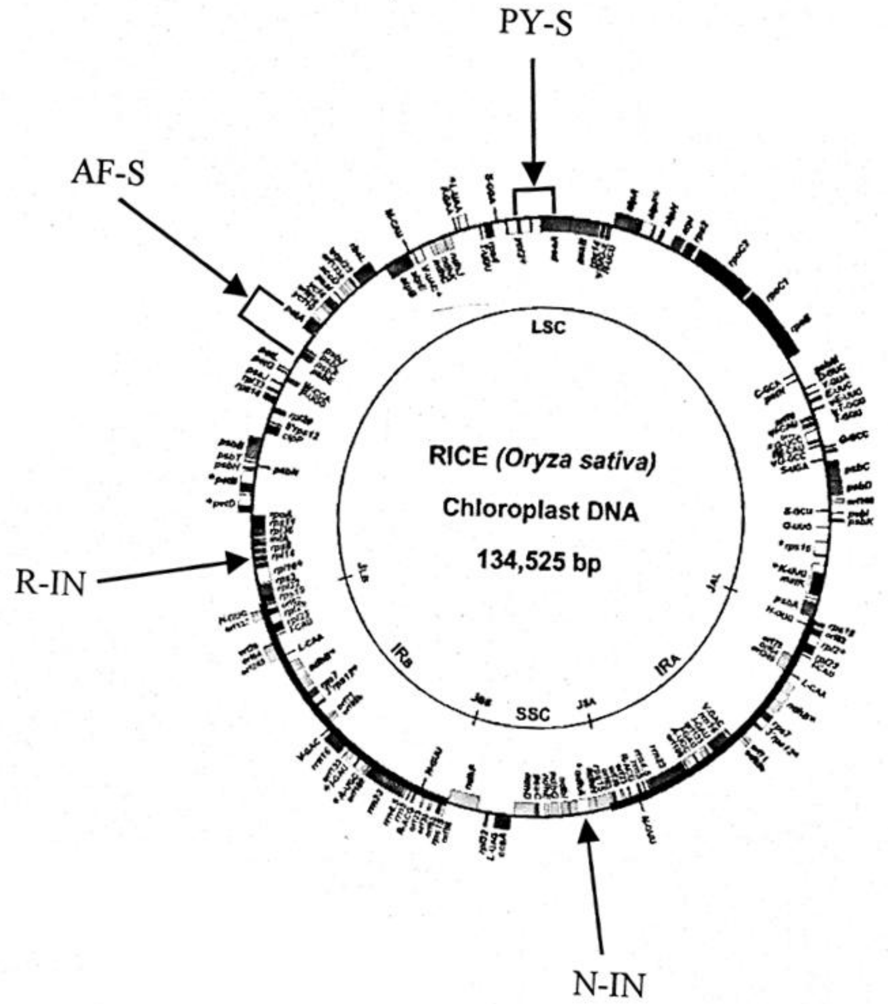


Figure 8 Location of four selected fragments for chloroplast sequence analyses in *Musa* (Chapter 4) on rice complete chloroplast genome (Tsudzuki et al.in press). The fragments indicated by arrows are (form top to bottom, counter clock-wise) PY-S = *psa*A-*ycf*3 intergenic spacer; AF-S = *pet*A-*psb*J-*psb*F intergenic spacers; R-IN= *rpl*16 intron; and N-IN = *ndh*A intron

Table 23 Details of primers used for amplifications. (Sawangpol, 2003)

Name	Nucleotide Sequence	Tm (°C)	Amplified Region	Sequence Code	Location [a]	Protein Encoded
*rpl*16-F	5’GCTATGCTTAGTGTGTGACT3’	55.3	*rpl*16 intron	R-IN	LSC	ribosomal protein L16
*rpl*16-R	5’CATTCTTCCTCTATGTTGTTT3’	52.0				
*psa*A-F	5’AAATCGTGAGCATCAGCATG3’	54.7	*psa*A-*ycf*3 exon3 intergenic spacer	PY-S	LSC	Photosystem I P700 apoprotein A1 and photosystem I assembly protein Ycf3
*psa*A-R	5’CCGAGGAGAACAGGCCATTC3’	58.6				
*ndh*A-F	5’GCTGCTCAATCTATTAGTTATGA3’	55.3	*ndh*A intron	N-IN	SSC	NADH dehygrogenase subunit 1
*ndh*A-R	5’TGTGCTTCAACTATATCAACTGT3’	53.7				
*pet*A-F	5’TATGAAAATCCACGAGAAGC3’	51.3	*pet*A-*psb*J-*psb*L-*psb*F intergenic spacer	AF-S	LSC	cytochrome f, photosystem II protein J and L, and cytochrome b559 beta chain, respectively
*pet*A-R	5’TATCAGCAATGCAGTTCATC3’	51.7				

[a] LSC= Large single copy chloroplast region and SSC= small single copy chloroplast region.

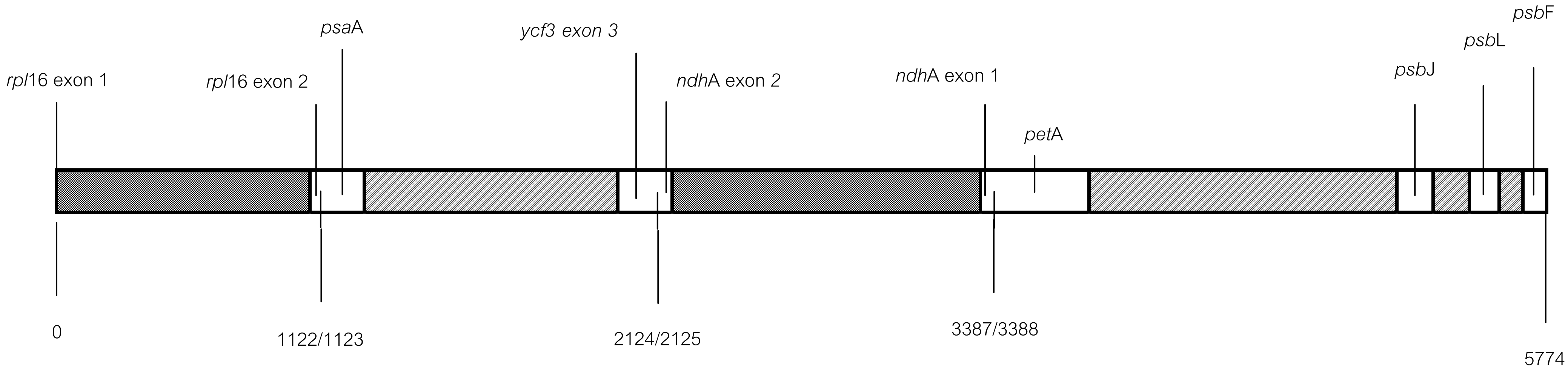


Figure 9 Diagram representation of the combined chloroplast sequence used in the phylogenetic analysis of *Musa*. The total of 5.4 - kb sequence contained 1.0 - kb *rpl*16 intron (R - IN), 1.0 - kb *psa*A - *ycf*3 intergenic spacer (PY - S), 1.1-kb *ndh*A (N - IN), and 2.3 - kb *pet*A - *psb*J - *psb*L - *psb*F intergenic spacer (AF - S) fragments. Numbers indicate positions on the aligned data matrix and boxes are exons (□), introns (▩), and intergenic spacers (▧) with minor modified from Sawangpol (2003).

Table 24 Average base composition and length composition of sequences and indels in combined chloroplast sequences of *Musa*. (Sawangpol, 2003). Aligned data matrix appears in Appendix 4.2. [a] Sequence code appears according to Figue 8.

Sequence Code [a]	Regions	Positions on Data Matrix	Aligned Length (bp)	No. of Indels	Indel Length (bp)	Average Base Composition			
						A	C	G	T
R-IN	*rpl*16 exons	1-12	54	-	-	0.48	0.19	0.19	0.14
		1081-1122							
	*rpl*16 intron	13-1080	1068	7	113	0.40	0.14	0.17	0.29
PY-S	*psa*A	1123-1289	167	-	-	0.25	0.23	0.23	0.29
	*psa*A-*rcf*3 spacer	1290-1970	681	3	51	0.31	0.18	0.14	0.37
	*rcf*3	1971-2124	154	-	-	0.26	0.27	0.16	0.30
N-IN	*ndh*A exons	2125-2185	102	-	-	0.33	0.18	0.14	0.35
		3347-3387							
	*ndh*A intron	2186-3346	1161	19	104	0.37	0.13	0.17	0.33
AF-S	*pet* A	3388-4219	832	-		0.31	0.18	0.22	0.29
	*pet*A-*psb*J spacer	4220-5358	1139	11	136	0.34	0.14	0.17	0.35
	*psb*J	5359-5481	123	-	-	0.41	0.26	0.17	0.16
	*psb*J-*psb*L spacer	5382-5606	125	-	-	0.27	0.22	0.15	0.36
	*psb*L	5607-5722	116	-	-	0.39	0.14	0.17	0.30
	*psb*L-*psb*F spacer	5723-5745	23	-	-	0.37	0.11	0.13	0.39
	*psb*F	5746-5774	29	-	-	0.34	0.16	0.18	0.32
-	Total	-	5774	39	404	0.34	0.16	0.18	0.32

Primer: *ndh*A

```
* 20 * 40 * 60 * 80 * 100 * 120 * 140 * 160 * 180
Aaw_Ranong: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---
GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166
Aaw_Yala : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT
: 166
M.laterita: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT :
166
AAw_Trang : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---
GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166
AAw_Prachu: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---
GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166
AAw_MW10 : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---
GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166
AAw_MW20 : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---
GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166
AAw_MW31 : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---
GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166
AAw_UP16 : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---
GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166
AAw_UP18 : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---
GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166
AAw_Rayong: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---
GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166
AAw_Chanth: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---
GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166
AAw_Mukdah: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---
GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166
M_rubra_Sa: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---
GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166
AAw_UP25 : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---
GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166
AAw_UP37 : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---
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M_x_rubra_: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

AAw_Salawe: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

M_terminif: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT

: 166

AAw_LN20 : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

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AAw_MaeYom: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

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AAw_NW22 : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

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AAw_NW33 : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

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AAw_NW38 : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

AAw_NW41 : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

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AAw_PH04 : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

AAw_PH05 : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

AAw_TL18 : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

AAw_UP36 : A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

AAw_Chanth: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

AAw_Chanth: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

AAw_Chanth: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

AAw_Chanth: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

AAw_Kancha: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

AAw_Kancha: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

AAw_Kancha: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

AAw_Trang1: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

AAw_Trang2: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

AAw_Trang3: A-ATA-CCA-TTA-ACT-CTA-TGT-GTG-TTA-TCA-ATA-TCT-CTA-C---

GTGTGATTCGTTGAACATGAACTTTATACTTCTTTCCTAGAAGTAAAGGAAAGAAGTTGAATGTAATGTATTGAATAGGTATTTTATTTTTTATTCATCATTCGGGTCAATGAGTTAAACCAGATAGT : 166

* 200 * 220 * 240 * 260 * 280 * 300 * 320 * 340 * 360

Aaw_Ranong:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

Aaw_Yala :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

M.laterita:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_Trang :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_Prachu:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_MW10 :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_MW20 :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_MW31 :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_UP16 :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_UP18 :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_Rayong:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_Chanth:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_Mukdah:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

M_rubra_Sa:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_UP25 :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_UP37 :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

M_x_rubra_:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_Salawe:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

M_terminif:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_LN20 :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_MaeYom:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_NW22 :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_NW33 :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_NW38 :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_NW41 :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_PH04 :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_PH05 :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_TL18 :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_UP36 :

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_Chanth:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_Chanth:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_Chanth:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_Chanth:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_Kancha:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_Kancha:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_Kancha:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_Trang1:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_Trang2:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

AAw_Trang3:

TATATGAGTGAAACAAAACAACTTAGAAGTTTGCAGTAAGAAGATAAAATCTCATTTCATATGTACAAGAATAAAGTTGAAGTAAACATAAGCAGTGTAAACTGTTTACCCCAAGATTAAGATTCTTTCATTAGTCATCATATCTTGGAGCGGGTGTAAAAGATCAACTGTATGGAGTT

TTC : 348

* 380 * 400 * 420 * 440 * 460 * 480 * 500 * 520 * 540

Aaw_Ranong:
ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA
GCA : 530

Aaw_Yala :
ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA
GCA : 530

M.laterita:
ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA
GCA : 530

AAw_Trang :
ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA
GCA : 530

AAw_Prachu:
ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA
GCA : 530

AAw_MW10 :
ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA
GCA : 530

AAw_MW20 :
ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA
GCA : 530

AAw_MW31 :
ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA
GCA : 530

AAw_UP16 :
ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA
GCA : 530

AAw_UP18 :
ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA
GCA : 530

AAw_Rayong:
ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA
GCA : 530

AAw_Chanth:

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_Mukdah:

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

M_rubra_Sa:

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_UP25 :

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_UP37 :

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

M_x_rubra_:

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_Salawe:

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

M_terminif:

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_LN20 :

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_MaeYom:

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_NW22 :

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_NW33 :

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_NW38 :

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_NW41 :

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_PH04 :

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_PH05 :

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_TL18 :

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_UP36 :

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_Chanth:

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_Chanth:

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_Chanth:

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_Chanth:

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_Kancha:

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_Kancha:

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_Kancha:

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_Trang1:

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GCA : 530

AAw_Trang2:

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

AAw_Trang3:

ATTACTGTCTTGTATTTATTACCATGCCGTAGATCAATCAAAAATCAGTGGACGGTTAGGAACACCAAAGTGCACAAAGGATTAGTAATAGAGATAATGTAAGGTATCAAAAAAAGAGATATTTCTACAATTTATAAAACGAATAAAAATAGGGACTTTAAGTTGGTAGAAATGATCAA

GCA : 530

* 560 * 580 * 600 * 620 * 640 * 660 * 680 * 700 * 720

Aaw_Ranong: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--

CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAATTAATAATGTAATAATCGAATTAAT : 710

Aaw_Yala : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTT---CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA----------

: 691

M.laterita: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA---------- :

692

AAw_Trang : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTTT-CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------

--- : 693

AAw_Prachu: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------

--- : 692

AAw_MW10 : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA------

---- : 692

AAw_MW20 : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA------

---- : 692

AAw_MW31 : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA------
---- : 692

AAw_UP16 : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 692

AAw_UP18 : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 692

AAw_Rayong: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTTTTCAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-----
----- : 694

AAw_Chanth: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTTT-CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA------
---- : 693

AAw_Mukdah: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTTTTCAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA----
------ : 694

M_rubra_Sa: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA--------
-- : 692

AAw_UP25 : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAATAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTTT-CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 693

AAw_UP37 : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAATAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTTT-CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 693

M_x_rubra_: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAATAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTTT-CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA--------
-- : 693

AAw_Salawe: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAATAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTTT-CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 693

M_terminif: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAATAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTTTTCAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA----------
: 694

AAw_LN20 : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTTT-CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 693

AAw_MaeYom: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTTT-CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA----
------ : 693

AAw_NW22 : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 692

AAw_NW33 : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 692

AAw_NW38 : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 692

AAw_NW41 : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 692

AAw_PH04 : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 692

AAw_PH05 : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 692

AAw_TL18 : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA--------
-- : 692

AAw_UP36 : GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 692

AAw_Chanth: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 692

AAw_Chanth: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 692

AAw_Chanth: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 692

AAw_Chanth: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTTTTCAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-----
----- : 694

AAw_Kancha: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA------
---- : 692

AAw_Kancha: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA------
---- : 692

AAw_Kancha: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA------
---- : 692

AAw_Trang1: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 692

AAw_Trang2: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 692

AAw_Trang3: GTACTTCCCTACGATTCCGATCTAGAGTATGCTCCTATTCACTGATTAAAGAAATGACTATCCAGAACGAATTAATCCCTTATTCTTTTTTTTT--CAAAGTACCCTCTTCTGAGATAGAAGAACAGGAACAAAAGAAATGGAATGTAATAATCGAAT--------TAATAA-------
--- : 692

* 740 * 760 * 780 * 800 * 820 * 840 * 860 * 880 * 900 *

Aaw_Ranong:

AAAAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

892

Aaw_Yala : --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

871

M.laterita: --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

872

AAw_Trang : --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

873

AAw_Prachu: --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

872

AAw_MW10 : --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

872

AAw_MW20 : --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

872

AAw_MW31 : --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

872

AAw_UP16 : --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

872

AAw_UP18 : --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

872

AAw_Rayong: --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

874

AAw_Chanth: --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

873

AAw_Mukdah: --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

874

M_rubra_Sa: --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

872

AAw_UP25 : --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

873

AAw_UP37 : --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

873

M_x_rubra_: --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

873

AAw_Salawe: --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

873

M_terminif: --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

874

AAw_LN20 : --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

873

AAw_MaeYom: --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

873

AAw_NW22 : --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGGCTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

872

AAw_NW33 : --
AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGGCTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :
872

AAw_NW38 : --
AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGGCTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :
872

AAw_NW41 : --
AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGGCTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :
872

AAw_PH04 : --
AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGGCTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :
872

AAw_PH05 : --
AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGGCTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :
872

AAw_TL18 : --
AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGGCTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :
872

AAw_UP36 : --
AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGGCTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :
872

AAw_Chanth: --
AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGATGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG : 872

AAw_Chanth: --
AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :
872

AAw_Chanth: --
AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :
872

AAw_Chanth: --
AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :
874

AAw_Kancha: --
AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGGCTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :
872

AAw_Kancha: --AAAAA-

GATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGGCTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG : 871

AAw_Kancha: --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGGCTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

872

AAw_Trang1: --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

872

AAw_Trang2: --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

872

AAw_Trang3: --

AAAAAAGATATTTATTTATTCTTTTTTCCCATCCATATGGGTGGAATTCCTATCACAATTAATGGACTAATTCCTAATTCTTTAAATTCTTTAGATTTATTGATATAACGAGTATTTTATTGAAGGGCTGAGTTATTACCGAACAAAGAAAAATACATTTTTATTATCATAAGGGATGAG :

872

920 * 940 * 960 * 980 * 1000 * 1020 * 1040 * 1060 * 1080 *

Aaw_Ranong:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1074

Aaw_Yala :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1053

M.laterita:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_Trang :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1055

AAw_Prachu:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_MW10 :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_MW20 :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_MW31 :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_UP16 :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_UP18 :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_Rayong:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1056

AAw_Chanth:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1055

AAw_Mukdah:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1056

M_rubra_Sa:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_UP25 :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1055

AAw_UP37 :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1055

M_x_rubra_:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1055

AAw_Salawe:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1055

M_terminif:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1056

AAw_LN20 :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1055

AAw_MaeYom:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1055

AAw_NW22 :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_NW33 :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_NW38 :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_NW41 :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_PH04 :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_PH05 :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_TL18 :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_UP36 :

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_Chanth:

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GTT :1054

AAw_Chanth:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_Chanth:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_Chanth:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1056

AAw_Kancha:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_Kancha:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1053

AAw_Kancha:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_Trang1:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_Trang2:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

AAw_Trang3:

ATTAATTCCGAAGCACTTTTTCTTATTCTAGCAAACGGAATTCCATTGGTTTAATTTCGGACTCTCTGATATATCTTTATTCTAGTTATCCCAAAAGAAAAGGGGTGATAATATCGAACTAGTCCTTACATTTATTTGTGGCCATAGAGGAGCCGTATGAAGCTGAGGTCTCATGTACG

GTT :1054

```
            1100        *       1120        *       1140        *       1160
Aaw_Ranong: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1134
Aaw_Yala  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1113
M.laterita: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_Trang : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1115
AAw_Prachu: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_MW10  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_MW20  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_MW31  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_UP16  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_UP18  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_Rayong: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1116
AAw_Chanth: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1115
AAw_Mukdah: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1116
M_rubra_Sa: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_UP25  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1115
AAw_UP37  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1115
M_x_rubra_: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1115
AAw_Salawe: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1115
M_terminif: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1116
AAw_LN20  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1115
AAw_MaeYom: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1115
AAw_NW22  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_NW33  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_NW38  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_NW41  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_PH04  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_PH05  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_TL18  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_UP36  : TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_Chanth: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_Chanth: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_Chanth: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
AAw_Chanth: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1116
AAw_Kancha: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114
```

AAw_Kancha: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1113

AAw_Kancha: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114

AAw_Trang1: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114

AAw_Trang2: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114

AAw_Trang3: TTGGAATAGCGATGGAAACAGTAATGTTATTATCGACTATAAT---TA-TCT-AAC-AGT-TCA-AGT :1114

Primer: *pet*A

* 20 * 40 * 60 * 80 * 100 * 120 * 140 * 160 * 180

AAw_Ranong :

AACGGGACGAATTGTATGTGCCAATTGCCATTTAGCTAATAAACCCGTGGATATTGAAGTTCCGCAAGCTGTGCTTCCTGATACTGTATTTGAAGCAGTTGTTCGAATCCCTTATGATAAGCAACTGAAACAAGTTCTTGCTAATGGTAAAAAGGGGACTTTGAATGTGGGGGCTGT

TCT : 180

AAw_Yala :

AACGGGACGAATTGTATGTGCCAATTGCCATTTAGCTAATAAACCCGTGGATATTGAAGTTCCGCAAGCTGTGCTTCCTGATACTGTATTTGAAGCAGTTGTTCGAATCCCTTATGATAAGCAACTGAAACAAGTTCTTGCTAATGGTAAAAAGGGGACTTTGAATGTGGGGGCTGT

TCT : 180

M_laterita :

AACGGGACGAATTGTATGTGCCAATTGCCATTTAGCTAATAAACCCGTGGATATTGAAGTTCCGCAAGCTGTGCTTCCTGATACTGTATTTGAAGCAGTTGTTCGAATCCCTTATGATAAGCAACTGAAACAAGTTCTTGCTAATGGTAAAAAGGGGACTTTGAATGTGGGGGCTGT

TCT : 180

AAw_Trang :

AACGGGACGAATTGTATGTGCCAATTGCCATTTAGCTAATAAACCCGTGGATATTGAAGTTCCGCAAGCTGTGCTTCCTGATACTGTATTTGAAGCAGTTGTTCGAATCCCTTATGATAAGCAACTGAAACAAGTTCTTGCTAATGGTAAAAAGGGGACTTTGAATGTGGGGGCTGT

TCT : 180

AAw_Prachuab:

AACGGGACGAATTGTATGTGCCAATTGCCATTTAGCTAATAAACCCGTGGATATTGAAGTTCCGCAAGCTGTGCTTCCTGATACTGTATTTGAAGCAGTTGTTCGAATCCCTTATGATAAGCAACTGAAACAAGTTCTTGCTAATGGTAAAAAGGGGACTTTGAATGTGGGGGCTGT

TCT : 180

AAw_MW10 : -- : -

AAw_MW20 : -- : -

AAw_MW31 : -- : -

AAw_UP16 : -- : -

AAw_UP18 : -- : -

AAw_Rayong : -- : -

AAw_Chanthab: -- : -

AAw_Mukdahan: -- : -

M_rubra_Sala: -- : -

AAw_UP25 : -- : -

AAw_UP37 : -- : -

M_x_rubra_Sa: -- : -
AAw_Salaween: -- : -
M.terminiflo: -- : -
AAw_LN20 : -- : -
AAw_MaeYom : -- : -
AAw_NW22 : -- : -
AAw_NW33 : -- : -
AAw_NW38 : -- : -
AAw_NW41 : -- : -
AAw_PH04 : -- : -
AAw_PH05 : -- : -
AAw_TL18 : -- : -
AAw_UP36 : -- : -
AAw_Chanthab: -- : -
AAw_Chanthab: -- : -
AAw_Chanthab: -- : -
AAw_Chanthab: -- : -
AAw_Kanchana: -- : -
AAw_Kanchana: -- : -
AAw_Kanchana: -- : -
AAw_Trang1 : -- : -
AAw_Trang2 : -- : -
AAw_Trang3 : -- : -

* 200 * 220 * 240 * 260 * 280 * 300 * 320 * 340 * 360

AAw_Ranong :
CATTTTACCCGACGGATTCGAATTAGCCCCCCTTGATCGTATTTCTCCTGAGTTGAAAGAAAAGATAGGAAATCTGTCTTTTCAGAGTTATCGTCCCAACAAAAGAAATATTATTGTGATAGGTCCTGTTCCCGGTCAGAAATATAGTGAAATCGTCTTTCCCATTCTTTCCCCCGAC
CC : 360
AAw_Yala :
CATTTTACCCGACGGATTCGAATTAGCCCCCCTTGATCGTATTTCTCCTGAGTTGAAAGAAAAGATAGGAAATCTGTCTTTTCAGAGTTATCGTCCCAACAAAAGAAATATTATTGTGATAGGTCCTGTTCCCGGTCAGAAATATAGTGAAATCGTCTTTCCCATTCTTTCCCCCGAC
CC : 360
M_laterita :
CATTTTACCCGACGGATTCGAATTAGCCCCCCTTGATCGTATTTCTCCTGAGTTGAAAGAAAAGATAGGAAATCTGTCTTTTCAGAGTTATCGTCCCAACAAAAGAAATATTATTGTGATAGGTCCTGTTCCCGGTCAGAAATATAGTGAAATCGTCTTTCCCATTCTTTCCCCCGAC
CC : 360

AAw_Trang :

CATTTTACCCGACGGATTCGAATTAGCCCCCCTTGATCGTATTTCTCCTGAGTTGAAAGAAAAGATAGGAAATCTGTCTTTTCAGAGTTATCGTCCCAACAAAAGAAATATTATTGTGATAGGTCCTGTTCCCGGTCAGAAATATAGTGAAATCGTCTTTCCCATTCTTTCCCCCGAC

CC : 360

AAw_Prachuab:

CATTTTACCCGACGGATTCGAATTAGCCCCCCTTGATCGTATTTCTCCTGAGTTGAAAGAAAAGATAGGAAATCTGTCTTTTCAGAGTTATCGTCCCAACAAAAGAAATATTATTGTGATAGGTCCTGTTCCCGGTCAGAAATATAGTGAAATCGTCTTTCCCATTCTTTCCCCCGAC

CC : 360

AAw_MW10 : -- : -

AAw_MW20 : -- : -

AAw_MW31 : -- : -

AAw_UP16 : -- : -

AAw_UP18 : -- : -

AAw_Rayong : -- : -

AAw_Chanthab: -- : -

AAw_Mukdahan: -- : -

M_rubra_Sala: -- : -

AAw_UP25 : -- : -

AAw_UP37 : -- : -

M_x_rubra_Sa: -- : -

AAw_Salaween: -- : -

M.terminiflo: -- : -

AAw_LN20 : -- : -

AAw_MaeYom : -- : -

AAw_NW22 : -- : -

AAw_NW33 : -- : -

AAw_NW38 : -- : -

AAw_NW41 : -- : -

AAw_PH04 : -- : -

AAw_PH05 : -- : -

AAw_TL18 : -- : -

AAw_UP36 : -- : -

AAw_Chanthab: -- : -

AAw_Chanthab: -- : -

AAw_Chanthab: -- : -

AAw_Chanthab: -- : -

AAw_Kanchana: -- : -

AAw_Kanchana: -- : -

AAw_Kanchana: -- : -

AAw_Trang1 : -- : -

AAw_Trang2 : -- : -

AAw_Trang3 : -- : -

* 380 * 400 * 420 * 440 * 460 * 480 * 500 * 520 * 540

AAw_Ranong :

TGCTACGAAGAAAGACGTTCACTTCTTAAAATATCCCATATACGTAGGTGGGAACAGAGGAAGGGGTCAGATTTATCCTGATGGTAGCAAAAGTAACAATACAGTCTATAATGCTACATCAGCAGGTATAGTAAGCAGAATAGTACGTAAAGAAAAAGGGGGATATGAAATAACC

ATAGT : 540

AAw_Yala :

TGCTACGAAGAAAGACGTTCACTTCTTAAAATATCCCATATACGTAGGTGGGAACAGAGGAAGGGGTCAGATTTATCCTGATGGTAGCAAAAGTAACAATACAGTCTATAATGCTACATCAGCAGGTATAGTAAGCAGAATAGTACGTAAAGAAAAAGGGGGATATGAAATAACC

ATAGT : 540

M_laterita :

TGCTACGAAGAAAGACGTTCACTTCTTAAAATATCCCATATACGTAGGTGGGAACAGAGGAAGGGGTCAGATTTATCCTGATGGTAGCAAAAGTAACAATACAGTCTATAATGCTACATCAGCAGGTATAGTAAGCAGAATAGTACGTAAAGAAAAAGGGGGATATGAAATAACC

ATAGT : 540

AAw_Trang :

TGCTACGAAGAAAGACGTTCACTTCTTAAAATATCCCATATACGTAGGTGGGAACAGAGGAAGGGGTCAGATTTATCCTGATGGTAGCAAAAGTAACAATACAGTCTATAATGCTACATCAGCAGGTATAGTAAGCAGAATAGTACGTAAAGAAAAAGGGGGATATGAAATAACC

ATAGT : 540

AAw_Prachuab:

TGCTACGAAGAAAGACGTTCACTTCTTAAAATATCCCATATACGTAGGTGGGAACAGAGGAAGGGGTCAGATTTATCCTGATGGTAGCAAAAGTAACAATACAGTCTATAATGCTACATCAGCAGGTATAGTAAGCAGAATAGTACGTAAAGAAAAAGGGGGATATGAAATAACC

ATAGT : 540

AAw_MW10 : -- : -

AAw_MW20 : -- : -

AAw_MW31 : -- : -

AAw_UP16 : -- : -

AAw_UP18 : -- : -

AAw_Rayong : -- : -

AAw_Chanthab: -- : -

AAw_Mukdahan: -- : -

M_rubra_Sala: -- : -

AAw_UP25 : -- : -

AAw_UP37 : -- : -

M_x_rubra_Sa: -- : -

AAw_Salaween: -- : -

M.terminiflo: -- : -

AAw_LN20 : -- : -

AAw_MaeYom : -- : -

AAw_NW22 : -- : -

AAw_NW33 : -- : -

AAw_NW38 : -- : -

AAw_NW41 : -- : -

AAw_PH04 : -- : -

AAw_PH05 : -- : -

AAw_TL18 : -- : -

AAw_UP36 : -- : -

AAw_Chanthab: -- : -

AAw_Chanthab: -- : -

AAw_Chanthab: -- : -

AAw_Chanthab: -- : -

AAw_Kanchana: -- : -

AAw_Kanchana: -- : -

AAw_Kanchana: -- : -

AAw_Trang1 : -- : -

AAw_Trang2 : -- : -

AAw_Trang3 : -- : -

* 560 * 580 * 600 * 620 * 640 * 660 * 680 * 700 * 720

AAw_Ranong :

TGATGCATCGGATGGACATCAAGTGGTTGATATTATACCTCCAGGACCAGAACTTCTTGTTTCAGAGGGTGAATCCATCAAGCTTGATCAACCATTAACAAGCAATCCCAATGTGGGAGGCTTTGGTCAGGGAGATGCAGAAATAGTGCTTCAAGACCCATTACGGGTCCAAGGT

CTTTT : 720

AAw_Yala :

TGATGCATCGGATGGACATCAAGTGGTTGATATTATACCTCCAGGACCAGAACTTCTTGTTTCAGAGGGTGAATCCATCAAGCTTGATCAACCATTAACAAGCAATCCCAATGTGGGAGGCTTTGGTCAGGGAGATGCAGAAATAGTGCTTCAAGACCCATTACGGGTCCAAGGT

CTTTT : 720

M_laterita :

TGATGCATCGGATGGACATCAAGTGGTTGATATTATACCTCCAGGACCAGAACTTCTTGTTTCAGAGGGTGAATCCATCAAGCTTGATCAACCATTAACAAGCAATCCCAATGTGGGAGGCTTTGGTCAGGGAGATGCAGAAATAGTGCTTCAAGACCCATTACGGGTCCAAGGT

CTTTT : 720

AAw_Trang :

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CTTTT : 720

AAw_Prachuab:

TGATGCATCGGATGGACATCAAGTGGTTGATATTATACCTCCAGGACCAGAACTTCTTGTTTCAGAGGGTGAATCCATCAAGCTTGATCAACCATTAACAAGCAATCCCAATGTGGGAGGCTTTGGTCAGGGAGATGCAGAAATAGTGCTTCAAGACCCATTACGGGTCCAAGGT

CTTTT : 720

AAw_MW10 : -- : -

AAw_MW20 : -- : -

AAw_MW31 : -- : -

AAw_UP16 : -- : -

AAw_UP18 : -- : -

AAw_Rayong : -- : -

AAw_Chanthab: -- : -

AAw_Mukdahan: -- : -

M_rubra_Sala: -- : -

AAw_UP25 : -- : -

AAw_UP37 : -- : -

M_x_rubra_Sa: -- : -

AAw_Salaween: -- : -

M.terminiflo: -- : -

AAw_LN20 : -- : -

AAw_MaeYom : -- : -

AAw_NW22 : -- : -

AAw_NW33 : -- : -

AAw_NW38 : -- : -

AAw_NW41 : -- : -

AAw_PH04 : -- : -

AAw_PH05 : -- : -

AAw_TL18 : -- : -

AAw_UP36 : -- : -

AAw_Chanthab: -- : -

AAw_Chanthab: -- : -

AAw_Chanthab: -- : -

AAw_Chanthab: -- : -

AAw_Kanchana: -- : -

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AAw_Kanchana: ------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------ :   -
AAw_Kanchana: ------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------ :   -
AAw_Trang1  : ------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------ :   -
AAw_Trang2  : ------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------ :   -
AAw_Trang3  : ------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------ :   -
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                 *    740     *    760     *    780     *    800     *    820     *    840     *    860     *    880     *    900
AAw_Ranong  :
GTTCTTCTTGGCATCTGTTATTTTGGCACAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA :
900
AAw_Yala    :
GTTCTTCTTGGCATCTGTTATTTTGGCACAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA :
900
M_laterita  :
GTTCTTCTTGGCATCTGTTATTTTGGCACAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA :
900
AAw_Trang   :
GTTCTTCTTGGCATCTGTTATTTTGGCACAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA :
900
AAw_Prachuab:
GTTCTTCTTGGCATCTGTTATTTTGGCACAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA :
900
AAw_MW10    : ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_MW20    : ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_MW31    : ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_UP16    : ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_UP18    : ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_Rayong  : ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_Chanthab: ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA :
152
AAw_Mukdahan: ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA :
152
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M_rubra_Sala: ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_UP25 : ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_UP37 : ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
M_x_rubra_Sa: ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_Salaween: ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
M.terminiflo: ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_LN20 : ------------------------------AGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 150
AAw_MaeYom : ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_NW22 : ------------------------------AGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 150
AAw_NW33 : ------------------------------AGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 150
AAw_NW38 : ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_NW41 : ------------------------------AGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 150
AAw_PH04 : ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_PH05 : ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_TL18 : ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_UP36 : ------------------------------AGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 150
AAw_Chanthab: ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_Chanthab: ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_Chanthab: ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_Chanthab: ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_Kanchana: ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_Kanchana: ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_Kanchana: ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_Trang1 : ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_Trang2 : ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152
AAw_Trang3 : ----------------------------CAAGTTTTTTTGGTTCTTAAAAAGAAACAGTTTGAAAAGGTTCAATTGTACGAAATGAATTTCTAGGTGCAGAGATTCCTTAACATCAAGTTGGTAAAAAGCGCCGAATTTTTTTTGATCCATACAATTATGTATGATCAAAAAATCTGTAA : 152

* 920 * 940 * 960 * 980 * 1000 * 1020 * 1040 * 1060 * 1080

AAw_Ranong : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC :1078

AAw_Yala : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC :1078

M_laterita : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC :1078

AAw_Trang : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

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AAw_Prachuab: ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC :1078

AAw_MW10 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

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AAw_MW20 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

AAw_MW31 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

AAw_UP16 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

AAw_UP18 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

AAw_Rayong : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

AAw_Chanthab: ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

AAw_Mukdahan: ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

M_rubra_Sala: ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

AAw_UP25 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

AAw_UP37 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

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M_x_rubra_Sa: ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

AAw_Salaween: ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

M.terminiflo: ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

AAw_LN20 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 328

AAw_MaeYom : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

AAw_NW22 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT-

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AAw_NW33 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT-

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AAw_NW38 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT-

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AAw_NW41 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT-

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AAw_PH04 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT-

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AAw_PH05 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT-

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AAw_TL18 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT-

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AAw_UP36 :

ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTTTTCGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC

: 330

AAw_Chanthab: ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

AAw_Chanthab: ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

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AAw_Chanthab: ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

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AAw_Chanthab: ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

AAw_Kanchana: ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT-

TCGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 331

AAw_Kanchana: ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT-

TCGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 331

AAw_Kanchana: ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT-

TCGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 331

AAw_Trang1 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

AAw_Trang2 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

AAw_Trang3 : ACCTTTTTGGTTGCTTTGTTTATACTTTTTTTT--

CGTTTTGCGGGATGTCTGGAATTCATTACTTGTATCCTATTCTTAGTAATAGACAATAGACATACAAAGAAAGAGAATACAGAGCAAGGATGGGAAAAATGAAAGAAAGAAATCCTTTTAGGAGGGATTACTAGTCTTACGAGTC : 330

* 1100 * 1120 * 1140 * 1160 * 1180 * 1200 * 1220 * 1240 * 1260

AAw_Ranong :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A :1258

AAw_Yala :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A :1258

M_laterita :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A :1258

AAw_Trang :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A :1258

AAw_Prachuab:

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A :1258

AAw_MW10 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_MW20 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_MW31 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_UP16 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_UP18 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_Rayong :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_Chanthab:

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_Mukdahan:

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

M_rubra_Sala:

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_UP25 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_UP37 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

M_x_rubra_Sa:

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_Salaween:

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

M.terminiflo:

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_LN20 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 508

AAw_MaeYom :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_NW22 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 509

AAw_NW33 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 509

AAw_NW38 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 511

AAw_NW41 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 509

AAw_PH04 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 511

AAw_PH05 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 511

AAw_TL18 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 511

AAw_UP36 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_Chanthab:

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_Chanthab:

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_Chanthab:

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_Chanthab:

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

AAw_Kanchana:

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 511

AAw_Kanchana:

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 511

AAw_Kanchana:

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A : 511

AAw_Trang1 :

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A : 510

AAw_Trang2 :

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A : 510

AAw_Trang3 :

TTCTATTCGACACAAGAAAAGGGCGGAAAATCCTTTTTCTTGTGTCGTCTTATATCGAAATAATAATGATTTTTTCTCCTGTTCGTCAAAGATTACCATTCCTTCTTTTCCGGGTCCACCAGAACTCTTTTGGTTAGATTCATAGGAAGTTGTGGACAAACAAAAAGAGAGAAAGGATT

A : 510

* 1280 * 1300 * 1320 * 1340 * 1360 * 1380 * 1400 * 1420 * 1440

AAw_Ranong : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T :1418

AAw_Yala : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T :1418

M_laterita : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T :1418

AAw_Trang : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T :1418

AAw_Prachuab: GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T :1418

AAw_MW10 : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T : 670

AAw_MW20 : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T : 670

AAw_MW31 : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T : 670

AAw_UP16 : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T : 670

AAw_UP18 : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T : 670

AAw_Rayong : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T : 670

AAw_Chanthab: GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T : 670

AAw_Mukdahan: GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T : 670

M_rubra_Sala: GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T : 670

AAw_UP25 : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T : 670

AAw_UP37 : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T : 670

M_x_rubra_Sa: GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T : 670

AAw_Salaween: GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T :
670

M.terminiflo: GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T : 670

AAw_LN20 : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATGA--------------------T :
668

AAw_MaeYom : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATGA--------------------T :
670

AAw_NW22 :
GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTAGTAGTTTAGTATAGAAATGAT :
689

AAw_NW33 :
GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTAGTAGTTTAGTATAGAAATGAT :
689

AAw_NW38 :
GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTAGTAGTTTAGTATAGAAATGAT :
691

AAw_NW41 :
GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTAGTAGTTTAGTATAGAAATGAT :
689

AAw_PH04 :
GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTAGTAGTTTAGTATAGAAATGAT :
691

AAw_PH05 :
GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTAGTAGTTTAGTATAGAAATGAT :
691

AAw_TL18 :
GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTAGTAGTTTAGTATAGAAATGAT :
691

AAw_UP36 : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATGA--------------------T :
670

AAw_Chanthab: GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T :
670

AAw_Chanthab: GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T :
670

AAw_Chanthab: GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T :
670

AAw_Chanthab: GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T :
670

AAw_Kanchana:
GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTAGTAGTTTAGTATAGAAATGAT :
691

AAw_Kanchana:
GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTAGTAGTTTAGTATAGAAATGAT :
691

AAw_Kanchana:
GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTAGTAGTTTAGTATAGAAATGAT :
691

AAw_Trang1 : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T :
670

AAw_Trang2 : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAAATTA--------------------T :
670

AAw_Trang3 : GGGGAATAATTGATTGAGCAAATAGAACTTCTTCAATTAACTTAAACTTTTAACTTAGAGAAATTATTCAAGAGAAATTATTCAAACAAATTATATTATAGAGTTTTATAGAGTAAGTTCTATAGAGTAAGTTCTATTAGTAGTTTAGTATAGAA--
TAGTAGTTTAGTATAGAAATTAT : 688

* 1460 * 1480 * 1500 * 1520 * 1540 * 1560 * 1580 * 1600 * 1620

AAw_Ranong :
TTGCAGGATGTCTCATGCGTAGAAATCTATATAATATTGTATTATTCAGAAAATCCATTGATTACTCTTTTCTTGTTTCTTCATAAGAGTTAATATTATGGAGGAAAGGAAGAACAGAGACTATGAATCAATCAATAGATTCAATTCTTCAAAAACATTATTAAGAAACAAAAGAATAGA
:1598

AAw_Yala :
TTGCAGGATGTCTCATGCGTAGAAATCTATATAATATTGTATTATTCAGAAAATCCATTGATTACTCTTTTCTTGTTTCTTCATAAGAGTTAATATTATGGAGGAAAGGAAGAACAGAGACTATGAATCAATCAATAGATTCAATTCTTCAAAAACATTATTAAGAAACAAAAGAATAGA
:1598

M_laterita :
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:1598

AAw_Trang :

TTGCAGGATGTCTCATGCGTAGAAATCTATATAATATTGTATTATTCAGAAAATCCATTGATTACTCTTTTCTTGTTTCTTCATAAGAGTTAATATTATGGAGGAAAGGAAGAACAGAGACTATGAATCAATCAATAGATTCAATTCTTCAAAAACATTATTAAGAAACAAAAGAATAGA

:1598

AAw_Prachuab:

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850

AAw_MW20 :

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850

AAw_MW31 :

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850

AAw_UP16 :

TTGCAGGATGTCTCATGCGTAGAAATCTATATAATATTGTATTATTCAGAAAATCCATTGATTACTCTTTTCTTGTTTCTTCATAAGAGTTAATATTATGGAGGAAAGGAAGAACAGAGACTATGAATCAATCAATAGATTCAATTCTTCAAAAACATTATTAAGAAACAAAAGAATAGA :

850

AAw_UP18 :

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850

AAw_Rayong :

TTGCAGGATGTCTCATGCGTAGAAATCTATATAATATTGTATTATTCAGAAAATCCATTGATTACTCTTTTCTTGTTTCTTCATAAGAGTTAATATTATGGAGGAAAGGAAGAACAGAGACTATGAATCAATCAATAGATTCAATTCTTCAAAAACATTATTAAGAAACAAAAGAATAGA :

850

AAw_Chanthab:

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850

AAw_Mukdahan:

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850

M_rubra_Sala:

TTGCAGGATGTCTCATGCGTAGAAATCTATATAATATTGTATTATTCAGAAAATCCATTGATTACTCTTTTCTTGTTTCTTCATAAGAGTTAATATTATGGAGGAAAGGAAGAACAGAGACTATGAATCAATCAATAGATTCAATTCTTCAAAAACATTATTAAGAAACAAAAGAATAGA :

850

AAw_UP25 :
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850

AAw_UP37 :
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850

M_x_rubra_Sa:
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850

AAw_Salaween:
TTGCAGGATGTCTCATGCGTAGAAATCTATATAATATTGTATTATTCAGAAAATCCATTGATTACTCTTTTCTTGTTTCTTCATAAGAGTTAATATTATGGAGGAAAGGAAGAACAGAGACTATGAATCAATCAATAGATTCAATTCTTCAAAAACATTATTAAGAAACAAAAGAATAGA :
850

M.terminiflo:
TTGCAGGATGTCTCATGCGTAGAAATCTATATAATATTGTATTATTCAGAAAATCCATTGATTACTCTTTTCTTGTTTCTTCATAAGAGTTAATATTATGGAGGAAAGGAAGAACAGAGACTATGAATCAATCAATAGATTCAATTCTTCAAAAACATTATTAAGAAACAAAAGAATAGA :
850

AAw_LN20 :
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848

AAw_MaeYom :
TTGCAGGATGTCTCATGCGTAGAAATCTATATAATATTGTATTATTCAGAAAATCCATTGATTACTCTTTTCTTGTTTCTTCATAAGAGTTAATATTATGGAGGAAAGGAAGAACAGAGACTATGAATCAATCAATAGATTCAATTCTTCAAAAACATTATTAAGAAACAAAAGAATAGA :
850

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869

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869

AAw_NW38 :
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871

AAw_NW41 :
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869

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871

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871

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850

AAw_Chanthab:
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850

AAw_Chanthab:
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850

AAw_Chanthab:
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850

AAw_Chanthab:
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850

AAw_Kanchana:
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871

AAw_Kanchana:
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871

AAw_Kanchana:
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871

AAw_Trang1 :

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850

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AAw_Trang3 :

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868

* 1640 * 1660 * 1680 * 1700 * 1720 * 1740 * 1760 * 1780 * 1800

AAw_Ranong : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

TCGCTCTAATTAGACAAAGGAGGGT :1772

AAw_Yala : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

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M_laterita : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTACCCTCCTTTGTCTAATTAGA------

GCGAT :1772

AAw_Trang : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTACCCTCCTTTGTCTAATTAGA---

---GCGAT :1772

AAw_Prachuab: GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

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AAw_MW10 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTACCCTCCTTTGTCTAATTAGA--

----GCGAT :1024

AAw_MW20 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTACCCTCCTTTGTCTAATTAGA--

----GCGAT :1024

AAw_MW31 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTACCCTCCTTTGTCTAATTAGA--

----GCGAT :1024

AAw_UP16 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTACCCTCCTTTGTCTAATTAGA---

---GCGAT :1024

AAw_UP18 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTACCCTCCTTTGTCTAATTAGA---

---GCGAT :1024

AAw_Rayong : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTACCCTCCTTTGTCTAATTAGA--

----GCGAT :1024

AAw_Chanthab: GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

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AAw_Mukdahan: GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

TCGCTCTAATTAGACAAAGGAGGGT :1024

M_rubra_Sala: GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTACCCTCCTTTGTCTAATTAGA---

---GCGAT :1024

AAw_UP25 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

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TCGCTCTAATTAGACAAAGGAGGGT :1024

M_x_rubra_Sa: GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

TCGCTCTAATTAGACAAAGGAGGGT :1024

AAw_Salaween: GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

TCGCTCTAATTAGACAAAGGAGGGT :1024

M.terminiflo: GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

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AAw_LN20 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

TCGCTCTAATTAGACAAAGGAGGGT :1022

AAw_MaeYom : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

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AAw_NW22 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

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AAw_NW33 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

TCGCTCTAATTAGACAAAGGAGGGT :1043

AAw_NW38 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

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AAw_NW41 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

TCGCTCTAATTAGACAAAGGAGGGT :1043

AAw_PH04 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

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AAw_PH05 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

TCGCTCTAATTAGACAAAGGAGGGT :1045

AAw_TL18 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------

TCGCTCTAATTAGACAAAGGAGGGT :1045

AAw_UP36 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------
TCGCTCTAATTAGACAAAGGAGGGT :1024
AAw_Chanthab: GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------
TCGCTCTAATTAGACAAAGGAGGGT :1024
AAw_Chanthab: GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------
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AAw_Chanthab: GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------
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AAw_Chanthab: GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------
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AAw_Kanchana: GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------
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AAw_Kanchana: GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------
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AAw_Trang1 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------
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AAw_Trang2 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------
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AAw_Trang3 : GTGGTTTGAAACATCAGAGCAAAGGATCCGTTTTGTCATTTCATTTCTACGAATATAATATTTTGATTATGTTGACTGGCCAATTTGTATGTTATGGAATAGATCATAATCTTCCTATAAGAGTAAGAAAAGAACTCAACGGGACCTTA------
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* 1820 * 1840 * 1860 * 1880 * 1900 * 1920 * 1940 * 1960 * 1980

AAw_Ranong :
AAGGTCCCGTTGAGTTCTTTTCTTACTCTTTCATGTCTACAATCCGGTTTATCCGATTACTAGAGAGATGAACCCAACCCAGAATATGAACCGTAAAAGAAAACACCTATTAAACCGATCACAGGAATACCAGTTACAGTACCAACCAGCCAAAGAGGAATCCTTCCAGTAGTATC
GGCC :1952
AAw_Yala :
AAGGTCCCGTTGAGTTCTTTTCTTACTCTTTCATGTCTACAATCCGGTTTATCCGATTACTAGAGAGATGAACCCAACCCAGAATATGAACCGTAAAAGAAAACACCTATTAAACCGATCACAGGAATACCAGTTACAGTACCAACCAGCCAAAGAGGAATCCTTCCAGTAGTATC
GGCC :1952
M_laterita :
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AAw_Trang :

AAGGTCCCGTTGAGTTCTTTTCTTACTCTTTCATGTCTACAATCCGGTTTATCCGATTACTAGAGAGATGAACCCAACCCAGAATATGAACCGTAAAAGAAAACACCTATTAAACCGATCACAGGAATACCAGTTACAGTACCAACCAGCCAAAGAGGAATCCTTCCAGTAGTATC

GGCC :1952

AAw_Prachuab:

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GGCC :1952

AAw_MW10 :

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GGCC :1204

AAw_UP16 :

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AAw_PH05 : AACCCCAGTATAGACTGGTACGATTCAATTCAACATTTTGTTCATTCGGGTTTGATTGTGTCATAGCTCTATAATTCAAATTAGGTTTATCGTTG :1500

AAw_TL18 : AACCCCAGTATAGACTGGTACGATTCAATTCAACATTTTGTTCATTCGGGTTTGATTGTGTCATAGCTCTATAATTCAAATTAGGTTTATCGTTG :1500

AAw_UP36 : AACCCCAGTATAGACTGGTACGATTCAATTCAACATTTTGTTCATTCGGGTTTGATTGTGTCATAGCTCTATAATTCAAATTAGGTTTATCGTTG :1479

AAw_Chanthab: AACCCCAGTATAGACTGGTACGATTCAATTCAACATTTTGTTCATTCGGGTTTGATTGTGTCATAGCTCTATMATTCAAATTAGGTTTATCGTTG :1479

AAw_Chanthab: AACCCCAGTATAGACTGGTACGATTCAATTCAACATTTTGTTCATTCGGGTTTGATTGTGTCATAGCTCTATMATTCAAATTAGGTTTATCGTTG :1479

AAw_Chanthab: AACCCCAGTATAGACTGGTACGATTCAATTCAACATTTTGTTCATTCGGGTTTGATTGTGTCATAGCTCTATMATTCAAATTAGGTTTATCGTTG :1479

AAw_Chanthab: AACCCCAGTATAGACTGGTACGATTCAATTCAACATTTTGTTCATTCGGGTTTGATTGTGTCATAGCTCTATMATTCAAATTAGGTTTATCGTTG :1479

AAw_Kanchana: AACCCCAGTATAGACTGGTACGATTCAATTCAACATTTTGTTCATTCGGGTTTGATTGTGTCATAGCTCTATCATTCAAATTAGGTTTATCGTTG :1500

AAw_Kanchana: AACCCCAGTATAGACTGGTACGATTCAATTCAACATTTTGTTCATTCGGGTTTGATTGTGTCATAGCTCTATMATTCAAATTAGGTTTATCGTTG :1500

AAw_Kanchana: AACCCCAGTATAGACTGGTACGATTCAATTCAACATTTTGTTCATTCGGGTTTGATTGTGTCATAGCTCTATAATTCAAATTAGGTTTATCGTTG :1500

AAw_Trang1 : AACCCCAGTATAGACTGGTACGATTCAATTCAACATTTTGTTCATTCGGGTTTGATTGTGTCATAGCTCTATMATTCAAATTAGGTTTATCGTTG :1479

AAw_Trang2 : AACCCCAGTATAGACTGGTACGATTCAATTCAACATTTTGTTCATTCGGGTTTGATTGTGTCATAGCTCTATAATTCAAATTAGGTTTATCGTTG :1479

AAw_Trang3 : AACCCCAGTATAGACTGGTACGATTCAATTCAACATTTTGTTCATTCGGGTTTGATTGTGTCATAGCTCTATMATTCAAATTAGGTTTATCGTTG :1497

Primer: *psa*A

* 20 * 40 * 60 * 80 * 100 * 120

AAw_Ranong : taggttccagatccaagtggtagtatcagggcccttagctattgttcttgagaaatggccgggtctggcccattcctcgaaagacgtttttatgggatccctatctacaacaattttcactt : 122

AAw_Yala : taggttccagatccaagtggtagtatcagggcccttagctattgttcttgagaaatggccgggtctggcccattcctcgaaagacgtttttatgggatccctatctacaacaattttcactt : 122

M_laterita : taggttccagatccaagtggtagtatcagggcccttagctattgttcttgagaaatggccgggtctggcccattcctcgaaagacgtttttatgggatccctatctacaacaattttcactt : 122

AAw_Trang : taggttccagatccaagtggtagtatcagggcccttagctattgttcttgagaaatggccgggtctggcccattcctcgaaagacgtttttatgggatccctatctacaacaattttcactt : 122

AAw_Prachuab : taggttccagatccaagtggtagtatcagggcccttagctattgttcttgagaaatggccgggtctggcccattcctcgaaagacgtttttatgggatccctatctacaacaattttcactt : 122

MW10-Musa-ps : -- : -

MW20-Musa-ps : -- : -

MW31-Musa-ps : -- : -

UP16-Musa-ps : -- : -

UP18-Musa-ps : -- : -

Aaw_Rayong : taggttccagatccaagtggtagtatcagggcccttagctattgttcttgagaaatggccgggtctggcccattcctcgaaagacgtttttatgggatccctatctacaacaattttcactt : 122

Aaw_Chanthab : taggttccagatccaagtggtagtatcagggcccttagctattgttcttgagaaatggccgggtctggcccattcctcgaaagacgtttttatgggatccctatctacaacaattttcactt : 122

Aaw_Mukdahan : taggttccagatccaagtggtagtatcagggcccttagctattgttcttgagaaatggccgggtctggcccattcctcgaaagacgtttttatgggatccctatctacaacaattttcactt : 122

M.laterita_S : taggttccagatccaagtggtagtatcagggcccttagctattgttcttgagaaatggccgggtctggcccattcctcgaaagacgtttttatgggatccctatctacaacaattttcactt : 122

UP25-Musa-ps : -- :   -

UP37-Musa-ps : -- :   -

M_x_laterita : taggttccagatccaagtggtagtatcagggcccttagctattgttcttgagaaatggccgggtctggcccattcctcgaaagacgtttttatgggatccctatctacaacaattttcactt : 122

Aaw_Salaween : taggttccagatccaagtggtagtatcagggcccttagctattgttcttgagaaatggccgggtctggcccattcctcgaaagacgtttttatgggatccctatctacaacaattttcactt : 122

M.terminiflo : taggttccagatccaagtggtagtatcagggcccttagctattgttcttgagaaatggccgggtctggcccattcctcgaaagacgtttttatgggatccctatctacaacaattttcactt : 122

LN20-Musa-ps : -- :   -

Aaw_MaeYom   : taggttccagatccaagtggtagtatcagggcccttagctattgttcttgagaaatggccgggtctggcccattcctcgaaagacgtttttatgggatccctatctacaacaattttcactt : 122

NW22-Musa-ps : -- :   -

NW33-Musa-ps : -- :   -

NW38-Musa-ps : -- :   -

NW41-Musa-ps : -- :   -

PH4-Musa-psa : -- :   -

PH5-Musa-psa : -- :   -

TL18-Musa-ps : -- :   -

UP36-Musa-ps : -- :   -

AAw_Chanthab : -- :   -

AAw_Chanthab : -- :   -

AAw_Chanthab : -- :   -

AAw_Chanthab : -- :   -

AAw_Kanchana : -- :   -

AAw_Kanchana : -- :   -

AAw_Kanchana : -- :   -

AAw_Trang1   : -- :   -

AAw_Trang2   : -- :   -

AAw_Trang3   : -- :   -

                    *   140   *   160   *   180   *   200   *   220   *   240

AAw_Ranong   : ctggttccggcgaacgaataatcattaagtcctcctctttccggacaacacatacaaagagacccgccaacagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 244

AAw_Yala   : ctggttccggcgaacgaataatcattaagtcctcctctttccggacaacacatacaaagagacccgccaacagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 244

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AAw_Trang   : ctggttccggcgaacgaataatcattaagtcctcctctttccggacaacacatacaaagagacccgccaacagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 244

AAw_Prachuab : ctggttccggcgaacgaataatcattaagtcctcctctttccggacaacacatacaaagagacccgccaacagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 244

MW10-Musa-ps : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

MW20-Musa-ps : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

MW31-Musa-ps : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

UP16-Musa-ps : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

UP18-Musa-ps : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

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UP25-Musa-ps : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

UP37-Musa-ps : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

M_x_laterita : ctggttccggcgaacgaataatcattaagtcctcctctttccggacaacacatacaaagagacccgccaacagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 244

Aaw_Salaween : ctggttccggcgaacgaataatcattaagtcctcctctttccggacaacacatacaaagagacccgccaacagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 244

M.terminiflo : ctggttccggcgaacgaataatcattaagtcctcctctttccggacaacacatacaaagagacccgccaacagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 244

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NW22-Musa-ps : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

NW33-Musa-ps : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

NW38-Musa-ps : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

NW41-Musa-ps : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

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UP36-Musa-ps : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

AAw_Chanthab : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

AAw_Chanthab : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

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AAw_Kanchana : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

AAw_Trang1   : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

AAw_Trang2   : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

AAw_Trang3   : --cagtttttagtgaacctctgaaagatagctattttatttatgttatgattag : 52

*   260   *   280   *   300   *   320   *   340   *   360

AAw_Ranong   : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 366

AAw_Yala   : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 366

M_laterita   : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 366

AAw_Trang   : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 366

AAw_Prachuab : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 366

MW10-Musa-ps : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 174

MW20-Musa-ps : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 174

MW31-Musa-ps : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 174

UP16-Musa-ps : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 174

UP18-Musa-ps : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 174

Aaw_Rayong   : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 366

Aaw_Chanthab : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 366

Aaw_Mukdahan : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 366

M.laterita_S : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 366

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UP37-Musa-ps : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 174

M_x_laterita : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 366

Aaw_Salaween : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 366

M.terminiflo : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 366

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NW22-Musa-ps : tccctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 174

NW33-Musa-ps : tccctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 174

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NW41-Musa-ps : tccctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 174

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AAw_Trang3 : tacctttctttcctatctcccatccatctattttatttagttattcactagagcaattatgatattgaagtcaatccgaggcaagtgttcggatctattatgacataacgattaggtgccca : 174

* 380 * 400 * 420 * 440 * 460 * 480

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AAw_Yala : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactattttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttccaataccta : 488

M_laterita : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactattttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttccaataccta : 488

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MW31-Musa-ps : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactattttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttccaataccta : 296

UP16-Musa-ps : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactattttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttccaataccta : 296

UP18-Musa-ps : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactattttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttccaataccta : 296

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UP37-Musa-ps : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactatttttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttccaatacctа : 296

M_x_laterita : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactatttttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttccaatacctа : 488

Aaw_Salaween : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactatttttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttccaatacctа : 488

M.terminiflo : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactatttttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttccaatacctа : 488

LN20-Musa-ps : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactatttttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttcca------- : 289

Aaw_MaeYom : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactatttttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttcca------- : 481

NW22-Musa-ps : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactatttttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttcca------- : 289

NW33-Musa-ps : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactatttttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttcca------- : 289

NW38-Musa-ps : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactatttttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttcca------- : 289

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PH5-Musa-psa : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactatttttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttcca------- : 289

TL18-Musa-ps : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactatttttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttcca------- : 289

UP36-Musa-ps : acggaccccttttctcttggaaagtcctttcccagcatgacgaaaaaactatttttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttcca------- : 289

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AAw_Trang1 : acggacccctttctcttggaaagtcctttcccagcatgacgaaaaaactattttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttccaatacccta : 296

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AAw_Trang3 : acggacccctttctcttggaaagtcctttcccagcatgacgaaaaaactattttttgtgcaaactagtgtacttatatctgaatgtataaatacctatatgaatctacttccaatacccta : 296

* 500 * 520 * 540 * 560 * 580 * 600 *

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AAw_Yala : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 587

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AAw_Prachuab : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 587

MW10-Musa-ps : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 395

MW20-Musa-ps : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 395

MW31-Musa-ps : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 395

UP16-Musa-ps : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 395

UP18-Musa-ps : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 395

Aaw_Rayong : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 587

Aaw_Chanthab : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 587

Aaw_Mukdahan : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 587

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UP25-Musa-ps : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 395

UP37-Musa-ps : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 395

M_x_laterita : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 587

Aaw_Salaween : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 587

M.terminiflo : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 587

LN20-Musa-ps : ---------------------------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 372

Aaw_MaeYom : ---------------------------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 564

NW22-Musa-ps : ---------------------------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 372

NW33-Musa-ps : ---------------------------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 372

NW38-Musa-ps : ---------------------------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 372

NW41-Musa-ps : ---------------------------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 372

PH4-Musa-psa : ---------------------------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 372

PH5-Musa-psa : ---------------------------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 372

TL18-Musa-ps : ---------------------------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 372

UP36-Musa-ps : ---------------------------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 372

AAw_Chanthab : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 395

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AAw_Kanchana : ---------------------------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 372

AAw_Kanchana : ---------------------------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 372

AAw_Kanchana : ---------------------------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 372

AAw_Trang1 : tatgaatctacttccaatacctatatgaatctacttccatggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 418

AAw_Trang2 : tatgaatctacttccaatacctatatgaatctacttccatggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 418

AAw_Trang3 : tatgaatctacttcca-----------------------tggaatatcttattactttactctaaattaaatcacaagaccattcattagaattaataagatccattcctatatcttatctg : 395

620 * 640 * 660 * 680 * 700 * 720 *

AAw_Ranong : tatttagtcattcgaaggtaccttttattagctttattagttttattctatactgtattcggatcatttatccctacgagataccatacaatgattttagaaggaagggatataataaaatt : 709

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NW22-Musa-ps : tatttagtcattcgaaggtaccttttattagctttattagttttattctatactgtattcggatcatttatccctacgagataccatacaatgattttagaaggaagggatataataaaatt : 494

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740 * 760 * 780 * 800 * 820 * 840 *

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MW10-Musa-ps : cttgattggatcttttcatgggaacgatctattttatttgattgatggatccaacaactaattttaatgaattaaaaaagagagtggttttattcgaaacgcctcgtgatcttcaaccaatt : 639

MW20-Musa-ps : cttgattggatcttttcatgggaacgatctattttatttgattgatggatccaacaactaattttaatgaattaaaaaagagagtggttttattcgaaacgcctcgtgatcttcaaccaatt : 639

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UP37-Musa-ps : cttgattggatcttttcatgggaacgatctattttatttgattgatggatccaacaactaattttaatgaattaaaaaagagagtggttttattcgaaacgcctcgtgatcttcaaccaatt : 639

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Aaw_MaeYom : cttgattggatcttttcatgggaacgatctattttatttgattgatggatccaacaactaattttaatgaattaaaaaagagagtggttttattcgaaacgcctcgtgatcttcaaccaatt : 808

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Primer: *rpl*16

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M_laterita: cgttaatttttctttagagtttagagttggaattaaaaaaaaa-tagactaaaccctacttaaacttaataactatataaaataaataaaaacaaaaataaaaacaaaataaactaataaccaac : 124

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UP18 : cgttaatttttctttagagtttagagttggaattaaaaaaaaa-tagactaaaccctacttaaacttaataactatataaaataaataaaaacaaaaataaaaacaaaataaactaataaccaac : 124

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UP25 : cgttaatttttctttagagtttagagttggaattaaaaaaaaa-tagactaaaccctacttaaacttaataactatataaaataaataaaaacaaaaataaaaacaaaataaactaataaccaac : 124

UP37 : cgttaatttttctttagagtttagagttggaattaaaaaaaaa-tagactaaaccctacttaaacttaataactatataaaataaataaaaacaaaaataaaaacaaaataaactaataaccaac :
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PH5 : cgttaatttttctttagagtttagagttggaattaaaaaaaaa-tagactaaaccctacttaaacttaataactatataaaataaataaaaacaaaaataaaaacaaaataaactaataaccaac : 124

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UP36 : cgttaatttttctttagagtttagagttggaattaaaaaaaaa-tagactaaaccctacttaaacttaataactatataaaataaataaaaacaaaaataaaaacaaaataaactaataaccaac :
124

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AAw_Chanth: --- : -

AAw_Chanth: --- : -

AAw_Chanth: --- : -

AAw_Kancha: --- : -

AAw_Kancha: --- : -

AAw_Kancha: --- : -

AAw_Trang1: --- : -

AAw_Trang2: --- : -

AAw_Trang3: --- : -

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                *       140        *       160        *       180        *       200        *       220        *       240        *
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AAw_Chanth: -- : -

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AAw_Chanth: -- : -

AAw_Kancha: -- : -

AAw_Kancha: -- : -

AAw_Kancha: -- : -

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AAw_Trang2: -- : -

AAw_Trang3: -- : -

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AAw_Yala :

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M_laterita:

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AAw_Kancha: -- : -

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380 * 400 * 420 * 440 * 460 * 480 * 500

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* 640 * 660 * 680 * 700 * 720 * 740 *

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749

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749

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749

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760 * 780 * 800 * 820 * 840 * 860 *

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880 * 900 * 920 * 940 * 960 * 980 * 1000

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* 1020 * 1040

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UP18 : aacgaccatcaactataaccccaaaagaaccagatttcgt :1032

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AAw_Salawe: aacgaccatcaactataaccccaaaagaaccagatttcgt :1032

M_terminif: aacgaccatcaactataaccccaaaagaaccagatttcgt :1032

LN20 : aacgaccatcaactataaccccaaaagaaccagatttcgt :1032

AAw_MaeYom: aacgaccatcaactataaccccaaaagaaccagatttcgt :1032

NW22 : aacgaccatcaactataaccccaaaagaaccagatttcgt :1032

NW33 : aacgaccatcaactataaccccaaaagaaccagatttcgt :1032

NW38 : aacgaccatcaactataaccccaaaagaaccagatttcgt :1032

NW41 : aacgaccatcaactataaccccaaaagaaccagatttcgt :1032

PH4 : aacgaccatcaactataaccccaaaagaaccagatttcgt :1032

PH5 : aacgaccatcaactataaccccaaaagaaccagatttcgt :1032

TL18 : aacgaccatcaactataaccccaaaagaaccagatttcgt :1032

UP36 : aacgaccatcaactataaccccaaaagaaccagatttcgt :1032

AAw_Chanth: aacgaccatcaactataaccccaaaagaaccagatttcgt : 652

AAw_Chanth: aacgaccatcaactataaccccaaaagaaccagatttcgt : 652

AAw_Chanth: aacgaccatcaactataaccccaaaagaaccagatttcgt : 645

AAw_Chanth: aacgaccatcaactataaccccaaaagaaccagatttcgt : 645

AAw_Kancha: aacgaccatcaactataaccccaaaagaaccagatttcgt : 645

AAw_Kancha: aacgaccatcaactataaccccaaaagaaccagatttcgt : 645

AAw_Kancha: aacgaccatcaactataaccccaaaagaaccagatttcgt : 645

AAw_Trang1: aacgaccatcaactataaccccaaaagaaccagatttcgt : 645

AAw_Trang2: aacgaccatcaactataaccccaaaagaaccagatttcgt : 645

AAw_Trang3: aacgaccatcaactataaccccaaaagaaccagatttcgt : 645

Tue Aug 29 14:02:38 GMT+07:00 2006

Datafile = F:\M_acuminata 4CP sequential.phy

Current OS = windows

Data in PHYLIP format

Number of sequences: 59

Length of sequences: 4333

PARSIMONY PROBABILITY

For 1 step(s), P(95%) = 0.9999932608050639

For 2 step(s), P(95%) = 0.9994874120992333

For 3 step(s), P(95%) = 0.998961200055099

For 4 step(s), P(95%) = 0.998410029646588

For 5 step(s), P(95%) = 0.9978130476697491

For 6 step(s), P(95%) = 0.997139900035412

For 7 step(s), P(95%) = 0.9963581477108122

For 8 step(s), P(95%) = 0.9954484528191389

For 9 step(s), P(95%) = 0.9944113542256892

For 10 step(s), P(95%) = 0.993256721282826

For 11 step(s), P(95%) = 0.9919913250792001

For 12 step(s), P(95%) = 0.9906160988935392

For 13 step(s), P(95%) = 0.9891293544424316

For 14 step(s), P(95%) = 0.9875298854281941

For 15 step(s), P(95%) = 0.9858178480835399

For 16 step(s), P(95%) = 0.9839941743607433

For 17 step(s), P(95%) = 0.9820598381461925

For 18 step(s), P(95%) = 0.9800155811363435

For 19 step(s), P(95%) = 0.9778619993565237

For 20 step(s), P(95%) = 0.9755997006380325

For 21 step(s), P(95%) = 0.9732293784029457

For 22 step(s), P(95%) = 0.9707518041026538

For 23 step(s), P(95%) = 0.9681677955221303

For 24 step(s), P(95%) = 0.965478198060437

For 25 step(s), P(95%) = 0.9626838831764848

For 26 step(s), P(95%) = 0.959785753617049

For 27 step(s), P(95%) = 0.9567847470900475

For 28 step(s), P(95%) = 0.9536818365243195

For 29 step(s), P(95%) = 0.9504780286044112

For 30 step(s), P(95%) = 0.9471743623402479

RUN SETTINGS

Calculated maximum connection steps at 95% = 29

Gaps treated as fifth state

HAPLOTYPES

Number of haplotypes = 33

Haplotype list :

- M_schizoca :
- AAw_Buiten :
- ABB_KHakMu :
- AAw_Cepu :
- AAw_Ranong :
- AAA-HomTho :
- AAw_Yala :
- AAw_trunca : AAw_Prachu AAw_3Chant AAA_Roning AA_P_oli
- AA_KluayKh : AAw_Mukdah AAw_4Chant
- AAB_NgaaCh :
- AA_Gwanhou :
- AAw_banksi :
- ABB_HinA :
- AB_Auko_IT :
- AAw_Pai :

- AAw_Trang :
- AAw_Rayong :
- AAw_Chanth :
- AAw_MaeYom : AAw_LN20
- M_rubra_Sa : AAw_MW10 AAw_MW20 AAw_MW31 AAw_UP16 AAw_UP18 M_rubra_Ku
- M_x_rubra_ : AAw_Salawe AAw_UP25 AAw_UP37
- AAw_NW22 : AAw_NW33 AAw_NW38 AAw_NW41 AAw_PH04 AAw_PH05 AAw_TL18

AAw_1Kanch AAw_3Kanch

- AAw_UP36 :
- AAw_1Chant :
- AAw_2Chant :
- AAw_2Kanch :
- AAw_Trang1 : AAw_Trang2
- AAw_Trang3 :
- A(A)B_Chen :
- AA_P_mas_S :
- ABB_Sulawe : AAB_P_tand
- AAw_Sulawe :
- AAw_zebrin :

CONNECTIONS

adding two min taxa 15[AAw_Trang] , 10[AA_Gwanhou]

In clusters 27, 31 distance 2

adding two min taxa 28[A(A)B_Chen] , 17[AAw_Chanth]

In clusters 2, 27 distance 4

adding two min taxa 32[AAw_zebrin] , 3[AAw_Cepu]

In clusters 1, 2 distance 5

adding two min taxa 32[AAw_zebrin] , 28[A(A)B_Chen]

In clusters 1, 2 distance 5

EAL DISTANCE MATRIX

pos :1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
31 32 33

[M_schizoca]1 : -- 29 29 28 26 24 25 23 25 25 24 23 24 28 24 24 24 24 21 22 25 22 21 25 24 23 24 25
28 26 24 26 28

[AAw_Buiten]2 : 29 -- 7 6 12 10 11 9 11 11 10 9 10 14 16 10 10 10 13 8 11 14 15 11 10 15 10 11 6
12 10 14 1

[ABB_KHakMu]3 : 29 7 -- 1 9 7 8 6 6 8 7 6 9 13 11 7 7 5 8 7 6 11 12 8 7 12 7 8 1 7 7 9 6

[AAw_Cepu]4 : 28 6 1 -- 8 6 7 5 7 9 8 7 8 12 12 8 8 6 9 6 7 10 11 7 6 11 6 7 2 8 8 10 5

[AAw_Ranong]5 : 26 12 9 8 -- 4 5 3 5 9 8 7 8 12 8 6 6 4 7 4 5 8 9 5 4 9 4 5 8 6 8 10 11

[AAA-HomTho]6 : 24 10 7 6 4 -- 1 1 3 7 6 5 6 10 8 4 4 2 5 2 3 6 7 3 2 7 2 3 6 4 6 8 9

[AAw_Yala]7 : 25 11 8 7 5 1 -- 2 4 8 7 6 7 11 9 5 5 3 6 3 4 7 8 4 3 8 3 4 7 5 7 9 10

[AAw_trunca]8 : 23 9 6 5 3 1 2 -- 2 6 5 4 5 9 7 3 3 1 4 1 2 5 6 2 1 6 1 2 5 3 5 7 8

[AA_KluayKh]9 : 25 11 6 7 5 3 4 2 -- 6 5 4 7 11 7 3 1 1 4 3 2 7 8 4 3 8 3 4 5 1 5 7 10

[AAB_NgaaCh]10 : 25 11 8 9 9 7 8 6 6 -- 1 2 1 5 9 3 5 5 6 5 6 9 10 8 7 10 7 8 7 7 1 7 10

[AA_Gwanhou]11 : 24 10 7 8 8 6 7 5 5 1 -- 1 2 6 8 2 4 4 5 4 5 8 9 7 6 9 6 7 6 6 2 6 9

[AAw_banksi]12 : 23 9 6 7 7 5 6 4 4 2 1 -- 3 7 7 3 3 3 4 3 4 7 8 6 5 8 5 6 5 5 1 5 8

[ABB_HinA]13 : 24 10 9 8 8 6 7 5 7 1 2 3 -- 4 10 4 6 6 7 4 7 8 9 7 6 9 6 7 8 8 2 8 9

[AB_Auko_IT]14 : 28 14 13 12 12 10 11 9 11 5 6 7 4 -- 14 8 10 10 11 8 11 12 13 11 10 13 10 11 12
12 6 12 13

[AAw_Pai]15 : 24 16 11 12 8 8 9 7 7 9 8 7 10 14 -- 8 8 6 3 8 7 8 7 9 8 9 8 9 10 8 8 10
15

[AAw_Trang]16 : 24 10 7 8 6 4 5 3 3 3 2 3 4 8 8 -- 2 2 5 2 3 8 9 5 4 9 4 5 6 4 4 8 9

[AAw_Rayong]17 : 24 10 7 8 6 4 5 3 1 5 4 3 6 10 8 2 -- 2 5 2 3 8 9 5 4 9 4 5 6 2 4 8 9

[AAw_Chanth]18 : 24 10 5 6 4 2 3 1 1 5 4 3 6 10 6 2 2 -- 3 2 1 6 7 3 2 7 2 3 4 2 4 6 9

[AAw_MaeYom]19 : 21 13 8 9 7 5 6 4 4 6 5 4 7 11 3 5 5 3 -- 5 4 5 4 6 5 6 5 6 7 5 5
7 12

[M_rubra_Sa]20 : 22 8 7 6 4 2 3 1 3 5 4 3 4 8 8 2 2 2 5 -- 3 6 7 3 2 7 2 3 6 4 4 8 7

[M_x_rubra_]21 : 25 11 6 7 5 3 4 2 2 6 5 4 7 11 7 3 3 1 4 3 -- 7 8 4 3 8 3 4 5 3 5 7 10

[AAw_NW22]22 : 22 14 11 10 8 6 7 5 7 9 8 7 8 12 8 8 8 6 5 6 7 -- 3 7 6 1 6 5 10 8 8 8 13

[AAw_UP36]23 : 21 15 12 11 9 7 8 6 8 10 9 8 9 13 7 9 9 7 4 7 8 3 -- 8 7 4 7 8 11 9 9 9
14

[AAw_1Chant]24 : 25 11 8 7 5 3 4 2 4 8 7 6 7 11 9 5 5 3 6 3 4 7 8 -- 1 8 3 4 7 5 7 9 10

[AAw_2Chant]25 : 24 10 7 6 4 2 3 1 3 7 6 5 6 10 8 4 4 2 5 2 3 6 7 1 -- 7 2 3 6 4 6 8 9

[AAw_2Kanch]26 : 23 15 12 11 9 7 8 6 8 10 9 8 9 13 9 9 9 7 6 7 8 1 4 8 7 -- 7 6 11 9 9 9
14

[AAw_Trang1]27 : 24 10 7 6 4 2 3 1 3 7 6 5 6 10 8 4 4 2 5 2 3 6 7 3 2 7 -- 3 6 4 6 8 9

[AAw_Trang3]28 : 25 11 8 7 5 3 4 2 4 8 7 6 7 11 9 5 5 3 6 3 4 5 8 4 3 6 3 -- 7 5 7 9 10

[A(A)B_Chen]29 : 28 6 1 2 8 6 7 5 5 7 6 5 8 12 10 6 6 4 7 6 5 10 11 7 6 11 6 7 -- 6 6 8 5

[AA_P_mas_S]30 : 26 12 7 8 6 4 5 3 1 7 6 5 8 12 8 4 2 2 5 4 3 8 9 5 4 9 4 5 6 -- 6 8 11

[ABB_Sulawe]31 : 24 10 7 8 8 6 7 5 5 1 2 1 2 6 8 4 4 4 5 4 5 8 9 7 6 9 6 7 6 6 -- 6 9

[AAw_Sulawe]32 : 26 14 9 10 10 8 9 7 7 7 6 5 8 12 10 8 8 6 7 8 7 8 9 9 8 9 8 9 8 8 6 -- 13

[AAw_zebrin]33 : 28 1 6 5 11 9 10 8 10 10 9 8 9 13 15 9 9 9 12 7 10 13 14 10 9 14 9 10 5
11 9 13 --

COMPUTED FROM THE NETWORK DISTANCE MATRIX

Pos : 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29
30 31 32 33

[M_schizoca]1 : -- 34 29 30 28 26 27 25 25 29 28 29 30 34 24 26 26 24 21 26 25 22 21 27 26 23 26 27 28
26 30 34 33

[AAw_Buiten]2 : 34 -- 7 6 14 12 13 11 11 15 14 15 16 20 16 12 12 10 13 12 11 18 17 13 12 19 12 13 6
12 16 20 1

[ABB_KHakMu]3 : 29 7 -- 1 9 7 8 6 6 10 9 10 11 15 11 7 7 5 8 7 6 13 12 8 7 14 7 8 1 7 11
15 6

[AAw_Cepu]4 : 30 6 1 -- 10 8 9 7 7 11 10 11 12 16 12 8 8 6 9 8 7 14 13 9 8 15 8 9 2 8
12 16 5

[AAw_Ranong]5 : 28 14 9 10 -- 4 5 3 5 9 8 9 10 14 10 6 6 4 7 4 5 12 11 5 4 13 4 5 8 6 10
14 13

[AAA-HomTho]6 : 26 12 7 8 4 -- 1 1 3 7 6 7 8 12 8 4 4 2 5 2 3 10 9 3 2 11 2 3 6 4 8 12 11

[AAw_Yala]7 : 27 13 8 9 5 1 -- 2 4 8 7 8 9 13 9 5 5 3 6 3 4 11 10 4 3 12 3 4 7 5 9 13
12

[AAw_trunca]8 : 25 11 6 7 3 1 2 -- 2 6 5 6 7 11 7 3 3 1 4 1 2 9 8 2 1 10 1 2 5 3 7 11 10

[AA_KluayKh]9 : 25 11 6 7 5 3 4 2 -- 6 5 6 7 11 7 3 1 1 4 3 2 9 8 4 3 10 3 4 5 1 7 11 10

[AAB_NgaaCh]10 : 29 15 10 11 9 7 8 6 6 -- 1 2 1 5 11 3 5 5 8 5 6 13 12 8 7 14 7 8 9 7 1 7
14

[AA_Gwanhou]11 : 28 14 9 10 8 6 7 5 5 1 -- 1 2 6 10 2 4 4 7 4 5 12 11 7 6 13 6 7 8 6 2 6
13

[AAw_banksi]12 : 29 15 10 11 9 7 8 6 6 2 1 -- 3 7 11 3 5 5 8 5 6 13 12 8 7 14 7 8 9 7 1 5 14

[ABB_HinA]13 : 30 16 11 12 10 8 9 7 7 1 2 3 -- 4 12 4 6 6 9 6 7 14 13 9 8 15 8 9 10 8 2 8 15

[AB_Auko_IT]14 : 34 20 15 16 14 12 13 11 11 5 6 7 4 -- 16 8 10 10 13 10 11 18 17 13 12 19 12 13 14 12 6 12 19

[AAw_Pai]15 : 24 16 11 12 10 8 9 7 7 11 10 11 12 16 -- 8 8 6 3 8 7 8 7 9 8 9 8 9 10 8 12 16 15

[AAw_Trang]16 : 26 12 7 8 6 4 5 3 3 3 2 3 4 8 8 -- 2 2 5 2 3 10 9 5 4 11 4 5 6 4 4 8 11

[AAw_Rayong]17 : 26 12 7 8 6 4 5 3 1 5 4 5 6 10 8 2 -- 2 5 2 3 10 9 5 4 11 4 5 6 2 6 10 11

[AAw_Chanth]18 : 24 10 5 6 4 2 3 1 1 5 4 5 6 10 6 2 2 -- 3 2 1 8 7 3 2 9 2 3 4 2 6 10 9

[AAw_MaeYom]19 : 21 13 8 9 7 5 6 4 4 8 7 8 9 13 3 5 5 3 -- 5 4 5 4 6 5 6 5 6 7 5 9 13 12

[M_rubra_Sa]20 : 26 12 7 8 4 2 3 1 3 5 4 5 6 10 8 2 2 2 5 -- 3 10 9 3 2 11 2 3 6 4 6 10 11

[M_x_rubra_]21 : 25 11 6 7 5 3 4 2 2 6 5 6 7 11 7 3 3 1 4 3 -- 9 8 4 3 10 3 4 5 3 7 11 10

[AAw_NW22]22 : 22 18 13 14 12 10 11 9 9 13 12 13 14 18 8 10 10 8 5 10 9 -- 3 11 10 1 10 11 12 10 14 18 17

[AAw_UP36]23 : 21 17 12 13 11 9 10 8 8 12 11 12 13 17 7 9 9 7 4 9 8 3 -- 10 9 4 9 10 11 9 13 17 16

[AAw_1Chant]24 : 27 13 8 9 5 3 4 2 4 8 7 8 9 13 9 5 5 3 6 3 4 11 10 -- 1 12 3 4 7 5 9 13 12

[AAw_2Chant]25 : 26 12 7 8 4 2 3 1 3 7 6 7 8 12 8 4 4 2 5 2 3 10 9 1 -- 11 2 3 6 4 8 12 11

[AAw_2Kanch]26 : 23 19 14 15 13 11 12 10 10 14 13 14 15 19 9 11 11 9 6 11 10 1 4 12 11 -- 11 12 13 11 15 19 18

[AAw_Trang1]27 : 26 12 7 8 4 2 3 1 3 7 6 7 8 12 8 4 4 2 5 2 3 10 9 3 2 11 -- 3 6 4 8 12 11

[AAw_Trang3]28 : 27 13 8 9 5 3 4 2 4 8 7 8 9 13 9 5 5 3 6 3 4 11 10 4 3 12 3 -- 7 5 9 13 12

[A(A)B_Chen]29 : 28 6 1 2 8 6 7 5 5 9 8 9 10 14 10 6 6 4 7 6 5 12 11 7 6 13 6 7 -- 6 10 14 5

[AA_P_mas_S]30 : 26 12 7 8 6 4 5 3 1 7 6 7 8 12 8 4 2 2 5 4 3 10 9 5 4 11 4 5 6 -- 8 12 11

[ABB_Sulawe]31 : 30 16 11 12 10 8 9 7 7 1 2 1 2 6 12 4 6 6 9 6 7 14 13 9 8 15 8 9 10 8 -- 6 15

[AAw_Sulawe]32 : 34 20 15 16 14 12 13 11 11 7 6 5 8 12 16 8 10 10 13 10 11 18 17 13 12 19 12 13 14 12 6 -- 19

[AAw_zebrin]33 : 33 1 6 5 13 11 12 10 10 14 13 14 15 19 15 11 11 9 12 11 10 17 16 12 11 18 11 12 5 11 15 19 --

DIFFERENCE MATRIX

Pos : 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33

[M_schizoca]1 : -- 5 0 2 2 2 2 2 2 0 4 4 6 6 6 0 2 2 0 0 4 0 0 0 2 2 0 2 2 0 0 6 8 5

[AAw_Buiten]2 : 5 -- 0 0 2 2 2 2 2 0 4 4 6 6 6 0 2 2 0 0 4 0 4 2 2 2 4 2 2 0 0 6 6 0

[ABB_KHakMu]3 : 0 0 -- 0 0 0 0 0 0 2 2 4 2 2 0 0 0 0 0 0 0 2 0 0 0 2 0 0 0 0 4 6 0

[AAw_Cepu]4 : 2 0 0 -- 2 2 2 2 0 2 2 4 4 4 0 0 0 0 0 2 0 4 2 2 2 4 2 2 0 0 4 6 0

[AAw_Ranong]5 : 2 2 0 2 -- 0 0 0 0 0 0 2 2 2 2 0 0 0 0 0 0 4 2 0 0 4 0 0 0 0 2 4 2

[AAA-HomTho]6 : 2 2 0 2 0 -- 0 0 0 0 0 2 2 2 0 0 0 0 0 0 0 4 2 0 0 4 0 0 0 0 2 4 2

[AAw_Yala]7 : 2 2 0 2 0 0 -- 0 0 0 0 2 2 2 0 0 0 0 0 0 0 4 2 0 0 4 0 0 0 0 2 4 2

[AAw_trunca]8 : 2 2 0 2 0 0 0 -- 0 0 0 2 2 2 0 0 0 0 0 0 0 4 2 0 0 4 0 0 0 0 2 4 2

[AA_KluayKh]9 : 0 0 0 0 0 0 0 0 -- 0 0 2 0 0 0 0 0 0 0 0 0 2 0 0 0 2 0 0 0 0 2 4 0

[AAB_NgaaCh]10 : 4 4 2 2 0 0 0 0 0 -- 0 0 0 0 2 0 0 0 2 0 0 4 2 0 0 4 0 0 2 0 0 0 4

[AA_Gwanhou]11 : 4 4 2 2 0 0 0 0 0 0 -- 0 0 0 2 0 0 0 2 0 0 4 2 0 0 4 0 0 2 0 0 0 4

[AAw_banksi]12 : 6 6 4 4 2 2 2 2 2 2 0 0 -- 0 0 4 0 2 2 4 2 2 6 4 2 2 6 2 2 4 2 0 0 6

[ABB_HinA]13 : 6 6 2 4 2 2 2 2 2 0 0 0 0 -- 0 2 0 0 0 2 2 0 6 4 2 2 6 2 2 2 0 0 0 6

[AB_Auko_IT]14 : 6 6 2 4 2 2 2 2 2 0 0 0 0 0 -- 2 0 0 0 2 2 0 6 4 2 2 6 2 2 2 0 0 0 6

[AAw_Pai]15 : 0 0 0 0 2 0 0 0 0 2 2 4 2 2 -- 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 4 6 0

[AAw_Trang]16 : 2 2 0 0 0 0 0 0 0 0 0 0 0 0 0 -- 0 0 0 0 0 2 0 0 0 2 0 0 0 0 0 0 2

[AAw_Rayong]17 : 2 2 0 0 0 0 0 0 0 0 0 2 0 0 0 0 -- 0 0 0 0 2 0 0 0 2 0 0 0 0 2 2 2

[AAw_Chanth]18 : 0 0 0 0 0 0 0 0 0 0 0 2 0 0 0 0 0 -- 0 0 0 2 0 0 0 2 0 0 0 0 2 4 0

[AAw_MaeYom]19 : 0 0 0 0 0 0 0 0 0 2 2 4 2 2 0 0 0 0 -- 0 0 0 0 0 0 0 0 0 0 0 4 6 0

[M_rubra_Sa]20 : 4 4 0 2 0 0 0 0 0 0 0 2 2 2 0 0 0 0 0 -- 0 4 2 0 0 4 0 0 0 0 2 2 4

[M_x_rubra_]21 : 0 0 0 0 0 0 0 0 0 0 0 2 0 0 0 0 0 0 0 0 -- 2 0 0 0 2 0 0 0 0 2 4 0

[AAw_NW22]22 : 0 4 2 4 4 4 4 4 2 4 4 6 6 6 0 2 2 2 0 4 2 -- 0 4 4 0 4 6 2 2 6 10 4

[AAw_UP36]23 : 0 2 0 2 2 2 2 2 0 2 2 4 4 4 0 0 0 0 0 2 0 0 -- 2 2 0 2 2 0 0 4 8 2

[AAw_1Chant]24 : 2 2 0 2 0 0 0 0 0 0 0 2 2 2 0 0 0 0 0 0 0 4 2 -- 0 4 0 0 0 0 2 4 2

[AAw_2Chant]25 : 2 2 0 2 0 0 0 0 0 0 0 2 2 2 0 0 0 0 0 0 0 4 2 0 -- 4 0 0 0 0 2 4 2

[AAw_2Kanch]26 : 0 4 2 4 4 4 4 4 2 4 4 6 6 6 0 2 2 2 0 4 2 0 0 4 4 -- 4 6 2 2 6 10 4

[AAw_Trang1]27 : 2 2 0 2 0 0 0 0 0 0 0 2 2 2 0 0 0 0 0 0 0 4 2 0 0 4 -- 0 0 0 2 4 2

[AAw_Trang3]28 : 2 2 0 2 0 0 0 0 0 0 0 2 2 2 0 0 0 0 0 0 0 6 2 0 0 6 0 -- 0 0 2 4 2

[A(A)B_Chen]29 : 0 0 0 0 0 0 0 0 0 0 2 2 4 2 2 0 0 0 0 0 0 0 2 0 0 0 2 0 0 -- 0 4 6 0

[AA_P_mas_S]30 : 0 0 0 0 0 0 0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 2 0 0 0 2 0 0 0 -- 2 4 0

[ABB_Sulawe]31 : 6 6 4 4 2 2 2 2 2 0 0 0 0 0 4 0 2 2 4 2 2 6 4 2 2 6 2 2 4 2 -- 0 6

[AAw_Sulawe]32 : 8 6 6 6 4 4 4 4 4 0 0 0 0 0 6 0 2 4 6 2 4 10 8 4 4 10 4 4 6 4 0 -- 6

[AAw_zebrin]33 : 5 0 0 0 2 2 2 2 0 4 4 6 6 6 0 2 2 0 0 4 0 4 2 2 2 4 2 2 0 0 6 6 --

The total positive difference matrix is 746.0

The total negative difference matrix is 0.0

OUTGROUP WEIGHTS

*** Network 1

AAw_Buiten weigth = 0.004347826086956522

AAw_zebrin weigth = 0.017391304347826087

ABB_KHakMu weigth = 0.02608695652173913

AAw_Cepu weigth = 0.017391304347826087

A(A)B_Chen weigth = 0.017391304347826087

AAw_Trang3 weigth = 0.004347826086956522

AAw_1Chant weigth = 0.004347826086956522

AAw_Pai weigth = 0.004347826086956522

M_schizoca weigth = 0.004347826086956522

AAw_MaeYom weigth = 0.017391304347826087

AAw_UP36 weigth = 0.004347826086956522

AAw_Trang weigth = 0.008695652173913044

AA_KluayKh weigth = 0.05217391304347826

AAA-HomTho weigth = 0.06086956521739131

AAw_Ranong weigth = 0.004347826086956522

AAw_trunca weigth = 0.14782608695652175

AAw_Yala weigth = 0.004347826086956522

AAw_Chanth weigth = 0.11304347826086956

AAw_2Chant weigth = 0.06086956521739131

AAw_Trang1 weigth = 0.008695652173913044

AAw_Rayong weigth = 0.034782608695652174

AA_P_mas_S weigth = 0.004347826086956522

M_rubra_Sa weigth = 0.10434782608695652

M_x_rubra_ weigth = 0.017391304347826087

AAw_NW22 weigth = 0.08695652173913043

AAw_2Kanch weigth = 0.004347826086956522

AAw_Sulawe weigth = 0.004347826086956522

AB_Auko_IT weigth = 0.004347826086956522

AAB_NgaaCh weigth = 0.043478260869565216

AA_Gwanhou weigth = 0.02608695652173913

ABB_HinA weigth = 0.017391304347826087

ABB_Sulawe weigth = 0.034782608695652174

AAw_banksi weigth = 0.034782608695652174

Total weight = 115.0

Biggest outgroup probability is AAw_trunca (0.14782608695652175)

Calculations are finished.

TCS v1.21

Tue Aug 29 14:02:51 GMT+07:00 2006

Datafile = F:\M_acuminata 4CP sequential.phy

It took 0.22248333333333334 minutes.

CURRICULUM VITAE

NAME	Mr. Det Wattanachaiyingcharoen
DATE OF BIRTH	11 Febuary 1963
EDUCATION BACKGROUND	
Bachelor Degree	Bachelor of Science (Biology) Srinakharinwirot University 1985
Master's Degree	Master of Science in Horticulture The University of Western Australia 1991
Postgraduate Certificate	Seed Science & Technology The University of Western Australia 1991
WORK EXPERIENCE	Associate Professor, Faculty of Agriculture Natural Resources and Environment Science 2000 - 2008 Naresuan University Council Member 2002 -2006 Head of Agriculture and Environment Integration R&D Unit. NU. 1998 - 2008 Assistant Professor 1996 - 1999 Vice-Dean for Academic Affair 1996 - 1999 Regional Advisory Committee Member of the INIBAP/IPGR/ CGIAR/UNDP for the Asia & Pacific Region 1991 - 2000 Head Department of Agricultural Science 1996 Agricultural Scientist, DOA 1988 - 1996 Residential Tutors. St'Catherine's College, UWA 1988-1991 Botanist, DOA 1985 - 1988