MICROSCOPIC AND MOLECULAR ANALYSES OF SELECTED *STRYCHNOS* SPECIES

Miss Kanittha Nakkliang

A Thesis Submitted in Partial Fulfillment of the Requirements
for the Degree of Master of Science Program in Public Health Sciences
College of Public Health Sciences
Chulalongkorn University
Academic Year 2015

ลักษณะทางจุลทรรศน์และอณูพันธุศาสตร์ของพืชสกุลสตริกโนส

นางสาวขนิษฐา นาคเกลี้ยง

วิทยานิพนธ์นี้เป็นส่วนหนึ่งของการศึกษาตามหลักสูตรปริญญาวิทยาศาสตรมหาบัณฑิต
สาขาวิชาวิทยาศาสตร์สาธารณสุข
วิทยาลัยวิทยาศาสตร์สาธารณสุข จุฬาลงกรณ์มหาวิทยาลัย
ปีการศึกษา 2558

Thesis Title	MICROSCOPIC AND MOLECULAR ANALYSES OF SELECTED *STRYCHNOS* SPECIES
By	Miss Kanittha Nakkliang
Field of Study	Public Health Sciences
Thesis Advisor	Assistant Professor Kanchana Rungsihirunrat, Ph.D.
Thesis Co-Advisor	Associate Professor Nijsiri Ruangrungsi, Ph.D.

Accepted by the College of Public Health Sciences, Chulalongkorn University in Partial Fulfillment of the Requirements for the Master's Degree

.....Dean of the College of Public Health Sciences
(Associate Professor Sathirakorn Pongpanich, Ph.D.)

THESIS COMMITTEE

.....Chairman
(Assistant Professor Naowarat Kanchanakhan, Ph.D.)
.....Thesis Advisor
(Assistant Professor Kanchana Rungsihirunrat, Ph.D.)
.....Thesis Co-Advisor
(Associate Professor Nijsiri Ruangrungsi, Ph.D.)
.....Examiner
(Assistant Professor Chanida Palanuvej, Ph.D.)
.....External Examiner
(Orawan Theanphong, Ph.D.)

ขนิษฐา นาคเกลี้ยง : ลักษณะทางจุลทรรศน์และอณูพันธุศาสตร์ของพืชสกุลสตริกโนส (MICROSCOPIC AND MOLECULAR ANALYSES OF SELECTED *STRYCHNOS* SPECIES) อ.ที่ปรึกษาวิทยานิพนธ์หลัก: ผศ. ดร. กาญจนา รังษีหิรัญรัตน์, อ.ที่ปรึกษาวิทยานิพนธ์ร่วม: รศ. ดร. นิจศิริ เรืองรังษี, หน้า.

พืชสกุลสตริกโนส 4 ชนิดที่พบในประเทศไทย ได้แก่ *Strychnos thorelii, S. lucida*, *S. nux vomica* และ *S. nux-blanda* เป็นพืชสมุนไพรที่สำคัญในการแพทย์พื้นบ้าน พืชสกุลตริกโนสมีฤทธิ์แก้ไข้ แก้ปวด แก้พิษงู และรักษาโรคไขข้อ เนื่องจากพืชสกุลสตริกโนส มีลักษณะทางพฤษศาสตร์และชื่อพื้นถิ่นที่คล้ายคลึงกัน ทำให้เกิดการใช้แทนที่โดยไม่ได้ตั้งใจ การศึกษาลักษณะทางจุลทรรศน์ และค่าคงที่ของใบ (จำนวนปากใบ ดัชนีปากใบ อัตราส่วนแพลิเสด จำนวนเส้นปลายใบ จำนวนเซลล์ผิวใบและพื้นที่ของเซลล์ผิวใบ) ทั้ง 4 ชนิด พบปากใบชนิด paracytic ไม่พบขนทั้งด้านบนและด้านล่างของใบ การหาคงที่ของใบระหว่างสตริกโนส 4 ชนิดพบว่าสามารถใช้จำแนกความแตกต่างของพืชสกุลสตริกโนสได้ โดยเฉพาะอย่างยิ่งดัชนีปากใบ ซึ่งพบค่าสูงสุดใน *S. nux-blanda* (ช่วง 15.24-16.44) และต่ำสุดใน *S. lucida* (ช่วง 6.77-7.52) การศึกษาลำดับนิวคลีโอไทด์ของบริเวณ ITS ยีน *rbc*L และยีน *mat*K พบความยาวของลำดับนิวคลีโอไทด์ประมาณ 700 1400 และ 1800 ตามลำดับ ความเหมือนของลำดับนิวคลีโอไทด์ของทั้ง 3 บริเวณภายในพืชชนิดเดียวกัน มีค่าร้อยละ 95 ถึง 99 และความเหมือนของลำดับนิวคลโอไทด์ระหว่างพืชต่างชนิดมีค่าร้อยละ 87 ถึง 99 เทคนิคพีซีอาร์-อาร์เอฟแอลพี (PCR-RFLP) ของยีน *mat*K ถูกพัฒนาขึ้น เมื่อตัดด้วยเอนไซม์ตัดจำเพาะ *Dra*I และ *Xba*I สามารถจำแนกสตริกโนสทั้ง 4 ได้ โดยดูจากความแตกต่างของขนาดชิ้นดีเอ็นเอ ผลการศึกษาสรุปได้ว่าลักษณะทางจุลทรรศน์และอณูพันธุศาสตร์สามารถใช้ในการจำแนกพืชสกุลสตริกโนสทั้ง 4 ชนิดที่พบในประเทศไทยได้

สาขาวิชา วิทยาศาสตร์สาธารณสุข ลายมือชื่อนิสิต .....

ปีการศึกษา 2558 ลายมือชื่อ อ.ที่ปรึกษาหลัก .....

ลายมือชื่อ อ.ที่ปรึกษาร่วม .....

5778952453 : MAJOR PUBLIC HEALTH SCIENCES
KEYWORDS:

KANITTHA NAKKLIANG: MICROSCOPIC AND MOLECULAR ANALYSES OF SELECTED *STRYCHNOS* SPECIES. ADVISOR: ASST. PROF. KANCHANA RUNGSIHIRUNRAT, Ph.D., CO-ADVISOR: ASSOC. PROF. NIJSIRI RUANGRUNGSI, Ph.D., pp.

There are four *Strychnos* species in Thailand including *Strychnos thorelii, S. lucida, S. nux-vomica and S. nux-blanda* which presented as important medicinal plants in folk medicine. *Strychnos* species have several ethnobotanical uses, they play an important role against fever, pain, antidote for snake poisoning and rheumatism. Many *Strychnos* species possess the similar morphology and vernacular name resulting in unintentional substitution. This current research aimed to investigate leaf microscopic characteristics and leaf measurement (stomatal number, stomatal index, palisade ratio, veinlet termination number, epidermal cell number and epidermal cell area) among four S*trychnos* species. The results showed paracytic type of stomata. There are no trichomes or cicatrices on both adaxial and abaxial epidermis. The leaf constants among four species are able to differentiate the *Strychnos* species, especially stomatal index which is highest in *S. nux-blanda* (range 15.24-16.44) and lowest in *S. lucida* (range 6.77-7.52). The full-length of nucleotide sequencing ITS region, *rbc*L and *mat*K gene were also evaluated and the result showed the sequence length in ITS region, *rbc*L and *mat*K gene were approximately 700, 1400 and 1800 base pairs respectively. The intra-species of three sequence shown 95-99% similarity and the inter-species of three sequence shown 87-99% similarity. PCR-RFLP method based on the *mat*K gene was developed. After digestion with specific restriction enzyme using *Dra*I and *Xba*I, four *Strychnos* species were easily distinguished based on the different sizes of the digested fragments. In conclusion, the use of both microscopic and molecular analyses are successful for the identification of *Strychnos* species in Thailand.

Field of Study: Public Health Sciences Student's Signature .....

Academic Year: 2015 Advisor's Signature .....

Co-Advisor's Signature .....

ACKNOWLEDGEMENTS

The author wishes to express her heartily gratitude and appreciation to her thesis advisor, Assistant Professor Dr. Kanchana Rungsihirunrat, for her guidance, suggestion, and support throughout the course of this study.

The author is sincerely grateful to her thesis co-advisor, Associate Professor Dr. Nijsiri Ruangrungsi, for his kindness and valuable suggestion to complete the study.

Gratitude is grateful to the thesis committee members, Dr. Orawan Theanphong, Assistant Professor Dr. Chanida Palanuvej and Assistant Professor Dr. Naowarat Kanchanakhan for their important and constructive suggestion in finalizing this thesis.

This research was supported by Research Assistant Scholarship, Chulalongkorn University. The authors appreciate all staff member of College of Public Health Sciences, Chulalongkorn University, Thailand for instrument supports.

The author's final thank goes to her family, especially her dear parents for their love, encourage, and support her to concentrate on her study.

CONTENTS

Page

THAI ABSTRACT iv

ENGLISH ABSTRACT v

ACKNOWLEDGEMENTS vi

CONTENTS vii

LIST OF TABLE x

LIST OF FIGURE xiii

LIST OF ABBREVIATIONS xvi

CHAPTER I INTRODUCTION 1

Research questions 3

Objectives of the study 3

The conceptual framework 4

CHAPTER II REVIEW OF RELATED LITERATURE 5

The genus *Strychnos* 5

Plant description 9

Strychnos thorelii Pierre ex Dop 9

Strychnos lucida R. Br. 10

Strychno nux-vomica L. 11

Strychnos nux-blanda A. W. Hill 12

Chemical constituent of *Strychnos* 13

Indole alkaloids 13

Strychnine and brucine 19

Pharmacological investigations of *Strychnos* genus 20

Page

Antimalarial activities 20
Antagonists of neuromuscular transmission activities 20
Analgesic and anti-inflammatory activities 21
Cytotoxic activities 21
Plant identification 22
Macroscopic and microscopic evaluation 22
Transverses section of midrib 23
Quantitative microscopy 23
Molecular evaluation 27
DNA isolation methods 27
CTAB method 28
DNA extraction kit 29
Determination of genomic DNA quantity and purity 29
Polymerase chain reaction (PCR) 34
DNA sequencing 37
PCR-RFLP analysis 40
CHAPTER III MATERIALS AND METHODS 41
Sample collection and authentication 43
Macroscopic evaluation 43
Microscopic evaluation 43
Methods for microscopic analysis 44
Transverse section of plant 44
Leaf constant numbers 45

Page

Molecular analysis 47
DNA extraction 47
PCR amplification 49
DNA sequencing analysis 52
PCR-RFLP method 53
CHAPTER IV RESULTS 54
Macroscopic evaluation 55
Microscopic evaluation 63
The stomatal classification 67
Leaf constant numbers 68
Molecular evaluation 76
The results of DNA extraction 77
PCR amplifications of ITS region, *rbc*L and *mat*K gene 78
DNA sequencing 81
PCR-RFLP method for species differentiation using *mat*K gene 81
REFERENCES 88
APPENDICES 97
Appendix A Microscopic evaluation 98
Appendix B Molecular evaluation 111
VITA 156

LIST OF TABLE

Table 1 List of 15 *Strychnos* species and their vernacular name found in Thailand.... 6

Table 2 Indole alkaloid from genus *Strychnos* 15

Table 3 Preparation of CTAB buffers 47

Table 4 The ITS primers used in this PCR amplification..... 49

Table 5 The *rbc*L primers used in this PCR amplification 50

Table 6 The *mat*K primers used in this PCR amplification 51

Table 7 List of restriction endonucleases in PCR-RFLP method 53

Table 8 Leaves of selected Strychnos species from difference locations in Thailand..... 54

Table 9 The stomatal number and stomatal index from four *Strychnos* species 68

Table 10 The palisade cells of four *Strychnos* species 69

Table 11 The epidermal cell number and epidermal cell area from four *Strychnos* species 71

Table 12 The veinlet termination number from four *Strychnos* species 73

Table 13 Summary of the leaf constant numbers consisting of stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number from four *Strychnos* species..... 75

Table 14 List of four *Strychnos* species collected from16 different locations in Thailand..... 76

Table 15 The size of restriction fragment of four *Strychnos* species digest 82

Table 16 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. thorelii,* collected from Chachoengsao province 1. 99

Table 17 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of S. *thorelii*, collected from Chachoengsao province 2. 100

Table 18 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. thorelii*, collected from Chonburi province..... 101

Table 19 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. lucida*, collected from Bangkok province. 102

Table 20 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. lucida*, collected from Pathum Thani province..... 103

Table 21 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. lucida*, collected from Nonthaburi province..... 104

Table 22 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. nux-vomica*, sample collected from Pathum Thani province. 105

Table 23 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. nux-vomica*, collected from Khon Kaen province. 106

Table 24 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. nux-vomica,* collected from Song khla province. 107

Table 25 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. nux-blanda*, collected from Chiang Mai province 1. 108

Table 26 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. nux-blanda*, collected from Chiang Mai province 2. 109

Table 27 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. nux-blanda*, collected from Chiang Mai province 3. 110

LIST OF FIGURE

Figure 1 Leaves and stem of *Strychnos thorelii* Pierre ex Dop 9

Figure 2 Leaves, berry and stem of *Strychnos lucida* R.Br. 10

Figure 3 Leaves, berries and seeds of *Strychnos nux-vomica* L. 11

Figure 4 Leaves and seed of *Strychnos nux-blanda* A. W. Hill 12

Figure 5 Chemical structure of Indole nucleus 14

Figure 6 Chemical structure of harman, koenigine, tryptamine and secologanin 14

Figure 7 Chemical structures of strychnine and brucine 19

Figure 8 Types of leaf stomata in ventral surface area: 25

Figure 9 Diagram illustrating the organization of the internal transcribed spacers (ITS) region of the nuclear ribosomal DNA 31

Figure 10 Structure of *mat*K gene which flanking between *trn*K gene regions 32

Figure 11 Structure of rbcL gene and atpB gene 33

Figure 12 Illustration of the polymerase chain reaction (PCR) 36

Figure 13 Maxam and Gilbert method 38

Figure 14 Sanger's method 40

Figure 15 The photomicroscope (Zeiss Image A.2 Axio, Germany) with an attached digital camera (Cannon Power shot A640, Japan) 44

Figure 16 Four upper contiguous epidermal cells with underlying palisade cells in surface view 46

Figure 17 The organization of plant ribosomal RNA gene 49

Figure 18 Structure of *rbc*L gene 50

Figure 19 Structure of *mat*K gene and the position of primer 51

Figure 20 Leaves of *Strychnos thorelii* Pierre ex Dop 55

Figure 21 The whole plant of *Strychnos thorelii* Pierre ex Dop 56

Figure 22 Leaves of *Strychnos lucida* R.Br. 57

Figure 23 The whole plant of *Strychnos lucida* R.Br. 58

Figure 24 Leaves of *Strychnos nux-vomica* L. 59

Figure 25 The whole plant of *Strychnos nux-vomica* L. 60

Figure 26 Leaves of *Strychnos nux-blanda* A. W. Hill 61

Figure 27 The whole plant of *Strychnos nux-blanda* A. W. Hill (A) 62

Figure 28 The transverse section of *S. thorelii* leaf through midrib 63

Figure 29 The transverse section of *S. lucida* leaf through midrib 64

Figure 30 The transverse section of *S. nux-vomica* leaf through midrib 65

Figure 31 The transverse section of *S. nux-blanda* leaf through midrib 66

Figure 32 Paracytic type stoma of four *Strychnos* species 67

Figure 33 Palisade cell of four *Strychnos* species 70

Figure 34 Upper epidermis cell of four *Strychnos* species 72

Figure 35 Veinlet termination of four *Strychnos* species 74

Figure 36 1.5% agarose gel electrophoresis of genomic DNA *Strychnos* species 77

Figure 37 PCR products of ITS on 1.5% agarose gel electrophoresis, stained with ethidium bromide and visualized under UV transilluminator 78

Figure 38 PCR products of *rbc*L gene on 1.5% agarose gel electrophoresis, stained with ethidium bromide and visualized under UV transilluminator 79

Figure 39 PCR products of *mat*K gene on 1.5% agarose gel electrophoresis, stained with ethidium bromide and visualized under UV transilluminator 80

Figure 40 PCR-RFLP pattern of four *Strychnos* species digested with *Xba*I 83

Figure 41 PCR-RFLP pattern of four *Strychnos* species digested with *Dra*I 84

Figure 42 The nucleotide sequence alignment of *mat*K gene from four *Strychnos* species 87

LIST OF ABBREVIATIONS

ºC	degree celsius
M	molarity
mg	milligram
$Mgcl_2$	magnesium chloride
min	minute
ml	milliliter
mm	millimeter
mM	millimolarity
mm^2	square millimeter
ng	nanogram
nm	nanometer
UV	ultraviolet
rpm	round per minute
SD	standard deviation
µl	microlitre
µm	micrometer
µM	micromolar
bp	base pair
cm	centimeter
DNA	deoxyribonucleic acid
Avg	average

LIST OF ABBREVIATIONS

DNA	deoxyribonucleic acid
dNTP	deoxyribonucleotide triphosphates (dATP, dTTP, dGTP, dCTP)
ddNTP	dideoxyribonucleotide triphosphates (ddATP, ddTTP, ddGTP, ddCTP)
EDTA	ethylenediaminetetraacetic acid
RFLP	restriction fragment length polymorphism
Taq	*Thermus aquaticus*
TBE buffer	tris-boric and EDTA buffer
PCR	polymerase chain reaction
A, T, C, G	nucleotide containing the base adenine, thymine, cytosine, and guanine, respectively

CHAPTER I

INTRODUCTION

World Health Organization (WHO) estimated that 80% of people worldwide rely on herbal medicines for some part of their primary health care including Thailand. There are various herbal plants are utilized as long as in Thai traditional medicine. The genus *Strychnos,* the largest genus of family Loganiaceae (Strychnaceae) [1] comprises about 200 species range from forest lianas to shrubs and trees, and can be subdivided into three geographically separated groups. There are at least 73 species of the South and Central America, 75 species of Africa and 44 species in Asia including Australia [2] Smitinand recorded the presence of 15 species in Thailand [3] including *S. thorelii, S. lucida, S. nux-vomica and S. nux-blanda* which presented as important medicinal plants in folk medicine. *Strychnos* species have several ethnobotanical uses. A few species are well known as arrow poison and also ordeal poison. However in ethnobotanical usage, they play an important role against fever, rheumatism, pain and antidote for snake poisoning [4-5]. The dried seeds of *Strychnos nux-vomica* contain 2.6-3% of total alkaloids. Major compounds are strychnine and brucine and other poisonous compounds which are responsible to pharmacological and toxicological activities.

There was the case of unintentional substitution of medicinal herbs from *Strychnos* species because many *Strychnos* species possess similar morphology and same vernacular name [6]. *Strychnos nux-vomica* has similar botanical characteristics with their closely related species; *S. nux-blanda*, and *S. lucida*. As a result, authentication is fundamental for standardization of herbal medicine. There are many methods used for examination of medicinal plant, ranging from simple morphological examination to physicochemical analysis, and DNA molecular method. Each method has their drawbacks and advantages. Sometimes two or several methods are applied for primary authentication. Macroscopic and microscopic examinations are still the most practical and standard method used for primary herbal plants authentication due to its simple, rapid and inexpensive. Macroscopic identities are based on the

authentication of their gross morphological characteristics and organoleptic properties such as size, shape, color, flowers or fruit that are visible with naked eye. Microscopic examination is also the method most commonly used to authenticate herbal medicine by observing cell structure and internal features under the microscope. Microscopic examination focuses on anatomical and histological structures of plant materials such as powdered drug characteristics, transverse section characteristics of leaf midrib and leaf constant characteristics; palisade cell, trichomes (hair), the arrangement of stomata in epidermis or the presence/absence of accumulated compounds. Quantitative measurements of their cell numbers offer specific leaf constants [7]. Their characteristics are capable to identify and authenticate plants species leading to plant material quality control.

In difficult or critical cases, some medicinal plants are not easily characterized by microscopy analysis because the adulterant may lead to confuse or misunderstand by authentication. In addition, a complementary with other analytical molecular methods provides important supporting evidence [8]. DNA-based molecular techniques have been proved to be the powerful way to discriminate species with high accuracy because DNA characteristics is the unique heredity of each species and is not affected from environmental factors. Plant genomes are more complex than other eukaryotic organisms due to present of multiple chromosome; nuclear genome, chloroplast genome and mitochondrial genome. A specific region of DNA sequence in plant genome has been used as a modern genomics tool for herbal plant identification. An internal transcribed spacer (ITS) region of nuclear ribosomal DNA is the most commonly used sequence for plant identification [9]. Many chloroplast, mitochondrial and nuclear gene have been utilized for studying sequence variation at genus/species level [10]. However, there are slightly previous studies and the data are still limited about *Strychnos* species existing in Thailand. As a result, it is essential for studying the pharmacognostic characteristics and the genetic information of *Strychnos* species. The information generate from this work can be useful for species identification and developing the more reproducible and robust PCR-RFLP for rapid identification.

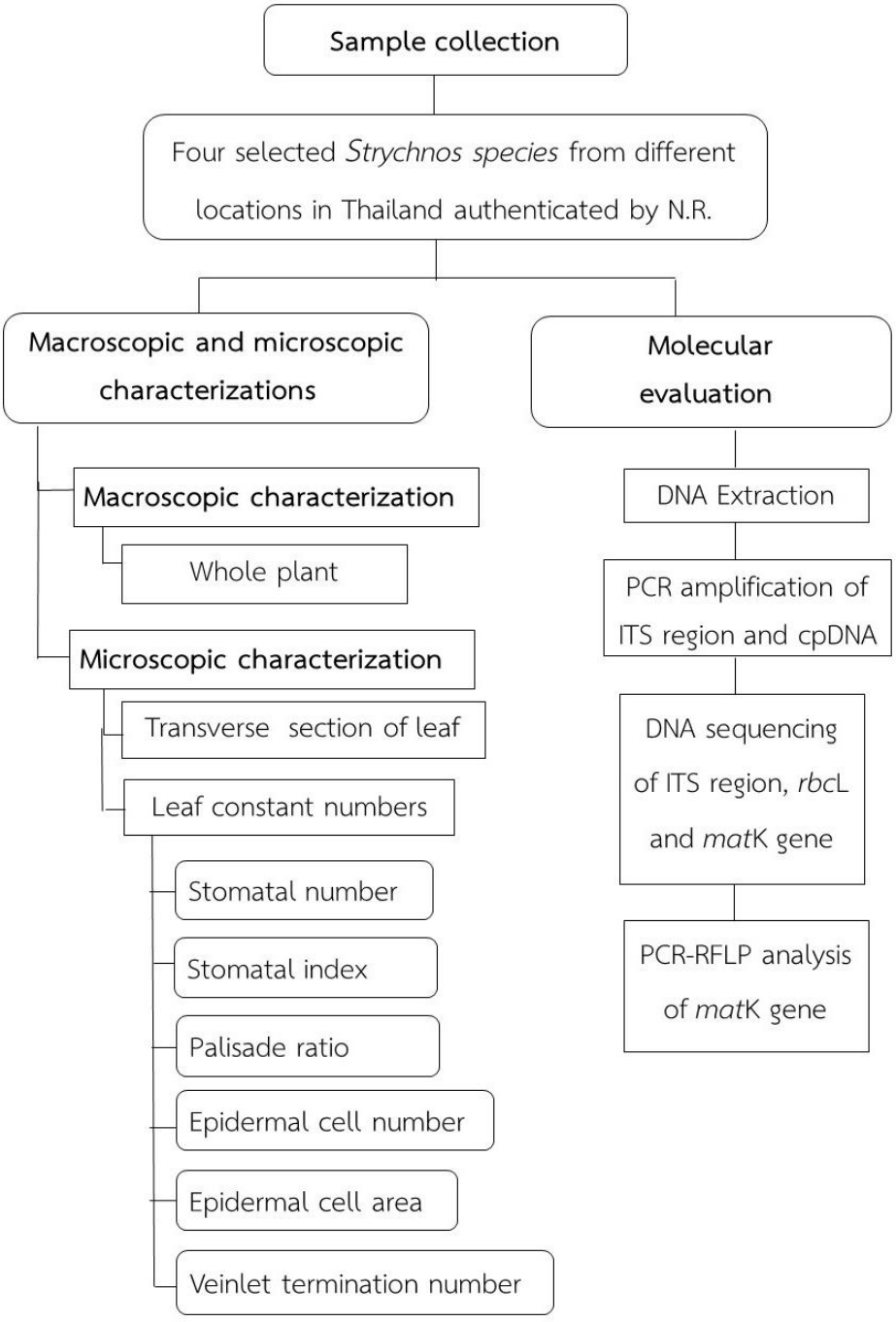
Research questions

1. Do the values of leaf constant numbers; stomatal number, stomatal index, palisade ratio, veinlet termination number, epidermal cell number and epidermal cell area of *S. thorelii, S. lucida, S. nux-vomica* and *S. nux-blanda* is useful to identify each species?
2. Do the differences sequence of ITS region, maturase K (*mat*K) gene and the large subunit of the ribulose-bisphosphate carboxylase (*rbc*L) gene of *S. thorelii, S. lucida, S. nux-vomica* and *S. nux-blanda* can be used to authenticate each species?
3. Does PCR-RFLP of *mat*K gene can be used as a species-specific marker of *S. thorelii, S. lucida, S. nux-vomica* and *S. nux-blanda*?

Objectives of the study

1. To study the leaf constants; stomatal number, stomatal index and palisade ratio, veinlet termination number, epidermal cell number and epidermal cell area of *S. thorelii, S. lucida, S. nux-vomica* and *S. nux-blanda*
2. To study the sequence variation of ITS region, maturase K (*mat*K) gene and the large subunit of the ribulose-bisphosphate carboxylase (*rbc*L) gene of *S. thorelii, S. lucida, S. nux-vomica* and *S. nux-blanda.*
3. To develop the PCR-RFLP method for species-specific marker of *S. thorelii, S. lucida, S. nux-vomica* and *S. nux-blanda.*

The conceptual framework



CHAPTER II

REVIEW OF RELATED LITERATURE

The genus *Strychnos*

Strychnos is a genus of flowering plants, belonging to family Loganiaceae (Strychnaceae). This genus comprises about 200 species range from forest lianas to shrubs and trees, all of which are pantropical in distribution and can be subdivided into three geographically separated groups of species. There are at least 73 species which are native of the south and Central America, 75 species of Africa and 44 species of Asia including Australia [2]. The only exception is *Strychnos potatorum* L. which is found both in Africa and Asia. Smitinand recorded the presence of 15 species of *Strychnos* in Thailand [3]. There are various Thai names for each species (the well-known vernacular name of each species are in bold printed) as shown in Table 1.

Table 1 List of 15 *Strychnos* species and their vernacular name found in Thailand

No.	*Strychnos* species	Vernacular name
1	*Strychnos axillaris* Colebr.	khwak kai (Chaiyaphum), kho bet (Nong Khai), **khi raet** (Prachin Buri), khiao ngu (Chumphon), tueng khruea dam tua mae (Lampang), ben (Northeastern), ben kho (Northeastern), lep khrut (Chanthaburi), lep rok (Phatthalung), nam khem (Chaiyaphum), mak ta kai (Loei)
2	*Strychnos cathayensis* Merr.	-
3	*Strychnos curtisii* King & Gamble	**Kluai khieo**
4	*Strychnos kerrii* A. W. Hill = *Strychnos nitida* G. Don	kluai khiao (Nakhon Ratchasima), **san di lok** (Chiang Mai)
5	*Strychnos krabiensis* A. W. Hill = *Strychnos ignatii* P. J. Bergius	**phaya mue lek** (Krabi)
6	*Strychnos lanata* A. W. Hill	-
7	*Strychnos lucida* R. Br.	**phaya mue lek** (Central), phaya mun lek (Central), ya mue lek (Krabi), siao duk (Northern), Strychnine bush
8	*Strychnos minor* Dennst.	tumka khao (Lampang), **tumka daeng** (Central, Northeastern, Lampang), thao kwang du thuk (Surat Thani), thao plong (Ranong)

Table 1 List of 15 *Strychnos* species and their vernacular name found in Thailand

No.	*Strychnos* species	Vernacular name
9	*Strychnos nux-blanda* A. W. Hill	klo-wo-sae (Karen-Mae Hong Son), klo-ue (Karen-Mae Hong Son), khi ka (Northeastern), **tumka khao** (Central), plu-wiat (Khmer), ma ting (Northern), ma ting ton (Northern), ma ting mak (Northern
10	*Strychnos nux-vomica* L	kra chi (Central), ka kling (Central), kot ka kling (Central), tumka daeng (Central), saeng buea (Ubon Ratchathani), **salaeng chai** (Central), salaeng thom (Nakhon Ratchasima), salaeng buea (Nakhon Ratchasima), hong-buai-chi (Chinese)
11	*Strychnos polyantha* Pierre ex Dop	
12	*Strychnos rupicola* Pierre ex Dop	**khi ka khruea** (Prachin Buri)
13	*Strychnos thorelii* Pierre ex Dop	khiao ngu (Chumphon), chong la a (Chanthaburi), **chong ra a** (Chanthaburi), thao sa em (Trat), lum nok (Chumphon), **sa eng** (Trat)
14	*Strychnos vanprukii* Craib	**thao chang** (Northern)
15	*Strychnos villosa* A. W. Hill	-

Botanical character

Strychnaceae family is shrubs, trees, or lianas. If then lianas with axillary simple or double curled tendrils, sometimes with axillary thorns. Stipules often reduced to a straight ciliate ridge connecting petiole bases. Leaves petiolate to sometimes subsessile; leaf blade margin entire, basal veins 3–7, secondary veins distinct 1–3 per side, from or near base and curved along margin. Inflorescences terminal and/or axillary, thyrsoid; bracts scalelike to sepal-like. Flowers pedicellate or sessile -4 or -5 merous. Corolla rotate to salverform; lobes valvate in bud, spreading to reflexed when open. Stamens inserted at corolla throat to middle of corolla tube, exserted to included; filaments long to short, mostly filiform; anthers orbicular to narrowly oblong, base mostly slightly -2 cleft, introrse, -2 locular and separate. Ovary 1 or -2 locular; ovules few to many per locule. Style cylindrical; stigma capitate or faintly -2cleft. Berry orange or red when ripe in species represented, usually globose to ellipsoid, thin to thick walled, outside smooth to minutely warty, glabrous; pulp fleshy, usually orange; 1-15 seeded. Seeds ± flattened to saucer-shaped, circular to elliptic in outline; seed coat sericeous, felty, or scabrous and glabrous; embryo spatulate; endosperm horny; cotyledon leaflike [11].

Plant description

***Strychnos thorelii* Pierre ex Dop**

Lianas to 18 m. Twing thingly patently pubescent, glabrescent. Leaves oblong-ovate to lanceolate, 4.5-10 by 2-4 cm, chartaceous to coriaceous, shining above, sometimes sparsely patently hairy on the midrib beneath, otherwise glabrous; base broadly cuneate to subcordate, slighty attenuatr, apex gradually acute-acuminate; 3-5 plinerved above the base; petiole 0.5-1 cm, pubescent Inflorescences axillary and terminal, up to 10 cm long, lax, minutely pubescent, with some fruit only, branches slender, torus somwhat broadened. Fruits ovoid to oblong-ellipsoid, 2.5 by 1.5 cm, thin-shelled. Seed 1, elliptic-lenticular, 2 by 1.25 [12].

Figure 1 Leaves and stem of *Strychnos thorelii* Pierre ex Dop

***Strychnos lucida* R. Br.**

Trees to 12 m tall, with spines when young. Branchlets sparsely pubescent or glabrous; branches grayish, rough with many small lenticels. Petiole 2–4 mm; leaf blade 2.5–10 × 1.5–6 cm, thin papery, glabrous, abaxially granular, base cuneate to slightly cordate, apex rounded, obtuse, or acute; basal veins 3–5. Thyrses terminal, ca. 9-flowered, pubescent. Calyx lobes broadly ovate. Corolla salverform, 1–1.5 cm; tube 7–12 mm, outside pubescent. Stamens inserted at corolla mouth, glabrous; filaments short; anthers oblong, 1.5–1.7 mm, apex exserted. Ovary globose, ca. 1 mm in diam. Style ca. 1.2 mm; stigma truncate. Berry globose, 2–2.5 cm in diam., smooth, glabrous, 2- or 3-seeded. Seeds shaped 1.2–1.5 × 1–1.2 cm [11].

Figure 2 Leaves, berry and stem of *Strychnos lucida* R.Br.

Strychno nux-vomica **L.**

Trees to 25 m tall. Branchlets slightly pubescent, glabrescent. Petiole 0.5–1.5 cm; leaf blade suborbicular, broadly elliptic, or ovate, 5–18 × 4–12.5 cm, papery, abaxially minutely hairy especially on veins, adaxially glabrous and shiny, base rounded to cordate, apex short acuminate to acute and often mucronulate; basal veins 3–5. Thyrses axillary, 3–6 cm; peduncle puberulent; bracteoles pubescent. Flowers 5 merous. Pedicel puberulent, calyx lobes ovate, corolla greenish white to white, salverform, ca. 1.3 cm. Stamens inserted at mouth or corolla tube; filaments very short; anthers elliptic, ca. 1.7 mm, apex exserted. Pistil 1–1.2 cm. Ovary ovoid, glabrous. Style to 1.1 cm, glabrous; stigma capitate. Berry orange when ripe, globose, 2–4 cm in diam., glabrous, 1–4 seeded. Seeds orbicular to elliptic, 2–4 cm wide [11].

Figure 3 Leaves, berries and seeds of *Strychnos nux-vomica* L.

***Strychnos nux-blanda* A. W. Hill**

Trees to 15 m. leaves simple, opposite broadly ovate, 9-22 cm wide, 7-16 cm long. Inflorescence in axillary cymose panicle; flowers greenish yellow. The fruit are orange with shiny surface and they are globular, 5-8 cm in diameter, with a hard pericarp 2-3 mm thick, and contain up 15 seed resembling those of S. nux-vomica L. but tending to be more irregular in shape, slightly larger in size [11].

Figure 4 Leaves and seed of *Strychnos nux-blanda* A. W. Hill

Medicinal uses

This plant has been recognized as medicinal plant whose parts have been used as components in traditional medicine of various purposes [13]

Roots: antimalarial, cathartic and external use as anti-inflammatory for snake bite

Wood: relief of muscular pain and fevers

Leaves: external use as anti-inflammatory for swelling

Stem: topically apply for sprains and antiphlogistic for snake bite,

Bark: in high doses, used as a poison which stimulates a central nervous system that can cause violent muscular convulsions

Chemical constituent of *Strychnos*

Strychnos plants are well-known as rich sources of bioactive indole alkaloids [14]. The Asian species are sources of strychnine and brucine, both of which obtained from seeds of *Strychnos ignatii* P. J. Bergius and *Strychnos nux-vomica* L. responsible for both the pharmacological and toxic properties, while the South American species are better known as the sources of certain types of curare [15].

Indole alkaloids

Indole alkaloid is an aromatic heterocyclic organic compound [1]. It has a bicyclic structure, consisting of a six-membered benzene ring fused to a five-membered nitrogen-containing pyrrole ring which can be substituted, either in oxidized or reduced forms, for example, *N*-acylindole, 2-acylindole, oxindole, pseudoindoxyl (*ψ*-indoxyl), indoline, *N*-acylindoline, methyleneindoline, indolenine, 7-hydroxy indolenine.

The indole alkaloids have been classified by their molecular skeletons into two types; simple indole alkaloids and complex or terpenoid indole alkaloids.

The simple indole alkaloids have uniformity structure. There are only indole nucleus (Figure 5) or derivatived indole nucleus, for example, harman and koenigine. Whereas the complex or terpenoid indole alkaloids are the derivation from a single precursor derived by the joining of an amino acid, tryptamine, a terpenoid and secologanin [16]. Chemical structure of harman, koenigine, tryptamine and secologanin were shown in Figure 6.

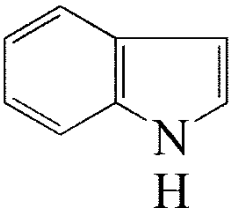


Figure 5 Chemical structure of Indole nucleus

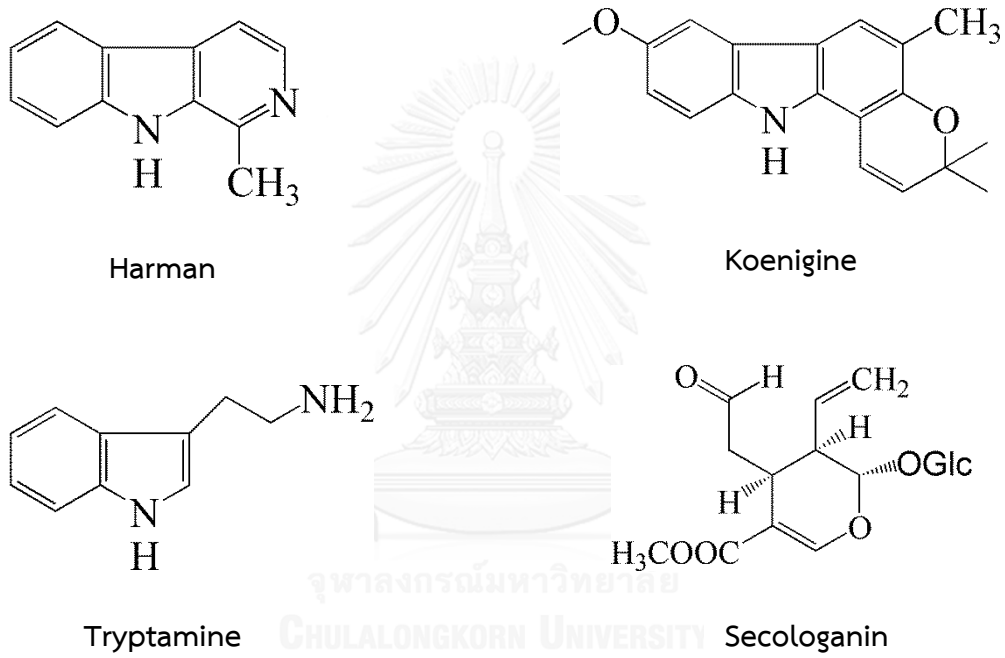


Figure 6 Chemical structure of harman, koenigine, tryptamine and secologanin

These complex indole alkaloids including monoterpenoid, bismonoterpenoid and trismonoterpenoid indole alkaloids found in *Strychnos* genus are summarized in Table 2.

Table 2 Indole alkaloid from genus *Strychnos*

Plant	Plant part	Compounds	References
		<u>Monoindole alkaloids</u>	
S. nux-vomica	Seed	Strychnine	[3], [17]
		Brucine	[3], [18]
		β-colubrine	[19]
		Pseudostrychnine	[11], [19]
		Pseudobrucine	[19]
		Strychnine *N*-oxide	[3], [18]
		Brucine *N*-oxide	[3],[18]
		16-hydroxy-α-colubrine	[19]
		2-hydroxy-3 methoxystrychnine	[19]
		Icajine	[11], [19]
		Vomicine	[19]
		Novacine	[19]
		Isostrychnine	[19]
		Isobrucine	[19]
		Isostrychnine *N*-oxide	[19]
		Isobrucine *N*-oxide	[19]
S. icaja	Root bark,	Strychnine	[20]
	Roots	Pseudostrychnine	[20]
		Protostrychnine	[20]
S. henning	Root bark	Diaboline	[11]
S. variabilis	Root bark	Retuline	[21]

Table 2 Indole alkaloid from genus *Strychnos* (Cont.)

Plant	Plant part	Compounds	References
S. panganensis	Root bark	*N*-desacetylisoretuline	[22]
		N-desacetylretuline	[22]
		12-hydroxy-11-methoxy-*N*-acetyl-nor-C-fluorocurarimine	[22]
		12-hydroxy-11-methoxy-nor-C-fluorocurarine	[22]
		N-desacetypermostrychnine	[22]
S. myrtodies	Stem bark	Strychnobrasiline	[23]
		Malagashanine	[23]
		12-hydroxymalagashanine	[23]
		Malagashanol	[23]
		Myrtoidine	[23]
		11-demethoxymyrtoidine	[23]
S. diplotricha	Stem bark	Myrtoidine	[23], [24]
		11-demethoxymyrtoidine	[24]
		3-epi-myrtoidine	[24]
S. lucida	Leaves	Brucine	[25]
		Pseudobrucine	[25]
		Brucine-*N*-oxide	[25]
		β-colubrine	[25]
		Strychnine	[25]
		Pseudostrychnine	[25]

Table 2 Indole alkaloid from genus *Strychnos* (Cont.)

Plant	Plant part	Compounds	References
S. usambarensis	Root bark, Roots	**Bisindole alkaloids**	
		Usambarensine	[26], [27]
		Dihydrousambarensine	[25],[26]
		10'-hydroxyusambarensine	[25]
		Methylusambarensine	[25]
		Usambarine	[25], [26]
	Leaves	Dihydrousambarine	[25]
		11-hydroxyusambarine	[25]
		10-hydroxyusambarine	[25]
		Strychnopentamine	[25], [28]
		Isostrychnopentamine	[25], [27]
		Chrysopentamine	[27]
		Longicaudatine	[26]
S. icaja	Roots	Bisnordihydrotoxiferine	[29],[30]
		C-dihydrotoxiferine	[11]
		C-toxiferine	[11]
		Sungucine	[20], [28-29]
		Isosungucine	[25], [29]
		18-hydroxyisosungucine	[25]
		Strychnogucine A	[31]
		Strychnogucine B	[20], [30]
		Strychnogucine C	[30]

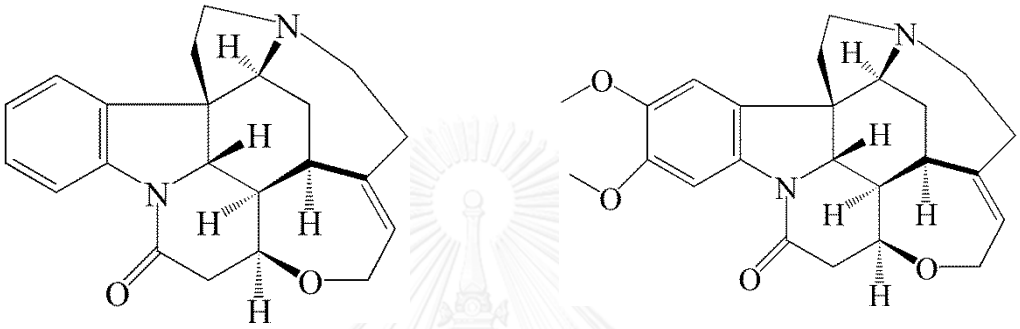
Table 2 Indole alkaloid from genus *Strychnos* (Cont.)

Plant	Plant part	Compounds	References
S. matopensis	Roots	Matopensine	[26]
S. kasengaensis	Root bark	Matopensine *N*-oxide	[26]
S. guianensis	Stem bark	Guiaflavine 5',6'-dehydroguiaflavine Guiachrysine	[32] [31] [33]
S. icaja	Roots	**Trisindol alkaloids** Strychnohexamine	[20],[29]

Although the indole alkaloids are abundant in *Strychnos* plants, there have been reports that these plants also contain other compounds such as terpenoids and lignan glucosides (in stem of *S. vanprukii*) [34]. Phenolic and compounds and glucosides isolated from bark and wood of *S. axillari* [35]. In addition, iridoid glucosides are also found in seeds of *S. nux-vomica* L. too and quinic acid in in bark and wood of *S. lucida* R. Br. [36-37].

Strychnine and brucine

Strychnine ($C_{21}H_{22}N_2O_2$, MW 334:41) is an indolomonoterpenic alkaloid possessing the strychnan group, which was isolated for the first time in 1818–1819 by Pelletier and Caventou [38] with brucine, its dimethoxylated analog. The chemical structure of strychnine and brucine were shown in Figure 7.



Strychnine **Brucine**

Figure 7 Chemical structures of strychnine and brucine

Strychnine, the most abundant alkaloid of *S. nux vomica* **L.**, is highly toxic to humans and most domestic animals. Strychnine is a well-known potent antagonist of glycine receptors in the vertebrate central nervous system and a strong blocker of various types of muscle and neuronal nicotinic acetylcholine receptors [39, 40]. Its poisoning is characterized by a short prodromal phase, after which there is an unusual combination of seizures with intact sensorium. Complications consist of hyperthermia, renal failure and rhabdomyolysis. The usual lethal dose of strychnine is reported to be between 50 and 100 mg, and the common cause of death is respiratory failure [41]. Brucine poisoning is rare, since it is usually ingested with strychnine, and strychnine is more toxic than brucine.

Pharmacological investigations of *Strychnos* genus

Antimalarial activities

The antimalarial activities of *Strychnos* alkaloids were further investigated in 2002 by Frederich and co-workers [27]. Sixty-nine alkaloids from various *Strychnos* species were subjected to *in vitro* antiplasmodial activities against chloroquine-resistant and chloroquine-sensitive lines of *Plasmodium falciparum*. The compounds, comprising mainly indolomonoterpenoid alkaloids, exhibited a wide range of biological potencies in the antiplasmodial assays. The most active alkaloids were also tested for cytotoxicity against HCT-116 colon cancer cells to determine their antiplasmodial selectivity. As a result of these studies, the alkaloids representing four types of bisindole skeleton exhibited potent and selective activities against plasmodium.

Philippe and co-workers [31] isolated a bisindole alkaloid, named strychnogucine C, and the first naturally occurring trimeric indolomonoterpenic alkaloid: strychnohexamine from the roots of *Strychnos icaja*. The *in vitro* antiplasmodial activities of these alkaloids have been determined against the FCA chloroquine-sensitive strain of *Plasmodium falciparum*. It was found that strychnogucine C possessed a weak activity (IC_{50} 16.1± 0.76 μM), which was notably less active than other sungucine type alkaloids: strychnogucine A (IC_{50} 2.3 ± 0.30 μM) and strychnogucine B (IC_{50} 0.6±0.07 μM). On the other hand, strychnohexamine presented a strong antiplasmodial activity with an IC_{50} of 1.1±0.10 μM, which was about two times more potent than bisnordihydrotoxiferine (IC_{50} 2.8±1.1 μM).

Antagonists of neuromuscular transmission activities

Wins and co-workers [42] presented the effective antagonists of nicotinic acetylcholine receptors in cultured human TE671 cells of constituents from the stem

bark of *Strychnos guianensis*. It was found that the most effective antagonist, guiachrysine, had an IC_{50} of 0.43 μM whereas another bisindole alkaloid, guiaflavine was slightly less effective (IC_{50} 0.70 μM). Moreover, monoindole compounds were 10 to 100 times less potent than bisindole alkaloids.

Analgesic and anti-inflammatory activities

Brucine and brucine N-oxide from seeds of *Strychnos nux-vomica* were reported that they possessed analgesic and anti-inflammatory activities. Both compounds significantly inhibited the released of prostaglandin E_2 in inflammatory tissue, reduced acetic acid-induced vascular permeability and the content of 6-keto-PGF_{1a} in Freund's complete adjuvant (FCA) induced arthritis rat's blood plasma [4].

Cytotoxic activities

The cytotoxic activity of two bisindolomonoterpenic alkaloids, viz. sungucine isolated from the roots of *Strychnos icaja* and isostrychnopentamine from the leaves and root bark of *Strychnos usambarensis* were studied. Isostrychnopentamine was found to induce apoptosis in HCT-116 colon cancer cells by classical pathways and sungucine was able to induce apoptosis in HL-60 leukemia cells. This has been observed by several apoptosis tests: morphology, induction of caspase 3, cleavage of RARP, and fragmentation of DNA [43].

Plant identification

The first step to categorize the herbal plant materials is the determination according to their macroscopic and microscopic characteristics for establishing the identity of herbal plant materials. Visual by eye based on the appearance of morphological characteristic provides the simplest and quickest inspection. However, macroscopic examination is sometime inadequate. It is often necessary to combine with other methods such as microscopic, chemical constituent or molecular analysis.

Previous studies refer to use of macroscopic and microscopic observation of the leaf morphological and anatomical characters for the *Strychnos* species identification and microscopic technique for comparative pharmacognostic studies and phytochemical studies on *Strychnos* specie [44-45].

Macroscopic and microscopic evaluation

The macroscopic study of medicinal plants was helpful in rapid identification of plant material and also played an important role in standardization of drugs. The fresh leaves were subject to macroscopic evaluation for the morphological characters such as size, shape, color etc.

Microscopic examination focused on anatomical structures of plant materials such as the arrangement of stomata in epidermis or the presence/absence of compounds by using microscope.

Transverses section of midrib

The qualitative microscopic evaluation of the transverse section of midribs and main veins demonstrated vascular tissues and particular surface cytomorphological characters such as trichomes, palisade cells, stomata, etc. Each cell type, form, size and its distribution within midrib cross section can provide distinguished identity for plant authentication. Moreover, midrib anatomical character enables to detect the contamination or adulteration in plant materials as well [46] .

Photomicroscope

Microscopic evaluation use a digital camera attached above the microscope. It is more convenient than camera lucida. Anyhow, the specimen has to be very thin and the optical part used should be of very high quality as any defects accentuate in the final print. The photograph is recorded by digital camera attached above the microscope by helping of the scale labeling program. The photomicrography is uniquely qualified to be used for routine and advanced microscopic investigation of medicinal plant materials [46].

Quantitative microscopy

In transverse sections it is not possible to study nature of epidermal cells, trichomes and stomata; stomatal index, vein islet number and veinlet termination number which play an important role in identifying characteristics of crude drugs and adulterants. However, these can be determined by quantitative microscopy. These quantitative microscopic values are comparatively constant for a particular species and can be used to make difference in closely related species.

Leaf measurement

The stomatal number and the stomatal index

The stomatal number and the stomatal index is very specific criteria for identification and characterization of crude drugs. Four different types of stoma are often available for matured leaves that are distinguished by there from and arrangement in the surrounding cells. Type of stoma were revealed in Figure 8.

1. The anomocytic (irregular-celled) types: the stoma is surrounded by varying number of cells, which generally not different from those of the epidermis.
2. The anisocytic or cruciferous (unequal-celled) type: the stoma is usually surrounded by three or four subsidiary cells which one is markedly smaller than the other.
3. The diacytic or caryophyllaceous (cross-celled) type: the stoma is accompanied by two subsidiary cells, the common wall of which is at right angle to the stoma.
4. The paracytic or rubiaceous (parallel-celled) type: the stoma has two subsidiary cells with the parallel to long axis of the stoma.

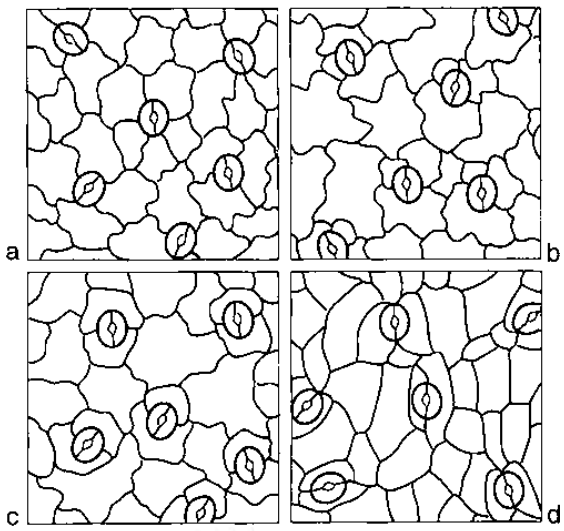


Figure 8 Types of leaf stomata in ventral surface area: a = Anomocytic type b = Anisocytic type, c = Diacytic type d = Paracytic type

Palisade ratio

Palisade cells are a type of photosynthetic cells of the mesophyll of leaf occurring mostly just beneath the upper epidermal surface layer. Palisade ratio can be defined as the average number of palisade cells present beneath each upper epidermal cell. This value remains constant within a range for a given plant species and is of diagnostic value in differentiating the species. This value does not alter by geographical variation and differ from species to species [46]. It is a very useful diagnostic feature for characterization and identification of different plant species.

Veinlet termination number

Veinlet termination number is defined as the number of veinlet termination per sq. mm of the leaf surface, midway between midrib of the leaf and its margin. It can be used as distinguishing character for the leaf of the same species or different species [47].

Epidermal cells area

The epidermal cell area is defined as the surface area of epidermal cells per sq.μm of leaf.

Clarification reagents for microscopic analysis

The presence of various contents within the cell such as starch grain, plastids, fat and oils etc., may give non-translucent section and obscure certain characteristics. There are some reagents that can dissolve of these contents and have been used to make a penetrating effect. Those sections may be more transparent and reveals details of the structures. Some of the reagents that most frequently used such as chloral hydrate and sodium hypochlorite are described below [47].

Chloral hydrate solution

Chloral hydrate is colorless hygroscopic crystal with melting point at 55°C. It's valuable and widely used as the best for clearing reagent. This solution dissolves starch, proteins, chlorophyll, resins, and volatile oils with the help of gentle warming. It does not dissolve calcium oxalate and causes the shrunken cells to expand without damage of cell wall or other tissue. Chloral hydrate is not only used for cross section, but also for whole leaves, flowers. [48]

Sodium hypochlorite solution

This solution is useful bleaching agent to remove deeply coloured sections such as many barks as well as for removing chlorophyll from the leaves [7]. The sections are immersed in the solution and left for a few minutes or until bleaching. The section should be removed from the solution and then washed with water when bleaching is completed.

Molecular evaluation

The molecular method or DNA-based techniques have been wildly used for herbal medicine technology and authentication of medicinal plant species. Some closely related species not easily characterized by general microscopy. Therefore, molecular methods are the most technique used for identification. These methods were useful in case of those that are frequently substituted or adulterated with other species. These techniques have been found to be useful and accurate for determination of genetic variation in plants [49].

DNA methods are suitable for identifying medicinal materials because genetic composition is unique for each individual irrespective of the physical forms of samples and are less affected by age, physiological conditions, environmental factors, harvest, storage and processing. Currently, sequence comparison or restriction analysis of fragments amplified with universal primers for organelle DNA has been widely used in species identification, genetic diversity and phylogenetic studies in many different plant species.

DNA isolation methods

DNA extraction is a routine step in many biological studies including molecular identification. In addition, DNA extraction is often used in medical examinations, clinical diagnostics, and forensic investigations. Therefore, a variety of methods have been established to isolate DNA molecules from biological materials [50]. Recently, many DNA extraction kits are commercially available. Different extraction methods have various effects on DNA quantity and quality. An ideal extraction technique should be optimize to obtain maximize DNA yield, minimize DNA degradation, and be efficient in terms of cost, time, labor, and supplies. It must also be suitable for extracting multiple samples and generate minimal hazardous waste [51].

The extraction of the nucleic acids is difficult in a variety of plants because of the presence of polyphenols and secondary metabolites that interfere with DNA isolation procedures and downstream reactions such as DNA restriction, amplification and cloning [52]. A large number of secondary metabolites such as tannins, alkaloids, phenolics and terpenes responsible for the valuable pharmacokinetic properties of medicinal plants which interfere with the isolation process, tend to co- purify with DNA and interact irreversibly with proteins and nucleic acids [53]. Examples, problems encountered in the isolation and purification of high molecular weight DNA from certain legume plant species include: degradation of DNA due to endonucleases, co-isolation of highly viscous polysaccharides and inhibitor compounds like polyphenols and other secondary metabolites which directly or indirectly interfere with subsequent enzymatic reactions [54]. The separation of DNA from cellular components can be divided into four stages: 1. Disruption, 2. Lysis, 3. Removal of proteins and contaminants and 4. Recovery of DNA. In some methods, stage 1 and 2 are combined [55]. In general, all methods involve disruption and lysis of the starting material followed by the removal of proteins and other contaminants and finally recovery of the DNA.

CTAB method

Doyle and Doyle have been used cetyltrimethyl ammoniumbromide (CTAB) to isolate DNA with the reducing agent β-mercaptoethanol in addition to proteinase K which removes protein [56]. CTAB is a cationic detergent, which solubilises membranes and forms a complex with DNA. Polyvinylpyrrolidone (PVP) has been also been used successfully to remove polyphenols along with a high molar concentration of NaCl to inhibit co-precipitation of polysaccharides and DNA. Most of the protocols recommend isolation of DNA from fresh tissues, but sometimes the samples collected from remote and rare locations may consist of plant parts in dry or semi-dry conditions [57]. Edwards

et al. have used Sodium dodecyl sulfate (SDS) and phenol instead of CTAB as a detergent for the same function of pure DNA isolation [58]. In the DNA preparation, it breaks up the lipids in the membranes to free the DNA from the cell.

DNA extraction kit

Some researcher use a commercial kit based methods to supplement CTAB based extractions to generate genomic DNA of high enough quality to pass stringent conditions for library preparation [59]. Kit based extraction methods are intended to easily remove contaminants, but are often expensive, particularly when many samples are required for analysis. For example, the problem of losing DNA through subsequent column washes or precipitations can be exacerbated when only small amount of leaf tissue is available for collection. Commercial column base extraction kits, such as DNeasy® (Qiagen, USA) or Wizard® (Promega, USA), a spin-column of DNA-binding membrane together with a buffer system for cell lysis, DNA binding and elution were used in DNA extraction procedure.

Determination of genomic DNA quantity and purity

DNA yield and purity were determined by two methods: agarose gel electrophoresis and spectrophotometer analysis. The yield was further measured by checking the optical density (OD) in a UV spectrophotometer at 260 nm. DNA purity determined by calculating the absorbance ratio at A260/A280 for pure DNA is approximately 1.8. Agarose gel electrophoresis is a method to separate DNA or RNA molecular by size. This is achieved by moving negatively charge nucleic acid molecular though an agarose matrix with an electric field. Shorter molecule move faster and migrate faster than longer ones.

The obtained genomic DNA is then used as a DNA template for amplified the interested region. There are several regions in the DNA from various origins that used for studying the divergence or identity of plants such as;

Nuclear genome

Nuclear genome is a linear DNA packed closely on the chromosome. It is the largest components in the nucleus. Nuclear genome is composed of information inherited equally from parents, one male, and one female. It is mostly used in forensic examinations. The regions of nuclear genome that commonly used in DNA fingerprint of herbal drug are;

Ribosomal DNA (rDNA)

Ribosomal DNA codes for ribosomal RNA. The ribosome is a macromolecule in the cell that is able to produce proteins or polypeptide chains. rDNA consists of a tandem repeat of a unit segment which comprises of non transcribed spacer (NTS), external transcribed spacer (ETS), 18S, ITS1, 5.8S, ITS2, and 28S tracts (Figure 9). In the large rDNA array, polymorphisms between rDNA repeat units are very low which means low rate of polymorphism among species, indicating that rDNA tandem arrays are evolving through concerted evolution, so comparison of the rDNA segment including ITS region of the related species and phylogenetic analysis are accomplished [60].

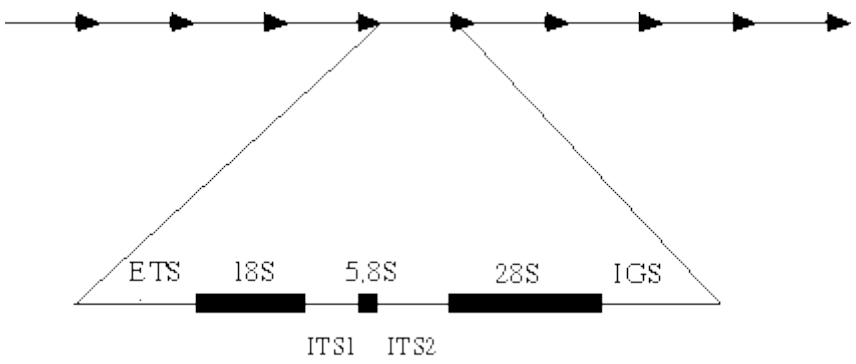


Figure 9 Diagram illustrating the organization of the internal transcribed spacers (ITS) region of the nuclear ribosomal DNA [61]

Internal transcribed spacers (ITS) are sequences located in eukaryotic ribosomal DNA (rDNA) genes between the 18S and 5.8S rDNA coding regions (ITS1) and between the 5.8S and 26S rDNA coding regions (ITS2) [62]. It has been found as parts of repeat units that are arranged in tandem arrays. The length and sequences of ITS regions of rDNA repeats are believed to be fast evolving. Universal PCR primers designed from highly conserved regions flanking the ITS and its relatively small size (600-700 base pairs) enable easy amplification of ITS region due to high copy of rDNA repeats. This makes the ITS region an interesting subject for evolutionary phylogenetic investigations [63]. The ITS region is typically been most useful for molecular systematics at the species level, and even within species

There are other regions in nuclear genome that are used in evolution analysis of plants but was not generally used in DNA fingerprint in herbal drug such as *phy* gene (phytochrome), *gap*A gene (glyceraldehydes-3-phosphate dehydrogenase), *adh* gene (alcohol dehydrogenase) and *pgi* gene (phosphoglucose isomerase).

Chloroplast genome

Chloroplast genomes (cpDNA) are relatively large, usually approximately 140 kb in higher plants. Chloroplast genome codes for all the ribosomal RNA (rRNA) and transfer RNA (tRNA) species needed for protein synthesis. It has been used extensively to infer plant phylogenies at different taxonomic levels. Direct sequencing of polymerase chain reaction (PCR) products is now becoming a rapidly expanding area of plant systematics and evolution [64]. Chloroplast DNA is uniparental inheritance, so its pattern is homozygous which mean identical copies are present in the entire of a gene made sequencing easier. Chloroplast genome such as;

*mat*K (Maturase K) gene is approximately 1500 base pairs in size, located within the intron of the chloroplast *trn*K gene (Figure 10). This gene can encode to enzyme maturase which presumably helps fold the intron RNA into the catalytically-active structure. The 3' end of the *mat*K was identified to contain a conserved region of about 100 base/aminoacid. The *mat*K gene is emerging as another valuable gene to study because of its reasonable size, high substitution rate, evenly distributed codon position variation, low transition and transversion ratio, and the easiness of amplification due to its two flanking coding *trn*K gene. The *mat*K gene has fast evolution so, it is not possible to use the universal primer [65].

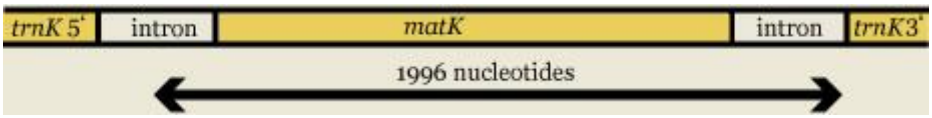


Figure 10 Structure of *mat*K gene which flanking between *trnK* gene regions [66]

The *rbc*L gene or RuBisCO (Ribulose-1,-5bisphosphate carboxylase/ oxygenase) is a single copy gene approximately 1430 base pairs in length. The *rbc*L gene is a gene coded for the large subunit of ribulose 1, 5 bisphosphate carboxylase/oxygenase and involved in catalyzing the primary chemical reaction by which inorganic carbon enters the biosphere which is first major step of carbon fixation. This gene has slow substitution rate and extensive database of sequences make *rbc*L sequence data well suited for phylogenetic studies at a variety of higher taxonomic levels, from interfamily to subclass [67].

*atp*B gene locates next to *rbc*L gene (Figure 11). Its common size is 1497 base pairs in plants. This gene encoded β-subunit of ATP synthase which is an enzyme catalyzes ATP synthesis. Their size, rate of evolution and lacking of intron, these are likewise to *rbc*L gene. Other chloroplast genomes are also used for investigating plants such as gene *ndh*F, the region in the area of gene *trn*T, *trn*L and *trn*F, *etc.* [68]

Figure 11 Structure of *rbc*L gene and *atp*B gene

Mitochondrial genome

Mitochondrial genome (mtDNA) is the DNA located in mitochondria which is involves in converting the chemical energy from food into adenosine triphosphate (ATP), an energy form that cells can use. Mitochondrial genome is large and vary in size, moreover, substitute rate of the nucleotide in plants mitochondrial genome is

slower than those of animals approximately 100-40 times and slower than those of nuclear genome and chloroplast genome around 12 and 4-3 times, respectively. Thus this genome is rarely used in authentication of herbal drugs [69].

Polymerase chain reaction (PCR)

PCR is a scientific technique in molecular biology developed in 1983 by Kary Mullis. PCR is based on using the ability of DNA polymerase to synthesize new strand of DNA complementary to the offered template strand. The PCR principle is to amplify a single or a few copies of a piece of DNA and generating thousands to millions of copies of a particular DNA sequence (Figure 12) [70]. A basic PCR set up requires several components and reagents such as, DNA template that contains the DNA region to be amplified, two primers that are complementary to the 3' ends of each of the sense and anti-sense strand of the DNA target, deoxynucleoside triphosphates (dNTPs; nucleotides containing triphosphate groups) which acts like the building-blocks from which the DNA polymerase synthesizes a new DNA strand, buffer solution, providing a suitable chemical environment for optimum activity and stability of the DNA polymerase, divalent cations, magnesium or manganese ions; generally Mg^{2+} is used, but Mg^{2+} can be utilized for PCR-mediated DNA mutagenesis, as higher Mg^{2+} concentration increases the error rate during DNA synthesis [71], monovalent cation potassium ions and *Taq* polymerase or another DNA polymerase with a temperature optimum at around 70 ºC. *Taq* DNA Polymerase is a highly thermostable DNA polymerase of the thermophilic bacterium *Thermus aquaticus*. The enzyme catalyzes 5' to 3' synthesis of DNA, it has no proofreading activity which is no detectable 3' to 5' exonuclease and possesses low 5' to 3' exonuclease activity. In addition, *Taq* DNA Polymerase exhibits deoxynucleotidyl transferase activity, which frequently results in the addition of extra adenines at the 3'-end of PCR products. Recombinant *Taq* DNA

Polymerase is ideal for standard PCR of templates 5 Kilo base (kb) or shorter. The error rate of *Taq* DNA Polymerase in PCR is $2.2x10^{-5}$ errors per nucleotide (nt) per cycle, as determined by a modified method that was described [72]. Accordingly, the accuracy of PCR is $4.5x10^{4}$. Accuracy is an inverse of the error rate and shows an average number of correct nucleotides incorporated before an error occurs. The PCR is commonly carried out in a reaction volume of 10–100 µl in small reaction tubes in a thermal cycler. The thermal cycler heats and cools the reaction tubes to achieve the temperatures required at each step of the reaction [73]. A typical set of reactions might have a pre denaturation then, followed by 30-40 cycles of each comprising denaturation, annealing and extension. Then, evaluate the PCR product in 1.5% agarose gel electrophoresis which can separate nucleic acid molecules by size. Agarose gel that contains buffer is formed by a meshwork of molecules, and nucleic acids are driven through it by an electric field from charge negative to charge positive then visualize by staining the gel in ethidium bromide and observed under UV light[74]. There are some factors affect to the PCR exponential progression such as existing phenol or enzymes found in the sample which are inhibitors of the polymerase reaction, reagent limitation, accumulation of pyrophosphate molecules, and self-annealing of the accumulating product. The advantage of PCR can lead to many applications such as sequencing, genetic engineering, cloning, forensic biology, etc.

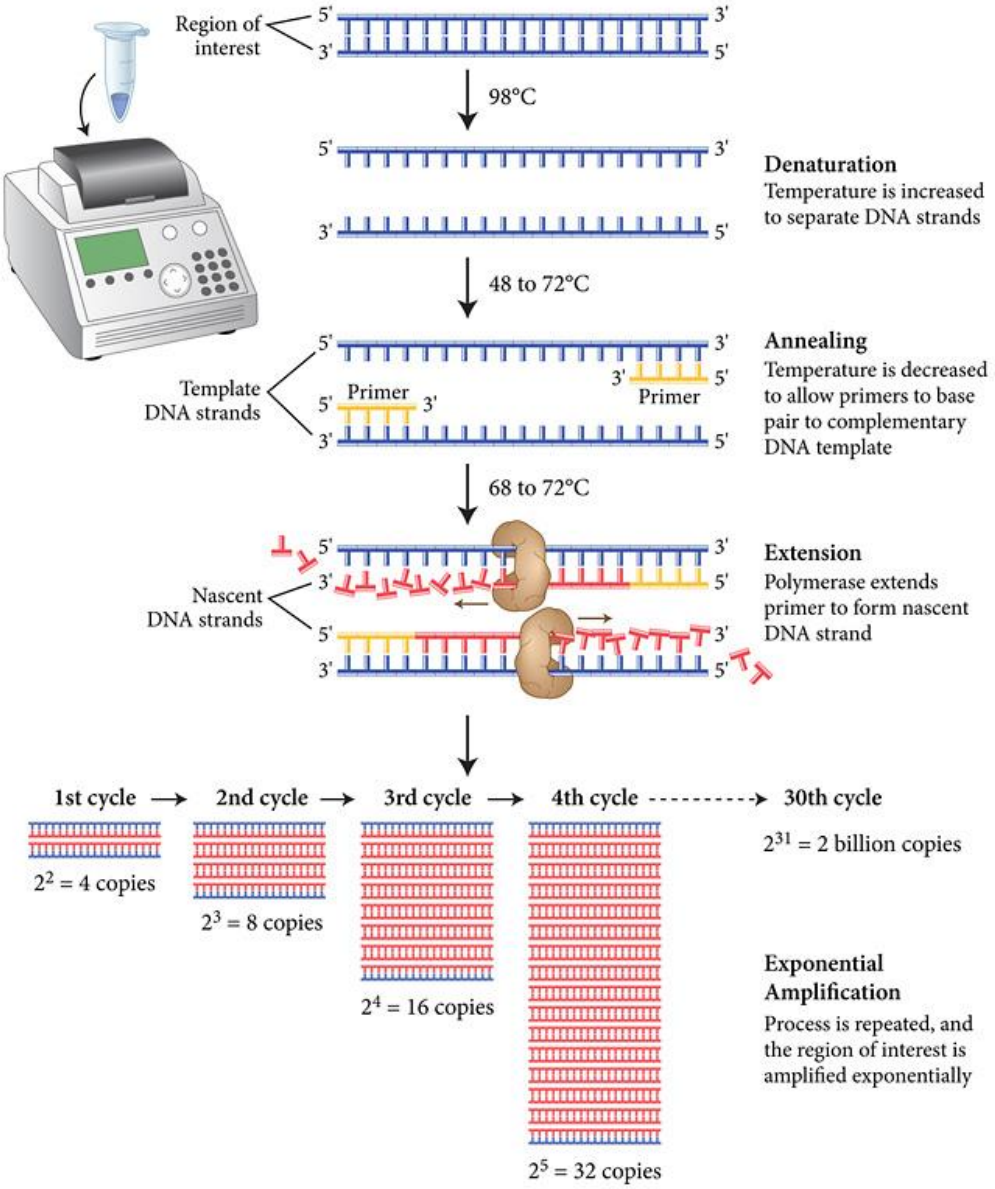


Figure 12 Illustration of the polymerase chain reaction (PCR) [75]

DNA sequencing

DNA sequencing is used for determining the order of the nucleotides which are adenine, guanine, cytosine, and thymine in a molecule of DNA. Polymorphism at the DNA level can be studied by several methods but the direct strategy is determination of nucleotide sequences of a defined region. Nowadays, DNA sequencing is a routine technique in molecular biology laboratories.

Knowledge of DNA sequences has become indispensable for basic biological research, other research branches utilizing DNA sequencing, and in numerous applied fields such as diagnostic, biotechnology, forensic biology and biological systematics. The advent of DNA sequencing has significantly accelerated biological research and discovery [76]. The methods can be categorized as two major methods as;

Maxam and Gilbert method

A sequencing method based on a chemical degradation was described by Maxam & Gilbert sequencing [77]. In this requires radioactive labeling at one 5' end of the DNA by a kinase reaction using gamma-32P ATP and purification of the DNA fragment. Chemical treatment generates breaks at a small proportion of one or two of the four nucleotide bases in each of four reactions (G, A+G, C, C+T) (Figure 13). For example, the purines (A+G) are depurinated using formic acid, the guanines (and to some extent the adenines) are methylated by dimethyl sulfate, and the pyrimidines (C+T) are methylated using hydrazine. The addition of salt (sodium chloride) to the hydrazine reaction inhibits the methylation of thymine for the C-only reaction. The modified DNAs are then cleaved by hot piperidine at the position of the modified base. The concentration of the modifying chemicals is controlled to introduce on average one modification per DNA molecule. Thus a series of labeled fragments is generated, from the radiolabeled end to the first "cut" site in each molecule. The fragments in

the four reactions are electrophoresed side by side in denaturing acrylamide gels for size separation. To visualize the fragments, the gel is exposed to X-ray film for autoradiography, yielding a series of dark bands each corresponding to a radiolabeled DNA fragment, from which the sequence may be inferred [78].

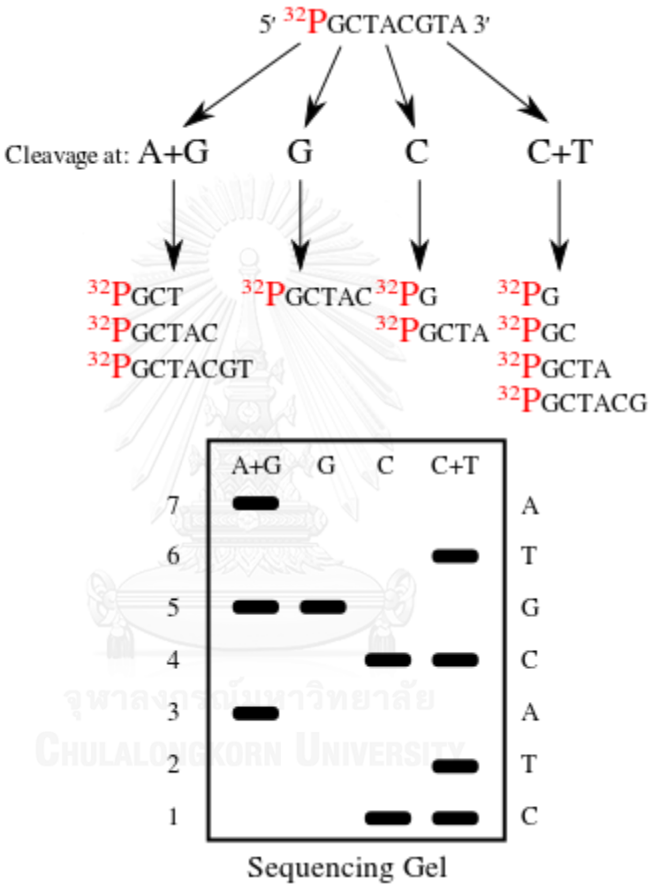


Figure 13 Maxam and Gilbert method [79]

Sanger'S method

Sanger sequencing is a method of DNA sequencing based on the selective incorporation of chain-terminating dideoxynucleotides by DNA polymerase during *in vitro* DNA replication. This method, developed by Frederick Sanger and colleagues in 1977, was initially known as the chain termination method or dideoxynuleotide method (Figure 14). This method is better than chemical method because of the lower of toxic chemicals and lower amount of radioactivity is used. The method requires a single-stranded DNA template, a DNA primer, a DNA polymerase, normal deoxynucleotidetriphosphates (dNTPs; dATP, dGTP, dCTP and dTTP), and modified nucleotides (dideoxyNTPs; (ddATP, ddGTP, ddCTP, or ddTTP), lacking a 3'-OH group required for the formation of a phosphodiester bond between two nucleotides, thus terminating DNA strand extension and resulting in DNA fragments of varying length. These ddNTPs will also be radioactively or fluorescently labelled for detection in automated sequencing machines. The DNA sample is divided into four separate sequencing reactions, containing all four of the standard deoxynucleotides and the DNA polymerase. To each reaction is added only one of the four dideoxynucleotides. The newly synthesized and labelled DNA fragments are heat denatured, and separated by size on a denaturing polyacrylamide-urea gel electrophoresis with each of the four reactions run in individual lanes (lanes A, T, G, C); the DNA bands are then visualized by autoradiography or UV light, and the DNA sequence can be directly read off the X-ray film or gel image. X-ray film was exposed to the gel, and the dark bands correspond to DNA fragments of different lengths. A dark band in a lane indicates a DNA fragment that is the result of chain termination after incorporation of a dideoxynucleotide (ddATP, ddGTP, ddCTP, or ddTTP). The relative positions of the different bands among the four lanes are then used to read (from bottom to top) the DNA sequence.

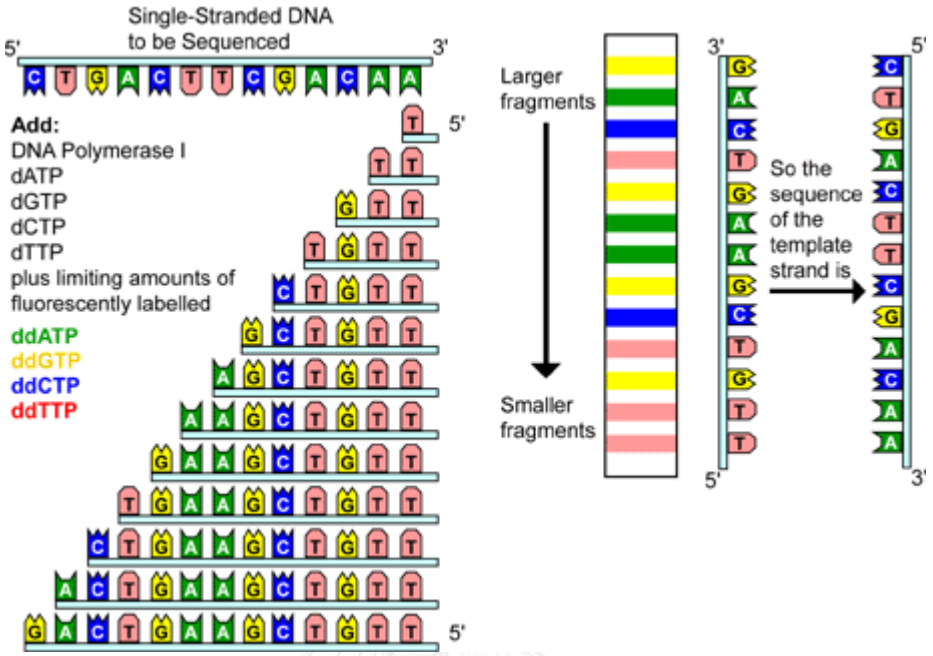


Figure 14 Sanger's method [80]

PCR-RFLP analysis

PCR-restriction fragment length polymorphism (RFLP)-based analysis is a popular technique for genetic analysis. It has been applied for the detection of intraspecies as well as interspecies variation. There exist several techniques that are related with PCR-RFLP and also involve gel electrophoresis including techniques for DNA fingerprinting and expression profiling. The first step in a PCR-RFLP analysis is amplification of a fragment containing the variation. This is followed by treatment of the amplified fragment with an appropriate restriction enzyme. Since the presence or absence of the restriction enzyme recognition site results in the formation of restriction fragments of different sizes, allele identification can be done by electrophoretic resolvement of the fragments. PCR-RFLP is an extremely valuable technique for genotyping of species-specific variations [81].

CHAPTER III

MATERIALS AND METHODS

Chemicals and Reagents

1. Ethanol (Merck, Germay)
2. Chloral hydrate (Ajax Finechem Pty Ltd., Australia)
3. sodium hypochlorite (Hiter Bleach, Kao industrial, Thailand)
4. CTAB: Hexadecyltrimethylammonium bromide (Sigma-Aldrich Company Co., St. Louis, MO, USA)
5. Liquid nitrogen
6. β-*m*ercaptoethanol (Sigma-Aldrich Company Co., St. Louis, MO, USA)
7. Chloroform (Merck, Darmstadt, Germany)
8. Isoamyl alcohol (Sigma-Aldrich Company Co., St. Louis, MO, USA)
9. Absolute ethanol (Merck, Darmstadt, Germany)
10. Sodium acetate (BDH Laboratory supplies, Poole, England)
11. Tris (hydroxymethyl)-aminomethane hydrochloride (Fluka, Biochemika, Germany)
12. EDTA: Ethylenediaminetetraacetic acid (Merck, Darmstadt, Germany)
13. NaCl: Sodium hydroxide (BDH Laboratory supplies, Poole, England)
14. Agarose (Ultrapure TM, Life technologies, USA)
15. Ethidium bromine (Sigma-Aldrich Company Co., St. Louis, MO, USA)
16. 1 kb DNA Ladder (Promega. USA)
17. Loading Dye (bromophenol blue, Fermentas, USA)
18. *Taq* DNA polymerase (Fermentas, USA)
19. forward - reverse primer primer (Operon Biotechnologies, Germany)
20. 10X PCR Buffer (Fermentas, USA)
21. $MgCl_2$ (Fermentas, USA)

22. Distilled water
23. DNA template

Materials

1. Microcentrifuge tube (Axygen, USA)
2. Pipet tips (Axygen, USA)
3. PCR tubes (Axygen, USA)
4. PCR purification kit (QIAGEN, USA)

Instrumentations

1. Microphotographs were taken using digital camera (Cannon Power shot A640, Japan) attached to the Photomicroscope (Zeiss Image A.2 Axio, Germany)
2. Micropipette (Eppendorf, Germany)
3. Mortar
4. UV transilluminator (AutoChem TM system, USA)
5. Thermal cycler (*Geneamp PCR 9700*, Applied Biosystems)
6. Gel electrophoresis apparatus and power supply
7. Centrifuge (*Biofuge Pico*, Kendro, Germany)
8. Vertex mixer
9. shaking incubator

Methods

Sample collection and authentication

The leaves of *S. thorelii, S. lucida*, *S. nux-vomica* and *S. nux-blanda* were collected from different locations in Thailand. They were authenticated by Associate Professor Dr. Nijsiri Ruangrungsi. Voucher specimens were deposited at College of Public Health Sciences, Chulalongkorn University, Thailand.

Macroscopic evaluation

Whole plant characters of *S. thorelii, S. lucida*, *S. nux-vomica* and *S. nux-blanda* were observed and recorded. The drawing outlines of whole plants were in proportion size which related to real size. Leaves morphological characteristic (leaves shape, base, texture, venations) were observed and recorded.

Microscopic evaluation

Microscope evaluation use a digital camera attached above the microscope (Figure 15). The photograph is recorded with an attached digital camera Cannon Power shot A640 and examining under the photomicroscope Zeiss Image A.2, Axio with objective lens. The images were recorded using AxioVision Release 4.8.3 software. This software was used for images alignment and labeling. The individual of each sample was studied under eyepiece lens of 10X magnifications and objectives with a 5X 10X, 20X and 40X magnifications.

Figure 15 The photomicroscope (Zeiss Image A.2 Axio, Germany) with an attached digital camera (Cannon Power shot A640, Japan)

Methods for microscopic analysis

Transverse section of plant

The fresh mature leaves were cleaned. Transverse section was prepared by cutting the leaves in parallel including the midrib and lamina into pieces as thin as possible and transferred these tissue sections by a brush moistened with water. Selected satisfactory sections were prepared and mounted onto a slide in glycerin for microscopic examination under photomicroscope, scaled for labeling size of each character. Transverse sections of midrib were drawn in the proportion size related to the original scale in drawing paper.

Stomata classification of leaves

The fresh mature leaves were cleaned and cut into small pieces (1x1 cm), in the central part of lamina, midway between the midrib and the margin. Small pieces of leaves were soaked in sodium hypochlorite solution (Haiter breaching solution: distilled water, 1:2) for 24 hour and cleared by gently warming with chloral hydrate

solution (chloral hydrate: distilled water, 9:1). The thin membranous layer which was sufficiently big enough for the field vision were taken on glass slide.

Leaf constant numbers

The fresh mature leaves were cleaned and clear with chloral hydrate solution using the same procedure as described in part stomata classification of leaves**.** Determined a total of 30 fields for the stomatal number, stomatal index, palisade ratio, veinlet termination number epidermal cell number and epidermal cell area. That were recorded and presented by mean and standard deviation (SD). Then, mean and SD of each sample were averaged as the constant number of each species. The methods were carried out as below;

a) Determination of stomatal number and stomatal index

Stomatal number is the average number of stomata per square mm of epidermis and the number on each surface of a leaf. Stomatal index (SI) is one of the more distinguishing characteristic for herbal leafy drugs. Stomatal is defined as the percentage of stomata from the total number of epidermal cell, which can be explained as:

$$SI = \frac{S}{E+S} \times 100$$

Where S = the number of stomata in a given area of leaf; and E = the number of epidermal cells in the same area of leaf

b) Determination of palisade ratio

Palisade ratio is the average number of palisade beneath one epidermal cell of a leaf. It is determined by counting the palisade cells beneath four continuous upper epidermal cell. The palisade cells in surface view were shown in Figure 16.

Figure 16 Four upper contiguous epidermal cells with underlying palisade cells in surface view

c) Determination of veinlet termination number

Small vascular bundle surrounded by many conducting tissue is call veinlet. The end termination of the vein is total number of veinlet termination point present per sq.mm on the surface of leaf.

d) Determination of epidermal cell number and epidermal cell area

Epidermal cell number was calculated by counting the number of each field (1 sq.mm), epidermal cell area was reported per sq.μm

Molecular analysis

DNA extraction

Preparation of CTAB buffer

Genomic DNA was individually extracted from the fresh young specimen leaves using a modified CTAB method. The preparation of CTAB buffers (4 µl of 2 mercaptoethanol was immediately added to each 1 ml of CTAB buffers before used) were shown in Table 3.

Table 3 Preparation of CTAB buffers

Stock reagent	Final concentration	Final amount
CTAB	2% (w/v)	2 g
1 M Tris-HCL pH8	100 mM	10 ml
0.5 M EDTA	20 mM	4 ml
5 M NaCl	1.4 M	28 ml

Make up with distilled water to 100 ml

Add 4 µl of 2 mercaptoethanol to each 1 ml of CTAB buffers before used.

Procedure

For DNA extraction procedure, fresh leaves were ground with liquid nitrogen to fine powder in mortar. The ground powders were transferred into 1.5 ml microcentrifuge tube using spatula. Then 500 µl of CTAB buffer, vortex and incubate the CTAB/plant mixture at 65 ºC for an hour in shaking incubator. After incubation, centrifuge for 10 minutes to spin down cell debris. Transfer the supernatant to a new microcentrifuge tube and 500 µl of chloroform was added. Vortex and then centrifuge

for 10 minutes. Transfer the aqueous phase (upper) to a new microcentifuge tube, 500 µl of chloroform/isoamyl alcohol (24:1) was added, vortex and then centrifuged for 10 minutes. Depending upon the purification of DNA, the aqueous phase may be re-extracted. Be carefully transferred the final upper aqueous phase to a clean microcentrifuge tube. Then 1:10 volume of 3M sodium acetate pH 5.0 was added followed by 2 volume of ice-cold (-20 ºC) absolute ethanol, and mix by slowly invert the tube. Let the tube stand at -20 ºC for an hour to precipitate DNA. After precipitation, centrifuge for 10 min and remove all of the supernatant. DNA was then washed with 1 ml of cold 70% ethanol and gently inverted the tube several times. Then centrifuge 10,000 rpm for 10 minutes and discard all the supernatant and allowed DNA pellet to dry at room temperature. Do not leaved the DNA to over dry because it will be hard to re-dissolve. Dissolved DNA in 100 µl TE buffer (10 mM Tris pH 8, 0.1 mM EDTA pH8) and stored at -20 ºC further use as templates in PCR amplification.

Determination of genomic DNA quantity

Five µl of genomic DNA were analyzed by 1.5% agarose gel electrophoresis and with 1 kb marker. Stained by ethidium bromide and visualized under UV illuminator.

PCR amplification

PCR amplification of ITS region

The ITS including ITS1 - 5.8S rDNA - ITS2 region was amplified using a pair of universal primer (ITS5 and ITS4) as shown in Figure 17 and Table 4. PCR amplification was performed in a 25 µl reaction volume, containing of 1X PCR buffer (100 mM) KCl, 20 mM Tris-HCl (pH 8), 2.5 mM $MgCl_2$, 0.2 mM dNTPs,0.2 µM of each primers, 0.5 unit of *Taq* DNA polymerase and 1 µl of DNA template. PCR amplification was performed in Thermal cycler under the following condition: initial denaturation step at 95 ºC for 5 minutes, followed by 30 cycles of denaturation at 95 ºC for 30 second, primer annealing at 55 ºC for 30 second, primer extension at 72 ºC for 30 second, a final extension at 72 ºC following 5 minutes, and then hold at 4 ºC. Five microliter of PCR product was separated by 1.5% agarose gels electrophoresis in 1XTBE buffer and stained with ethidium bromide.

Figure 17 The organization of plant ribosomal RNA gene

Table 4 The ITS primers used in this PCR amplification

Primer	Direction	Sequencing (5'-3')	Length (bp)	Tm (ºC)
ITS5	Forward	GGAAGTAAAAGTCGTAACAAG G	22	55
ITS4	Reverse	TCCTCCGCTTATTGAGC	20	56

PCR amplification of *rbc*L gene

*rbc*L gene was amplified using a pair of primer as shown in Figure 18 and Table 5. PCR amplification was performed in a 25 µl reaction volume, containing of 1X PCR buffer (100 mM KCl, 20 mM Tris-HCl (pH 8.0), 2.5 mM $MgCl_2$, 0.2 mM dNTPs, 0.2 µM of each primers, 0.5 unit of *Taq* DNA polymerase and 1 µl of DNA template. PCR amplification was performed in Thermal cycler under the following condition: initial denaturation step at 95 ºC for 5 minutes, followed by 30 cycles of denaturation at 95 ºC for 30 second, primer annealing at 55 ºC for 30 second, primer extension at 72 ºC for 30 second, and a final extension at 72 ºC for 5 minutes, and then hold at 4 ºC. Five microliter of PCR product was separated by 1.5% agarose gels electrophoresis in 1X TBE buffer and stained with ethidium bromide.

Figure 18 Structure of *rbc*L gene

Table 5 The *rbc*L primers used in this PCR amplification

Primer	Direction	Sequencing (5'-3')	Length (bp)	Tm (ºC)
*rbc*L	Forward	TGTCACCACAAACAGAGACTAAAGCA	29	62
*rbc*L	Reverse	AGTCTTTTAGTAAAGATTGGGCCGAG	23	59

PCR amplification of *mat*K gene

*mat*K gene was amplification using a pair of primer as shown in Figure 19 and Table 6. PCR amplification was performed in a 25 µl reaction volume, containing of 1X PCR buffer (100 mM KCl, 20 mM Tris-HCl (pH 8.0), 2.5 mM $MgCl_2$, 0.2 mM dNTPs, 0.2 µM of each primers, 0.5 unit of *Taq*DNA polymerase and 1 µl of DNA template. PCR amplification was performed in Thermal cycler under the following condition: initial denaturation step at 95 C for 5 minutes, followed by 30 cycles of denaturation at 95 ºC for 30 second, primer annealing at 54 ºC for 30 second, primer extension at 72 ºC for 1 minute, a final extension at 72 ºC following 5 minutes, and then hold at 4 ºC. . Five microliter of PCR product was separated by 1.5% agarose gels electrophoresis in 1X TBE buffer and stained with ethidium bromide.

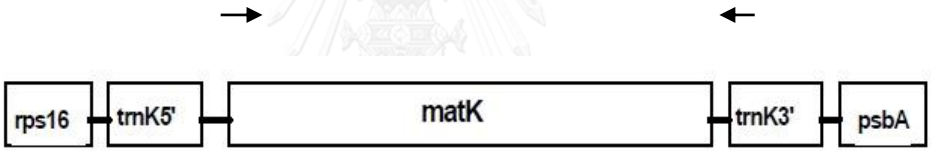


Figure 19 Structure of *mat*K gene and the position of primer

Table 6 The *mat*K primers used in this PCR amplification

Primer	Direction	Sequencing (5'-3')	Length (bp)	Tm (ºC)
*trn*K	Forward	CTGTTGATAAGTTTACCTGCCTCCG	25	70
*trn*K	Reverse	ATTGCACACGGCTTTCCCTATG	22	66

Preparation of 1.5 %agarose gel

Weight 1.5 g of agarose in 100 ml of 1X TBE buffer and solubilized by heating in microwave. Then, let the gel solution to warm before pouring into a plastic tray. After the gel was solid, removed the comb and put the tray into a gel electrophoresis apparatus fulfilled with 1X TBE buffer in chamber. Five microliter of each amplified PCR products was analyzed in 1.5% agarose gel electrophoresis comparison with 1 kb molecular weight marker. Electrophoresis was performed at constant voltage of 100 volts until the faster migration dye (bromophenol blue) has traveled at the end of gel and then stained with ethidium bromide. The agarose gel was visualized under UV transilluminator and photographed.

DNA sequencing analysis

Procedure

The PCR products were purified by PCR purification kit (QIAGEN) according to the manufacturer's protocol prior sequencing (ABI system). The ITS region, *rbc*L and *mat*K sequences from both sense and antisense stand were sequenced and analyzed using BioEdit sequence alignment version 7.0.9 for Windows.

PCR-RFLP method

The *mat*K sequences data were analyzed and the PCR products were digested with restriction enzymes (*Dra*I, *Xba*I) according to manufacturer's instructions. Restriction endonucleases recognition site of *Dra*I and *Xba*I were shown in Table 7.

Table 7 List of restriction endonucleases in PCR-RFLP method

Restriction enzyme	Genomic source	Sequencing	Restriction condition
*Dra*I	*Deinococcus radiophilus*	5′...TTT▼AAA...3′ 3′...AAA▲TTT...5′	37 ºC
*Xba*I	*Xanthomonas badrii*	5′...T▼CTAGA...3′ 3′...AGATC▲T...5′	37 ºC

Procedure

The digestion of PCR products was performed according to instructions from the manufacturer. The reaction mixture was carried out in 20 µl which consisting of 10 µl of *mat*K gene PCR amplification product, 2 µl of restriction buffer, 10 U/µl restriction enzyme. The reaction was incubated at temperature 37 ºC for 30 minute in shaking incubator. Ten microliter of the restriction reaction were separated through their length by 1% agarose gel electrophorese along with 1 kb DNA ladder. Electrophoresis was performed in 1X TBE buffer at constant voltage of 80 volts until the faster migration dye (bromophenol blue) has traveled to two-third of gel and then stained with ethidium bromide. Fragment patterns were analyzed under UV transilluminator and photographed.

CHAPTER IV

RESULTS

Sample collection

Total twelve specimens of *S. thorelii, S. lucida*, *S. nux-vomica* and *S. nux-blanda* were collected from Bangkok, Chachoengsao, Songkla, Chonburi, Nonthaburi, Chiangmai and Pathum Thani provinces in Thailand, during August, 2014 to February, 2015. The collecting locality details were shown in Table 8.

Table 8 Leaves of selected *Strychnos* species from difference locations in Thailand

Strychnos Species	Sample no	Location	Collecting date	Voucher ID
S. thorelii	1	Chachoengsao	Aug, 2014	St1
	2	Chachoengsao	Aug, 2014	St2
	3	Chonburi	Oct, 2014	St3
S. lucida	1	Bangkok	Sep,2014	Sl1
	2	Pathum Thani	Sep,2014	Sl2
	3	Nonthaburi	Feb, 2015	Sl3
S. nux-vomica	1	Pathum Thani	Sep, 2014	Sv1
	2	Khon Kaen	Nov, 2014	Sv2
	3	Songkhla	Nov, 2014	Sv3
S. nux- blanda	1	Chiang Mai	Nov, 2014	Sb1
	2	Chiang Mai	Nov, 2014	Sb2
	3	Chiang Mai	Nov, 2014	Sb3

Macroscopic and microscopic evaluations

Macroscopic evaluation

Macroscopic evaluation of four *Strychnos* species were revealed as followed;

***Strychnos thorelii* Pierre ex Dop**

Leaves oblong-ovate to lanceolate, 4.5 to 14 long, 2 to 5 cm wide, chartaceous to coriaceous, shining above, sometimes sparsely patently hairy on the midrib beneath, otherwise glabrous; base broadly cuneate to cordate, apex gradually acute-acuminate, , basal veins 3-5. Leaves of *S. thorelii* were shown in Figure 20. The whole plant of *S. thorelii* was demonstrated in Figure 21.

Figure 20 Leaves of *Strychnos thorelii* **Pierre ex Dop**

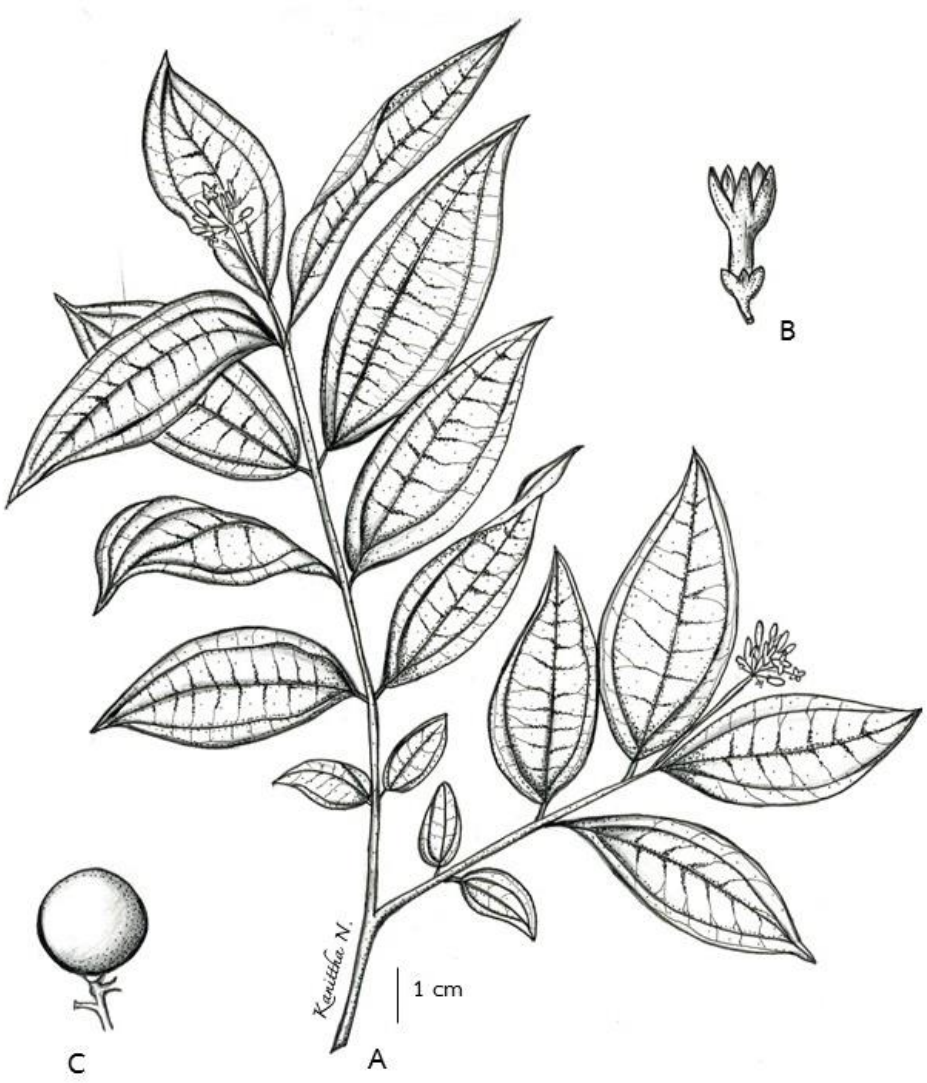


Figure 21 The whole plant of *Strychnos thorelii* Pierre ex Dop (A) flower (B) and berry (C)

***Strychnos lucida* R.Br.**

Leaf blade 2.5 to 10 long, 1.5 to 6 cm wide, thin papery, glabrous, abaxially granular, base cuneate to cordate, apex rounded, obtuse, or acute, basal veins 3-5. Leaves of S. lucida in Figure 22. The whole plant of *S. lucida* was demonstrated in Figure 23.

Figure 22 Leaves of *Strychnos lucida* R.Br.

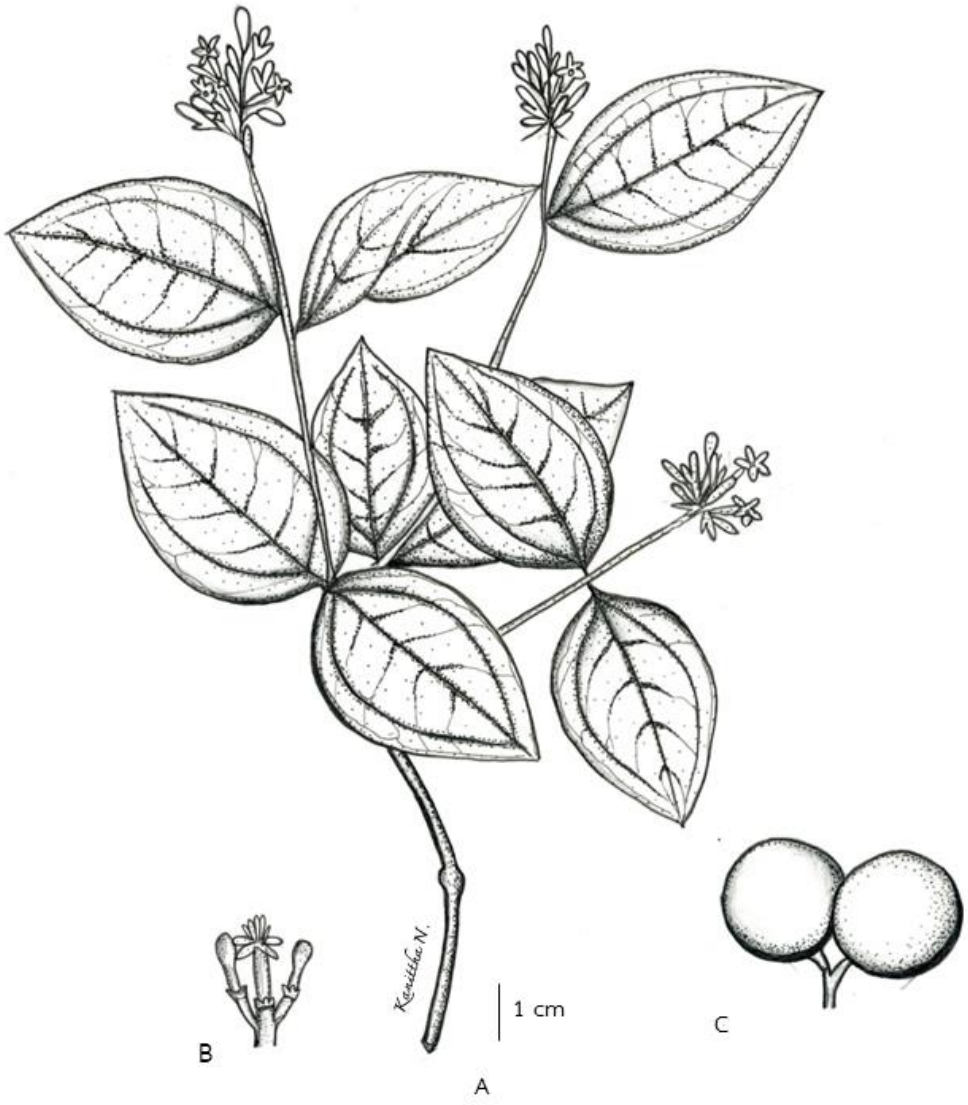


Figure 23 The whole plant of *Strychnos lucida* R.Br.(A), flower (B) and berries (C)

***Strychnos nux-vomica* L.**

Leaf blade suborbicular, broadly elliptic, or ovate, 5 to 18 long, 4 to 12.5 cm wild, papery, abaxially minutely hairy especially on veins, adaxially glabrous and shiny, base rounded to cordate, apex short acuminate to acute and often mucronulate, basal veins 3-5. Leaves of *S. nux-vomica* were shown in Figure 24. The whole plant of *S. nux-vomica* was demonstrated in Figure 25.

Figure 24 Leaves of *Strychnos nux-vomica* L.

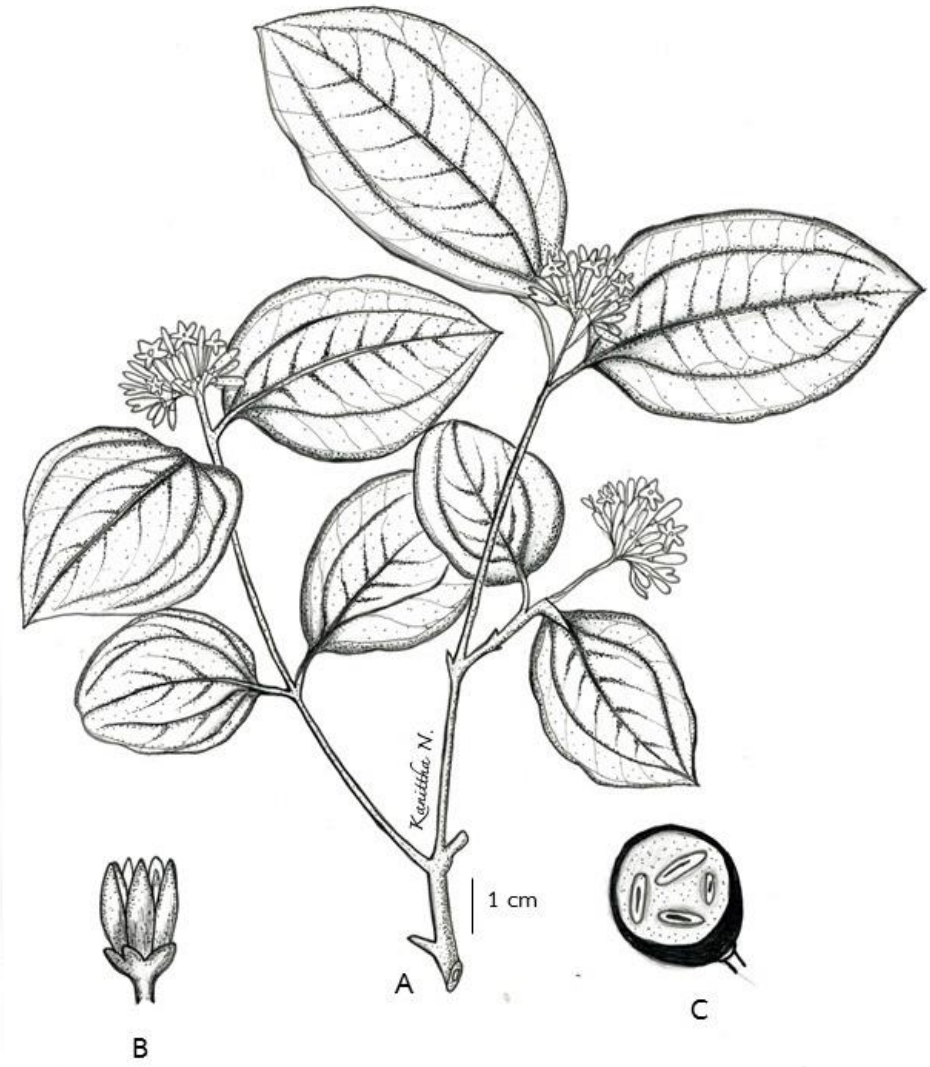


Figure 25 The whole plant of *Strychnos nux-vomica* L. (A), flower (B) and berry (C)

***Strychnos nux-blanda* A. W. Hill**

Leaves simple, opposite broadly ovate, 7 to 16 cm long. 9 to 22 cm wide, base broadly cuneate to cordate, apex gradually acute-acuminate. Laves are three to five veined from the base. Leaves of S. nux-blanda were shown in Figure 26. The whole plant of *S. nux-blanda* was demonstrated in Figure 27.

Figure 26 Leaves of *Strychnos nux-blanda* A. W. Hill

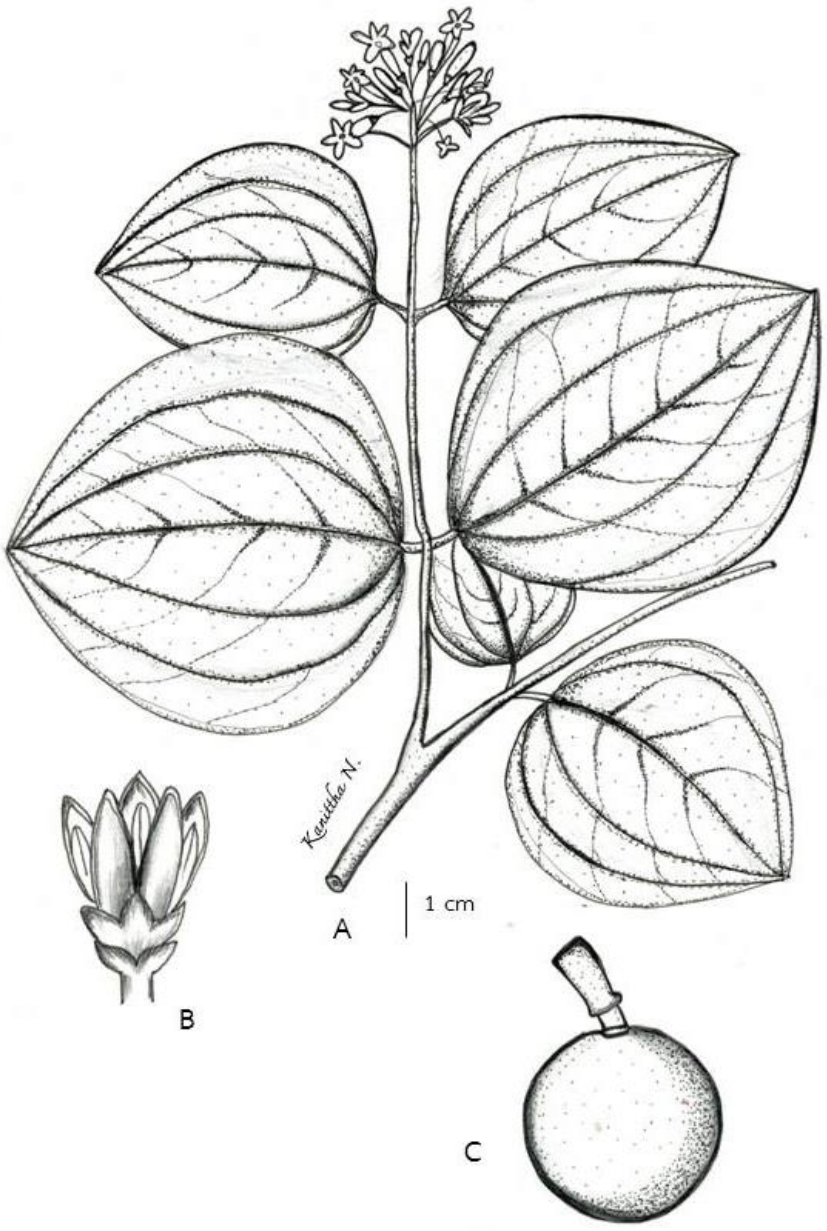


Figure 27 The whole plant of *Strychnos nux-blanda* A. W. Hill (A) flower (B) and berry (C)

Microscopic evaluation

Microscopic character of four *Strychnos* species were examined in both upper and lower epidermis, and transverse section of midrib. The outline drawings of midrib transvers sectional view of each species the feature characteristics were found and described as below

a) *S. thorelii;* the upper and lower surface is covered by single layer of epidermis. The upper epidermis showed the presence of well-developed cuticle without any trichomes. The midrib was composed of one collenchyma layer cells underneath the epidermis of both upper and lower epidermal. The mesophyll showed the presence of distinct one palisade layer and spongy parenchyma. Vascular bundles are conjoint, bi-collateral and exarch. All these vascular bundle are surrounded by sclerenchyma tissue as illustrated in Figure 28.

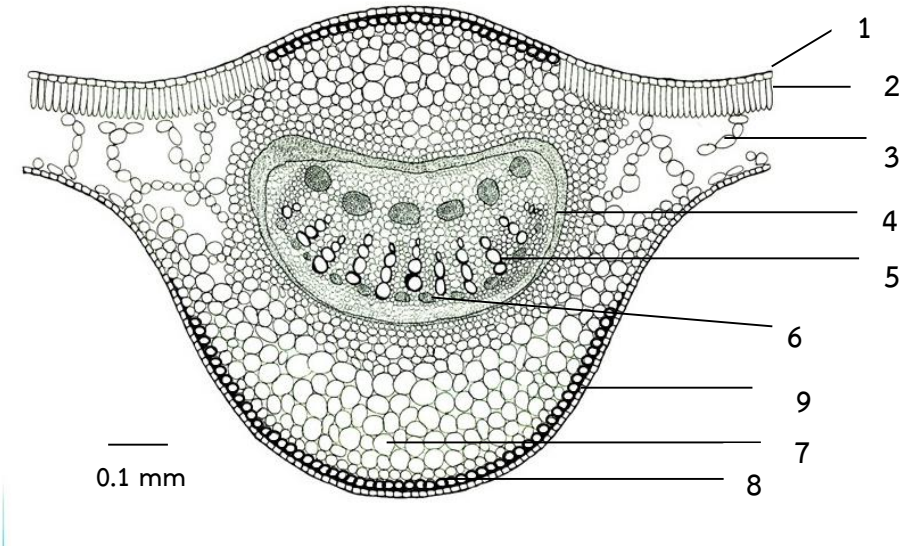


Figure 28 The transverse section of *S. thorelii* leaf through midrib
1. Upper epidermis, 2. Palisade cell, 3. Spongy cell, 4. Sclerenchyma (fiber), 5. Xylem, 6. Phloem, 7. Parenchyma, 8. Collenchyma, 9. Lower epidermis

b) *S. lucida;* the upper and lower surface is covered by single layer of epidermis. The upper epidermis showed the presence of well-developed cuticle without any trichomes. The midrib was composed of 2-3 collenchyma layer cells underneath the epidermis of both upper and lower epidermal. The mesophyll was composed of two palisade layers and various spongy cells. Vascular bundles are conjoint, bi-collateral and exarch. The vascular bundles were towards the dorsal side two big vascular are also present. All these vascular bundle are surrounded by sclerenchyma tissue as shown in Figure 29.

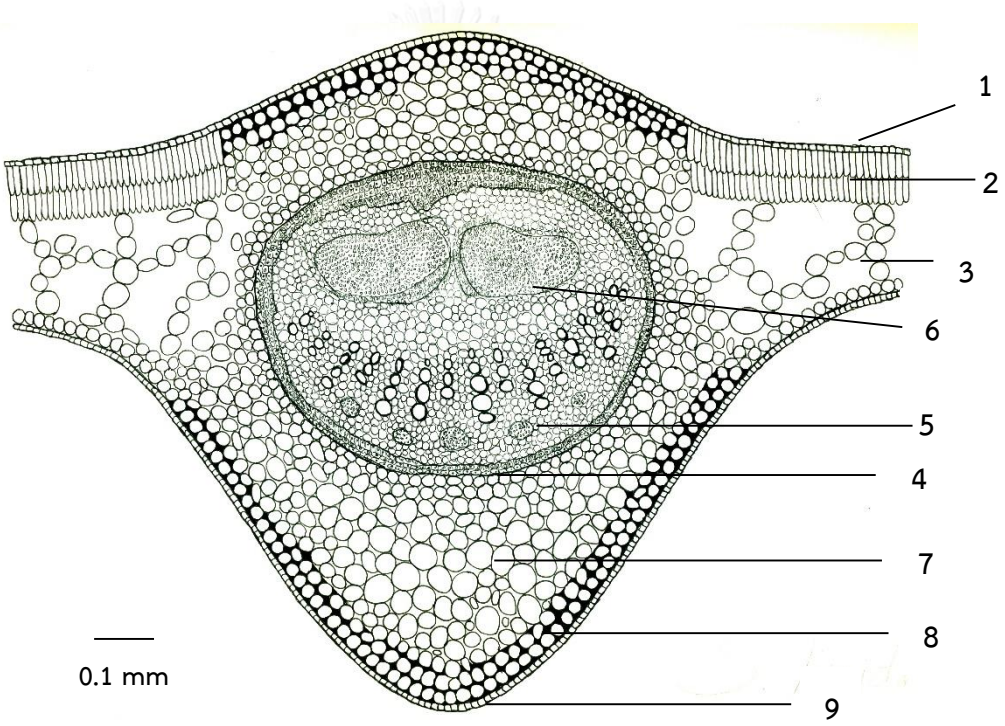


Figure 29 The transverse section of *S. lucida* leaf through midrib
1. Upper epidermis, 2. Palisade cell, 3. Spongy cell, 4. Sclerenchyma (fiber), 5. Xylem, 6. Phloem, 7. Parenchyma, 8. Collenchyma, 9. Lower epidermis

c) *S. nux-vomica*; the upper and lower surface is covered by single layer of epidermis. The upper epidermis showed the presence of well-developed cuticle without any trichomes. The midrib was composed of 2-3 collenchyma layer cells underneath the epidermis of both upper and lower epidermal. The mesophyll showed the presence of distinct two palisade layer and spongy parenchyma. Vascular bundles are conjoint, bi-collateral and exarch. All these vascular bundle are surrounded by sclerenchyma tissue as shown in Figure 30.

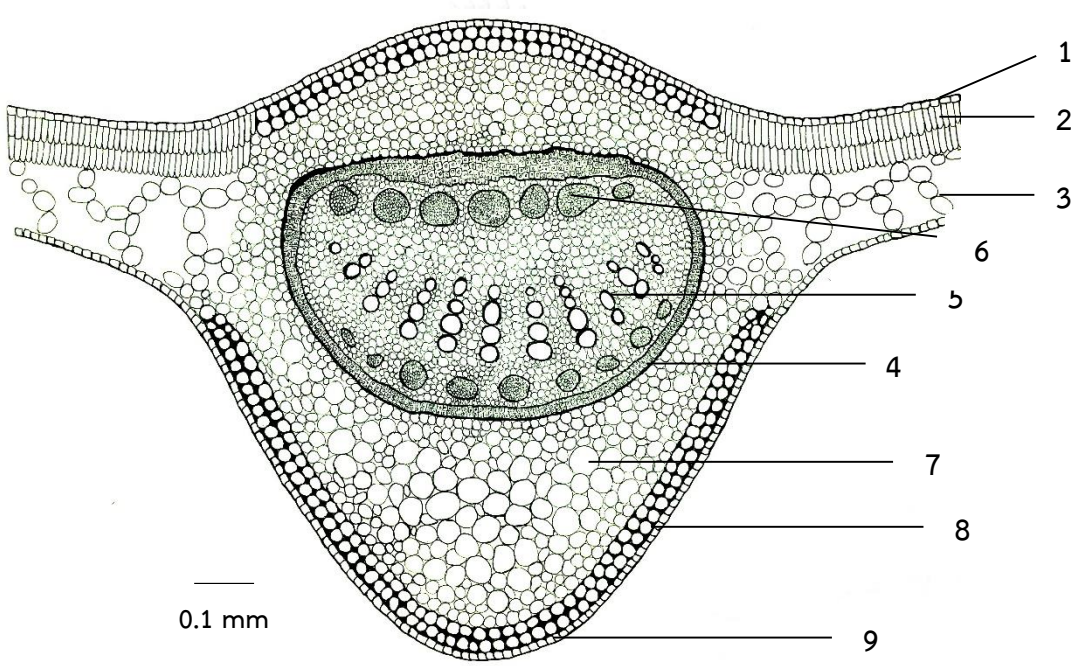


Figure 30 The transverse section of *S. nux-vomica* leaf through midrib
1. Upper epidermis, 2. Palisade cell, 3. Spongy cell, 4. Sclerenchyma (fiber), 5. Xylem, 6. Phloem, 7. Parenchyma, 8. Collenchyma, 9. Lower epidermis

d) *S. nux-blanda;* the upper and lower surface is covered by single layer of epidermis. The upper epidermis showed the presence of thick cuticle, without any trichomes. The midrib was composed of 3-4 collenchyma layer cells underneath the epidermis of both upper and lower epidermal. The mesophyll showed the presence of distinct two palisade layer and spongy parenchyma. Vascular bundles are conjoint, bi-collateral and exarch. All these vascular bundle are surrounded by sclerenchyma tissue as shown in Figure 31.

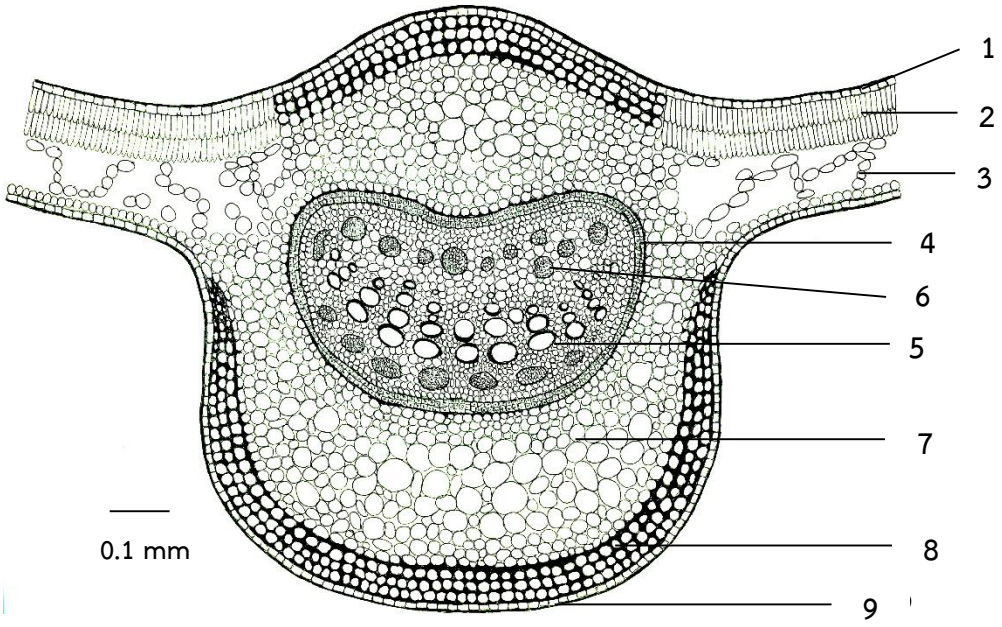


Figure 31 The transverse section of *S. nux-blanda* leaf through midrib
1. Upper epidermis, 2. Palisade cell, 3. Spongy cell, 4. Sclerenchyma (fiber), 5. Xylem, 6. Phloem, 7. Parenchyma, 8. Collenchyma, 9. Lower epidermis

According to the following characteristics of midrib transverse section of each species, the xylem, phloem, parenchyma and sclerenchyma are arranged together to form a vascular bundle. There are different type of vascular bundle depending on arrangement of conducting tissues. Layer of palisade and collenchyma cell was different.

The stomatal classification

The stoma type of four *Strychnos* species were classified as paracytic type, consisting of two subsidiary cells with the parallel to long axis of the stoma. The lower epidermis characteristics and of stomata among four *Strychnos* species were demonstrated in Figure 32.

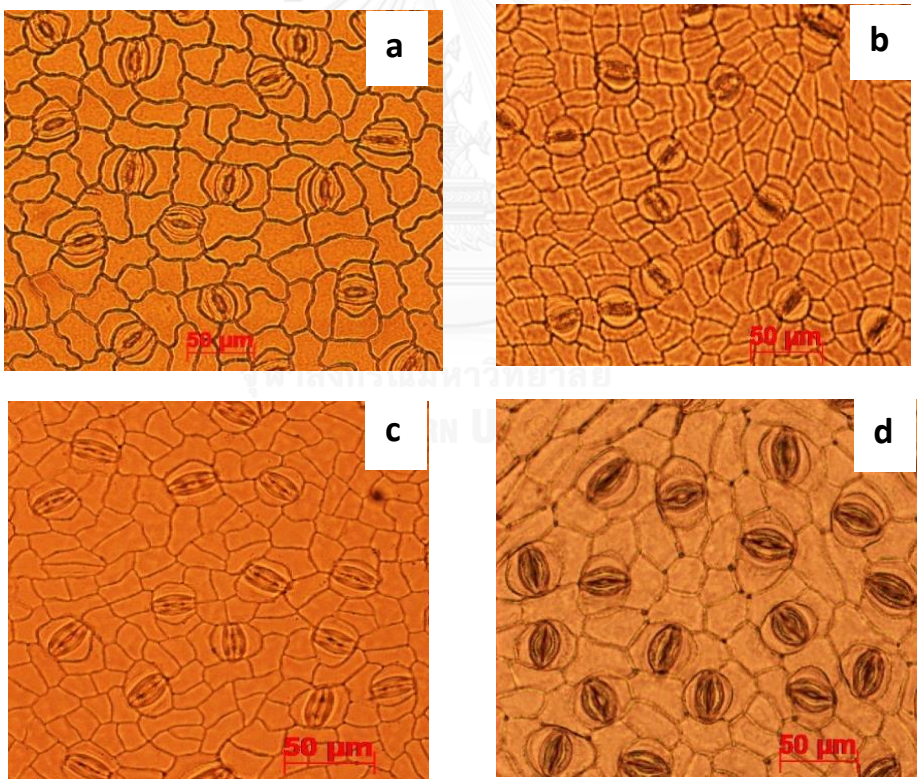


Figure 32 Paracytic type stoma of four *Strychnos* species

(a) *S. thorelii,* (b) *S. lucida,* (c) *S. nux-vomica and* (*d) S. nux-blanda*

Leaf constant numbers

The leaf constant numbers consisting of stomatal number, stomatal index, palisade ratio, veinlet termination number, epidermal cell number and epidermal cell area by microscopic analyses were as mean ±SD of each sample.

Stomatal number and stomatal index

The results of stomatal number and stomatal index of *S. thorelii, S. lucida, S. nux-vomica and S. nux-blanda* from three different locations were illustrated in Table 9. The stomatal index among four species were different from each other with the highest value of *S. nux-blanda* (15.98±1.0) and the lowest value of *S. lucida (*7.11±0.51).

Table 9 The stomatal number and stomatal index from four *Strychnos* species

Strychnos species	Sample no.	Stomatal number (sq.mm)	Stomatal index
S. thorelii	1	154.27±9.95	11.72±0.66
	2	164.93±11.51	11.51±0.85
	3	166.67±13.13	11.98±0.99
	Avg.	161.96±11.53	11.74±0.83
S. lucida	1	167.47±15.16	6.77±0.73
	2	177.87±14.16	7.52±0.64
	3	170.40±14.16	7.35±0.50
	Avg.	171.91±13.31	7.11±0.51
S. nux-vomica	1	214.93±14.13	8.71±0.51
	2	202.93±11.16	8.74±0.48
	3	196.40±11.95	8.56±0.50
	Avg.	204.75±12.41	8.67±0.50
S. nux-blanda	1	239.33±13.62	15.24±0.68
	2	257.33±18.03	16.44±1.14
	3	254.93±20.37	16.26±1.18
	Avg.	250.53±17.34	15.98±1.0

Palisade ratio

The palisade ratio of four *strychnos* species from three different locations were shown in Table 10. The highest value of palisade ratio was found in *S. nux-blanda (*12.29±0.82) and the lowest value was found in *S. thorelii* (4.42±0.49). The palisade cells of four *Strychnos* species was shown in Figure 33.

Table 10 The palisade cells of four *Strychnos* species

Strychnos species	Sample no.	Palisade ratio
S. thorelii	1	4.41±0.48
	2	4.44±0.48
	3	4.42±0.58
	Avg.	4.42±0.49
S. lucida	1	6.50±0.73
	2	6.79±0.78
	3	6.78±0.69
	Avg.	6.69±0.73
S. nux-vomica	1	7.98±0.75
	2	9.36±0.72
	3	9.45±0.82
	Avg.	8.93±0.76
S. nux-blanda	1	12.08±0.81
	2	12.53±0.81
	3	12.27±0.85
	Avg.	12.29±0.82

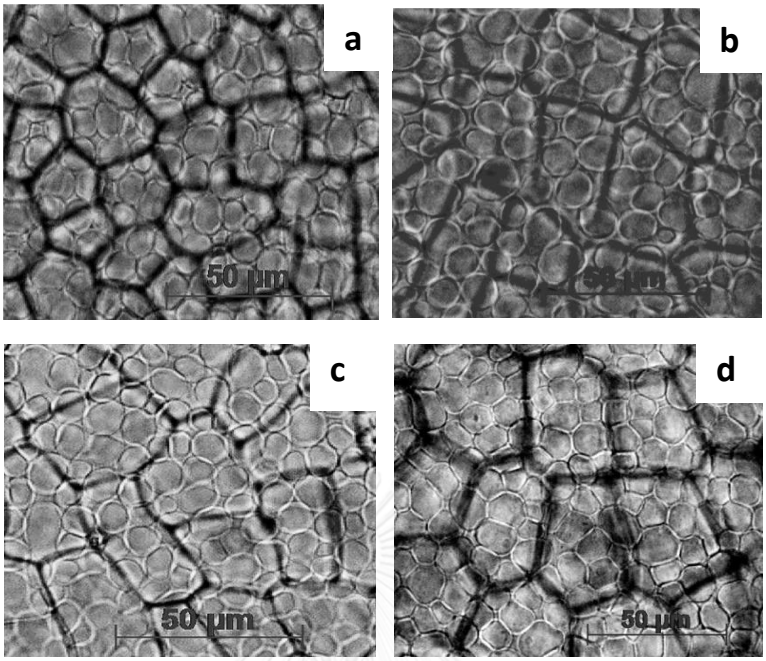


Figure 33 Palisade cell of four *Strychnos* species (a) *S. thorelii* (b) *S. lucida* (c) *S. nux-vomica* and (d) *S. nux-blanda*

Epidermal cell number and epidermal cell area

Epidermal cell area was examined on upper epidermis among four *Strychnos* species. The highest epidermal cell area per square micrometer was found in *S. nux-blanda (*1102.71±24.74). The lowest epidermal cell area was found in *S. lucida* (422.47±8.04). The epidermal cell number and epidermal cell area of four *Strychnos* species from three locations was shown in Table 11 and the epidermal cells characteristics was shown in Figure 34.

Table 11 The epidermal cell number and epidermal cell area from four *Strychnos* species

Strychnos species	Sample no.	Epidermal cell number (sq.mm)	Epidermal cell area (sq.μm)
S. thorelii	1	1628.40±37.89	614.31±13.85
	2	1648.93±38.25	606.77±14.00
	3	1658.67±46.26	598.83±12.89
	Avg.	1645.33±40.80	606.64±13.58
S. lucida	1	2386.35±47.57	419.32±8.32
	2	2349.75±45.05	425.75±8.10
	3	2368.53±43.23	422.34±7.69
	Avg.	2368.22±43.28	422.47±8.04
S. nux-vomica	1	1411.93±30.79	709.16±15.30
	2	1398.00±34.53	724.61±17.79
	3	1310.13±31.87	710.23±18.04
	Avg.	1374.35±32.40	711.05±17.04
S. nux-blanda	1	884.67±20.75	1130.95±25.82
	2	940.53±18.84	1063.64±21.57
	3	898.53±21.37	1113.56±26.82
	Avg.	907.91±20.37	1102.71±24.74

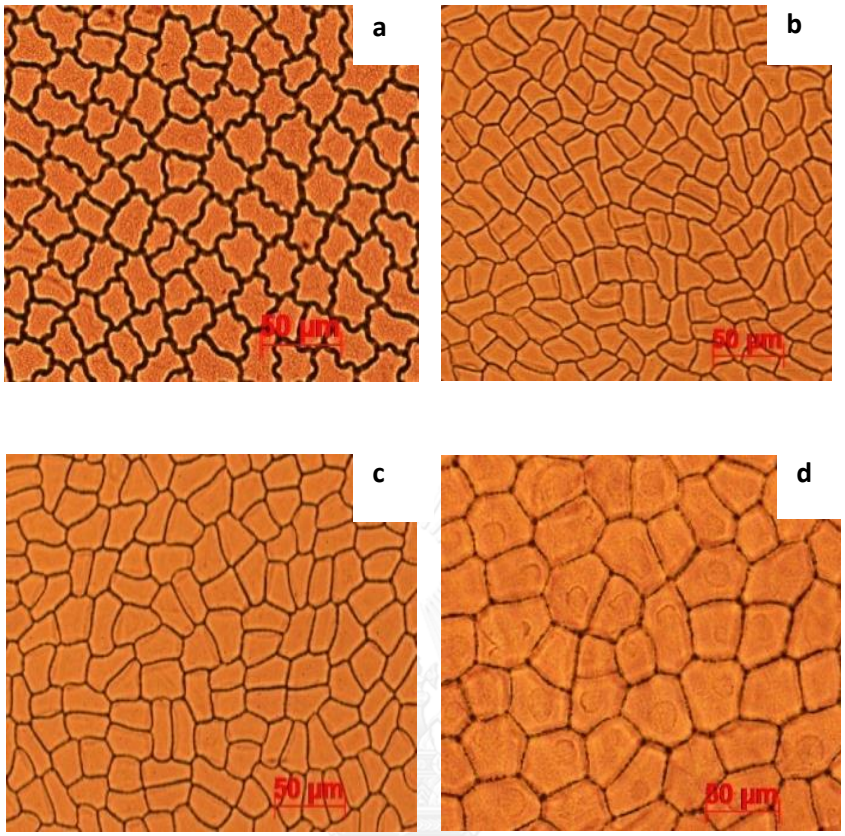


Figure 34 Upper epidermis cell of four *Strychnos* species
(a) S. thorelii, (b) S. lucida, (c) S. nux-vomica and (d) S. nux-bland

Veinlet termination number

Veinlet termination numbers of four *Strychnos* species were shown in Table 12. The highest veinlet termination number was found in *S. nux-blanda* (17.93±1.75) and the lowest epidermal cell area was found in *S. thorelii* (15.47 ±1.13), the veinlet termination characters were in Figure 35.

Table 12 The veinlet termination number from four *Strychnos* species

***Strychnos* species**	**Sample no.**	**Veinlet termination number (sq.mm)**
S. thorelii	1	16.18±1.14
	2	14.57±1.13
	3	15.65±1.13
	Avg.	15.47 ±1.13
S. lucida	1	16.42±1.51
	2	16.66±1.63
	3	16.63±1.96
	Avg.	16.57±1.80
S. nux-vomica	1	19.22±1.84
	2	17.06±1.65
	3	17.78±1.95
	Avg.	17.93±1.75
S. nux-blanda	1	16.35±1.66
	2	16.92±1.29
	3	15.49±1.21
	Avg.	16.25±1.39

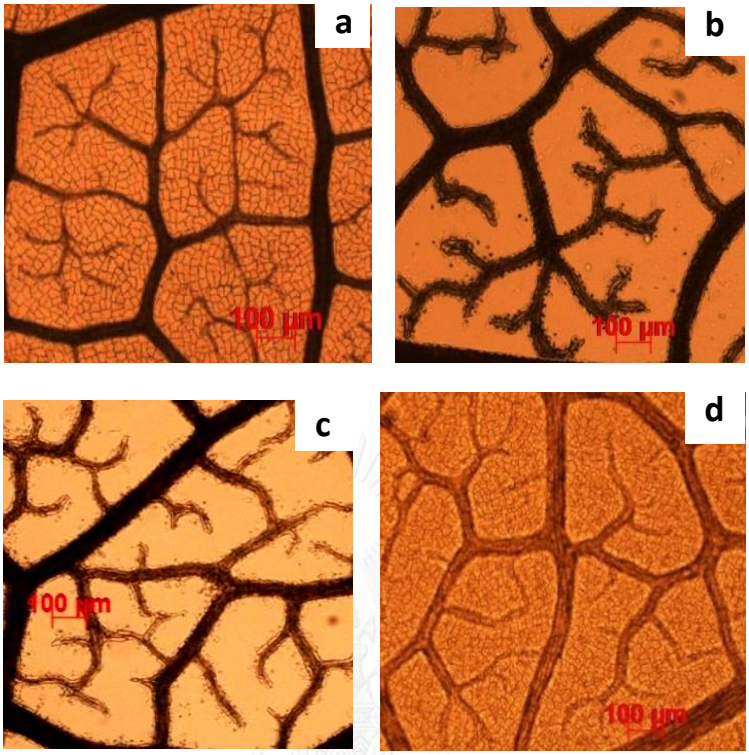


Figure 35 Veinlet termination of four *Strychnos* species

(a) *S. thorelii* (b) *S. lucida* (c) *S. nux-vomica* and (d) *S. nux-blanda*

The summary of leaf constant numbers consisting of stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of four *Strychnos* species were shown in Table 13 and the raw data of each parameters were shown in appendix A.

Table 13 Summary of the leaf constant numbers consisting of stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number from four *Strychnos* species

Strychnos species	Sample no.	Stomatal number (sq.mm)	Stomatal index	Palisade ratio	Epidermal cell number (sq.mm)	Epidermal cell area (sq.µm)	Veinlet termination number (sq.mm)
S. thorelii	1	154.27±9.95	11.72±0.66	4.41±0.48	1628.40±37.89	614.31±13.85	16.18±1.14
	2	164.93±11.51	11.51±0.85	4.44±0.48	1648.93±38.25	606.77±14.00	14.57±1.13
	3	166.67±13.13	11.98±0.99	4.42±0.58	1658.67±46.26	598.83±12.89	15.65±1.13
	avg.	161.96±11.53	11.74±0.83	4.42±0.49	1645.33±49.54	606.64±13.58	15.47±1.13
S. lucida	1	167.47±15.16	6.77±0.73	6.50±0.73	2386.35±47.57	419.32±8.32	16.42±1.51
	2	177.87±14.16	7.52±0.64	6.79±0.78	2349.75±45.05	425.75±8.10	16.66±1.63
	3	170.40±14.16	7.35±0.50	6.78±0.69	2368.53±43.23	422.34±7.69	16.63±1.96
	avg.	171.91±13.31	7.11±0.51	6.69±0.73	2368.22±43.28	422.47±8.04	16.57±1.80
S. nux-vomica	1	214.93±14.13	8.71±0.51	7.98±0.75	1411.93±30.79	709.16±15.30	19.22±1.84
	2	202.93±11.16	8.74±0.48	9.36±0.72	1398.00±34.53	724.61±17.79	17.06±1.65
	3	196.40±11.95	8.56±0.50	9.45±0.82	1310.13±31.87	710.23±18.04	17.78±1.95
	avg.	204.75±12.41	8.67±0.50	8.93±0.76	1374.35±32.40	711.05±17.04	17.93±1.75
S. nux-blanda	1	239.33±13.62	15.24±0.68	12.08±0.81	884.67±20.75	1130.95±25.82	16.35±1.66
	2	257.33±18.03	16.44±1.14	12.53±0.81	940.53±18.84	1063.64±21.57	16.92±1.29
	3	254.93±20.37	16.26±1.18	12.27±0.85	898.53±21.37	1113.56±26.82	15.49±1.21
	avg.	250.53±17.34	15.98±1.0	12.29±0.82	907.91±20.37	1102.71±24.74	16.25±1.39

Molecular evaluation

Young fresh leaves of four *Strychnos* species were collected from 16 different locations in Thailand as shown in Table 14.

Table 14 List of four *Strychnos* species collected from16 different locations in Thailand

Strychnos species	Sample no	Location	Collecting date	Voucher ID
S. thorelii	1	Chachoengsao	Aug, 2014	St1
	2	Chachoengsao	Aug, 2014	St2
	3	Chonburi	Oct, 2014	St3
	4	Chonburi	Oct, 2014	St4
S. lucida	1	Bangkok	Sep,2014	Sl1
	2	Pathum Thani	Sep,2014	Sl2
	3	Nonthaburi	Feb, 2015	Sl3
S. nux-vomica	1	Pathum Thani	Sep, 2014	Sv1
	2	Khon Kaen	Nov, 2014	Sv2
	3	Songkhla	Nov, 2014	Sv3
	4	Chachoengsao	Dec, 2014	Sv4
	5	Chanthaburi	Feb, 2015	Sv5
S. nux- blanda	1	Chiang Mai	Nov, 2014	Sb1
	2	Chiang Mai	Nov, 2014	Sb2
	3	Chiang Mai	Nov, 2014	Sb3
	4	Chiang Mai	Nov, 2014	Sb4

The results of DNA extraction

The total genomic DNA was individually isolated from young leaves using modified CTAB method as described in chapter 3. The genomic DNA was examined on 1.5% agarose gel electrophoresis after straining with ethidium bromide as shown in Figure 36. The extracted total DNA was then stored at -20 ºC for further use as DNA templates in PCR amplification.

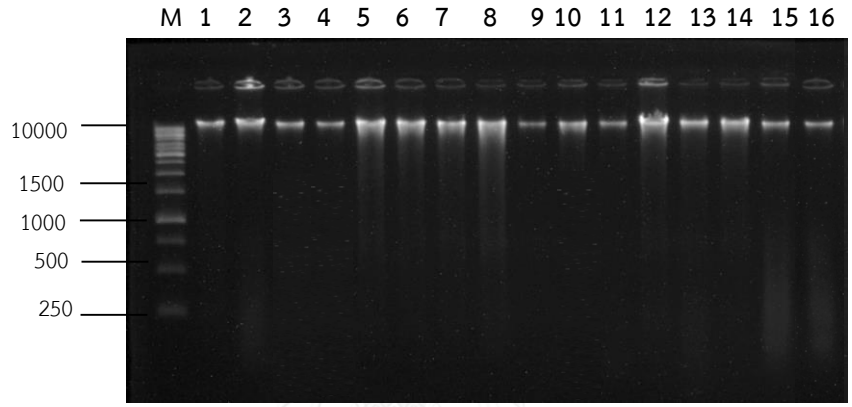


Figure 36 1.5% agarose gel electrophoresis of genomic DNA *Strychnos* species

Lane M: 1 Kb DNA ladder

Lane 1-4: *S. thorelii*

Lane 5-7: *S. lucida*

Lane 8-12: *S. nux-vomica*

Lane 13-16: *S. nux-blanda*

PCR amplifications of ITS region, *rbc*L and *mat*K gene

For amplification of ITS region, a pair of universal PCR primers (ITS5 and ITS4) designed from highly conserved regions flanking the Internal transcribe spacer (ITS) region were used for PCR amplification. The PCR products were dispersed in 1.5% agarose gel electrophoresis. When compared to 1 kb DNA ladder the PCR products were approximately 700 base pairs (bp) in size as shown in Figure 37.

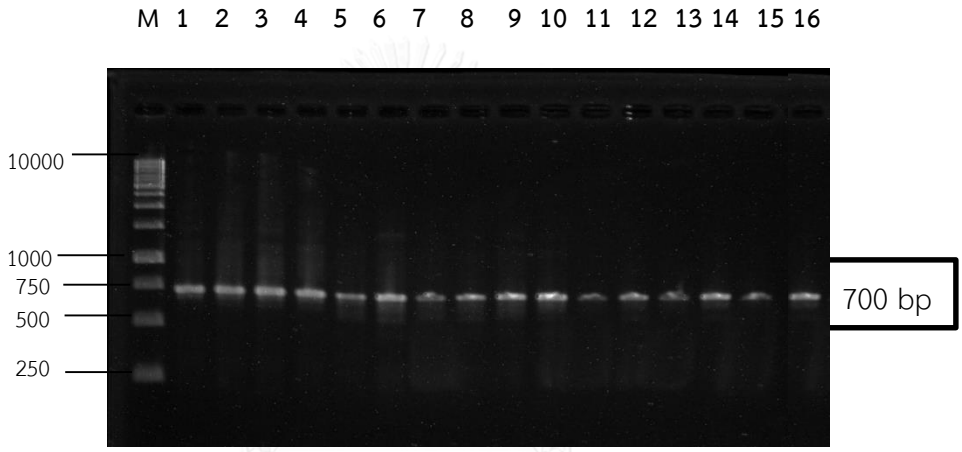


Figure 37 PCR products of ITS on 1.5% agarose gel electrophoresis, stained with ethidium bromide and visualized under UV transilluminator

Lane M: 1 Kb DNA ladder

Lane 1-4: *S. thorelii*

Lane 5-7: *S. lucida*

Lane 8-12: *S. nux-vomica*

Lane 13-16: *S. nux-blanda*

For amplification of *rbc*L gene, a pair of specific *rbc*L PCR primers was used for *rbc*L gene for PCR amplification. The PCR products were dispersed in 1.5% agarose gel electrophoresis. When compared to 1 kb DNA ladder, the PCR products were approximately 1400 bp in size as shown in Figure 38.

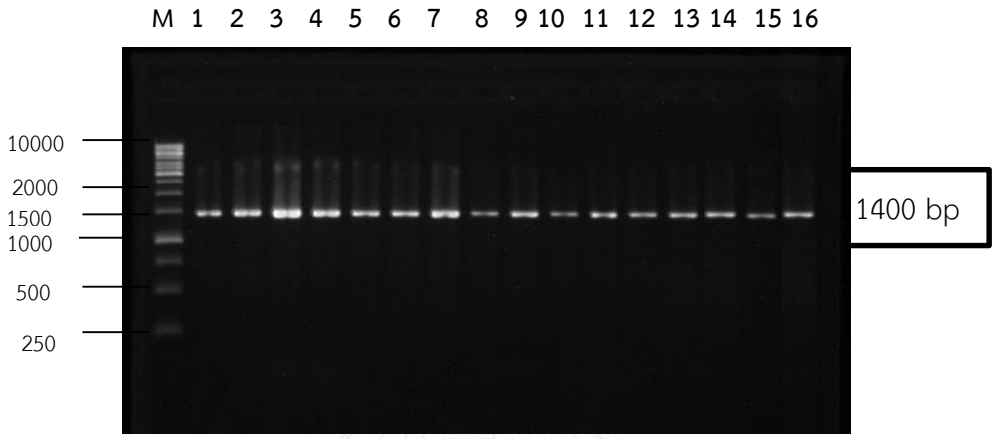


Figure 38 PCR products of *rbc*L gene on 1.5% agarose gel electrophoresis, stained with ethidium bromide and visualized under UV transilluminator

Lane M: 1 Kb DNA ladder

Lane 1-4: *S. thorelii*

Lane 5-7: *S. lucida*

Lane 8-12: *S. nux-vomica*

Lane 13-16: *S. nux-blanda*

For amplification of *mat*K gene, a pair of specific *mat*K PCR primer was used for amplification. The PCR products were dispersed in 1.5% agarose gel electrophoresis. When compared to 1 kb DNA ladder, the PCR products gene were approximately 1800 bp in size shown in Figure 39.

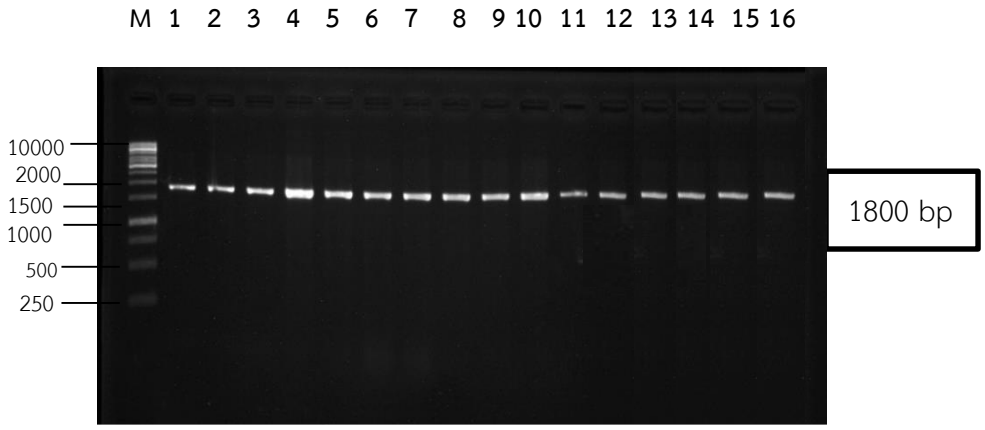


Figure 39 PCR products of *mat*K gene on 1.5% agarose gel electrophoresis, stained with ethidium bromide and visualized under UV transilluminator

Lane M: 1 Kb DNA ladder

Lane 1-4: *S. thorelii*

Lane 5-7: *S. lucida*

Lane 8-12: *S. nux-vomica*

Lane 13-16: *S. nux-blanda*

DNA sequencing

The raw data of DNA sequences of ITS region, *rbc*L gene and *mat*K gene from *S. thorelii, S. lucida, S. nux-vomica* and *S. nux-blanda* were included in Appendix B.

The length of the ITS sequence among four *Strychnos* species were 730-738 bp The similarity of the ITS region nucleotide sequence among the intra-species range from 98 % to 99% while the inter-species range from 87% to 99%.

The length of the *rbc*L sequence among four *Strychnos* species, were from 1440

to 1463 bp. The similarity of the *rbc*L nucleotide sequence among the intra-species range from 95 % to 99% while the inter-species range from 94% to 97%.

The length of the *mat*K sequence among four *Strychnos* species 1808 to 1815 bp in length. The similarity of the *mat*K nucleotide sequence among the intraspecies range from 96 % to 99% while the interspecies range from 90% to 95%.

PCR-RFLP method for species differentiation using *mat*K gene

Based on the alignment of the *mat*K gene of four *Strychnos* species, the polymorphic nucleotides were observed at different positions as shown in Figure 42. The PCR products were digested with two restriction enzymes, *Dra*I and *Xba*I. The restriction fragments were separated on 1% agarose gel electrophoresis along with the 1 Kb ladder molecular marker. The PCR-RFLP pattern of the *mat*K gene was shown in Figure 40-41. When the PCR product was digested with *Xba*I, the PCR-RFLP restriction pattern can be distinguished *S. thorelii* from the other three *Strychnos* species by observing the single uncut 1800 bp band while the other three *Strychnos* species shows the 1400 and 400 bp bands as shown in Figure 40 and Table 15.

To distinguish the three *Strychnos* species, the PCR product was digested with *Dra*I restriction enzyme. The PCR-RFLP restriction pattern can be distinguished *S. nux-vomica, S. lucida* and *S. nux-bland*.

In *S. nux-vomica*, there are two bands of 1620 and 180 fragments in size were observed after digestion with *Dra*I. For *S. lucida,* there are three bands of 1150, 360 and 290 fragments in size while *S. nux-blanda* showed the three bands of 1210, 380 and 210 fragments in size after digestion with *Dra*I restriction enzyme as shown in Figure 41 and Table 15.

Table 15 The size of restriction fragment of four *Strychnos* species digest with *Xba*I and *Dra*I

Strychnos **Species**	**Restriction fragment (base pair)**	
	***Xba*I**	***Dra*I**
S. thorelii	1800	1210, 380, 210
S. lucida	1400, 400	1150, 360, 290
S. nux-vomica	1400, 400	1620, 180
S. nux-blanda	1400, 400	1210, 380, 210

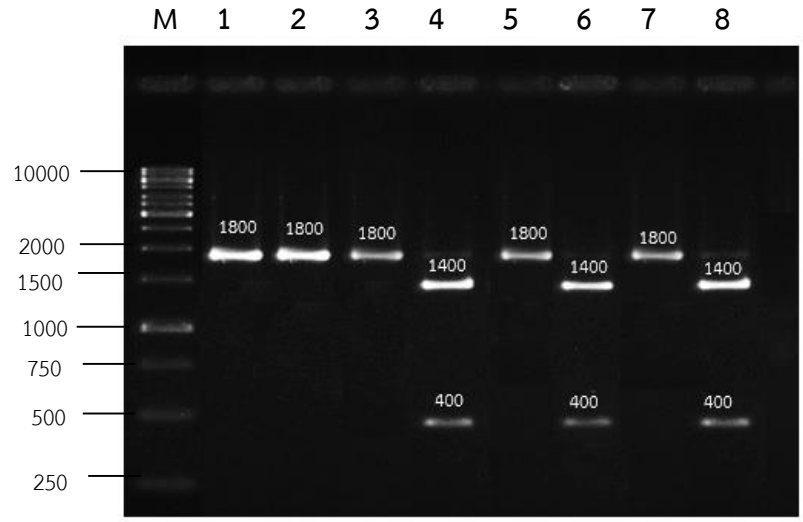


Figure 40 PCR-RFLP pattern of four *Strychnos* species digested with *Xba*I

Lane M: 1 Kb DNA ladder

Lane 1: undigested PCR product of *S. thorelii*

Lane 2: *Xba*I digested PCR product of *S. thorelii*

Lane 3: undigested PCR product of *S. nux-vomica*

Lane 4: *Xba*I digested PCR product of *S. nux-vomica*

Lane 5: undigested PCR product of *S. lucida*

Lane 6: *Xba*I digested PCR product of *S. lucida*

Lane 7: undigested PCR product of *S. nux- blanda*

Lane 8: *Xba*I digested PCR product of *S. nux- blanda*

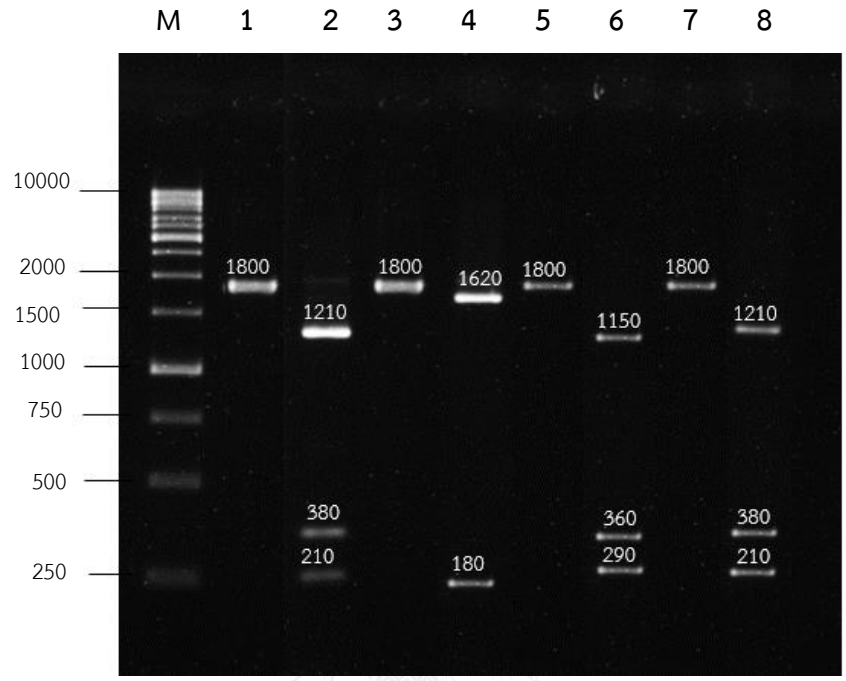


Figure 41 PCR-RFLP pattern of four *Strychnos* species digested with *Dra*I

Lane M: 1 Kb DNA ladder

Lane 1: undigested PCR product of *S. thorelii*

Lane 2: *Dra*I digested PCR product of *S. thorelii*

Lane 3: undigested PCR product of *S. nux-vomica*

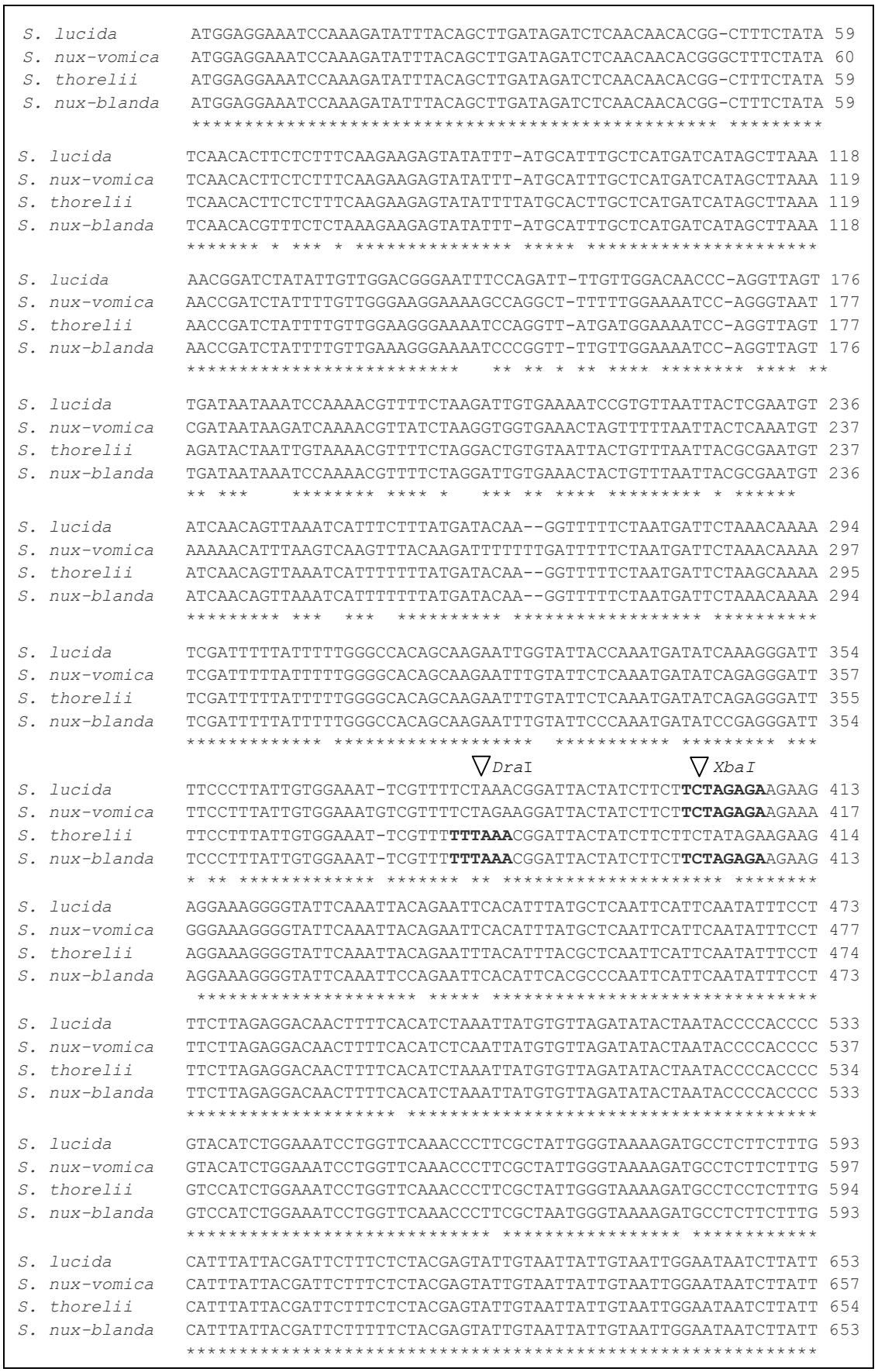
Lane 4: *Dra*I digested PCR product of *S. nux-vomica*

Lane 5: undigested PCR product of *S. lucida*

Lane 6: *Dra*I digested PCR product of *S. lucida*

Lane 7: undigested PCR product of *S. nux- blanda*

Lane 8: *Dra*I digested PCR product of *S. nux- blanda*


S. lucida ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGG-CTTTCTATA 59
S. nux-vomica ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGGCTTTCTATA 60
S. thorelii ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGG-CTTTCTATA 59
S. nux-blanda ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGG-CTTTCTATA 59
S. lucida TCAACACTTCTCTTTCAAGAAGAGTATATTT-ATGCATTTGCTCATGATCATAGCTTAAA 118
S. nux-vomica TCAACACTTCTCTTTCAAGAAGAGTATATTT-ATGCATTTGCTCATGATCATAGCTTAAA 119
S. thorelii TCAACACTTCTCTTTCAAGAAGAGTATATTTTATGCACTTGCTCATGATCATAGCTTAAA 119
S. nux-blanda TCAACACGTTTCTCTAAAGAAGAGTATATTT-ATGCATTTGCTCATGATCATAGCTTAAA 118
S. lucida AACGGATCTATATTGTTGGACGGGAATTTCCAGATT-TTGTTGGACAACCC-AGGTTAGT 176
S. nux-vomica AACCGATCTATTTTGTTGGGAAGGAAAAGCCAGGCT-TTTTTGGAAAATCC-AGGGTAAT 177
S. thorelii AACCGATCTATTTTGTTGGAAGGGAAAATCCAGGTT-ATGATGGAAAATCC-AGGTTAGT 177
S. nux-blanda AACCGATCTATTTTGTTGAAAGGGAAAATCCCGGTT-TTGTTGGAAAATCC-AGGTTAGT 176
S. lucida TGATAATAAATCCAAAACGTTTTCTAAGATTGTGAAAATCCGTGTTAATTACTCGAATGT 236
S. nux-vomica CGATAATAAGATCAAAACGTTATCTAAGGTGGTGAAACTAGTTTTTAATTACTCAAATGT 237
S. thorelii AGATACTAATTGTAAAACGTTTTCTAGGACTGTGTAATTACTGTTTAATTACGCGAATGT 237
S. nux-blanda TGATAATAAATCCAAAACGTTTTCTAGGATTGTGAAACTACTGTTTAATTACGCGAATGT 236
S. lucida ATCAACAGTTAAATCATTTCTTTATGATACAA--GGTTTTTCTAATGATTCTAAACAAAA 294
S. nux-vomica AAAAACATTTAAGTCAAGTTTACAAGATTTTTTTGATTTTTCTAATGATTCTAAACAAAA 297
S. thorelii ATCAACAGTTAAATCATTTTTTTTATGATACAA--GGTTTTTCTAATGATTCTAAGCAAAA 295
S. nux-blanda ATCAACAGTTAAATCATTTTTTTTATGATACAA--GGTTTTTCTAATGATTCTAAACAAAA 294
DraI
XbaI
S. lucida TCGATTTTTATTTTTGGGCCACAGCAAGAATTGGTATTACCAAATGATATCAAAGGGATT 354
S. nux-vomica TCGATTTTTATTTTTGGGGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATT 357
S. thorelii TCGATTTTTATTTTTGGGGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATT 355
S. nux-blanda TCGATTTTTATTTTTGGGCCACAGCAAGAATTTGTATTCCCAAATGATATCCGAGGGATT 354
S. lucida TTCCCTTATTGTGGAAAT-TCGTTTTCTAAACGGATTACTATCTTCTTCTAGAGAAGAAG 413
S. nux-vomica TTCCTTTATTGTGGAAATGTCGTTTTCTAGAAGGATTACTATCTTCTTCTAGAGAAGAAA 417
S. thorelii TTCCTTTATTGTGGAAAT-TCGTTTTTTAAACGGATTACTATCTTCTTCTATAGAAGAAG 414
S. nux-blanda TCCCTTTATTGTGGAAAT-TCGTTTTTTAAACGGATTACTATCTTCTTCTAGAGAAGAAG 413
S. lucida AGGAAAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCT 473
S. nux-vomica GGGAAAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCT 477
S. thorelii AGGAAAGGGGTATTCAAATTACAGAATTTACATTTACGCTCAATTCATTCAATATTTCCT 474
S. nux-blanda AGGAAAGGGGTATTCAAATTCCAGAATTCACATTCACGCCCAATTCATTCAATATTTCCT 473
S. lucida TTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTAATACCCCACCCC 533
S. nux-vomica TTCTTAGAGGACAACTTTTCACATCTCAATTATGTGTTAGATATACTAATACCCCACCCC 537
S. thorelii TTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTAATACCCCACCCC 534
S. nux-blanda TTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTAATACCCCACCCC 533
S. lucida GTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTG 593
S. nux-vomica GTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTG 597
S. thorelii GTCCATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCCTCTTTG 594
S. nux-blanda GTCCATCTGGAAATCCTGGTTCAAACCCTTCGCTAATGGGTAAAAGATGCCTCTTCTTTG 593
S. lucida CATTTATTACGATTCTTTCTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 653
S. nux-vomica CATTTATTACGATTCTTTCTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 657
S. thorelii CATTTATTACGATTCTTTCTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 654
S. nux-blanda CATTTATTACGATTCTTTTTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 653

```
S. lucida       TCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTC 713
S. nux-vomica   TCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTC 717
S. thorelii     GCTACAAAGAAACCCAGTTTTTCTTTTTTACCAAAAAGAAATAAAAGATTATTCTTCTTC 714
S. nux-blanda   TCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAACGAAATAAAAGATTATTCTTCTTC 713
                 **************************** ****************************

S. lucida       TTAAATAATTCTTAAGTATGTGAATACGAATCCATTTTCGTCTTTCTACATAACCAATCT 773
S. nux-vomica   TTAAATAATTCTTAATAAGGTCAATACGAATCCATTTTCGTCTTTCTACATAACCAATCT 777
S. thorelii     TTATATAATTCTTATGTATGTGAATACGAATCCATTTTCCTCTTTCTACATAACCAATCT 774
S. nux-blanda   TTAAAAAATCCTTAAGTATGTGAATACGAATCCATTTTCGTCTTTCTACATAACCAATCT 773
                *** * *** ****  ** ****************************************

S. lucida       TCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATGGAAAA 833
S. nux-vomica   TCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATGGAAAA 837
S. thorelii     TCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCTATTTCTATGGAAAA 834
S. nux-blanda   TCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCCATTTCTATGGAAAA 833
                ************************************************************

S. lucida       ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAA 893
S. nux-vomica   ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAA 897
S. thorelii     ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAAGCCAAACTACGGTTGTTCAAA 894
S. nux-blanda   ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAA 893
                ************************************************************

S. lucida       GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAGGGGACG 953
S. nux-vomica   GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 957
S. thorelii     GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 954
S. nux-blanda   GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 953
                ************************************************************

S. lucida       GCTCCTTTGATGAATAAATGGAAATCTTACCTTGGCAATTTTTGGCAATGTCATTTTGAC 1013
S. nux-vomica   GCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGAC 1017
S. thorelii     GCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGGCATTTTGAC 1014
S. nux-blanda   GCTCCTTTGATGAATAAATGGAAATCTTACCTTGGCAATTTTTGGCAATGTCATTTTGAC 1013
                ************************************************************

S. lucida       CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACCAATCATTCCCCTGGAC 1073
S. nux-vomica   CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACCAATCATTCCCTTTGAC 1077
S. thorelii     CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACCAATCATTCCCCTTGAC 1074
S. nux-blanda   CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACCAATCATTCCCCTTGAC 1073
                ************************************************************

S. lucida       TTTATGGGGCTATCTTTCAGAAGGGGTCCGACTAAACCTTTTCAATGGGTACGGGAGTCC 1133
S. nux-vomica   TTTATGGGGCTATCTTTTAGAAGTGGCGCGTCTAAACCCTTTCAATGGGTACGGAAGTCC 1137
S. thorelii     TTTATGGGGCTATCTTTCAGAAGTGTGGCGACTAAACCCTTTCAATGGGTACGGGAGTCC 1134
S. nux-blanda   TTTATGGGGCTATCTTTCAGAAGGGGGGCGACTAAACCCCTTCAATGGGTACCGGAGTCC 1133
                ***************** ****  ****** ****************************
                                  ∇ DraI
S. lucida       AAATGGAAAGAA**TTTAAA**CATTTCC-TAAACCAAATAATGCCCATTAGGAAAAAAATGGG 1192
S. nux-vomica   AAATGAAAAGAATTAATTCATTTTC-TAATCCAAATAAGGGCTATTATAGGAAAATTGGG 1196
S. thorelii     AAATGGAAAGAATTAAAACATTTCCCTAATCCAATAATGGCCTTTTAGGAAAAAATTGGG 1194
S. nux-blanda   AAATGGAAAGAATTAAAACATTTTCCCAAACCAAAAAAGGCCTATTAGGAGAAAATTGGG 1193
                ************** *  *****     ** ****  *         *      *  ***

S. lucida       AAACCCCTTGGTCCAAAAATTATTCCCTCCTGGGGGGGTGGGACCATTGGTGGTTAAAACC 1252
S. nux-vomica   AAACCCCTTGGTCCAAAATTATTTCCCCTCTGGGTGTGGGAAACATATGGGGTTATAAGC 1256
S. thorelii     AAACCCTTTGGTCCAAAAATTATCCCCCCCTGGGGGGGTGGGAACATTGGGGGTTAAAAGC 1254
S. nux-blanda   AAACCCCTTGGTCCAAAAATTATTCCCCCCTGGGGGGGTGGGAACATTGGGGGTTAAAAGC 1253
                ********************  * ***  ***** *  ** * **** ********** *

S. lucida       CAAAAGTTTGTGAACCCACCTTAAGGGGCATCCCATTAGTTAAAGCCGGTTTGGACTGAT 1312
S. nux-vomica   GAAAAGTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAAGCCGGTTTGGACTGAT 1316
S. thorelii     GAAATTTTTTGGAAACCCCTTAGGGGGGCATCCCATTTAGTAAGCCGGATTTGAACTGAT 1314
S. nux-blanda   GAAAATTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAGCCGGGTTTGGACTGAT 1313
                 ***  ***  * * **   *   ****************** **** ***********
```

```
S. lucida       TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1372
S. nux-vomica   TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1376
S. thorelii     TTATCAGATTCGGATATTATTGACCGGGTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1374
S. nux-blanda   TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1373
                ************************************************************

S. lucida       CATAGCGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCT 1432
S. nux-vomica   CATAGTGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCT 1436
S. thorelii     CATAGCGGATCTTCCAAAAAAGTGAGTTTGTATCGAATAAAGTATATACTTCGGTTTTCT 1434
S. nux-blanda   CATAGCGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCT 1433
                ************************************************************

S. lucida       TGTGCTAAAATTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1492
S. nux-vomica   TGTGCTAAAACTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1496
S. thorelii     TGTGCTAAAACTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1494
S. nux-blanda   TGTGCTAAAACTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1493
                ********** ************************************************
                           ▽ DraI
S. lucida       GGGTCGGAATTTTTGGAA**TTTAAA**CTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTC 1552
S. nux-vomica   GGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTC 1556
S. thorelii     GGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGTCCTTTCTTTGAACTTC 1554
S. nux-blanda   GGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTC 1553
                ******************  ********************* ****************
                                                          ▽ DraI
S. lucida       CCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTGG-ATTTTGATATT 1611
S. nux-vomica   CCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTGGTATTTTGGTATT 1616
S. thorelii     CCAAGAGTTTCTTCTCCCTTTTGGGGGGTGTATAGAAGTCGGA**TTTA**--**AA**TTTGGTATT 1612
S. nux-blanda   CCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGA**TTTA**--**AA**TTTGGTATT 1611
                ******************************************   * **** * **
                        ▽ DraI
S. lucida       TGGAATTGTATAACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTGAGACCTTGT 1671
S. nux-vomica   TGGAATA**TTTAAA**CTGATCTGGTGAATCAGCAATGATTCATATTCATTCTGAGACCTTGT 1676
S. thorelii     TGGA-TATTATAACTGATCTGGTGAATCATCAATGATTCATATTCATTCTGAGACCTTGT 1671
S. nux-blanda   TGGA-TATTATAACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTGAGACCTTGT 1670
                **** ** *  ***************   ******************************

S. lucida       AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1731
S. nux-vomica   AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1736
S. thorelii     AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1731
S. nux-blanda   AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1730
                ************************************************************

S. lucida       AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTCTAAACTA 1791
S. nux-vomica   AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTTCTAAATA 1796
S. thorelii     AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTCTAAATTA 1791
S. nux-blanda   AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTTTGAAATA 1790
                ************************************************   ** **

S. lucida       AAGTTTAAATGAGTTATCA 1810
S. nux-vomica   AAGTCTAAAAAAGGAAAAA 1815
S. thorelii     AAGTCTAAAAAAAAAGAAA 1810
S. nux-blanda   AAGTCTTAAAAAGGAAACA 1809
                **** * **  *      *
```

Figure 42 The nucleotide sequence alignment of *mat*K gene from four *Strychnos* species (Bole letter indicated the Recognition site, ▽ indicated the positon of restriction site)

REFERENCES

1. Panya R, *Isolation and structure elucidation of alkaloids from the roots of Strychnos nux-bland* in *Chemistry, Faculty of cience* 2014, Chiang Mai University.
2. Neuwinger H D, *African Ethnobotany : Poisons and Drugs, Chemistry, Pharmacology, Toxicology.* 1996: p. 569-578.
3. Smitinand T, *Thai Plant Names,*. 2001, the Forest Herbarium, Royal Forest Department, Bangkok, Thailand. .
4. Yin W, et al., *Analgesic and anti-inflammatory properties of brucine and brucine N-oxide extracted from seeds of Strychnos nux-vomica.* Journal of Ethnopharmacology, 2003. **88**: p. 205-214.
5. Grieve M, *A modern herbal medicine, Poison and Antidotes.* 2007.
6. Chanthornteptawan V and Ngearndee P, *The phamacognostical studies on "Phayaa mue lek" Strychnos lucida R. Br.* Bull Dept Med Sci, 1988. **30**.
7. Trease G E and Evans W C, *Pharmacognosy.* 2002, 15 th ed. London: W.B. Saunders.
8. Joshi K, Chavan P, and Warude D, *Molecular markers in herbal drug technology.* Current Science, 2004. **87**: p. 159-165.
9. He Y, et al., *Internal transcribed spacers (ITS) identification of Angelica anomala Lallem Chuanbaizhi (in Chinese) cultivars collected in Sichuan and their molecular phylogenetic analysis with other Angelica L. species.* Journal of Medicinal Plants Research 2011. **5**(16): p. 3653-3659.
10. Randall S L, Richard C C, and Jonathan F W, *Use of nuclear genes for pylogeny reconstruction un plant.* Australian Systematic Botany 2004: p. 145-170.
11. shu, m.q., *Flora of China STRYCHNOS Linnaeus*. Vol. 15. 1996. 324-327.
12. Sukhul T, *PHYTOCHEMICAL STUDY OF STRYCHNOS THORELII STEM*. 1990, Chulalongkorn University: Bangkok. p. 140.
13. Chayamarit K and Phuphatanapong L, *Medicinal Plants of Thailand (part seven: Strychnaceae(Loganiceae).* 2002. 2002, the Forest Herbarium, Royal Forest Department , Bangkok, Thailand. 12-13.
14. Bisset N G, Phillipson J D, and Zenk M. H, *Indole and Biogenetically Related Alkaloids*. 1980, Acadermic Press, New YorK. 27-33.

15. Philippe G, et al., *About the toxicity of some Strychnos species and their alkaloids.* Toxicon, 2004. **44**: p. 405-416.
16. Phongluck T, *Indole Alkaloids*. 1977, Chulalongkorn University. 1-6.
17. Philippe G and Angenot L, *Recent developments in the field of arrow and dart poisons.* Ethnopharmacol, 2005. **100**(1-2): p. 85-91.
18. Deng X K, et al., *The anti-tumor effects of alkaloids from the seeds of Strychnos nux-vomica on HepG2 cells and its possible mechanism.* Ethnopharmacol, 2006. **106**: p. 179-186.
19. Wua W, et al., *AlkaloidprofilingincrudeandprocessedStrychnosnux-vomicaseedsbymatrix-assistedlaserdesorption/ionization-time offlightmassspectrometry.* Pharmaceutical and BiomedicalAnalysis, 2007: p. 430-436.
20. Philippe G, et al., *Study of the interaction of antiplasmodial strychnine derivatives with the glycine receptor.* Eur J Pharmacol, 2006. **530**(1-2): p. 15-22.
21. Tits M, Tavernier D, and Angenot L, *Indole alkaloids of Strychnos variabilis.* Phytochemistry 1980 **19**: p. 1531-1534.
22. Nuzillard J M, et al., *Alkaloids from root bark of Strychnos panganensis.* Phytochemistry. **43**: p. 897-902.
23. Martin M T, et al., *Minor N-b,C(21)-secocuran alkaloids of Strychnos myrtoides* PHYTOCHEMISTRY 1999. **51**(3): p. 479-486.
24. Rasoanaivo P, et al., *The co-occurrence of C(3) epimer N-b,C(21)-secocuran alkaloids in Strychnos diplotricha and Strychnos myrtoides* PHYTOCHEMISTRY 2001. **56**(8): p. 863 - 867.
25. Asai F, et al., *Study on the components of the folk medicine.* Shoyakugaku Xasshi, 1982. **102**: p. 690-694.
26. Frederich M, et al., *In Vitro Activities of Strychnos Alkaloids and Extracts against Plasmodium falciparum.* Antimicrob Agents Chemother., 1999. **43**(9): p. 2328-2331.
27. Frederich M, Tits P, and Grellier G, *Antiplasmodial Activity of Alkaloids from Various Strychnos species.* Journal of Natural Product, 2002. **65**.

28. Frédérich M, et al., *Chrysopentamine, an Antiplasmodial Anhydronium Base from Strychnos usambarensis leaves.* Planta Medica, 2004. **70**: p. 72-76.

29. Kambu K, Coune C, and Angenot L, *New Alkaloids from the Roots of Strychnos icaja.* Planta Medicad, 1979. **37**(10): p. 61-164.

30. Philippe G, et al., *Strychnohexamine from Strychnos icaja, a naturally occuring trimeric indolomonoterpenic alkaloid.* Tetrahedron Lett, 2002. **43**: p. 3387-3390.

31. Philippe G, et al., *Indolomonoterpenic alkaloids from Strychnos icaja roots. .* Phytochemistry, 2003. **62**(4): p. 632-639.

32. Penelle J, et al., *5 ',6 '-dehydroguiachrysine and 5 ',6 '-dehydroguiaflavine, two curarizingquaternary indole alkaloids from the stem bark of Strychnos guianensis.* PHYTOCHEMISTRY 2001. **58**(4): p. 619-626.

33. Penelle J, et al., *Quaternary indole alkaloids from the stem bark of Strychnos guianensis.* PHYTOCHEMISTRY 2000. **53**(8): p. 1057-1066.

34. Thongphasuka P, et al., *Antioxidant lignan glucosides from Strychnos vanprukii.* Fitoterapia 2004. **75**(7-8): p. 623 - 628.

35. Itoha A, et al., *Phenolic and iridoid glycosides from Strychnos axillaris.* Phytochemistry, 2008. **69**(5): p. 1208-1214.

36. Zhang X, et al., *Iridoid glucosides from Strychnos nux-vomica.* Phytochemistry, 2003. **64**(8): p. 1341-1344.

37. Itoh A, et al., *A quinic acid ester from Strychnos lucida.* J Nat Med 2006. **60**: p. 146-148.

38. Pelletier PJ and Caventou J B, *Note sur un nouvel alcali. .* Annales de Chimie et de Physique 1818. **8**: p. 323-324.

39. García A G, MartínezT, and Miledi A R, *Strychnine induces embryo toxicity in rat neurulation.* Neurotoxicol. Teratol., 2005. **27**: p. 855-859.

40. McCool B A and Chappell A, *Strychnine and taurine modulation of amygdala-associated anxiety-like behavior is "state" dependent*
Behav. Brain. Res, 2007. **178**(1): p. 70-81.

41. Perper J and A J, *Fatal strychnine poisoning-A case report and review of the literature.* Forensic. Sci., 1985. **30**: p. 1248-1255. .

42. Wins P, et al., *Bisindole alkaloids from Strychnos guianensis are effective antagonists of nicotinic acetylcholine receptors in cultured human TE671 cells.* Naunyn-Schmiedeberg's Archives Pharmacology. **367**: p. 253-259.

43. Frederich M, Tits M, and Angenot L, *Chemistry of Natural Compounds.* 2003. **39**: p. 513-519.

44. Kagithoju S, et al., *Pharmacognostic and phytochemical investigations in Strychnos potatorum Linn.F.* Pharmacognosy and Phytochemistry, 2013. **2**(4): p. 46-51.

45. BINU T V and VIJAYAKUMARI B, *Pharmacognostical and anatomical evaluation of the selected part of Strychnos potatorum L.f.* Int J Pharm Bio Sci 2014. **5**(2): p. 251-258.

46. Ferguson N M, *A textbook of Pharmacognosy*. 1956, New York, The Macmillan.

47. KHANDELWAL, D.K.R., *PRACTICAL PHARMACOGNOSY TECHNIQUES AND EXPERIMENTS*. 2011, India.

48. World Health Organization.WHO Guidelines, *Quality control methods for medicinal plant materials.* 2011.

49. Mukherjee P K, *Quality control of herbal drugs: an approach to evaluation of botanicals. .* 2007: p. 131-182.

50. Milligan B G, *Total DNA isolation. In: Hoelzel AR, ed. Molecular Genetic Analysis of Population: A Practical Approach*, ed. n. Edition. 1998, Oxford, New York, Tokyo: Oxford University Press.

51. Chen H, et al., *Evaluation of Five Methods for Total DNA Extraction from Western Corn Rootworm Beetles.* Plos one, 2010. **5**(8).

52. Sghaier Z A and M. C, *Genomic DNA extraction method from pearl millet (Pennisetum glaucum) leaves.* African Journal of Biotechnology, 2005. **4**(8): p. 862-866.

53. Katterman F, R H, and hattuck V I S, *An effective method of DNA isolation from the mature leaves of Gossypium species that contain large amounts of phenolics, terpeniodes and tannins.* Preparative Biochemistry, 1983(13): p. 347-359.

54. Weishing K, et al., *DNA isolation and purification. In DNA fingerprinting in plants and fungi*. . 1995, Boca Raton, Florida.

55. Sadasivam S and Manickam, *A Biochemical Methods (Revised 2 ed).* . 1996, New Delhi, New Age International (P) Ltd. Publishers.

56. Doyle J J and Doyle J L, *Isolation of plantDNA from fresh tissue.* Focus, 1990(12): p. 13-15.

57. Khanuja S, et al., *Rapid Isolation of DNA from Dry and Fresh Samples of plants producing Large Amounts of Secondary Metabolites and essential oils.* Plants Molecular Biology Report, 1990. **17**(1): p. 74.

58. Edwards K, Johnstone C, and Thompson C, *A simple and rapid method for the preparation of plant Research genomic DNA for PCR analysis. Nucleic Acid.* 1991.

59. Tibbits J F, et al., *A rapid method for tissue collection and high-throughput isolation of genomic DNA frommature trees.* Plant Mol Biol Report, 2006. **24**: p. 81-91.

60. Hillis D M and Davis S K, *Ribosomal DNA: intraspecific polymorphism, concerted evolution, and phylogeny reconstruction.* Syst Zool 1988. **37**: p. 163-66.

61. Muir G and Schlötterer C. *Limitations to the phylogenetic use of ITS sequences in closely related species and populations*. 1999; Available from: http://webdoc.sub.gwdg.de/ebook/y/1999/whichmarker/index.htm

62. Souframanien J, Joshi A, and Gopalakrishna T, *Intraspecific variation in the internal transcribed spacer region of rDNA in black gram (Vigna mungo (L.) Hepper).* Curr Sci 2003. **85**(6): p. 798-802.

63. Sharma S, et al., *Internal transcribed spacer (ITS) sequences of ribosomal DNA of wild barley and their comparison with ITS sequences in common wheat.* Barley Genetics Newsletter 2002. **32**: p. 38-45.

64. Gielly L and Taberlet P, *The use of chloroplast DNA to resolve plant phylogenies: noncoding versus rbcL sequences. .* Mol Biol Evo, 1994. **11**(5): p. 769-777.

65. Hilu K W and Hongping L, *he matK gene: sequence variation and application in plant systematics. .* TAm J Bot, 1997. **84**(6).

66. Carol A and Wilson. *Based on chloroplast matK gene and trnK intron sequence data.* 2004; Available from: http://www.rsabg.org/iris/research/systematics/13-phylogeny-of-the-genus-iris-based-on-dna-sequence-data.

67. Frascaria N, et al., *he rbcL gene sequence from chestnut indicates a slow rate of evolution in the Fagaceae.* Genome 36,, 1993. **4**.

68. Hoot S B, Cullman A, and Crane P R, *The utility of atpB gene sequences in resolving phylogenetic relationships: comparison with rbcL and 18S ribosomal DNA sequences in the Lardizabalaceae.* Ann Missouri Bot Gar, 1995. **82**: p. 194-207.

69. Palmer J D, *Mitochondria DNA in plant systematic: applications and limitations. In molecular systematics of plants 2.* . 1992. , New York, Kluwer academic publishe.

70. Bartlett J, M S, and Stirling D, *A short history of the polymerase chain reaction.* Methods Mol Bio, 2003. **226**: p. -6.

71. Pavlov A R, et al., *Recent developments in the optimization of thermostable DNA polymerases for efficient applications.* Trends in Biotechnology, 2004. **22**(5): p. 253-260.

72. Lundberg K S, *High-fidelity amplification using a thermostable DNA plymerase isolated from Pyrococcus furiosu.* Gene 108, 1991. **1**: p. 1-6.

73. Sambrook J and Russel D W, *Molecular Cloning: A Laboratory Manual. 3 ed.* . 2001, New York, Cold Spring Harbor Laboratory Press.

74. Howe C J, *Gene cloning and Manipulation. 2nd ed.* . 2007.

75. Sriprapun M. *Basic and principles of PCR and advanced PCR techniques*. 2014; Available from: http://www.slideshare.net/MetheeSri/principle-of-pcr.

76. Olsvik O, *Use of automated sequencing of polymerase chain reaction-generated amplicons to identify three types of cholera toxin subunit B in Vibrio cholerae O1 strains.* Clin Microbiol 1993. **31**(1): p. 22-25.

77. Maxam A M and Gilbert W, *A new method for sequencing DNA.* Proc. Natl. Acad. Sci., 1977. **74**(2).

78. Gaastra W, *Chemical cleavage (Maxam and Gilbert) method for DNA sequence determination.* 2012.

79. *Maxam–Gilbert sequencing*. 2015; Available from: https://en.wikipedia.org/wiki/Maxam%E2%80%93Gilbert_sequencing#cite_note-Maxam77-1.

80. Kevin. *PCR vs DNA Sequencing*. 2010; Available from: http://kevinlee-sbi4u.blogspot.com/.

81. Rasmussen H B, *Restriction Fragment Length Polymorphism Analysis of PCR-Amplified Fragments (PCR-RFLP) and Gel Electrophoresis -Valuable Tool for Genotyping and Genetic Fingerprinting. In S. Magdeldin (Ed.* Biochemistry, Genetics and Molecular Biology 2012: p. 315-330.

82. Akbar S, et al., *Pharmacognostic studies of stem, roots and leaves of Malva parviflora L.* Asian Pac J Biomed, 2014. **4**(5): p. 410-415.

83. Kumar S, Kumar V, and Prakah O, *Microscopic evaluation and physiochemical analysis of Dillenia indica leaf.* Asian Pac J Biomed, 2011. **1**(5): p. 337-340.

84. Oduoye O T and Ogundie O T, *Macro and morphological evaluation of Loganiaceae liana as medicinal plant in South-Western nigeria.* THE IJES, 2013. **2**(7): p. 47-52.

85. Oduoye O T, Ogundipe O T, and Olowokudejo J D, *Leaf epidermal analysis for diagnosos of enigmatic Strychnos specices in Nigeria.* THE IJES, 2013. **2**(7): p. 109-119.

86. Balasubramani P S, et al., *Development of ITS sequence based molecular marker to distinguish,Tribulus terrestris L. (Zygophyllaceae) from its adulterants.* Fitoterapia., 2010. **81**(6): p. 503-508.

87. Laprise S, R., *Analysis of purative DNA barcodes for identification and distinction of native and invasive plans species*. 2010, Babson Faculty Research Fund.

88. Hui X, et al., *Identification of Crude Drugs from Chinese Medicinal Plants of the Genus Bupleurum Using Ribosomal DNA ITS Sequences.* Planta Med, 2009. **75**: p. 89-93.

89. Dubouzet J G and Shinoda K, *Relationships among old and new world Alliums according to ITS DNA sequence analysis.* Theor Appl Genet, 1999. **98**: p. 422-433.

90. Kikkawa S H, et al., *Potential utility of DNA sequence analysis of ling-term-stored plant leaf fragment for forensic dicrimination and identification.* analytical sciences, 2010. **26**(913-916).

91. Asahina H, et al., *Identification of medicinal Dendrobium species by phylogenitic analyses using matK and rbcl sequences.* J Nat Med, 2010. **64**: p. 133-138.

92. Wei W, et al., *PCR-RFLP analysis of cpDNA and mtDNA in the genus Houttuynia in some areas of China.* Hereditas, 2005. **142**: p. 24-32.

93. Chen S, et al., *PCR-RFLP Analysis of cpDNA in Tea Cultivars (Camellia sinensis L.) in Sichuan of China* Journal of Agricultural Science 2012. **4**.

94. Gao T, et al., *Idwntification of Fabaceae plants using the DNA barcode matK.* Planta Med, 2011. **77**: p. 92-94.

95. Zhao Z, et al., *Authentication is fundamental for standardization of chainese medicine.* Planta Med, 2006. **72**: p. 865-874.

APPENDICES

Appendix A Microscopic evaluation

The raw data of leaf constant numbers

Table 16 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. thorelii,* collected from Chachoengsao province 1.

File	Stomatal cell			Palisade cell		Epidermal cell		Veinlet termination number (sq.mm)
	Number of epidermal cells (sq.mm)	Stomatal number (sq.mm)	Stomatal index	Number of beneath 4 epidermal ell	Palisade ratio	Number of epidermal cells (sq.mm)	epidermal cell area (sq.μm)	
1	1132	152	11.84	16	4	1704	586.85	16.50
2	1168	144	10.98	19	4.75	1724	580.05	15.50
3	1116	144	11.43	19	4.75	1580	632.91	16.00
4	1140	148	11.49	16	4	1560	641.03	18.00
5	1172	176	13.06	15	3.75	1512	661.38	16.75
6	1124	156	12.19	19	4.75	1500	666.67	18.25
7	1160	156	11.85	16	4	1584	631.31	15.25
8	1088	156	12.54	14	3.5	1600	625.00	16.25
9	1180	144	10.88	16	4	1624	615.76	17.75
10	1196	136	10.21	21	5.25	1640	609.76	17.00
11	1144	156	12.00	18	4.5	1556	642.67	18.75
12	1116	144	11.43	17	4.25	1644	608.27	16.00
13	1176	164	12.24	15	3.75	1608	621.89	16.50
14	1160	140	10.77	17	4.25	1536	651.04	16.25
15	1188	176	12.90	18	4.5	1676	596.66	16.00
16	1232	144	10.47	17	4.25	1588	629.72	15.00
17	1240	168	11.93	18	4.5	1596	626.57	16.00
18	1200	152	11.24	20	5	1496	668.45	17.00
19	1156	160	12.16	19	4.75	1584	631.31	17.50
20	1168	152	11.52	18	4.5	1548	645.99	15.50
21	1240	164	11.68	17	4.25	1492	670.24	16.00
22	1204	164	11.99	21	5.25	1636	611.25	17.75
23	1124	144	11.36	18	4.5	1596	626.57	15.50
24	1144	152	11.73	19	4.75	1572	636.13	15.00
25	1148	156	11.96	21	5.25	1532	652.74	15.00
26	1144	164	12.54	16	4	1504	664.89	15.25
27	1148	148	11.42	20	5	1716	582.75	14.50
28	1112	156	12.30	18	4.5	1628	614.25	15.00
29	1124	152	11.91	16	4	1652	605.33	14.75
30	1216	160	11.63	15	3.75	1572	636.13	15.00
	Mean	154.27	11.72	Mean	4.41	Mean	614.40	16.18
	S.D.	9.95	0.66	S.D.	0.48	S.D.	13.85	1.14

Table 17 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of S. *thorelii*, collected from Chachoengsao province 2.

File	Stomatal cell			Palisade cell		Epidermal cell		Veinlet termination number (sq.mm)
	Number of epidermal cells (sq.mm)	Stomatal number (sq.mm)	Stomatal index	Number of beneath 4 epidermal ells	Palisade ratio	Number of epidermal cells (sq.mm)	epidermal cell area (sq.μm)	
1	1172	180	13.31	17	4.25	1556	642.67	14.00
2	1300	160	10.96	19	4.75	1624	615.76	14.50
3	1204	152	11.21	19	4.75	1692	591.02	14.75
4	1228	172	12.29	18	4.5	1504	664.89	14.25
5	1320	148	10.08	17	4.25	1580	632.91	13.50
6	1200	160	11.76	18	4.5	1648	606.80	15.25
7	1208	152	11.18	19	4.75	1504	664.89	13.75
8	1296	164	11.23	18	4.5	1536	651.04	16.75
9	1316	172	11.56	19	4.75	1636	611.25	14.00
10	1384	156	10.13	19	4.75	1716	582.75	14.50
11	1388	180	11.48	18	4.5	1660	602.41	14.00
12	1244	164	11.65	19	4.75	1696	589.62	14.75
13	1284	172	11.81	17	4.25	1604	623.44	13.50
14	1348	148	9.89	18	4.5	1708	585.48	13.25
15	1264	152	10.73	20	5	1492	670.24	15.50
16	1248	180	12.61	16	4	1576	634.52	13.50
17	1348	176	11.55	16	4	1700	588.24	13.75
18	1244	160	11.40	17	4.25	1684	593.82	14.25
19	1280	164	11.36	17	4.25	1600	625.00	15.00
20	1320	180	12.00	18	4.5	1488	672.04	13.50
21	1340	152	10.19	19	4.75	1612	620.35	14.25
22	1276	168	11.63	18	4.5	1512	661.38	14.75
23	1344	152	10.16	17	4.25	1520	657.89	16.25
24	1320	164	11.05	20	5	1480	675.68	17.00
25	1336	152	10.22	15	3.75	1652	605.33	17.25
26	1356	184	11.95	16	4	1624	615.76	13.50
27	1352	168	11.05	20	5	1512	661.38	14.00
28	1364	156	10.26	17	4.25	1672	598.09	13.25
29	1268	176	12.19	17	4.25	1636	611.25	15.75
30	1292	184	12.47	15	3.75	1648	606.80	13.50
	Mean	164.93	11.51	Mean	4.44	Mean	606.77	14.57
	S.D.	11.54	0.85	S.D.	0.48	S.D.	13.58	1.13

Table 18 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. thorelii*, collected from Chonburi province.

File	Stomatal cell			Palisade cell		Epidermal cell		Veinlet termination number
	Number of epidermal cells (sq.mm)	Stomatal number (sq.mm)	Stomatal index (sq.mm)	Number of beneath 4 epidermal ells	Palisade ratio	Number of epidermal cells (sq.mm)	epidermal cell area (sq.μm)	
1	1268	176	12.19	15	3.75	1680	595.24	17.25
2	1300	148	10.22	19	4.75	1656	603.86	15.75
3	1232	144	10.47	22	5.5	1736	576.04	15.00
4	1208	164	11.95	18	4.5	1676	596.66	16.75
5	1204	180	13.01	17	4.25	1612	620.35	17.25
6	1220	184	13.11	18	4.5	1544	647.67	15.75
7	1208	160	11.70	19	4.75	1688	592.42	15.00
8	1240	188	13.17	20	5	1600	625.00	16.25
9	1300	172	11.68	17	4.25	1612	620.35	15.50
10	1216	164	11.88	22	5.5	1648	606.80	16.00
11	1196	180	13.08	19	4.75	1588	629.72	15.75
12	1196	156	11.54	18	4.5	1672	598.09	16.25
13	1168	176	13.10	19	4.75	1704	586.85	13.75
14	1216	184	13.14	23	5.75	1684	593.82	15.25
15	1252	188	13.06	16	4	1616	618.81	16.50
16	1324	152	10.30	25	5.25	1592	628.14	17.50
17	1264	148	10.48	19	4.75	1736	576.04	15.50
18	1252	164	11.58	15	3.75	1608	621.89	16.00
19	1248	168	11.86	18	4.5	1716	582.75	14.00
20	1256	160	11.30	18	4.5	1740	574.71	17.00
21	1140	156	12.04	17	4.25	1700	588.24	16.50
22	1244	168	11.90	20	5	1708	585.48	17.75
23	1204	176	12.75	16	4	1580	632.91	15.00
24	1288	152	10.56	23	5.75	1676	596.66	15.25
25	1180	164	12.20	18	4.5	1648	606.80	14.75
26	1188	148	11.08	22	5.5	1676	596.66	15.25
27	1104	176	13.75	23	5.75	1648	606.80	14.50
28	1240	180	12.68	18	4.5	1704	586.85	15.00
29	1212	152	11.14	19	4.75	1604	623.44	13.25
30	1188	172	12.65	17	4.25	1708	585.48	14.25
	Mean	166.67	11.98	Mean	4.42	Mean	598.83	15.65
	S.D.	13.13	0.99	S.D.	0.58	S.D.	13.58	1.13

Table 19 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. lucida*, collected from Bangkok province.

File	Stomatal cell			Palisade cell		Epidermal cell		Veinlet termination number (sq.mm)
	Number of epidermal cells (sq.mm)	Stomatal number (sq.mm)	Stomatal index	Number of beneath 4 epidermal ells	Palisade ratio	Number of epidermal cells (sq.mm)	epidermal cell area (sq.μm)	
1	2784	160	5.43	30	7.5	2464	405.84	15.00
2	2804	184	6.16	28	7	2412	414.59	16.25
3	2988	184	5.80	26	6.5	2524	396.20	16.75
4	2860	184	6.04	27	6.75	2472	404.53	17.50
5	2776	196	6.59	23	5.75	2496	400.64	17.25
6	2796	176	5.92	24	6	2432	411.18	18.50
7	2716	152	5.30	28	7	2492	401.28	17.75
8	2688	168	5.88	24	6	2212	452.08	15.75
9	2832	168	5.60	27	6.75	2432	411.18	20.25
10	2676	148	5.24	25	6.25	2324	430.29	16.25
11	2656	176	6.21	26	6.5	2516	397.46	16.00
12	2840	152	5.08	23	5.75	2508	398.72	13.75
13	2704	152	5.32	29	7.25	2340	427.35	17.50
14	2732	164	5.66	30	7.5	2444	409.17	17.25
15	2640	140	5.04	30	7.5	2192	456.20	18.00
16	2876	180	5.89	24	6	2356	424.45	18.50
17	2608	144	5.23	26	6.5	2212	452.08	17.00
18	2592	144	5.26	25	6.25	2348	425.89	15.25
19	2740	148	5.12	21	5.25	2200	454.55	17.00
20	2628	164	5.87	26	6.5	2360	423.73	16.25
21	2696	180	6.26	22	5.5	2196	455.37	17.50
22	2860	184	6.04	24	6	2312	432.53	14.50
23	2816	176	5.88	23	5.75	2236	447.23	16.75
24	2756	160	5.49	23	5.75	2376	420.88	14.25
25	2700	176	6.12	29	7.25	2200	454.55	15.00
26	2892	164	5.37	25	6.25	2388	418.76	15.50
27	2856	180	5.93	28	7	2296	435.54	15.00
28	2956	192	6.10	33	8.25	2276	439.37	14.75
29	2688	152	5.35	29	7.25	2224	449.64	14.00
30	2888	176	5.74	22	5.5	2268	440.92	16.50
	Mean	167.47	6..77	Mean	6.50	Mean	419.32	16.42
	S.D.	15.61	0.73	S.D.	0.73	S.D.	8.32	1.51

Table 20 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. lucida*, collected from Pathum Thani province.

File	Stomatal cell			Palisade cell		Epidermal cell		Veinlet termination number (sq.mm)
	Number of epidermal cells (sq.mm)	Stomatal number (sq.mm)	Stomatal index	Number of beneath 4 epidermal ells	Palisade ratio	Number of epidermal cells (sq.mm)	epidermal cell area (sq.μm)	
1	1888	164	7.99	31	7.75	2200	454.55	15.75
2	1804	180	9.07	23	5.75	2208	452.90	19.50
3	1892	160	7.80	25	6.25	2328	429.55	17.25
4	2204	184	7.71	28	7	2100	476.19	18.50
5	1876	184	8.93	22	5.5	2100	476.19	17.50
6	1844	160	7.98	24	6	2212	452.08	18.25
7	2188	172	7.29	26	6.5	2504	399.36	15.00
8	2212	164	6.90	27	6.75	2256	443.26	15.00
9	2008	196	8.89	28	7	2512	398.09	17.50
10	1872	184	8.95	29	7.25	2132	469.04	16.50
11	1864	188	9.16	23	5.75	2448	408.50	14.50
12	2156	188	8.02	23	5.75	2108	474.38	14.00
13	2196	196	8.19	30	7.5	2164	462.11	15.75
14	2120	196	8.46	26	6.5	2184	457.88	16.25
15	2184	192	8.08	27	6.75	2120	471.70	15.50
16	1744	180	9.36	29	7.25	2144	466.42	16.75
17	1780	156	8.06	30	7.5	2112	473.48	15.25
18	1792	152	7.82	32	8	2148	465.55	14.25
19	1824	160	8.06	24	6	2244	445.63	20.00
20	1736	176	9.21	30	7.5	2128	469.92	18.75
21	1756	156	8.16	26	6.5	2132	469.04	17.25
22	2052	184	8.23	36	9	2296	435.54	18.25
23	2296	176	7.12	25	6.25	2268	440.92	15.25
24	2220	192	7.96	24	6	2396	417.36	16.50
25	2208	184	7.69	29	7.25	2412	414.59	16.00
26	2008	168	7.72	27	6.75	2304	434.03	16.25
27	2232	192	7.92	28	7	2468	405.19	19.00
28	2204	192	8.01	29	7.25	2492	401.28	18.50
29	2184	196	8.24	26	6.5	2320	431.03	15.00
30	1768	164	8.49	28	7	2352	425.17	16.00
	Mean	177.87	7.52	Mean	6.79	Mean	425.75	16.66
	S.D.	14.16	0.64	S.D.	0.78	S.D.	8.10	1.63

Table 21 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. lucida*, collected from Nonthaburi province.

File	Stomatal cell			Palisade cell		Epidermal cell		Veinlet termination number (sq.mm)
	Number of epidermal cells (sq.mm)	Stomatal number (sq.mm)	Stomatal index	Number of beneath 4 epidermal ells	Palisade ratio	Number of epidermal cells (sq.mm)	epidermal cell area (sq.μm)	
1	2104	156	6.90	26	6.5	2088	478.93	13.50
2	2032	164	7.47	28	7	2036	491.16	15.50
3	2080	176	7.80	22	5.5	2456	407.17	15.00
4	2268	168	6.90	27	6.75	2452	407.83	17.75
5	2000	164	7.58	28	7	2840	352.11	15.75
6	2044	172	7.76	30	7.5	2076	481.70	16.50
7	2396	180	6.99	25	6.25	2256	443.26	14.50
8	2140	164	7.12	30	7.5	2560	390.63	17.50
9	2240	168	6.98	25	6.25	2380	420.17	18.75
10	2220	176	7.35	27	6.75	1940	515.46	19.00
11	1816	184	9.20	24	6	2096	477.10	14.75
12	2064	172	7.69	30	7.5	2392	418.06	16.25
13	2212	160	6.75	26	6.5	2656	376.51	18.00
14	2196	172	7.26	28	7	2324	430.29	15.75
15	2160	176	7.53	25	6.25	2280	438.60	19.00
16	2108	168	7.38	29	7.25	2356	424.45	14.75
17	2064	152	6.86	26	6.5	2732	366.03	15.00
18	1972	168	7.85	24	6	2340	427.35	16.75
19	2136	152	6.64	25	6.25	2476	403.88	19.75
20	2060	192	8.53	23	5.75	2688	372.02	19.25
21	2192	160	6.80	31	7.75	2852	350.63	17.75
22	2168	164	7.03	29	7.25	2556	391.24	14.00
23	2252	160	6.63	32	8	2396	417.36	12.00
24	2180	188	7.94	28	7	1944	514.40	12.75
25	2112	184	8.01	32	8	2336	428.08	18.50
26	2040	164	7.44	27	6.75	2612	382.85	13.75
27	2072	168	7.50	26	6.5	2524	396.20	14.75
28	2132	184	7.94	25	6.25	2720	367.65	19.25
29	1984	188	8.66	32	8	1960	510.20	18.00
30	2128	168	7.32	23	5.75	2128	469.92	12.25
	Mean	170.40	7.35	Mean	6.78	Mean	422.34	17.78
	S.D.	10.64	0.50	S.D.	0.69	S.D.	8.04	1.95

Table 22 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. nux-vomica*, sample collected from Pathum Thani province.

File	Stomatal cell			Palisade cell		Epidermal cell		Veinlet termination number (sq.mm)
	Number of epidermal cells (sq.mm)	Stomatal number (sq.mm)	Stomatal index	Number of beneath 4 epidermal ells	Palisade ratio	Number of epidermal cells (sq.mm)	epidermal cell area (sq.μm)	
1	2320	220	8.66	26	6.5	1424	702.25	20.50
2	2160	204	8.63	30	7.5	1504	664.89	22.50
3	2140	232	9.78	29	7.25	1492	670.24	19.75
4	2144	212	9.00	36	9	1428	700.28	16.50
5	2052	196	8.72	37	9.25	1368	730.99	20.75
6	2288	212	8.48	30	7.5	1476	677.51	21.00
7	1996	200	9.11	34	8.5	1392	718.39	18.00
8	2052	204	9.04	36	9	1500	666.67	18.50
9	2056	196	8.70	32	8	1248	801.28	21.00
10	2340	212	8.31	30	7.5	1508	663.13	22.75
11	2368	224	8.64	25	6.25	1272	786.16	22.25
12	2204	192	8.01	31	7.75	1376	726.74	18.75
13	2284	208	8.35	31	7.75	1320	757.58	16.75
14	2240	196	8.05	28	7	1460	684.93	17.50
15	2108	216	9.29	33	8.25	1432	698.32	16.75
16	2292	224	8.90	30	7.5	1364	733.14	18.50
17	2196	192	8.04	37	9.25	1316	759.88	18.00
18	2440	208	7.85	30	7.5	1456	686.81	21.50
19	2336	224	8.75	32	8	1432	698.32	19.00
20	2476	204	7.61	31	7.75	1368	730.99	17.25
21	2388	220	8.44	30	7.5	1360	735.29	17.00
22	2396	240	9.10	32	8	1380	724.64	17.75
23	2324	224	8.79	32	8	1424	702.25	16.50
24	2296	228	9.03	30	7.5	1504	664.89	19.00
25	2160	216	9.09	30	7.5	1432	698.32	20.00
26	2220	244	9.90	35	8.75	1316	759.88	20.25
27	2240	216	8.79	35	8.75	1368	730.99	19.00
28	2388	220	8.44	33	8.25	1424	702.25	20.50
29	2300	228	9.02	35	8.75	1388	720.46	18.75
30	2484	236	8.68	34	8.5	1508	663.13	20.25
	Mean	214.93	8.71	Mean	7.98	Mean	709.16	19.22
	S.D.	14.13	0.51	S.D.	0.75	S.D.	15.30	1.84

Table 23 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. nux-vomica*, collected from Khon Kaen province.

File	Stomatal cell			Palisade cell		Epidermal cell		Veinlet termination number (sq.mm)
	Number of epidermal cells (sq.mm)	Stomatal number (sq.mm)	Stomatal index	Number of beneath 4 epidermal ells	Palisade ratio	Number of epidermal cells (sq.mm)	epidermal cell area (sq.μm)	
1	2148	188	8.05	40	10	1420	704.23	16.25
2	2272	192	7.79	36	9	1464	683.06	15.25
3	2100	200	8.70	34	8.5	1368	730.99	16.00
4	2108	220	9.45	40	10	1452	688.71	15.00
5	2132	200	8.58	34	8.5	1440	694.44	14.75
6	2212	208	8.60	39	9.75	1432	698.32	18.25
7	2184	236	9.75	34	8.5	1460	684.93	18.25
8	2172	188	7.97	38	9.5	1404	712.25	18.75
9	2172	204	8.59	37	9.25	1444	692.52	15.50
10	2128	208	8.90	37	9.25	1420	704.23	20.75
11	2100	224	9.64	36	9	1340	746.27	16.50
12	2048	212	9.38	35	8.75	1404	712.25	17.00
13	2092	204	8.89	40	10	1348	741.84	15.25
14	2016	196	8.86	37	9.25	1396	716.33	18.50
15	2096	200	8.71	33	8.25	1396	716.33	17.25
16	2136	208	8.87	39	9.75	1352	739.64	17.5
17	2160	200	8.47	40	10	1340	746.27	15.00
18	2100	196	8.54	42	10.5	1364	733.14	16.25
19	2060	212	9.33	33	8.25	1284	778.82	15.25
20	2112	188	8.17	38	9.5	1228	814.33	18.25
21	2052	208	9.20	41	10.25	1412	708.22	17.25
22	2052	188	8.39	31	7.75	1368	730.99	20.00
23	2056	196	8.70	38	9.5	1292	773.99	16.75
24	2108	200	8.67	36	9	1352	739.64	15.50
25	2140	196	8.39	37	9.25	1392	718.39	16.50
26	2128	196	8.43	37	9.25	1400	714.29	20.25
27	2052	196	8.72	43	10.75	1320	757.58	18.00
28	2096	212	9.19	39	9.75	1368	730.99	18.75
29	2188	200	8.38	40	10	1372	728.86	16.00
30	2196	212	8.80	39	9.75	1324	755.29	17.00
	Mean	202.93	8.74	Mean	9.36	Mean	724.61	17.06
	S.D.	11.16	0.48	S.D.	0.72	S.D.	17.79	1.65

Table 24 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. nux-vomica*, collected from Song khla province.

File	Stomatal cell			Palisade cell		Epidermal cell		Veinlet termination number (sq.mm)
	Number of epidermal cells (sq.mm)	Stomatal number (sq.mm)	Stomatal index	Number of beneath 4 epidermal ells	Palisade ratio	Number of epidermal cells (sq.mm)	epidermal cell area (sq.μm)	
1	2092	180	7.92	39	8.75	1252	798.72	19.50
2	2156	200	8.49	36	9	1244	803.86	20.25
3	2184	196	8.24	36	9	1252	798.72	20.00
4	2076	196	8.63	44	11	1280	781.25	17.25
5	2032	208	9.29	38	9.5	1272	786.16	16.25
6	2048	200	8.90	39	9.75	1268	788.64	19.00
7	2096	180	7.91	37	9.25	1252	798.72	20.75
8	2156	192	8.18	35	8.75	1240	806.45	21.50
9	2120	208	8.93	32	8	1260	793.65	14.75
10	2108	232	9.91	38	9.5	1308	764.53	17.75
11	2036	212	9.43	36	9	1288	776.40	14.50
12	2124	220	9.39	40	10	1320	757.58	15.75
13	2120	196	8.46	38	9.5	1372	728.86	15.25
14	2116	188	8.16	39	9.75	1224	816.99	18.25
15	2044	208	9.24	44	11	1364	733.14	17.25
16	2084	184	8.11	35	8.75	1352	739.64	15.75
17	2168	192	8.14	38	9.5	1280	781.25	21.50
18	2156	200	8.49	34	8.5	1316	759.88	16.75
19	2212	196	8.14	41	10.25	1280	781.25	17.50
20	2168	188	7.98	39	9.75	1264	791.14	18.25
21	2160	184	7.85	43	10.75	1236	809.06	14.25
22	2116	196	8.48	40	10	1296	771.60	15.00
23	2124	204	8.76	36	9	1336	748.50	18.50
24	2120	192	8.30	33	8.25	1408	710.23	16.50
25	2080	188	8.29	38	9.5	1260	793.65	16.25
26	2052	180	8.06	33	8.25	1268	788.64	14.75
27	2052	200	8.88	37	9.25	1284	778.82	19.75
28	2092	192	8.41	42	10.5	1224	816.99	19.50
29	2020	196	8.84	43	10.75	1224	816.99	16.00
30	2052	184	8.23	35	8.75	1284	778.82	18.75
	Mean	196.40	8.56	Mean	9.45	Mean	710.23	17.78
	S.D.	11.95	0.52	S.D.	0.82	S.D.	18.04	1.95

Table 25 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. nux-blanda*, collected from Chiang Mai province 1.

File	Stomatal cell			Palisade cell		Epidermal cell		Veinlet termination number (sq.mm)
	Number of epidermal cells (sq.mm)	Stomatal number (sq.mm)	Stomatal index	Number of beneath 4 epidermal ells	Palisade ratio	Number of epidermal cells (sq.mm)	epidermal cell area (sq.μm)	
1	1296	236	15.40	45	11.25	856	1168.22	18.00
2	1348	252	15.75	49	12.25	952	1050.42	18.00
3	1332	224	14.40	51	12.75	852	1173.71	17.75
4	1396	244	14.88	48	12	844	1184.83	17.00
5	1308	244	15.72	50	12.5	884	1131.22	17.00
6	1264	264	17.28	45	11.25	856	1168.22	15.75
7	1364	240	14.96	52	13	868	1152.07	13.75
8	1264	236	15.73	46	11.5	868	1152.07	15.00
9	1380	224	13.97	45	11.25	852	1173.71	15.50
10	1356	220	13.96	53	13.25	888	1126.13	16.75
11	1284	240	15.75	49	12.25	852	1173.71	18.50
12	1344	268	16.63	52	13	840	1190.48	17.75
13	1388	240	14.74	50	12.5	912	1096.49	15.75
14	1336	248	15.66	44	11	860	1162.79	16.75
15	1292	212	14.10	48	12	864	1157.41	19.25
16	1404	252	15.22	47	11.75	844	1184.83	14.75
17	1324	252	15.99	43	10.75	872	1146.79	15.50
18	1272	220	14.75	45	11.25	912	1096.49	15.50
19	1396	216	13.40	51	12.75	844	1184.83	19.50
20	1328	224	14.43	55	13.75	888	1126.13	14.25
21	1312	240	15.46	47	11.75	916	1091.70	16.25
22	1276	244	16.05	50	12.5	880	1136.36	14.50
23	1288	236	15.49	48	12	900	1111.11	15.50
24	1356	252	15.67	49	12.25	884	1131.22	15.00
25	1300	236	15.36	51	12.75	828	1207.73	12.50
26	1316	236	15.21	43	10.75	908	1101.32	15.25
27	1256	248	16.49	49	12.25	852	1173.71	17.50
28	1388	232	14.32	48	12	884	1131.22	16.75
29	1408	252	15.18	53	13.25	832	1201.92	18.25
30	1372	248	15.31	43	10.75	876	1141.55	17.00
	Mean	239.33	15.24	Mean	12.08	Mean	1130.95	16.35
	S.D.	13.62	0.86	S.D.	0.81	S.D.	25.82	1.66

Table 26 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. nux-blanda*, collected from Chiang Mai province 2.

File	Stomatal cell			Palisade cell		Epidermal cell		Veinlet termination number (sq.mm)
	Number of epidermal cells (sq.mm)	Stomatal number (sq.mm)	Stomatal index	Number of beneath 4 epidermal ells	Palisade ratio	Number of epidermal cells (sq.mm)	epidermal cell area (sq.μm)	
1	1200	288	19.35	55	13.75	980	1020.41	17.50
2	1284	256	16.62	53	13.25	924	1082.25	18.75
3	1264	256	16.84	57	14.25	960	1041.67	15.00
4	1332	260	16.33	49	12.25	996	1004.02	16.75
5	1404	248	15.01	52	13	952	1050.42	17.75
6	1344	236	14.94	55	13.75	1000	1000.00	16.25
7	1300	252	16.24	51	12.75	908	1101.32	17.50
8	1252	240	16.09	55	13.75	1000	1000.00	17.25
9	1304	268	17.05	47	11.75	984	1016.26	17.50
10	1284	216	14.40	53	13.25	1004	996.02	18.50
11	1276	268	17.36	52	13	960	1041.67	15.75
12	1304	228	14.88	50	12.5	956	1046.03	18.75
13	1332	276	17.16	49	12.25	900	1111.11	17.50
14	1236	264	17.60	53	13.25	916	1091.70	16.00
15	1332	268	16.75	46	11.5	984	1016.26	17.75
16	1328	220	14.21	51	12.75	956	1046.03	17.50
17	1360	264	16.26	53	13.25	948	1054.85	15.50
18	1260	252	16.67	48	12	992	1008.06	14.25
19	1280	284	18.16	46	11.5	980	1020.41	16.25
20	1328	276	17.21	46	11.5	924	1082.25	17.25
21	1320	264	16.67	50	12.5	956	1046.03	14.75
22	1372	228	14.25	48	12	972	1028.81	17.25
23	1308	260	16.58	47	11.75	916	1091.70	19.00
24	1300	256	16.45	51	12.75	940	1063.83	17.75
25	1320	256	16.24	45	11.25	956	1046.03	17.00
26	1368	264	16.18	49	12.25	988	1012.15	16.25
27	1288	256	16.58	46	11.5	980	1020.41	17.50
28	1328	276	17.21	47	11.75	880	1136.36	16.00
29	1348	280	17.20	51	12.75	864	1157.41	18.75
30	1300	260	16.67	48	12	908	1101.32	14.75
	Mean	257.33	16.44	Mean	12.53	Mean	1063.64	16.92
	S.D.	18.08	1.14	S.D.	0.81	S.D.	21.57	1.29

Table 27 Stomatal number, stomatal index, palisade ratio, epidermal cell number, epidermal cell area and veinlet termination number of *S. nux-blanda*, collected from Chiang Mai province 3.

File	Stomatal cell			Palisade cell		Epidermal cell		Veinlet termination number (sq.mm)
	Number of epidermal cells (sq.mm)	Stomatal number (sq.mm)	Stomatal index	Number of beneath 4 epidermal ells	Palisade ratio	Number of epidermal cells (sq.mm)	epidermal cell area (sq.μm)	
1	1352	260	16.13	50	12.5	908	1101.32	15.25
2	1316	240	15.42	52	13	944	1059.32	14.75
3	1308	232	15.06	51	12.75	980	1020.41	14.25
4	1304	224	14.66	47	11.75	936	1068.38	15.00
5	1292	236	15.45	54	13.5	908	1101.32	14.75
6	1364	268	16.42	48	12	876	1141.55	14.50
7	1328	244	15.52	47	11.75	868	1152.07	15.25
8	1296	252	16.28	45	11.25	864	1157.41	15.75
9	1320	256	16.24	54	13.5	876	1141.55	16.75
10	1332	280	17.37	44	11	848	1179.25	17.50
11	1284	264	17.05	50	12.5	880	1136.36	14.00
12	1280	272	17.53	48	12	848	1179.25	16.25
13	1292	228	15.00	57	14.25	896	1116.07	14.50
14	1340	220	14.10	50	12.5	872	1146.79	13.50
15	1360	240	15.00	46	11.5	888	1126.13	15.75
16	1284	276	17.69	44	11	884	1131.22	17.00
17	1356	224	14.18	49	12.25	856	1168.22	14.25
18	1300	284	17.93	48	12	960	1041.67	15.00
19	1316	256	16.28	51	12.75	852	1173.71	17.50
20	1340	284	17.49	46	11.5	844	1184.83	15.50
21	1320	272	17.09	47	11.75	860	1162.79	16.00
22	1264	272	17.71	52	13	916	1091.70	14.75
23	1316	224	14.55	44	11	844	1184.83	15.00
24	1284	244	15.97	50	12.5	936	1068.38	17.75
25	1292	280	17.81	49	12.25	872	1146.79	15.75
26	1340	244	15.40	52	13	896	1116.07	14.75
27	1300	276	17.51	45	11.25	880	1136.36	16.00
28	1292	256	16.54	45	11.25	844	1184.83	14.00
29	1296	268	17.14	54	13.5	908	1101.32	15.50
30	1308	272	17.22	51	12.75	928	1077.59	18.25
	Mean	254.93	16.26	Mean	12.27	Mean	1113.36	15.49
	S.D.	20.31	1.18	S.D.	0.85	S.D.	26.82	1.21

Appendix B Molecular evaluation

(The ITS, *rbc*L and *mat*K sequence and the multiple sequence alignment of four *Strychnos* species collected from different locations of Thailand)

The ITS sequence of *S. thorelii, S. nux-vomica, S. lucida and S. nux-blanda*

>ITS–St1

TTTCTTCCGAATAATGTTATGCTTAAACTCAACGGGTAGTACCGCCTGACCTGGGGTCGCGGTCGTAGCCGAGCATCAAAGAGATGCTGGCTTCAGGGTCATG
GCAGTCCACACGAGCAACGGGTTTTCACACGACAGATATGCGAGTTGAGGCATTCAACCACCACTTGTCGTGACGCCCGTCGGGAGGGACTCTCATTTAGGC
CAACCGCACGCTGGCACGGGAGGCCAATATCCGTCCCCCGCACACGGCATAAGTTGGCGTGTTAGGGGATCGACGTGATGCGTGACGCCCAGGCAGACGTGC
CCTCGACCTAGTGGCTTCAGGCGCAACTTGCGTTCAAAGACTCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCATCG
ATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCATTTTAGTTTAGGTAGAAGCCGAACTCCCGCCGAGTGCGCACCGCGAACGGGGACCGACGGGGCAGGCT
ATCAGTGAAAGTTTTCCTTGGCGCTTTCCGCGCCGGGGTTCAATTGTTTGCGCACGGCCTGGCACCCGAGGGTGCAAGCCGGTCGCGGAACGAGGCCGAGAA
AGGGTTGCCCCCGCCCGGCGCCCGTGGGAAGAAACGAGTTCGCGGGTCATCTGCAGGATTCGTCAATGATCCTTCCGCAGGTACACCTACGGAAACCTTGTT
ACGATTTTTAACTTCCAA

>ITS–St2

TTTCTTCCGGCCTATGATATGCTTAAACTCAGCTGGGAAGTCCCGCCTGACCTGGGGTCGCGGTCGTAGCCGAGCATCAAAGAGATGCTGGCTTCAGGGTCA
TGGCAGTCCACACGAGCAACGGGTTTTCACACGACAGATATGCGAGTTGAGGCATTCAACCACCACTTGTCGTGACGCCCGTCGGGAGGGACTCTCATTTAG
GCCAACCGCACGCTGGCACGGGAGGCCAATATCCGTCCCCCGCACACGGCATAAGTTGGCGTGTTAGGGGATCGACGTGATGCGTGACGCCCAGGCAGACGT
GCCCTCGACCTAGTGGCTTCAGGCGCAACTTGCGTTCAAAGACTCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCAT
CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCATTTTAGTTTAGGTAGAAGCCGAACTCCCGCCGAGTGCGCACCGCGAACGGGGACCGACGGGGCAGG
CTATCAGTGAAAGTTTTCCTTGGCGCTTTCCGCGCCGGGGTTCAATTGTTTGCGCACGGCCTGGCACCCGAGGGTGCAAGCCGGTCGCGGAACGAGGCCGAG
AAAGGGTTGCCCCCGCCCGGCGCCCGTGGGAAGAAACGAGTTCGCGGGTCATCTGCAGGATTCGTCAATGATCCTTCCGCAGGTTCACCTACGGAAACCTTG
TTACATTTTTTACTTTCAA

>ITS–St3

TTTCTTCCGACTTATTGATATGCTTAAACTCAGCGGGAAGTCCCGCCTGACCTGGGGTCGCGGTCGTAGCCGAGCATCAAAGAGATGCTGGCTTCAGGGTCAT
GGCAGTCCACACGAGCAACGGGTTTTCACACGACAGATATGCGAGTTGAGGCATTCAACCACCACTTGTCGTGACGCCCGTCGGGAGGGACTCTCATTTAGG
CCAACCGCACGCTGGCACGGGAGGCCAATATCCGTCCCCCGCACACGGCATAAGTTGGCGTGTTAGGGGATCGACGTGATGCGTGACGCCCAGGCAGACGTG
CCCTCGACCTAGTGGCTTCAGGCGCAACTTGCGTTCAAAGACTCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCATC
GATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCATTTTAGTTTAGGTAGAAGCCGAACTCCCGCCGAGTGCGCACCGCGAACGGGGACCGACGGGGCAGGC
TATCAGTGAAAGTTTTCCTTGGCGCTTTCCGCGCCGGGGTTCAATTGTTTGCGCACGGCCTGGCACCCGAGGGTGCAAGCCGGTCGCGGAACGAGGCCGAGA
AAGGGTTGCCCCCGCCCGGCGCCCGTGGGAAGAAACGAGTTCGCGGGTCATCTGCAGGATTCGTCAATGATCCTTCCGCAGGTTCACCTACGGAAACCTTGT
TACGATTTTTTACTTCCAA

>ITS–St4

TTTCTTCCGGCTATGATATGCTTAAACTCAAGCGGGTAATCCCGCCTGACCTGGGGTCGCGGTCGTAGCCGAGCATCAAAGAGATGCTGGCTTCAGGGTCAT
GGCAGTCCACACGAGCAACGGGTTTTCACACGACAGATATGCGAGTTGAGGCATTCAACCACCACTTGTCGTGACGCCCGTCGGGAGGGACTCTCATTTAGG
CCAACCGCACGCTGGCACGGGAGGCCAATATCCGTCCCCCGCACACGGCATAAGTTGGCGTGTTAGGGGATCGACGTGATGCGTGACGCCCAGGCAGACGTG
CCCTCGACCTAGTGGCTTCAGGCGCAACTTGCGTTCAAAGACTCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCATC
GATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCATTTTAGTTTAGGTAGAAGCCGAACTCCCGCCGAGTGCGCACCGCGAACGGGGACCGACGGGGCAGGC
TATCAGTGAAAGTTTTCCTTGGCGCTTTCCGCGCCGGGGTTCAATTGTTTGCGCACGGCCTGGCACCCGAGGGTGCAAGCCGGTCGCGGAACGAGGCCGAGA
AAGGGTTGCCCCCGCCCGGCGCCCGTGGGAAGAAACGAGTTCGCGGGTCATCTGCAGGATTCGTCAATGATCCTTCCGCAGGTTCCACCTACGGAAACCTTGT
TACGATTTTTTACTTCCAA

>ITS-Sl1

TTTCCTCCGGCTTATTGATATGCTTAAACTCAGCGGTGTAGTCCCGCCTGACCTGGGGTCGCGGTCGTGGCCGAGCGTCCTCGGGACGCCTGGCGGCAGGGT
CGCGGCAGCCCGCTCGAGCGACGGGTTCCGGGACGACAGCTATGCGAGTTGAGGCATTCAACCACCACTTGTCGTGACGCCCGTCGTGAGGGACTCTCATTT
AGGCCAACCGCGCGCTAGCACGGGAGGCCATTATCCGTCCCCTCCCGCACGGCCCGAGAGGGCGTGTGGGGGGAGCGACGCGATGCGTGACGCCCAGGCAG
ACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAAGACTCGATGGTTCACGGGATTCTGCAATTCACACCAAGTTTCGCAGTTTGCTACGTTCT
TCATCGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTTTAGGTAGATGCCGATCGCCCCCGGGCGCACCGCGAACGGGGCCACGAGGGGCGG
GCTATCCGTGAAAGTTTTCCTTGGCGCTTTCCGCGCCGGGGTTCGTTGTTTGCGCGCGGCCCGGCACCCGAGGGATCGGGCCGCTCGCGAGACGGGGCCGAG

GCGGGGTTGCCCCCTCCCGACGCCCGTGGAGAGAAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTCCACCTAAGGGAACCTTG
TTACGATTTTTACTTCCAA

>ITS-Sl2

TTTCCTCCGCTTATTGATATGCTTAACTCAACGGGTAGTCCCGCCTGACCTGGGGTCGCGGTCGTGGCCGAGCGTCCTCGGGACGCCTGGCGGCAGGGTCGC
GGCAGCCCGCTCGAGCGACGGGTTCCGGGACGACAGCTATGCGAGTTGAGGCATTCAACCACCACTTGTCGTGACGCCCGTCGTGAGGGACTCTCATTTAGG
CCAACCGCGCGCTAGCACGGGAGGCCATTATCCGTCCCCTCCCGCACGGCCCGAGAGGGCGTGTGGGGGGAGCGACGCGATGCGTGACGCCCAGGCAGACG
TGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAAGACTCGATGGTTCACGGGATTCTGCAATTCACACCAAGTTTCGCAGTTTGCTACGTTCTTCA
TCGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTTTAGGTAGATGCCGATCGCCCCCGGGCGCACCGCGAACGGGGCCACGAGGGGCGGGC
TATCCGTGAAAGTTTTCCTTGGCGCTTTCCGCGCCGGGGTTCGTTGTTTGCGCGCGGCCCGGCACCCGAGGGATCGGGCCGCTCGCGAGACGGGGCCGAGGC
GGGGTTGCCCCCTCCCGACGCCCGTGGAGAGAAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTCCACCTACGGGAACCTTGTT
ACGATTTTTACTTCCAA

>ITS-Sl3

TTTCCTCCGGCTTATTGATATGCTTAAACTCAACGGGTAGTCCCGCCTGACCTGGGTTCGCGGTCGTGGCCGAGCGTCCTCGGGACGCCTGGCGGCAGGGTC
GCGGCAGCCCGCTCGAGCGACGGGTTCCGGGACGACAGCTATGCGAGTTGAGGCATTCAACCACCACTTGTCGTGACGCCCGTCGTGAGGGACTCTCATTTA
GGCCAACCGCGCGCTAGCACGGGAGGCCATTATCCGTCCCCTCCCGCACGGCCCGAGAGGGCGTGTGGGGGGAGCGACGCGATGCGTGACGCCCAGGCAGA
CGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAAGACTCGATGGTTCACGGGATTCTGCAATTCACACCAAGTTTCGCAGTTTGCTACGTTCTT
CATCGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTTTAGGTAGATGCCGATCGCCCCCGGGCGCACCGCGAACGGGGCCACGAGGGGCGG
GCTATCCGTGAAAGTTTTCCTTGGCGCTTTCCGCGCCGGGGTTCGTTGTTTGCGCGCGGCCCGGCACCCGAGGGATCGGGCCGCTCGCGAGACGGGGCCGAG
GCGGGGTTGCCCCCTCCCGACGCCCGTGGAGAGAAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTCCACCTACGGAAACCTTG
TTACGATTTTTACTTCCAA

>ITS-Sv1

TTTCTTCCGGCCTATTGATATGCTTAAACTCAGCGGGTAATCCCGCCTGACCTGGGGTCGCGGTCGTGGCCGAGCGTCCTCGGGACGCCTGGCGGCAGGGTC
GCGGCAGTCCGCTCGAGCGACGGGCTCCGACACGACAGCTATGCGAGTTGAGGCATTCAACCACCACTTGTCGTGACGCCCGTCGTGAGGGACTCTCATTTA
GGCCAACCGCGCGCTAGCACGGGAGGCCATTGTCCGTCCCCTCCCGCACGGCCCGAGAGAGCGTGTGGGGGGAGCGACGCGATGCGTGACGCCCAGGCAGA
CGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAAGACTCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTT
CATCGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTTTAGGTAGATGCCGATCGCCCCCGGGCGCACCGCGAACTTGGCCGCGAGGGGCGGG
CTATCCGTGAAAGTTTTCCTTGGCGCTTTCCGCGCCGGGGTTCGTTGTTTGCGCGCGGCCCGGCACCCGAGGGATCGGGCCGCTCGCGAGACGGTGCCGAGG
CGGGGTTGCCCCCTCCCGACGCCCGTGGAGAGTAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTCCACCTACGGAAACCTTGT
TACGATTTTTACTTCCAA

>ITS-Sv2

TTTCTTCCGGCCTATTGATATGCTTAAACTCAGCGGGTAATCCCGCCTGACCTGGGGTCGCGGTCGTGGCCGAGCGTCCTCGGGACGCCTGGCGGCAGGGTC
GCGGCAGTCCGCTCGAGCGACGGGCTCCGACACGACAGCTATGCGAGTTGAGGCATTCAACCACCACTTGTCGTGACGCCCGTCGTGAGGGACTCTCATTTA
GGCCAACCGCGCGCTAGCACGGGAGGCCATTGTCCGTCCCCTCCCGCACGGCCCGAGAGGGCGTGTGGGGGGAGCGACGCGATGCGTGACGCCCAGGCAGA
CGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAAGACTCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTT
CATCGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTTTAGGTAGATGCCGATCGCCCCCGGGCGCACCGCGAACGGGGCCGCGAGGGGCGG
GCTATCCGTGAAAGTTTTCCTTGGCGCTTTCCGCGCCGGGGTTCGTTGTTTGCGCGCGGCCCGGCACCCGAGGGATCGGGCCGCTCGCGAGACGGGGCCGAG
GCGGGGTTGCCCCCTCCCGACGCCCGTGGAGAGTAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTCCACCTACGGAAACCTTG
TTACGATTTTTACTTCCAA

>ITS-Sv3

TTTCCTCCCGCCTATTGATATGCTTAAACTCAGCGGGTATTGGATCCCGCCTGACCTGGGGTCGCGGTCGTGGCCGAGCGTCCTCGGGACGCCTGGCGGCAG
GGTCGCGGCAGTCCGCTCGAGCGACGGGCTCCGACACGACAGCTATGCGAGTTGAGGCATTCAACCACCACTTGTCGTGACGCCCGTCGTGAGGGACTCTCA
TTTAGGCCAACCGCGCGCTAGCACGGGAGGCCATTGTCCGTCCCCTCCCGCACGGCCCGAGAGGGCGTGTGGGGGGAGCGACGCGATGCGTGACGCCCAGG
CAGACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAAGACTCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGT
TCTTCATCGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTTTAGGTAGATGCCGATCGCCCCCGGGCGCACCGCGAACGGGGCCGCGAGGGG

CGGGCTATCCGTGAAAGTTTTCCTTGGCGCTTTCCGCGCCGGGGTTCGTTGTTTGCGCGCGGCCCGGCACCCGAGGGATCGGGCCGCTCGCGAGACGGGGCC
GAGGCGGGGTTGCCCCCTCCCGACGCCCGTGGAGAGTAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTCCACCTACGGAAACC
TTGTTACGATTTTTACTTCCAA

>ITS-Sv4

TTTCCTCCGGGCTATTGATATGCTTAAACTCAGCGTTGGTAATCCCACCTGACCTGGGGTCGCGGTCGTGGCCGAGCGTCCTCGGGACGCCTGGCGGCAGGG
TCGCGGCAGTCCGCTCGAGCGACGGGCTCCGACACGACAGCTATGCGAGTTGAGGCATTCAACCACCACTTGTCGTGACGCCCGTCGTGAGGGACTCTCATT
TAGGCCAACCGCGCGCTAGCACGGGAGGCCATTGTCCGTCCCCTCCCGCACGGCCCGAGAGGGCGTGTGGGGGGAGCGACGCGATGCGTGACGCCCAGGCA
GACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAAGACTCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTC
TTCATCGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTTTAGGTAGATGCCGATCGCCCCCGGGCGCACCGCGAACGGGGCCGCGAGGGGCG
GGCTATCCGTGAAAGTTTTCCTTGGCGCTTTCCGCGCCGGGGTTCGTTGTTTGCGCGCGGCCCGGCACCCGAGGGATCGGGCCGCTCGCGAGACGGGGCCGA
GGCGGGGTTGCCCCCTCCCGACGCCCGTGGAGAGTAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTTCACCTACGGAAACCTT
GTTACGATTTTTACTTCCAA

>ITS-Sv5

TTTCCTCCGGCCTATTGATATGCTTAAACTCAGCCGGTATATCCCACCTGACCTGGGGTCGCGGTCGTGGCCGAGCGTCCTCGGGACGCCTGGCGGCAGGGT
CGCGGCAGTCCGCTCGAGCGACGGGCTCCGACACGACAGCTATGCGAGTTGAGGCATTCAACCACCACTTGTCGTGACGCCCGTCGTGAGGGACTCTCATTT
AGGCCAACCGCGCGCTAGCACGGGAGGCCATTGTCCGTCCCCTCCCGCACGGCCCGAGAGGGCGTGTGGGGGGAGCGACGCGATGCGTGACGCCCAGGCAG
ACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAAGACTCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCT
TCATCGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTTTAGGTAGATGCCGATCGCCCCCGGGCGCACCGCGAACGGGGCCGCGAGGGGCG
GGCTATCCGTGAAAGTTTTCCTTGGCGCTTTCCGCGCCGGGGTTCGTTGTTTGCGCGCGGCCCGGCACCCGAGGGATCGGGCCGCTCGCGAGACGGGGCCGA
GGCGGGGTTGCCCCCTCCCGACGCCCGTGGAGAGTAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCACGTTCACCTACGGAAACCTT
GTTACGATTTTTACTTCCAA

>ITS-Sb1

TTTCCTCCGGCCTATTGATATGCTTAAACTCAGCGGGTTTTAGTCACGCCTGAACTGGGGTCGCGGTCGTGGCCGAGCGTCCACGGGACGCCTGGCAGAAGG
GTCACGGCAGTCCGCTCGAACGACGGGTTCCAACACGACAACTATGCGAGTTGAGGCATTCAACCACCACTTGTCGTGACGCCCATCGGGAGGGACTCTCAT
TTAGGCCAACCGCACGATAGCACGGGAGGCCATTATCCGTCCCCCCTCGCACGGCCCGAGCAGGCGTGTGGGGGGAGAGACGCGATGCGTGACGCCCAGGC
AGACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAAGACTCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTT
CTTCATCGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTGTAGGTAGATGCCGATCGCCCCCGGGCGCACCGCGAACGGGGCCACGAGGGGC
GGGCTATCCGTGAAAGTTTTCCTTGGCGCTTTCCGCGCCGGGGTTCGTTGTTTGCGCGCGGCCTGGCACCCGAGGGACCGGGCCGCTCGCGAAACGGGGCCG
AGACGGGGTTGCCCCCCTCCCGACGCCCGCGGAGAGAAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTTCACCTACGGAAACC
TTGTTACGATTTTTACTTCCAA

>ITS-Sb2

TTTCCTCCGGCTAATGATATGCTTAAACTCAGCGGGTTTAGTCCCGCCTGACCTGGGGTCGCTGGTCGTGGCCGAGCGTCCACGGGACGCCTGGGCAGAAGG
GTCACGGCAGTCCGCTCGAACGACGGGTTCCAACACGACAACTATGCGAGTTGAGGCATTCAACCACCACTTGTCGTGACGCCCATCGGGAGGGACTCTCAT
TTAGGCCAACCGCACGATAGCACGGGAGGCCATTATCCGTCCCCCCTCGCACGGCCCGAGCAGGCGTGTGGGGGGAGAGACGCGATGCGTGACGCCCAGGC
AGACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAAGACTCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTT
CTTCATCGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTGTAGGTAAGATGCCGATCGCCCCCGGGCGCACCGCGAACGGGTGCCACGAGGG
GCGGGCTATCCGTGAAAGTTTTCCTTGGCGCTTTCCGCGCCGGGGTTCGTTGTTTGCGCGCGGCCTGGCACCCGAGGGACCGGGCCGCTCGCGAAACGGGGC
CGAGACGGGGTTGCCCCCCTCCCGACGCCCGCGGAGAGAAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTACACCTACGGAAA
CCTTGTTACGATTTTTACTTCCAA

>ITS-Sb3

TTTCCTCCGGCTATGATATGCTTAAACTCAGCGGGTAGTCCCGCCTGACCTGGGGTCGCGGTCGTGGCCGAGCGTCCACGGGACGCCTGGCAGAAGGGTCAC
GGCAGTCCGCTCGAACGACGGGTTCCAACACGACAACTATGCGAGTTGAGGCATTCAACCACCACTTGTCGTGACGCCCATCGGGAGGGACTCTCATTTAGG
CCAACCGCACGATAGCACGGGAGGCCATTATCCGTCCCCCCTCGCACGGCCCGAGCAGGCGTGTGGGGGGAGAGACGCGATGCGTGACGCCCAGGCAGACG
TGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAATGACTCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTC
ATCGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTGTAGGTAGATGCCGATCGCCCCCGGGCGCACCGCGAACGGGGCCACGAGGGGCGGG
CTATCCGCTGAAAGTTTTCCTTGGCGCTTTCCGCGCCGGGGTTCGTTGTTTGCGCGCGGCCTGGCACCCGAGGGACCGGGCCGCTCGCGAAACGGGGCCGAG
ACGGGGTTGCCCCCCTCCCGACGCCCGCGGAGAGAAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTACACCTACGGAAACCTT
GTTACGATTTTTACTTCCAA

>ITS-Sb4

TTTCCTTCGGCTATTGATATGCTTAAACTCAGCGGGTATTTGTACCGCCTGACCTGGGGTCGCGGTCGTGGCCGAGCGTCCACGGGACGCCTGGCAGAAGGG
TCACGGCAGTCCGCTCGAACGACGGGTTCCAACACGACAACTATGCGAGTTGAGGCATTCAACCACCACTTGTCGTGACGCCCATCGGGAGGGACTCTCATT
TAGGCCAACCGCACGATAGCACGGGAGGCCATTATCCGTCCCCCCTCGCACGGCCCGAGCAGGCGTGTGGGGGGAGAGACGCGATGCGTGACGCCCAGGCA
GACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAAGACTCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTC
TTCATCGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTGTAGGTAGATGCCGATCGCCCCCGGGCGCACCGCGAACGAGGCCACGAGGGGCG
GGCTATCCGTGAAAGTTTTCCTTGGCGCTTTCCGCGCCGGGGTTCGTTGTTTGCGCGCGGCCTGGCACCCGAGGGACCGGGCCGCTCGCGAAACGGGGCCGA
GACGGGGTTGCCCCCCTCCCGACGCCCGCGGAGAGAAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTTCACCTACGGAAACCT
TGTTACGATTTTTTACTTCCAA

The multiple sequence alignment of ITS region

```
ITS-Sv4         TTTCCTCCGGGCTATTGATATGCTTAAACTCAGCGTTGGTA----ATCCCACCTGACCTG 56
ITS-Sv5         TTTCCTCCGGCCTATTGATATGCTTAAACTCAGC--CGGTAT---ATCCCACCTGACCTG 55
ITS-Sv1         TTTCTTCCGGCCTATTGATATGCTTAAACTCAGCG--GGTA----ATCCCGCCTGACCTG 54
ITS-Sv2         TTTCTTCCGGCCTATTGATATGCTTAAACTCAGCG--GGTA----ATCCCGCCTGACCTG 54
ITS-Sv3         TTTCCTCCCGCCTATTGATATGCTTAAACTCAGCG--GGTATTGGATCCCGCCTGACCTG 58
ITS-Sl1         TTTCCTCCGGCTTATTGATATGCTTAAACTCAGCG-GTGTA----GTCCCGCCTGACCTG 55
ITS-Sl2         TTTCCTCCG-CTTATTGATATGCTTAA-CTCAACG-G-GTA----GTCCCGCCTGACCTG 52
ITS-Sl3         TTTCCTCCGGCTTATTGATATGCTTAAACTCAACG-G-GTA----GTCCCGCCTGACCTG 54
ITS-Sb2         TTTCCTCCGGC-TAATGATATGCTTAAACTCAGCG--GGTTT--AGTCCCGCCTGACCTG 55
ITS-Sb3         TTTCCTCCGGC-TA-TGATATGCTTAAACTCAGCG--GGT----AGTCCCGCCTGACCTG 52
ITS-Sb1         TTTCCTCCGGCCTATTGATATGCTTAAACTCAGCG--GGTTTT-AGTCACGCCTGAACTG 57
ITS-Sb4         TTTCCTTCGGC-TATTGATATGCTTAAACTCAGCG--GGTATT-TGTACCGCCTGACCTG 56
ITS-St1         TTTCTTCCGAATAAT-GTTATGCTTAAACTCAA-C-GGGTA----GTACCGCCTGACCTG 53
ITS-St4         TTTCTTCCGGCTA-T-GATATGCTTAAACTCAAGC-GGGTA----ATCCCGCCTGACCTG 53
ITS-St2         TTTCTTCCGGCCTAT-GATATGCTTAAACTCAGCT-GGGAA----GTCCCGCCTGACCTG 54
ITS-St3         TTTCTTCCGACTTATTGATATGCTTAAACTCAGC--GGGAA----GTCCCGCCTGACCTG 54
                **** * *        * ********* ****      *       *  * ***** ***

ITS-Sv4         GGGTCGC-GGTCGTGGCCGAGCGTCCTCGGGACGCCTGG-CGGCAGGGTCGCGGCAGTCC 114
ITS-Sv5         GGGTCGC-GGTCGTGGCCGAGCGTCCTCGGGACGCCTGG-CGGCAGGGTCGCGGCAGTCC 113
ITS-Sv1         GGGTCGC-GGTCGTGGCCGAGCGTCCTCGGGACGCCTGG-CGGCAGGGTCGCGGCAGTCC 112
ITS-Sv2         GGGTCGC-GGTCGTGGCCGAGCGTCCTCGGGACGCCTGG-CGGCAGGGTCGCGGCAGTCC 112
ITS-Sv3         GGGTCGC-GGTCGTGGCCGAGCGTCCTCGGGACGCCTGG-CGGCAGGGTCGCGGCAGTCC 116
ITS-Sl1         GGGTCGC-GGTCGTGGCCGAGCGTCCTCGGGACGCCTGG-CGGCAGGGTCGCGGCAGCCC 113
ITS-Sl2         GGGTCGC-GGTCGTGGCCGAGCGTCCTCGGGACGCCTGG-CGGCAGGGTCGCGGCAGCCC 110
ITS-Sl3         GGTTCGC-GGTCGTGGCCGAGCGTCCTCGGGACGCCTGG-CGGCAGGGTCGCGGCAGCCC 112
ITS-Sb2         GGGTCGCTGGTCGTGGCCGAGCGTCCACGGGACGCCTGGGCAGAAGGGTCACGGCAGTCC 115
ITS-Sb3         GGGTCGC-GGTCGTGGCCGAGCGTCCACGGGACGCCTGG-CAGAAGGGTCACGGCAGTCC 110
ITS-Sb1         GGGTCGC-GGTCGTGGCCGAGCGTCCACGGGACGCCTGG-CAGAAGGGTCACGGCAGTCC 115
ITS-Sb4         GGGTCGC-GGTCGTGGCCGAGCGTCCACGGGACGCCTGG-CAGAAGGGTCACGGCAGTCC 114
ITS-St1         GGGTCGC-GGTCGTAGCCGAGCATCAAAGAGATGC-TGG-CTTCAGGGTCATGGCAGTCC 110
ITS-St4         GGGTCGC-GGTCGTAGCCGAGCATCAAAGAGATGC-TGG-CTTCAGGGTCATGGCAGTCC 110
ITS-St2         GGGTCGC-GGTCGTAGCCGAGCATCAAAGAGATGC-TGG-CTTCAGGGTCATGGCAGTCC 111
ITS-St3         GGGTCGC-GGTCGTAGCCGAGCATCAAAGAGATGC-TGG-CTTCAGGGTCATGGCAGTCC 111
                ** **** ****** ******* **   * ** ** *** *   ******  ***** **

ITS-Sv4         GCTCGAGCGACGGGCTCCGACACGACAGCTATGCGAGTTGAGGCATTCAACCACCACTTG 174
ITS-Sv5         GCTCGAGCGACGGGCTCCGACACGACAGCTATGCGAGTTGAGGCATTCAACCACCACTTG 173
ITS-Sv1         GCTCGAGCGACGGGCTCCGACACGACAGCTATGCGAGTTGAGGCATTCAACCACCACTTG 172
ITS-Sv2         GCTCGAGCGACGGGCTCCGACACGACAGCTATGCGAGTTGAGGCATTCAACCACCACTTG 172
ITS-Sv3         GCTCGAGCGACGGGCTCCGACACGACAGCTATGCGAGTTGAGGCATTCAACCACCACTTG 176
ITS-Sl1         GCTCGAGCGACGGGTTCCGGGACGACAGCTATGCGAGTTGAGGCATTCAACCACCACTTG 173
ITS-Sl2         GCTCGAGCGACGGGTTCCGGGACGACAGCTATGCGAGTTGAGGCATTCAACCACCACTTG 170
ITS-Sl3         GCTCGAGCGACGGGTTCCGGGACGACAGCTATGCGAGTTGAGGCATTCAACCACCACTTG 172
ITS-Sb2         GCTCGAACGACGGGTTCCAACACGACAACTATGCGAGTTGAGGCATTCAACCACCACTTG 175
ITS-Sb3         GCTCGAACGACGGGTTCCAACACGACAACTATGCGAGTTGAGGCATTCAACCACCACTTG 170
ITS-Sb1         GCTCGAACGACGGGTTCCAACACGACAACTATGCGAGTTGAGGCATTCAACCACCACTTG 175
ITS-Sb4         GCTCGAACGACGGGTTCCAACACGACAACTATGCGAGTTGAGGCATTCAACCACCACTTG 174
ITS-St1         ACACGAGCAACGGGTTTTCACACGACAGATATGCGAGTTGAGGCATTCAACCACCACTTG 170
ITS-St4         ACACGAGCAACGGGTTTTCACACGACAGATATGCGAGTTGAGGCATTCAACCACCACTTG 170
ITS-St2         ACACGAGCAACGGGTTTTCACACGACAGATATGCGAGTTGAGGCATTCAACCACCACTTG 171
ITS-St3         ACACGAGCAACGGGTTTTCACACGACAGATATGCGAGTTGAGGCATTCAACCACCACTTG 171
                 * *** * ***** *     ******  ******************************

ITS-Sv4         TCGTGACGCCCGTCGTGAGGGACTCTCATTTAGGCCAACCGCGCGCTAGCACGGGAGGCC 234
ITS-Sv5         TCGTGACGCCCGTCGTGAGGGACTCTCATTTAGGCCAACCGCGCGCTAGCACGGGAGGCC 233
ITS-Sv1         TCGTGACGCCCGTCGTGAGGGACTCTCATTTAGGCCAACCGCGCGCTAGCACGGGAGGCC 232
ITS-Sv2         TCGTGACGCCCGTCGTGAGGGACTCTCATTTAGGCCAACCGCGCGCTAGCACGGGAGGCC 232
ITS-Sv3         TCGTGACGCCCGTCGTGAGGGACTCTCATTTAGGCCAACCGCGCGCTAGCACGGGAGGCC 236
ITS-Sl1         TCGTGACGCCCGTCGTGAGGGACTCTCATTTAGGCCAACCGCGCGCTAGCACGGGAGGCC 233
ITS-Sl2         TCGTGACGCCCGTCGTGAGGGACTCTCATTTAGGCCAACCGCGCGCTAGCACGGGAGGCC 230
ITS-Sl3         TCGTGACGCCCGTCGTGAGGGACTCTCATTTAGGCCAACCGCGCGCTAGCACGGGAGGCC 232
```

```
ITS-Sb2         TCGTGACGCCCATCGGGAGGGACTCTCATTTAGGCCAACCGCACGATAGCACGGGAGGCC 235
ITS-Sb3         TCGTGACGCCCATCGGGAGGGACTCTCATTTAGGCCAACCGCACGATAGCACGGGAGGCC 230
ITS-Sb1         TCGTGACGCCCATCGGGAGGGACTCTCATTTAGGCCAACCGCACGATAGCACGGGAGGCC 235
ITS-Sb4         TCGTGACGCCCATCGGGAGGGACTCTCATTTAGGCCAACCGCACGATAGCACGGGAGGCC 234
ITS-St1         TCGTGACGCCCGTCGGGAGGGACTCTCATTTAGGCCAACCGCACGCTGGCACGGGAGGCC 230
ITS-St4         TCGTGACGCCCGTCGGGAGGGACTCTCATTTAGGCCAACCGCACGCTGGCACGGGAGGCC 230
ITS-St2         TCGTGACGCCCGTCGGGAGGGACTCTCATTTAGGCCAACCGCACGCTGGCACGGGAGGCC 231
ITS-St3         TCGTGACGCCCGTCGGGAGGGACTCTCATTTAGGCCAACCGCACGCTGGCACGGGAGGCC 231
                *********** *** ************************* ** * ************

ITS-Sv4         ATTGTCCGTCCCCTCCCGCACGGCCCGAGAGGGCGTGTGGGGGGAGCGACGCGATGCGTG 294
ITS-Sv5         ATTGTCCGTCCCCTCCCGCACGGCCCGAGAGGGCGTGTGGGGGGAGCGACGCGATGCGTG 293
ITS-Sv1         ATTGTCCGTCCCCTCCCGCACGGCCCGAGAGAGCGTGTGGGGGGAGCGACGCGATGCGTG 292
ITS-Sv2         ATTGTCCGTCCCCTCCCGCACGGCCCGAGAGGGCGTGTGGGGGGAGCGACGCGATGCGTG 292
ITS-Sv3         ATTGTCCGTCCCCTCCCGCACGGCCCGAGAGGGCGTGTGGGGGGAGCGACGCGATGCGTG 296
ITS-Sl1         ATTATCCGTCCCCTCCCGCACGGCCCGAGAGGGCGTGTGGGGGGAGCGACGCGATGCGTG 293
ITS-Sl2         ATTATCCGTCCCCTCCCGCACGGCCCGAGAGGGCGTGTGGGGGGAGCGACGCGATGCGTG 290
ITS-Sl3         ATTATCCGTCCCCTCCCGCACGGCCCGAGAGGGCGTGTGGGGGGAGCGACGCGATGCGTG 292
ITS-Sb2         ATTATCCGTCCCCCCTCGCACGGCCCGAGCAGGCGTGTGGGGGGAGAGACGCGATGCGTG 295
ITS-Sb3         ATTATCCGTCCCCCCTCGCACGGCCCGAGCAGGCGTGTGGGGGGAGAGACGCGATGCGTG 290
ITS-Sb1         ATTATCCGTCCCCCCTCGCACGGCCCGAGCAGGCGTGTGGGGGGAGAGACGCGATGCGTG 295
ITS-Sb4         ATTATCCGTCCCCCCTCGCACGGCCCGAGCAGGCGTGTGGGGGGAGAGACGCGATGCGTG 294
ITS-St1         AATATCCGTCCCC-CGCACACGGCATAAGTTGGCGTGTTAGGGGATCGACGTGATGCGTG 289
ITS-St4         AATATCCGTCCCC-CGCACACGGCATAAGTTGGCGTGTTAGGGGATCGACGTGATGCGTG 289
ITS-St2         AATATCCGTCCCC-CGCACACGGCATAAGTTGGCGTGTTAGGGGATCGACGTGATGCGTG 290
ITS-St3         AATATCCGTCCCC-CGCACACGGCATAAGTTGGCGTGTTAGGGGATCGACGTGATGCGTG 290
                * * ********* * * ******   **   ******  *****  **** ********

ITS-Sv4         ACGCCCAGGCAGACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAA-GAC 353
ITS-Sv5         ACGCCCAGGCAGACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAA-GAC 352
ITS-Sv1         ACGCCCAGGCAGACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAA-GAC 351
ITS-Sv2         ACGCCCAGGCAGACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAA-GAC 351
ITS-Sv3         ACGCCCAGGCAGACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAA-GAC 355
ITS-Sl1         ACGCCCAGGCAGACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAA-GAC 352
ITS-Sl2         ACGCCCAGGCAGACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAA-GAC 349
ITS-Sl3         ACGCCCAGGCAGACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAA-GAC 351
ITS-Sb2         ACGCCCAGGCAGACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAA-GAC 354
ITS-Sb3         ACGCCCAGGCAGACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAATGAC 350
ITS-Sb1         ACGCCCAGGCAGACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAA-GAC 354
ITS-Sb4         ACGCCCAGGCAGACGTGCCCTCGGCCTAACGGCTTCGGGCGCAACTTGCGTTCAAA-GAC 353
ITS-St1         ACGCCCAGGCAGACGTGCCCTCGACCTAGTGGCTTCAGGCGCAACTTGCGTTCAAA-GAC 348
ITS-St4         ACGCCCAGGCAGACGTGCCCTCGACCTAGTGGCTTCAGGCGCAACTTGCGTTCAAA-GAC 348
ITS-St2         ACGCCCAGGCAGACGTGCCCTCGACCTAGTGGCTTCAGGCGCAACTTGCGTTCAAA-GAC 349
ITS-St3         ACGCCCAGGCAGACGTGCCCTCGACCTAGTGGCTTCAGGCGCAACTTGCGTTCAAA-GAC 349
                ********************** ****  ****** ****************** ***

ITS-Sv4         TCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCAT 413
ITS-Sv5         TCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCAT 412
ITS-Sv1         TCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCAT 411
ITS-Sv2         TCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCAT 411
ITS-Sv3         TCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCAT 415
ITS-Sl1         TCGATGGTTCACGGGATTCTGCAATTCACACCAAGTTTCGCAGTTTGCTACGTTCTTCAT 412
ITS-Sl2         TCGATGGTTCACGGGATTCTGCAATTCACACCAAGTTTCGCAGTTTGCTACGTTCTTCAT 409
ITS-Sl3         TCGATGGTTCACGGGATTCTGCAATTCACACCAAGTTTCGCAGTTTGCTACGTTCTTCAT 411
ITS-Sb2         TCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCAT 414
ITS-Sb3         TCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCAT 410
ITS-Sb1         TCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCAT 414
ITS-Sb4         TCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCAT 413
ITS-St1         TCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCAT 408
ITS-St4         TCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCAT 408
ITS-St2         TCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCAT 409
ITS-St3         TCGATGGTTCACGGGATTCTGCAATTCACACCAAGTATCGCAGTTTGCTACGTTCTTCAT 409
                ********************************** **********************
```

```
ITS-Sv4         CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTTTAGGTA-GATGCCGAT 472
ITS-Sv5         CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTTTAGGTA-GATGCCGAT 471
ITS-Sv1         CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTTTAGGTA-GATGCCGAT 470
ITS-Sv2         CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTTTAGGTA-GATGCCGAT 470
ITS-Sv3         CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTTTAGGTA-GATGCCGAT 474
ITS-Sl1         CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTTTAGGTA-GATGCCGAT 471
ITS-Sl2         CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTTTAGGTA-GATGCCGAT 468
ITS-Sl3         CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTTTAGGTA-GATGCCGAT 470
ITS-Sb2         CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTGTAGGTAAGATGCCGAT 474
ITS-Sb3         CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTGTAGGTA-GATGCCGAT 469
ITS-Sb1         CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTGTAGGTA-GATGCCGAT 473
ITS-Sb4         CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTTTTAGTGTAGGTA-GATGCCGAT 472
ITS-St1         CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCATTTTAGTTTAGGTA-GAAGCCGAA 467
ITS-St4         CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCATTTTAGTTTAGGTA-GAAGCCGAA 467
ITS-St2         CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCATTTTAGTTTAGGTA-GAAGCCGAA 468
ITS-St3         CGATGCGAGAGCCGAGATATCCGTTGCCGAGAGTCATTTTAGTTTAGGTA-GAAGCCGAA 468
                ********************************** ******* ****** ** *****

ITS-Sv4         CGCCCCCGG---GCGCACCGCGAACGGG-GCCGCGAGGGGCGGGCTATCCG-TGAAAGTT 527
ITS-Sv5         CGCCCCCGG---GCGCACCGCGAACGGG-GCCGCGAGGGGCGGGCTATCCG-TGAAAGTT 526
ITS-Sv1         CGCCCCCGG---GCGCACCGCGAACTTG-GCCGCGAGGGGCGGGCTATCCG-TGAAAGTT 525
ITS-Sv2         CGCCCCCGG---GCGCACCGCGAACGGG-GCCGCGAGGGGCGGGCTATCCG-TGAAAGTT 525
ITS-Sv3         CGCCCCCGG---GCGCACCGCGAACGGG-GCCGCGAGGGGCGGGCTATCCG-TGAAAGTT 529
ITS-Sl1         CGCCCCCGG---GCGCACCGCGAACGGG-GCCACGAGGGGCGGGCTATCCG-TGAAAGTT 526
ITS-Sl2         CGCCCCCGG---GCGCACCGCGAACGGG-GCCACGAGGGGCGGGCTATCCG-TGAAAGTT 523
ITS-Sl3         CGCCCCCGG---GCGCACCGCGAACGGG-GCCACGAGGGGCGGGCTATCCG-TGAAAGTT 525
ITS-Sb2         CGCCCCCGG---GCGCACCGCGAACGGGTGCCACGAGGGGCGGGCTATCCG-TGAAAGTT 530
ITS-Sb3         CGCCCCCGG---GCGCACCGCGAACGGG-GCCACGAGGGGCGGGCTATCCGCTGAAAGTT 525
ITS-Sb1         CGCCCCCGG---GCGCACCGCGAACGGG-GCCACGAGGGGCGGGCTATCCG-TGAAAGTT 528
ITS-Sb4         CGCCCCCGG---GCGCACCGCGAACGAG-GCCACGAGGGGCGGGCTATCCG-TGAAAGTT 527
ITS-St1         CTCCCGCCGAGTGCGCACCGCGAACGGGGACCG-ACGGGGCAGGCTATCAG-TGAAAGTT 525
ITS-St4         CTCCCGCCGAGTGCGCACCGCGAACGGGGACCG-ACGGGGCAGGCTATCAG-TGAAAGTT 525
ITS-St2         CTCCCGCCGAGTGCGCACCGCGAACGGGGACCG-ACGGGGCAGGCTATCAG-TGAAAGTT 526
ITS-St3         CTCCCGCCGAGTGCGCACCGCGAACGGGGACCG-ACGGGGCAGGCTATCAG-TGAAAGTT 526
                 * *** * *   *************  *  **    ***** ******* * ********

ITS-Sv4         TTCCTTGGCGCTTTCCGCGCCGGGGTTCG-TTGTTTGCGCGCGGCCCGGCACCCGAGGGA 586
ITS-Sv5         TTCCTTGGCGCTTTCCGCGCCGGGGTTCG-TTGTTTGCGCGCGGCCCGGCACCCGAGGGA 585
ITS-Sv1         TTCCTTGGCGCTTTCCGCGCCGGGGTTCG-TTGTTTGCGCGCGGCCCGGCACCCGAGGGA 584
ITS-Sv2         TTCCTTGGCGCTTTCCGCGCCGGGGTTCG-TTGTTTGCGCGCGGCCCGGCACCCGAGGGA 584
ITS-Sv3         TTCCTTGGCGCTTTCCGCGCCGGGGTTCG-TTGTTTGCGCGCGGCCCGGCACCCGAGGGA 588
ITS-Sl1         TTCCTTGGCGCTTTCCGCGCCGGGGTTCG-TTGTTTGCGCGCGGCCCGGCACCCGAGGGA 585
ITS-Sl2         TTCCTTGGCGCTTTCCGCGCCGGGGTTCG-TTGTTTGCGCGCGGCCCGGCACCCGAGGGA 582
ITS-Sl3         TTCCTTGGCGCTTTCCGCGCCGGGGTTCG-TTGTTTGCGCGCGGCCCGGCACCCGAGGGA 584
ITS-Sb2         TTCCTTGGCGCTTTCCGCGCCGGGGTTCG-TTGTTTGCGCGCGGCCTGGCACCCGAGGGA 589
ITS-Sb3         TTCCTTGGCGCTTTCCGCGCCGGGGTTCG-TTGTTTGCGCGCGGCCTGGCACCCGAGGGA 584
ITS-Sb1         TTCCTTGGCGCTTTCCGCGCCGGGGTTCG-TTGTTTGCGCGCGGCCTGGCACCCGAGGGA 587
ITS-Sb4         TTCCTTGGCGCTTTCCGCGCCGGGGTTCG-TTGTTTGCGCGCGGCCTGGCACCCGAGGGA 586
ITS-St1         TTCCTTGGCGCTTTCCGCGCCGGGGTTCAATTGTTTGCGCACGGCCTGGCACCCGAGGGT 585
ITS-St4         TTCCTTGGCGCTTTCCGCGCCGGGGTTCAATTGTTTGCGCACGGCCTGGCACCCGAGGGT 585
ITS-St2         TTCCTTGGCGCTTTCCGCGCCGGGGTTCAATTGTTTGCGCACGGCCTGGCACCCGAGGGT 586
ITS-St3         TTCCTTGGCGCTTTCCGCGCCGGGGTTCAATTGTTTGCGCACGGCCTGGCACCCGAGGGT 586
                 ***************************  ********** ***** ************

ITS-Sv4         TCGGGCCGCTCGCGAGACGGGGCCGAGGCGGGGTTGCCCCC-TCCCGACGCCCGTGGAGA 645
ITS-Sv5         TCGGGCCGCTCGCGAGACGGGGCCGAGGCGGGGTTGCCCCC-TCCCGACGCCCGTGGAGA 644
ITS-Sv1         TCGGGCCGCTCGCGAGACGGTGCCGAGGCGGGGTTGCCCCC-TCCCGACGCCCGTGGAGA 643
ITS-Sv2         TCGGGCCGCTCGCGAGACGGGGCCGAGGCGGGGTTGCCCCC-TCCCGACGCCCGTGGAGA 643
ITS-Sv3         TCGGGCCGCTCGCGAGACGGGGCCGAGGCGGGGTTGCCCCC-TCCCGACGCCCGTGGAGA 647
ITS-Sl1         TCGGGCCGCTCGCGAGACGGGGCCGAGGCGGGGTTGCCCCC-TCCCGACGCCCGTGGAGA 644
ITS-Sl2         TCGGGCCGCTCGCGAGACGGGGCCGAGGCGGGGTTGCCCCC-TCCCGACGCCCGTGGAGA 641
```

```
ITS-Sl3         TCGGGCCGCTCGCGAGACGGGGCCGAGGCGGGGTTGCCCCC-TCCCGACGCCCGTGGAGA 643
ITS-Sb2         CCGGGCCGCTCGCGAAACGGGGCCGAGACGGGGTTGCCCCCCTCCCGACGCCCGCGGAGA 649
ITS-Sb3         CCGGGCCGCTCGCGAAACGGGGCCGAGACGGGGTTGCCCCCCTCCCGACGCCCGCGGAGA 644
ITS-Sb1         CCGGGCCGCTCGCGAAACGGGGCCGAGACGGGGTTGCCCCCCTCCCGACGCCCGCGGAGA 647
ITS-Sb4         CCGGGCCGCTCGCGAAACGGGGCCGAGACGGGGTTGCCCCCCTCCCGACGCCCGCGGAGA 646
ITS-St1         GCAAGCCGGTCGCGGAACGAGGCCGAGAAAGGGTTGCCCCC-GCCCGGCGCCCGTGGGAA 644
ITS-St4         GCAAGCCGGTCGCGGAACGAGGCCGAGAAAGGGTTGCCCCC-GCCCGGCGCCCGTGGGAA 644
ITS-St2         GCAAGCCGGTCGCGGAACGAGGCCGAGAAAGGGTTGCCCCC-GCCCGGCGCCCGTGGGAA 645
ITS-St3         GCAAGCCGGTCGCGGAACGAGGCCGAGAAAGGGTTGCCCCC-GCCCGGCGCCCGTGGGAA 645
                 *  **** *****  ***  ******   ***********  **** ****** **  *

ITS-Sv4         GTAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTTCACCTAC 705
ITS-Sv5         GTAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCACGTTCACCTAC 704
ITS-Sv1         GTAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTCCACCTAC 703
ITS-Sv2         GTAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTCCACCTAC 703
ITS-Sv3         GTAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTCCACCTAC 707
ITS-Sl1         GAAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTCCACCTAA 704
ITS-Sl2         GAAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTCCACCTAC 701
ITS-Sl3         GAAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTCCACCTAC 703
ITS-Sb2         GAAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTACACCTAC 709
ITS-Sb3         GAAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTACACCTAC 704
ITS-Sb1         GAAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTTCACCTAC 707
ITS-Sb4         GAAACGAGTTCGCGGGTCGTCTGCAGGATTCGACAATGATCCTTCCGCAGGTTCACCTAC 706
ITS-St1         GAAACGAGTTCGCGGGTCATCTGCAGGATTCGTCAATGATCCTTCCGCAGGTACACCTAC 704
ITS-St4         GAAACGAGTTCGCGGGTCATCTGCAGGATTCGTCAATGATCCTTCCGCAGGTCCACCTAC 704
ITS-St2         GAAACGAGTTCGCGGGTCATCTGCAGGATTCGTCAATGATCCTTCCGCAGGTTCACCTAC 705
ITS-St3         GAAACGAGTTCGCGGGTCATCTGCAGGATTCGTCAATGATCCTTCCGCAGGTTCACCTAC 705
                * ***************** ************* **************** ** ******

ITS-Sv4         GGAAACCTTGTTACGATTTTT-ACTTCCAA 734
ITS-Sv5         GGAAACCTTGTTACGATTTTT-ACTTCCAA 733
ITS-Sv1         GGAAACCTTGTTACGATTTTT-ACTTCCAA 732
ITS-Sv2         GGAAACCTTGTTACGATTTTT-ACTTCCAA 732
ITS-Sv3         GGAAACCTTGTTACGATTTTT-ACTTCCAA 736
ITS-Sl1         GGGAACCTTGTTACGATTTTT-ACTTCCAA 733
ITS-Sl2         GGGAACCTTGTTACGATTTTT-ACTTCCAA 730
ITS-Sl3         GGAAACCTTGTTACGATTTTT-ACTTCCAA 732
ITS-Sb2         GGAAACCTTGTTACGATTTTT-ACTTCCAA 738
ITS-Sb3         GGAAACCTTGTTACGATTTTT-ACTTCCAA 733
ITS-Sb1         GGAAACCTTGTTACGATTTTT-ACTTCCAA 736
ITS-Sb4         GGAAACCTTGTTACGATTTTTTACTTCCAA 736
ITS-St1         GGAAACCTTGTTACGATTTTTAACTTCCAA 734
ITS-St4         GGAAACCTTGTTACGATTTTTA-CTTCCAA 733
ITS-St2         GGAAACCTTGTTAC-ATTTTTTACTTTCAA 734
ITS-St3         GGAAACCTTGTTACGATTTTTTACTTCCAA 735
                  ** ********** ******  *** ***
```

The size of the ITS region

Sequence 1: ITS–St1 734 bp

Sequence 2: ITS–St2 734 bp

Sequence 3: ITS–St3 735 bp

Sequence 4: ITS–St4 733 bp

Sequence 5: ITS-Sl1 733 bp

Sequence 6: ITS-Sl2 730 bp

Sequence 7: ITS-Sl3 732 bp

Sequence 8: ITS-Sv1 732 bp

Sequence 9: ITS-Sv2 732 bp

Sequence 10: ITS-Sv3 736 bp

Sequence 11: ITS-Sv4 734 bp

Sequence 12: ITS-Sv5 733 bp

Sequence 13: ITS-Sb1 736 bp

Sequence 14: ITS-Sb2 738 bp

Sequence 15: ITS-Sb3 733 bp

Sequence 16: ITS-Sb4 736 bp

The pairwise of similarity score

Sequences (1:2) Aligned. Score: 98	Sequences (4:6) Aligned. Score: 88	Sequences (8:9) Aligned. Score: 99
Sequences (1:3) Aligned. Score: 98	Sequences (4:7) Aligned. Score: 88	Sequences (8:10) Aligned. Score: 99
Sequences (1:4) Aligned. Score: 99	Sequences (4:8) Aligned. Score: 88	Sequences (8:11) Aligned. Score: 98
Sequences (1:5) Aligned. Score: 87	Sequences (4:9) Aligned. Score: 89	Sequences (8:13) Aligned. Score: 95
Sequences (1:6) Aligned. Score: 88	Sequences (4:10) Aligned. Score: 88	Sequences (8:14) Aligned. Score: 95
Sequences (1:7) Aligned. Score: 88	Sequences (4:11) Aligned. Score: 88	Sequences (8:15) Aligned. Score: 95
Sequences (1:8) Aligned. Score: 87	Sequences (4:12) Aligned. Score: 88	Sequences (8:16) Aligned. Score: 95
Sequences (1:9) Aligned. Score: 88	Sequences (4:13) Aligned. Score: 88	Sequences (9:10) Aligned. Score: 99
Sequences (1:10) Aligned. Score: 88	Sequences (4:14) Aligned. Score: 89	Sequences (9:11) Aligned. Score: 99
Sequences (1:11) Aligned. Score: 88	Sequences (4:15) Aligned. Score: 89	Sequences (9:12) Aligned. Score: 99
Sequences (1:12) Aligned. Score: 87	Sequences (4:16) Aligned. Score: 88	Sequences (9:13) Aligned. Score: 95
Sequences (1:13) Aligned. Score: 88	Sequences (5:6) Aligned. Score: 99	Sequences (9:14) Aligned. Score: 95
Sequences (1:14) Aligned. Score: 88	Sequences (5:7) Aligned. Score: 99	Sequences (9:15) Aligned. Score: 95
Sequences (1:15) Aligned. Score: 88	Sequences (5:8) Aligned. Score: 97	Sequences (9:16) Aligned. Score: 95
Sequences (1:16) Aligned. Score: 88	Sequences (5:9) Aligned. Score: 98	Sequences (10:11) Aligned. Score: 99
Sequences (2:3) Aligned. Score: 99	Sequences (5:10) Aligned. Score: 98	Sequences (10:12) Aligned. Score: 99
Sequences (2:4) Aligned. Score: 98	Sequences (5:11) Aligned. Score: 97	Sequences (10:13) Aligned. Score: 95
Sequences (2:5) Aligned. Score: 87	Sequences (5:12) Aligned. Score: 97	Sequences (10:14) Aligned. Score: 95
Sequences (2:6) Aligned. Score: 87	Sequences (5:13) Aligned. Score: 95	Sequences (10:15) Aligned. Score: 95
Sequences (2:7) Aligned. Score: 88	Sequences (5:14) Aligned. Score: 95	Sequences (10:16) Aligned. Score: 95
Sequences (2:8) Aligned. Score: 88	Sequences (5:15) Aligned. Score: 95	Sequences (11:12) Aligned. Score: 99
Sequences (2:9) Aligned. Score: 88	Sequences (5:16) Aligned. Score: 95	Sequences (11:13) Aligned. Score: 95
Sequences (2:10) Aligned. Score: 88	Sequences (6:7) Aligned. Score: 99	Sequences (11:14) Aligned. Score: 95
Sequences (2:11) Aligned. Score: 88	Sequences (6:8) Aligned. Score: 97	Sequences (11:15) Aligned. Score: 95
Sequences (2:12) Aligned. Score: 88	Sequences (6:9) Aligned. Score: 98	Sequences (11:16) Aligned. Score: 95
Sequences (2:13) Aligned. Score: 88	Sequences (6:10) Aligned. Score: 98	Sequences (12:13) Aligned. Score: 95
Sequences (2:14) Aligned. Score: 88	Sequences (6:11) Aligned. Score: 97	Sequences (12:14) Aligned. Score: 95
Sequences (2:15) Aligned. Score: 88	Sequences (6:12) Aligned. Score: 97	Sequences (12:15) Aligned. Score: 95
Sequences (2:16) Aligned. Score: 88	Sequences (6:13) Aligned. Score: 95	Sequences (12:16) Aligned. Score: 95
Sequences (3:4) Aligned. Score: 99	Sequences (6:14) Aligned. Score: 95	Sequences (13:14) Aligned. Score: 99
Sequences (3:5) Aligned. Score: 88	Sequences (6:15) Aligned. Score: 95	Sequences (13:15) Aligned. Score: 99
Sequences (3:6) Aligned. Score: 88	Sequences (6:16) Aligned. Score: 95	Sequences (13:16) Aligned. Score: 98
Sequences (3:7) Aligned. Score: 88	Sequences (7:8) Aligned. Score: 97	Sequences (14:15) Aligned. Score: 99
Sequences (3:8) Aligned. Score: 88	Sequences (7:9) Aligned. Score: 98	Sequences (14:16) Aligned. Score: 98
Sequences (3:9) Aligned. Score: 89	Sequences (7:10) Aligned. Score: 98	Sequences (15:16) Aligned. Score: 99
Sequences (3:10) Aligned. Score: 88	Sequences (7:11) Aligned. Score: 97	
Sequences (3:11) Aligned. Score: 88	Sequences (7:12) Aligned. Score: 97	
Sequences (3:12) Aligned. Score: 88	Sequences (7:13) Aligned. Score: 95	
Sequences (3:13) Aligned. Score: 88	Sequences (7:14) Aligned. Score: 95	
Sequences (3:14) Aligned. Score: 88	Sequences (7:15) Aligned. Score: 95	
Sequences (3:15) Aligned. Score: 88	Sequences (7:16) Aligned. Score: 95	
Sequences (3:16) Aligned. Score: 88	Sequences (8:12) Aligned. Score: 98.	
Sequences (4:5) Aligned. Score: 88		

The *rbc*L sequence of *S. thorelii, S. nux-vomica,*

S. lucida and S. nux-blanda

>*rbc*L-St1

GCTGGTGTTAAGAGTACAAATTGACATTATTATACTCCTCAATACGAAACCAAAGATACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCCGGAGTTC
CACCTGAAAAAGCAGGGGCCCCAGTAGCTGCCGGAATCTTCTACTGGTACATGGACAAACTGTGTGGACCGATGGACTTACCAGCCTTGATCGTTACAAAGG
GCGCTGCTAGATATTCCACCCTGTTGCTGGAGAAGAAGACCAATAAATTGCTTAAGTAGCTTATCCCTTAGACCTTTTTGAAGAAGGTTCTGTTACTAACATG
TTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAGCCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCCAAGGCC
CGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCCCTGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTA
CGGTAGGGCAGTTTATGAATGTCTTCGTGGTGGACTTGATTTTACCAAAGATGATGAAAACGTGAACTCCCAACCATTTATGCGTTGGAGAGATCGTTTCTTA
TTTTGTGCCGAAGCACTTTATAAAGCACAGGCTGAAACCGGTGAAATCAAAGGACATTACTTGAATGCTACTGCAGGTACATGCGAAGAAATGATGAAAAGAG
CTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGACTACTTAACCGGGGGATTCACTGCAAATACTACCTTAGCTCATTATTGCCGAGATAATGG
CCTACTTCTTCACATCCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGTATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGT
GGAGATCATGTTCACGCTGGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTACTGGCGGGAGGATTTTATTGAAAAA
GATCCAAACCCGCGGTGTTTATTTCACTCAAGATTGGGGTCTCTCTACCGGGGGGTTATACCTGGTGGCTTCAGGGGGGTATTCACGTTTGGGCATATGCCTG
CTCCTGACCCAGAATTTTTGGGGGATAGAAGCTGTAACTTACAGTTTCGGGGGGAGAGAACTTTTAGGACACCCCTTGGGGGGAAAATGCGCCCAGGGTGCC
GTTAGCGAAAAACAAGGTATCTCCTAAAAAACTGTGGTTAAAAAACCTCCTATTATGAAGGGCGTGATCTTGCTGCTGAGGGTAATGATATTATCCGTGAGGC
TAGCAAATGGAGTCCTGAACTCGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTACCAAGCAGTGGATACTTTGGATCCGCTTAAGTCTTAATTA
CCTTTGTCTCGTAGTGAATTAAA

>*rbc*L-St2

GCTGGTGTTAAGAGTACAAATTGACTTTATTATACTCCTCAATACGAAACCAAAGATACTGATATCTTGGCACCATTCCGAGTAACCTCCTCAACCCGGAGTT
CCACCTGAAAAAGCAGGGGCCGCAGTAGCTGCCGAATCTTCTACTGGTACATGGACAACTGTGTGGACCGATGGACTTACCAGCCTTGATCGTTACAAAGGG
CGCTGCTACCATATCGAGCCTGTTGCTGGAGAAGAAGATCAATATATTGCTTATGTAGCTTATCCCTTAGACCTTTTTGAAGAAGGTTCTGTTACTAACATGTT
TACTTCCATTGTAGGTAATGTATTTGGGTTCAAAGCCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCCAAGGCCCG
CCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCCCTGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACG
GTAGGGCAGTTTATGAATGTCTTCGTGGTGGACTTGATTTTACCAAAGATGATGAAAACGTGAACTCCCAACCATTTATGCGTTGGAGAGATCGTTTCTTATT
TTGTGCCGAAGCACTTTATAAAGCACAGGCTGAAACCGGTGAAATCAAAGGACATTACTTGAATGCTACTGCAGGTACATGCGAAGAAATGATGAAAAGAGCT
GTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGACTACTTAACCGGGGGATTCACTGCAAATACTACCTTAGCTCATTATTGCCGAGATAATGGCC
TACTTCTTCACATCCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGTATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGG
AGATCATGTTCACGCTGGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTACTGGCGTGATGATTTTATTGAAAAAGA
TCGAAGCCCCCGGTGTTTATTTCACTCAAAAATTGGGTCTCTCTACCGGGGTGTTATACCTGTGGGCTTCAGGGGGGTATTCACGTTTGGGCATATGCCTGGC
TCTGACCCAAAATTTTTGGGGGATGAAGCCTGAACTACAGTTCCGGTGGAAGGAACTTTAAGGACACCCCTTGGGGGTAAATGGCGCCAAGGTGCCCTTAGC
CGAAACCAGGGTATCTCCTAAAAAACCATTGTGTAAAAAACTCCCTAAATGGAAGGGCTGTGAACTTTGGCCCCCTAGAGGGGAAAGATATTATCCGGGAGG
CTAGCAAATGGAGTCCTGAACTCGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTACCAAGCAGTGGATACTTTGGATCCGCTTAAGTCTTAATT
ACCTTTGTCTCGTAGTAATGAAA

>*rbc*L-St3

GCTGGTGTTAAGAGTACAAATTGACTTTATTATACTCCTCAATACGAAACCAAAAGATACTGATATCTTGGGCAGCATTCCGAGTAACTCCTCAACCCGGAGA
TTCCACCTGAAGAAGCAGGGGCCGCAGTAGCTGCCGAATCTTCTACTGGTACATGGACAACTGTGTGGACCGAATGGACTTACCAGCCCTTGATCGTTACAAA
GGGCGCTGCTACCATATCGAGCCTGTTGCTGGAGAAGAAGATCAATATATTGCTTATGTAGCTTATCCCTTAGACCTTTTTGAAGAAGGTTCTGTTACTAACA
TGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAGCCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCCAAGGC
CCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCCCTGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACT
ACGGTAGGGCAGTTTATGAATGTCTTCGTGGTGGACTTGATTTTACCAAAGATGATGAAAACGTGAACTCCCAACCATTTATGCGTTGGAGAGATCGTTTCTT
ATTTTGTGCCGAAGCACTTTATAAAGCACAGGCTGAAACCGGTGAAATCAAAGGACATTACTTGAATGCTACTGCAGGTACATGCGAAGAAATGATGAAAAGA
GCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGACTACTTAACCGGGGGATTCACTGCAAATACTACCTTAGCTCATTATTGCCGAGATAATG
GCCTACTTCTTCACATCCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGTATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGG

TGGAGATCATGTTCACGCTGGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAGACATCACTTTGGGCTTTGTTGATTTACTGCCGGGATGATTTTATTGAAAA
AGATCGAAACCCCCGGTGTTTATTTCACTCAAGATTGGGTCTCTCTACCGGGGGTTATACCTGTGGCTTCAGGGGGTATTCACGTTTGGCATATGCCTGGCTC
TGACCCAAATTTTTGGGGGATGAAGCCTGTACCTACAGTTCCGGTGGAGGGAACTTTAAGGACACCCCTTGGGGGAAATGGCCCCAGGTGCCCCTTACCCAA
TCCAGGTATCTCTTAAGAACCATGTGTAAAAAACTCTGTAATTGAAAGGGCGTGGATCTTTTGCCGCTAAAAGGTAATGATATTATCCGTGAGGCTAGCAAAT
GGAGTCCTGAACTCGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTACCAAGCAGTGGATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTC
TCGTAGTAATGAAA

>*rbc*L-St4

GCTGGTGTTAAGAGCACAATTGACTTATTATACTCCTCAATACGAAACCAAAGATACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCCGGAGTTCCA
CCTGAAGAACCAGGGGCCGCGAGTAGCTGCCGAATCTTCTACTGGTACATGGAAAACTGTGTGGACCGATGGACTTACCAGCCTTGATCGTTACAAAGGCCG
CTGCTACAATATCGAGCCTGTTGCTGGAGAAGAAGATCAATATATTGCTTATGTAGCTTATCCCTTAGACCTTTTTGAAGAAGGTTCTGTTACTAACATGTTTA
CTTCCATTGTAGGTAATGTATTTGGGTTCAAAGCCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCCAAGGCCCGCC
TCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCCCTGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGT
AGGGCAGTTTATGAATGTCTTCGTGGTGGACTTGATTTTACCAAAGATGATGAAAACGTGAACTCCCAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTT
GTGCCGAAGCACTTTATAAAGCACAGGCTGAAACCGGTGAAATCAAAGGACATTACTTGAATGCTACTGCAGGTACATGCGAAGAAATGATGAAAAGAGCTGT
ATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGACTACTTAACCGGGGGATTCACTGCAAATACTACCTTAGCTCATTATTGCCGAGATAATGGCCTA
CTTCTTCACATCCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGTATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAG
ATCATGTTCACGCTGGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTACTGCGGGATGATTTTATTGAAAAAGATCC
AAACCCGCGGTGTTTATTTCACTCAAGATTGGGGTCTCTCTACCGGGGGGTTATACCTTGTGGCTTCAGGGGGGTATTCACGTTTGGGCATATGCCTGGCTCT
GACCCAGAATTTTTGGGGGATGAAGCTTGTACCTCACAGTTCGGGGGAAGGAAACTTTAGGACACCCTCTGGGGGAAAAGGCCCCAGGGGCCCGTACCCAAT
CCAGGAATCTCCTGAAAACCATGTGTTAAAAAGCTCGTAATGAAGGGCGTGATCTTGCTGCTGAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGTCC
TGAACTCGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTACCAAGCAGTGGATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTCTCGTAGT
GAATTAAA

>*rbc*L-Sl1

GCTGGTGTTAAGAGTACAAATTGACTTATTATACTCCTGAATACGAAACCAAAGATACTGATATCTTGGGCACCATTCCGAGTAACTCCTCAACCCGGAGTTC
CCACCTGAAGAAACAGGGGCCGCAGTAGCTGCCGAATCTTCTACTGGTACATGGACAACTGTGTGGACCGATGGACTTACCAGCCTTGATCGTTACAAAGGG
CGCTGCTACAATATCGACCCTGTTGCTGGAGAAGAAGACCAATATATTGCTTAAGTAGCTTACCCCTTAGACCTTTTTGAAGAAGGTTCTGTTACTAACATGT
TTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAGCCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCCAAGGCCC
GCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTCTGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTAC
GGTAGGGCAGTTTATGAATGTCTTCGTGGTGGACTTGATTTTACCAAAGATGATGAAAACGTGAACTCCCAACCATTTATGCGTTGGAGAGATCGTTTCTTAT
TTTGTGCCGAAGCACTTTATAAAGCACAGGCTGAAACCGGTGAAATCAAAGGGCATTACTTGAATGCTACTGCAGGTACATGCGAAGAAATGATCAAAAGAGC
TGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGACTACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGC
CTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGTATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTG
GAGATCATATTCACGCTGGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAGACATCACTTTGGGCTTTGTTGATTTACTGCCGTGATGATTTTATTGAAAAAG
ATCGAAGTCCCCGTATTTATTTCACTCAAAGATGGGGTCTCTCTACCGGGGGGTTATACCTGGTGGCTTCAGGGGGGTATTCACCGTTTGGCCATATGCCTGG
CTCTGACCCAAAATTTTTGGGGGATAGAGCCTGTACCTACAGTTCCGGTGGGAGGGAACTTTAAGGACACCCCTTGGGGGGAAATGGCCCCCAAGGGGCCCT
TAACCAAATCCAGGTAACCTCTTAAAAAACATTGTGTAAAAAACCTCCCTTAATGAAGGGCGTGATCTTGCTGCTGAGGGTAATGATATTATCCGTGAGGCTA
GCAAATGGAGTCCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTTTCAAGCAGTGGATACTTTGGATCCGCTTAAGTCTTAATTACC
TTTGTCTCGTAGTGAATTAAA

>*rbc*L-Sl2

GCTGGTGTTAAGAGTACAAATTGACTTATTATACTCCTGAATACGAAACCAAAGATACTGATATCTTGGGCAGCATTCCGAGTAACTCCTCAACCCGGAGTTC
CACCTTGAAGAAGCAAGGGCCCCAGTAGCTGCCGAATCTTCTACTGGTACATGGACAACTGTGTGGGACCGATGGACTTACCAGCCCTTGATCGTTACAAAG
GGCGCTGCTACCATATCGAGCCTGTTGCTGGAGAAGAAGATCAATATATTGCTTAAGTAGCTTACCCCTTAGACCTTTTTGAAGAAGGTTCTGTTACTAACAT
GTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAGCCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCCAAGGC
CCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTCTGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACT
ACGGTAGGGCAGTTTATGAATGTCTTCGTGGTGGACTTGAATTTTACCAAAGATGATGAAAACGTGAACTCCCAACCATTTATGCGTTGGAGAGATCGTTTCT
TATTTTGTGCCGAAGCACTTTATAAAGCACAGGCTGAAACCGGTGAAATCAAAGGGCATTACTTGAATGCTACTGCAGGTACATGCGAAGAAATGATCAAAAG
AGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGACTACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAAT
GGCCTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGTATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTG
GTGGAGATCATATTCACGCTGGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTACTGCCGGGATGATTTTATTGAAA
AAGATCGAAGTCCCCGTATTTATTTCACTCAAGATTGGGGTCTCTCTACCGGGGGGGTTATACCTGGTGGCTTCAGGGGGGTATTCACCGTTTGGCCATATGCC
TTGCTCTGACCCAAAATTTTTGGGGGATGAAGCCTGAACTAACAGTTCCGGTGGAAGGAACTTTAAGGAACACCCTTGGGGGGAAATGGCCCCCAAGTGGCC
CTTTAGCAAATCGAGGTAACCTCTTAAAAAACATTGTGTAAAAAACCTCCCTTAATGAAGGGCGTGATCTTGCTGCTGAGGGTAATGATATTATCCGTGAGGC
TAGCAAATGGAGTCCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTTTCAAGCAGTGGATACTTTGGATCCGCTTAAGTCTTAATTA
CCTTTGTCTCGTAGTTAATTAAT

>*rbc*L-Sl3

GCTGGTGTTAAGAGTACAAATTGACTTATTATACTCCTGAATACGAAACCAAAGATACTGATATCTTGGGCAGCATTCCGAGTAACTCCTCAACCCGGAGTTC
CACCTTGAAGAAGCAAGGGCCCCAGTAGCTGCCGAATTTTCTACTGGTACATGGACAACTGTGTGGGACCGATGGACTTACCAGCCCTTGATCGTTACAAAG
GGCGCTGCTACCATATCGAGCCTGTTGCTGGAGAAGGAGATCAATATATTGCTTAAGTAGCTTACCCCTTAGACCTTTTTGAAGAAGGTTCTGTTACTAACAT
GTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAGCCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCCAAGGC
CCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTCTGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACT
ACGGTAGGGCAGTTTATGAATGTCTTCGTGGTGGACTTGATTTAACCAAAGATGATGAAAACGTGAACTCCCAACCATTTATGCGTTGGAGAGATCGTTTCTT
ATTTTGTGCCGAAGCACTTTATAAAGCACAGGCTGAAACCGGTGAAATCAAAGGGCATTACTTGAATGCTACTGCAGGTACATGCGAAGAAATGATCAAAAGA
GCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGACTACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATG
GCCTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGTATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGG
TGGAGATCATTTTCACGCTGGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTACTGCCGGGATGATTTTATTGAAAA
AGATCGAAGTCCCCGTATTTATTTCACTCAAGATTGGGGTCTCTCTACCGGGGGGTTATACCTGGTGGCTTCAGGGGGGTATTCACCGTTTGGCCATATGCCT
TGCTCTGACCCAAAATTTTTGGGGGATGAAGCCTGAACTAACAGTTCCGGTGGAAGGAACTTTAAGGAACACCCTTGGGGGGAAATGGCCCCCAAGTGGCCC
TTTAGCAAATCGAGGTAACCTCTTAAAAAACATTGTGTAAAAAACCTCCCTTAATGAAGGGCGTGATCTTGCTGCTGAGGGTAATGATATTATCCGTGAGGCT
AGCAAATGGAGTCCTGAACTTGCTGCTGCTTGTGAGGTATGGGAGGAGATCAGATTTAATTTTCAAGCAGTGGATACTTTGGATCCGCTTAAGTCTTAATTAC
CTTTGTCTCGTAGTTAATTAAT

>*rbc*L-Sv1

GCTGGTGTTAAGAGTACAATTGACTTATTATACTCCTGAATACGAAACCAAAGATACTGATATCTTGGCAGCATTCCGGAGTAACTCCTCAACCCGGAGTTCC
ACCTGAAAAACCAGGGGCCCCAGTAGCTGCCGAATCTTCTACTGGGACATGGAAAACTGTGTGGACCGATGGACTTACCAGCCTTGATCGTTACAAAGGGCG
CTGCTACAATATCGAGCCTGTTGCTGGAGAAGAAGATCAATATATTGCTTATGTAGCTTACCCCTTAGACCTTTTTGAAGAAGGTTCTGTTACTAACATGTTTA
CTTCCATTGTAGGTAATGTATTTGGGTTCAAAGCCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCCAAGGCCCGCC
TCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTCTGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGT
AGGGCAGTTTATGAATGTCTTCGTGGTGGACTTGATTTTACCAAAGATGATGAAAACGTGAACTCCCAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTT
GTGCCGAAGCACTTTATAAAGCACAGACTGAAACCGGTGAAATCAAAGGGCATTACTTGAATGCTACTGCAGGTACATGCGAAGAAATGATCAAAAGAGCTGT

ATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGACTACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGCCTA
CTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGTATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAG
ATCATATTCACGCTGGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAGACATCACTTTGGGCTTTGTTGATTTACTGCGTGATGATTTTATTGAAAAAGATCG
AAGTCCCGGTATTTATTTCACTCAAGATTGGGTCTCTCTACCGGGGGTGTTATACCTGTGGGCTTCAGGGGGGTATTCACGTTTGGGCATATGCCTGGCTCTGA
CCCAAGATTTTTGGGGGATAGAGGCTGGACCTACAGTTCCGGTGGGAGGAACTTTTAGGACACCCTTTGGGGGAAAAGGCCCCAAGGGGCCCTTAAGCGAAT
CGAGTAGCTCTAGAAGCATGTGTAAAAGCTCGTAATGAAGGGCGTGATCTTGCTGCTGAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGTCCTGAAC
TTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGGTTTAATTTTCAAGCAGTGGATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTCTCGTAGTGAATTA
AA

>*rbc*L-Sv2

GCTGGTGTTAAGAGTACACTTGACTTATTATACTCCTGGAATACGAAACCAAAGTTACTGATATCTTGGGCAGCATTCCGAGTAACTCCTCAACCCGGAGATT
CCACCTGAAGAAGCAGGGGCCCCAGTAGCTGCCGAATCTTCTACTGGTACATGGACAACTGTGTGGACCGATGGACTTACCAGCCTTGATCGTTACAAAAGG
GCGCTGCTACCCATAATCGAGCCTGTTGCTGGAGAAGAAGATCAATATAATTGCTTAAGTAGCTTACCCCTTAGACCTTTTTGAAGAAGGTTCTGTTACTAAC
ATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAGCCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCCAAGG
CCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTCTGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAAC
TACGGTAGGGCAGTTTATGAATGTCTTCGTGGTGGACTTGATTTTACCAAAGATGATGAAAACGTGAACTCCCAACCATTTATGCGTTGGAGAGATCGTTTCT
TATTTTGTGCCGAAGCACTTTATAAAGCACAGACTGAAACCGGTGAAATCAAAGGGCATTACTTGAATGCTACTGCAGGTACATGCGAAGAAATGATCAAAAG
AGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGACTACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAAT
GGCCTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGTATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTG
GTGGAGATCATATTCACGCTGGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTACTGCGGGATGATTTTATTGAAAA
AAAATCGAAGTCCCGGTATTTATTTCACTCAAGATTTGGTCTCTCTACCGGGGGTGTTATACCTGTAGGCTTCAGGGGGGTATTCCACGTTTTGGCAATATGCC
TGGCTCTGACCCAAAATTTTTGGGGGATGAATGCTTGTACCTACAGTTCCGGTGGGAGGAACTTTTAGGAACACCCTTGGGGGGAAAGCGCCCCAGGTGCCC
GTTACCGAAATCAGAGAAGCGTCTAGAAGCATGTGTAAAAGCTCGTAATGAAGGGCGTGATCTTGCTGCTGAGGGTAATGATATTATCCGTGAGGCTAGCAAA
TGGAGTCCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGGTTTAATTTTCAAGCAGTGGATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGT
CTCGTAGTTAATTAAA

>*rbc*L-Sv3

GCTGGTGTTAAGAGTACAATTGACTTATTATACTCCTGGAATACGAAACCAAAGATACTGATATCTTGGGCAGCATTCCGAGTAACTCCTCAACCCGGAGATT
CCACCTGAAGAAGCAGGGGCCCCAGTAGCTGCCGAATCTTCTACTGGTACATGGACAACTGTGTGGACCGATGGACTTACCAGCCTTGATCGTTACAAAAGG
GCGCTGCTACCATAATCGAGCCTGTTGCTGGAGAAGAAGATCAATATAATTGCTTAAGTAGCTTACCCCTTAGACCTTTTTGAAGAAGGTTCTGTTACTAACA
TGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAGCCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCCAAGGC
CCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTCTGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACT
ACGGTAGGGCAGTTTATGAATGTCTTCGTGGTGGACTTGATTTTACCAAAGATGATGAAAACGTGAACTCCCAACCATTTATGCGTTGGAGAGATCGTTTCTT
ATTTTGTGCCGAAGCACTTTATAAAGCACAGACTGAAACCGGTGAAATCAAAGGGCATTACTTGAATGCTACTGCAGGTACATGCGAAGAAATGATCAAAAGA
GCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGACTACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATG
GCCTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGTATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGG
TGGAGATCATATTCACGCTGGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTACTGCGGGATGATTTTATTGAAAAA
AAATCGAAGTCCCGGTATTTATTTCACTCAAGATTGGGTCTCTCTACCGGGGGTGTTATACCTGTGGGCTTCAGGGGGGTATTCCACGTTTTGGCAATATGCCT
GGCTCTGACCCAAAATTTTTGGGGGATGAATGCTTGTACCTACAGTTCCGGTGGGAGGAACTTTTAGGAACACCCTTGGGGGGAAAGCGCCCCAGGTGCCCG
TTACCGAAATCAGAGAAGCGTCTAGAAGCATGTGTAAAAGCTCGTAATGAAGGGCGTGATCTTGCTGCTGAGGGTAATGATATTATCCGTGAGGCTAGCAAAT
GGAGTCCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGGTTTAATTTTCAAGCAGTGGATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTC
TCGTAGTTAATTAAA

>*rbc*L-Sv4

GCTGGTGTAAGAGGACAAATTGACATTATTATACTCCGGAATACGAAACCAAAAATATCTGATATCTTGGCAACATTCCGAGTAACTCCTCAACCCGGAGTTC
CACCTTGAAGAAGCAGGGGCCCCAGTAGCTGCCGAATCTTCTACTGGTACATGGACAACTGTGTGGACCGATGGACTTACCAGCCTTGATCGTTACAAAGGG
CGCTGCTACCATATCGAGCCTGTTGCTGGAGAAGAAGATCAATATATTGCTTAAGTAGCTTACCCCTTAGACCTTTTTGAAGAAGGTTCTGTTACTAACATGT
TTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAGCCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCCAAGGCCC
GCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTCTGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTAC
GGTAGGGCAGTTTATGAATGTCTTCGTGGTGGACTTGATTTTACCAAAGATGATGAAAACGTGAACTCCCAACCATTTATGCGTTGGAGAGATCGTTTCTTAT
TTTGTGCCGAAGCACTTTATAAAGCACAGACTGAAACCGGTGAAATCAAAGGGCATTACTTGAATGCTACTGCAGGTACATGCGAAGAAATGATCAAAAGAGC
TGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGACTACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGC
CTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGTATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTG
GAGATCATATTCACGCTGGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTACTGGCGGGATGATTTTATTGAAAAAA
GATCGAAGTCCCCGGTATTTATTTTCACTCAAGATTGGGGTCTCTCTACCGGGGTGTTATACCTGTGGGCTTCAGGGGGGTATTCACGTTTGGGCATATGCCT
TGCCTCTGACCCAAAATTTTTGGGGGATAGATGCTTACTTACAGTTTCGGTGGGAGGAACTTTTAAGGACACCCTTGGGGGGAAATGGCCCCAAGGGGGCCC
TAACCAAATCCAGGAAAACTCTAGAAGCATGTGTAAAAGCTCGTAATGAAGGGCGTGATCTTGCTGCTGAGGGTAATGATATTATCCGTGAGGCTAGCAAATG
GAGTCCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGGTTTAATTTTCAAGCAGTGGATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTCT
CGTAGTGAATTAAA

>*rbc*L-Sv5

GCTGGTGTTAAAAGGACAAATTGACTTATTATACTCCTGAATACGAAACCAAAGATACTGATATCTTGGCACCATTCCGAGTAACTCCTCAACCCGGAGATTC
CACCTGAAGAAGCAGGGGCCCCAGTAGCTGCCGGAATCTTCTACTGGTACATGGACAACTGTGTGGACCGATGGACTTACCAGCCTTGATCGTTACAAAGGG
CGCTGCTACCATATCGAGCCTGTTGCTGGAGAAGAAGATCAATATATTGCTTAAGTAGCTTACCCCTTAGACCTTTTTGAAGAAGGTTCTGTTACTAACATGT
TTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAGCCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCCAAGGCCC
GCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTCTGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTAC
GGTAGGGCAGTTTATGAATGTCTTCGTGGTGGACTTGATTTTACCAAAGATGATGAAAACGTGAACTCCCAACCATTTATGCGTTGGAGAGATCGTTTCTTAT
TTTGTGCCGAAGCACTTTATAAAGCACAGACTGAAACCGGTGAAATCAAAGGGCATTACTTGAATGCTACTGCAGGTACATGCGAAGAAATGATCAAAAGAGC
TGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGACTACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGC
CTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGTATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTG
GAGATCATATTCACGCTGGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAGACATCACTTTGGGCTTTGTTGATTTACTGCGGGGATGATTTTATTGAAAAAG
ATCGAAGTCCCGGTATTTATTTCACTCAAGATTGGGGTCTCTCTACCGGGGTGTTATACCTGTGGGCTTCAGGGGGGTATTCCACGTTTGGGCATATGCCTGG
CCTCTGACCCAAGATTTTTGGGGGATAGATGCCTGGACCTACAAGTTCCGGTGGAAGGAACTTTTAGGAACACCCTTGGGGGGAAATGGCCCCAAGGGGCCC
TTAACCAATCGAGTAGCTCTAGAAGCATGTGTAAAAGCTCGTAATGAAGGGCGTGATCTTGCTGCTGAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGA
GTCCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGGTTTAATTTTCAAGCAGTGGATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTCTCG
TAGTGAATTAAA

>*rbc*L-Sb1

GCTGGTGTAAAGAGTACAAATTGACATTATATACTCCTGAATACGAAACCAAAGATACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCCGGAGTTCC
ACCTTGAAGAAGCAGGGGCCGCAGTAGCTGCCGAATCTTCTAATGGTACATGGACAAATGGGTGGACCGATGGACTTACCAGCCTTGATCGTTACAAAGGGC
GCTGCTACAATATCGAGCCTGTTGCTGGAGAAGAAGATCAATTTATTGCTTATGTAGCTTACCCCTTAGACCTTTTTGAAGAAGGTTCTGTTACTAACATGTTT
ACTTCCATTGTAGGTAATGTATTTGGGTTCAAAGCCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCCAAGGCCCGC
CTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTCTGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGG
TAGGGCAGTTTATGAATGTCTTCGTGGTGGACTTGATTTTACCAAAGATGATGAAAACGTGAACTCCCAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTT
GTGCCGAAGCACTTTATAAAGCACAGGCTGAAACCGGTGAAATCAAAGGACATTACTTGAATGCTACTGCAGGTACATGCGAAGAAATGATCAAAAGAGCTGT

ATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGACTACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGCCTA
CTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGTATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAG
ATCATATTCACGCTGGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTACTGCGGGGATGATTTTATTGAAAAAGATC
GAAATCCCGGTATTTATTTCACTCAAGATTGGGTCTCTCTACCGGGGTGTTATACCTGGTGGCTTCAGGGGGGTATTCACGTTTGGCCATATGCCTGGCTCTT
GACCCAGAATTTTTGGGGGATGAAGGCTTGTACCTACAGGTTCCGGTGGGAAGGAACTTTTAGGAACACCCTTGGGGGGAAATGCGCCCAGGGTGCCCTAAC
CCGAATCCGAGTAGCCCTCATAAAACCATGTGTAAAAGCTCGTAATGAAGGGCGTGATCTTGCTGCTGAGGGTAATGATATTATCCGTGAGGCTAGCAAATGG
AGTCCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTTTCAAGCAGTGGATACTTTGGATCCGCTTAAGGCTTAATTACCTTTGTCTC
GTAGTGAATTAAA

>*rbc*L-Sb2

GCTGGTGTAAAGAGTACAAATTGACATATTATACTCCTGAATACGAAACCAAAGATACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCCGGAGTTCC
ACCTTGAAAAAGCAGGGCCCGCAGTAGCTGCCGAATCTTCTAATGGTACATGGACAAATGTGTGGACCGATGGACTTACCAGCCTTGATCGTTACAAAGGCC
GCTGCTACCATATCGAGCCTGTTGCTGGAGAAGAAGATCAATTTATTGCTTAAGTAGCTTACCCCTTAGACCTTTTTGAAGAAGGTTCTGTTACTAACATGTTT
ACTTCCATTGTAGGTAATGTATTTGGGTTCAAAGCCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCCAAGGCCCGC
CTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTCTGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGG
TAGGGCAGTTTATGAATGTCTTCGTGGTGGACTTGATTTTACCAAAGATGATGAAAACGTGAACTCCCAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTT
GTGCCGAAGCACTTTATAAAGCACAGGCTGAAACCGGTGAAATCAAAGGACATTACTTGAATGCTACTGCAGGTACATGCGAAGAAATGATCAAAAGAGCTGT
ATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGACTACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGCCTA
CTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGTATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAG
ATCATATTCACGCTGGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTACTGCGTGATGATTTTATTGAAAAAGATCG
AAGTCCCGGTATTTATTTCACTCAAGATTGGGTCTCTCTACCGGGTGTTATACCTGTGGCTTCAGGGGGTATTCACGTTTGGCATATGCCTTGCTCTGACCCA
AGATTTTTGGGGGATGAATCCTTGTACCTACAGTTCCGGGGGAGGAACCTTAAGGACACCCCTTGGGGGAATAGCGCCCAAGGGGCCCTAACCAAAACCAGG
AGCTCTAGAAGCATGTGTAAAAGCTCGTAATGAAGGGCGTGATCTTGCTGCTGAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGTCCTGAACTTGCT
GCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTTTCAAGCAGTGGATACTTTGGATCCGCTTAAGGCTTAATTACCTTTGTCTCGTAGTGAATGAAA

>*rbc*L-Sb3

GCTGGTGTTAAGAGGACAATTGACATATTATACTCCGGAATACGAAACCAAAGATACTGATATCTTGGCACCATTCCGAGTAACTCCTCAACCCGGAATTCCA
CCTTGAAGAAACAGGGGCCGCAGTAGCTGCCGAATCTTCTACTGGGACATGGACAAATGTGTGGACCGATGGACTTACCAGCCTTGATCGTTACAAAGGGCG
CTGCTACAATATCGACCCTGTTGCTGGAGAAGAAGATCAATTTATTGCTTAAGTAGCTTACCCCTTAGACCTTTTTGAAGAAGGTTCTGTTACTAACATGTTTA
CTTCCATTGTAGGTAATGTATTTGGGTTCAAAGCCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCCAAGGCCCGCC
TCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTCTGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGT
AGGGCAGTTTATGAATGTCTTCGTGGTGGACTTGATTTTACCAAAGATGATGAAAACGTGAACTCCCAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTT
GTGCCGAAGCACTTTATAAAGCACAGGCTGAAACCGGTGAAATCAAAGGACATTACTTGAATGCTACTGCAGGTACATGCGAAGAAATGATCAAAAGAGCTGT
ATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGACTACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGCCTA
CTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGTATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAG
ATCATATTCACGCTGGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAGACATCACTTTGGGCTTTGTTGATTTACTGGCGGGATGATTTTATTGAAAAAGATC
GAAGTCCCGGTATTTATTTCACTCAAAGATTGGGTCTCTCTACCGGGGTGTTATACCTGTGGGCTTCGGGGGGGTATTCCACGTTTTGGGCATATGCCTGGCT
CTGACCCAAAATTTTTGGGGAATAAAGCCTTGTACTTACAGGTTCCGGTGGAGGGAAACTTTTAGGGACACCCTTGGGGTAATGCGCCAGGTGCCGTAGCGA
ATCGAGTAGCTCTAGAAGCATGTGTAAAAGCTCGTAATGAAGGGCGTGATCTTGCTGCTGAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGTCCTGA
ACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTTTCAAGCAGTGGATACTTTGGATCCGCTTAAGGCTTAATTACCTTTGTCTCGTAGTGAA
TTAAA

>*rbc*L-Sb4

GCTGGTGTAAAGAGGACAATTGACTTATTATACTCCGGAATACGAAACCAAAGATACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCCGGGAGTTCC
ACCTGAAGAAGCAAGGGCCCCAGTAGCTGCCGAATCTTCTACTGGTACATGGACAACTGTGTGGACCGATGGACTTACCAGCCTTGATCGTTACAAAGGGCG
CTGCTACCATATCGAGCCTGTTGCTGGAGAAGAAGATCAATTTATTGCTTAAGTAGCTTACCCCTTAGACCTTTTTGAAGAAGGTTCTGTTACTAACATGTTTA
CTTCCATTGTAGGTAATGTATTTGGGTTCAAAGCCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCCAAGGCCCGCC
TCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTCTGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGT
AGGGCAGTTTATGAATGTCTTCGTGGTGGACTTGATTTTACCAAAGATGATGAAAACGTGAACTCCCAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTT
GTGCCGAAGCACTTTATAAAGCACAGGCTGAAACCGGTGAAATCAAAGGACATTACTTGAATGCTACTGCAGGTACATGCGAAGAAATGATCAAAAGAGCTGT
ATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGACTACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGCCTA
CTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGTATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAG
ATCATATTCACGCTGGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAGACATCACTTTGGGCTTTGTTGATTTACTGGCGGGATGATTTTATTGAAAAAGATC
GAAGTCCCGGTATTTATTTCACTCAAGATTGGGTCTCTCTACCGGGGGTGTTATACCTGGGGGCTTCAGGGGGGTATTCACCGTTTGGGCATATGCCTGGCTCT
GACCCAAAATTTTTGGGGGATAGAGGCTGGACCTAACAGTTCCGGGGGGAGGAACTTTATGGACACCCTTGGGGTAATGCGCCAGGTGCCGTAGCGAATCGA
GTAGCTCTAGAAGCATGTGTAAAAGCTCGTAATGAAGGGCGTGATCTTGCTGCTGAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGTCCTGAACTTG
CTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTTTCAAGCAGTGGATACTTTGGATCCGCTTAAGGCTTAATTACCTTTGTCTCGTAGTTAATTAAA

The multiple sequence alignment of *rbc*L gene

```
rbcL-Sb3        GCTGGTGTTAAGAGGACAA-TTGAC-ATATTATACTCC-GGAATACGAAACCAAA-GATA 56
rbcL-Sb4        GCTGGTGTAAAGAGGACAA-TTGAC-TTATTATACTCC-GGAATACGAAACCAAA-GATA 56
rbcL-Sv1        GCTGGTGTTAAGAGTACAA-TTGAC-TTATTATACTCC-TGAATACGAAACCAAA-GATA 56
rbcL-Sv5        GCTGGTGTTAAAAGGACAAATTGAC-TTATTATACTCC-TGAATACGAAACCAAA-GATA 57
rbcL-Sv4        GCTGGTGT-AAGAGGACAAATTGACATTATTATACTCC-GGAATACGAAACCAAA-AATA 57
rbcL-Sv2        GCTGGTGTTAAGAGTACAC-TTGAC-TTATTATACTCCTGGAATACGAAACCAAA-GTTA 57
rbcL-Sv3        GCTGGTGTTAAGAGTACAA-TTGAC-TTATTATACTCCTGGAATACGAAACCAAA-GATA 57
rbcL-Sb1        GCTGGTGTAAAGAGTACAAATTGAC-ATTATATACTCC-TGAATACGAAACCAAA-GATA 57
rbcL-Sb2        GCTGGTGTAAAGAGTACAAATTGAC-ATATTATACTCC-TGAATACGAAACCAAA-GATA 57
rbcL-Sl2        GCTGGTGTTAAGAGTACAAATTGAC-TTATTATACTCC-TGAATACGAAACCAAA-GATA 57
rbcL-Sl3        GCTGGTGTTAAGAGTACAAATTGAC-TTATTATACTCC-TGAATACGAAACCAAA-GATA 57
rbcL-Sl1        GCTGGTGTTAAGAGTACAAATTGAC-TTATTATACTCC-TGAATACGAAACCAAA-GATA 57
rbcL-St1        GCTGGTGTTAAGAGTACAAATTGACATTATTATACTCC-TCAATACGAAACCAAA-GATA 58
rbcL-St4        GCTGGTGTTAAGAGCACAA-TTGAC-TTATTATACTCC-TCAATACGAAACCAAA-GATA 56
rbcL-St2        GCTGGTGTTAAGAGTACAAATTGACTTTATTATACTCC-TCAATACGAAACCAAA-GATA 58
rbcL-St3        GCTGGTGTTAAGAGTACAAATTGACTTTATTATACTCC-TCAATACGAAACCAAAAGATA 59
                ******** ** ** ***  *****  *  ********   **************   **

rbcL-Sb3        -CTGATATCTTGG-CACCATTCCG-AGTAAC-TCCTCAACCCGGAATTCCACCTTGAAGA 112
rbcL-Sb4        -CTGATATCTTGG-CAGCATTCCG-AGTAAC-TCCTCAACCCGGGAGTTCCACCTGAAGA 112
rbcL-Sv1        -CTGATATCTTGG-CAGCATTCCGGAGTAAC-TCCTCAACCCGGAG-TTCCACCTGAAAA 112
rbcL-Sv5        -CTGATATCTTGG-CACCATTCCG-AGTAAC-TCCTCAACCCGGAGATTCCACCTGAAGA 113
rbcL-Sv4        TCTGATATCTTGG-CAACATTCCG-AGTAAC-TCCTCAACCCGGAGTTCCACCTTGAAGA 114
rbcL-Sv2        -CTGATATCTTGGGCAGCATTCCG-AGTAAC-TCCTCAACCCGGAGATTCCACCTGAAGA 114
rbcL-Sv3        -CTGATATCTTGGGCAGCATTCCG-AGTAAC-TCCTCAACCCGGAGATTCCACCTGAAGA 114
rbcL-Sb1        -CTGATATCTTGG-CAGCATTCCG-AGTAAC-TCCTCAACCCGGAGTTCCACCTTGAAGA 113
rbcL-Sb2        -CTGATATCTTGG-CAGCATTCCG-AGTAAC-TCCTCAACCCGGAGTTCCACCTTGAAAA 113
rbcL-Sl2        -CTGATATCTTGGGCAGCATTCCG-AGTAAC-TCCTCAACCCGGAGTTCCACCTTGAAGA 114
rbcL-Sl3        -CTGATATCTTGGGCAGCATTCCG-AGTAAC-TCCTCAACCCGGAGTTCCACCTTGAAGA 114
rbcL-Sl1        -CTGATATCTTGGGCACCATTCCG-AGTAAC-TCCTCAACCCGGAGTTCCCACCTGAAGA 114
rbcL-St1        -CTGATATCTTGG-CAGCATTCCG-AGTAAC-TCCTCAACCCGGAG-TTCCACCTGAAAA 113
rbcL-St4        -CTGATATCTTGG-CAGCATTCCG-AGTAAC-TCCTCAACCCGGAG-TTCCACCTGAAGA 111
rbcL-St2        -CTGATATCTTGG-CACCATTCCG-AGTAACCTCCTCAACCCGGAG-TTCCACCTGAAAA 114
rbcL-St3        -CTGATATCTTGGGCAGCATTCCG-AGTAAC-TCCTCAACCCGGAGATTCCACCTGAAGA 116
                 ************ ** ******* ****** ************   * *  * **** *

rbcL-Sb3        AACAGGGGCCGC-AGTAGCTGCCG-AATCTTCTACTGGGACATGGA-CAAATGTGTGG-A 168
rbcL-Sb4        AGCAAGGGCCCC-AGTAGCTGCCG-AATCTTCTACTGGTACATGGA-CAACTGTGTGG-A 168
rbcL-Sv1        ACCAGGGGCCCC-AGTAGCTGCCG-AATCTTCTACTGGGACATGGA-AAACTGTGTGG-A 168
rbcL-Sv5        AGCAGGGGCCCC-AGTAGCTGCCGGAATCTTCTACTGGTACATGGA-CAACTGTGTGG-A 170
rbcL-Sv4        AGCAGGGGCCCC-AGTAGCTGCCG-AATCTTCTACTGGTACATGGA-CAACTGTGTGG-A 170
rbcL-Sv2        AGCAGGGGCCCC-AGTAGCTGCCG-AATCTTCTACTGGTACATGGA-CAACTGTGTGG-A 170
rbcL-Sv3        AGCAGGGGCCCC-AGTAGCTGCCG-AATCTTCTACTGGTACATGGA-CAACTGTGTGG-A 170
rbcL-Sb1        AGCAGGGGCCGC-AGTAGCTGCCG-AATCTTCTAATGGTACATGGA-CAAATGGGTGG-A 169
rbcL-Sb2        AGCAGGGCCCGC-AGTAGCTGCCG-AATCTTCTAATGGTACATGGA-CAAATGTGTGG-A 169
rbcL-Sl2        AGCAAGGGCCCC-AGTAGCTGCCG-AATCTTCTACTGGTACATGGA-CAACTGTGTGGGA 171
rbcL-Sl3        AGCAAGGGCCCC-AGTAGCTGCCG-AATTTTCTACTGGTACATGGA-CAACTGTGTGGGA 171
rbcL-Sl1        AACAGGGGCCGC-AGTAGCTGCCG-AATCTTCTACTGGTACATGGA-CAACTGTGTGG-A 170
rbcL-St1        AGCAGGGGCCCC-AGTAGCTGCCGGAATCTTCTACTGGTACATGGACAAACTGTGTGG-A 171
rbcL-St4        ACCAGGGGCCGCGAGTAGCTGCCG-AATCTTCTACTGGTACATGGA-AAACTGTGTGG-A 168
rbcL-St2        AGCAGGGGCCGC-AGTAGCTGCCG-AATCTTCTACTGGTACATGGA-CAACTGTGTGG-A 170
rbcL-St3        AGCAGGGGCCGC-AGTAGCTGCCG-AATCTTCTACTGGTACATGGA-CAACTGTGTGG-A 172
                * ** ** ** * ************ *** ***** *** *******  ** ** **** *

rbcL-Sb3        CCGA-TGGACTTACCAGCC-TTGATCGTTACAAA-GGGCGCTGCTACA-ATA-TCGACCC 223
rbcL-Sb4        CCGA-TGGACTTACCAGCC-TTGATCGTTACAAA-GGGCGCTGCTACC-ATA-TCGAGCC 223
rbcL-Sv1        CCGA-TGGACTTACCAGCC-TTGATCGTTACAAA-GGGCGCTGCTACA-ATA-TCGAGCC 223
rbcL-Sv5        CCGA-TGGACTTACCAGCC-TTGATCGTTACAAA-GGGCGCTGCTACC-ATA-TCGAGCC 225
rbcL-Sv4        CCGA-TGGACTTACCAGCC-TTGATCGTTACAAA-GGGCGCTGCTACC-ATA-TCGAGCC 225
rbcL-Sv2        CCGA-TGGACTTACCAGCC-TTGATCGTTACAAAAGGGCGCTGCTACCCATAATCGAGCC 228
rbcL-Sv3        CCGA-TGGACTTACCAGCC-TTGATCGTTACAAAAGGGCGCTGCTACC-ATAATCGAGCC 227
rbcL-Sb1        CCGA-TGGACTTACCAGCC-TTGATCGTTACAAA-GGGCGCTGCTACA-ATA-TCGAGCC 224
```

```
rbcL-Sb2        CCGA-TGGACTTACCAGCC-TTGATCGTTACAAA-GGCCGCTGCTACC-ATA-TCGAGCC 224
rbcL-Sl2        CCGA-TGGACTTACCAGCCCTTGATCGTTACAAA-GGGCGCTGCTACC-ATA-TCGAGCC 227
rbcL-Sl3        CCGA-TGGACTTACCAGCCCTTGATCGTTACAAA-GGGCGCTGCTACC-ATA-TCGAGCC 227
rbcL-Sl1        CCGA-TGGACTTACCAGCC-TTGATCGTTACAAA-GGGCGCTGCTACA-ATA-TCGACCC 225
rbcL-St1        CCGA-TGGACTTACCAGCC-TTGATCGTTACAAA-GGGCGCTGCTAGA-TAT-TCCACCC 226
rbcL-St4        CCGA-TGGACTTACCAGCC-TTGATCGTTACAAA-GGCCGCTGCTACA-ATA-TCGAGCC 223
rbcL-St2        CCGA-TGGACTTACCAGCC-TTGATCGTTACAAA-GGGCGCTGCTACC-ATA-TCGAGCC 225
rbcl-St3        CCGAATGGACTTACCAGCCCTTGATCGTTACAAA-GGGCGCTGCTACC-ATA-TCGAGCC 229
                **** ************** ************** ** ********       ** * **

rbcL-Sb3        TGTTGCTGGAGAAGAAGATCAATTTA-TTGCTTAAGTAGCTTACCCCTTAGACCTTTTTG 282
rbcL-Sb4        TGTTGCTGGAGAAGAAGATCAATTTA-TTGCTTAAGTAGCTTACCCCTTAGACCTTTTTG 282
rbcL-Sv1        TGTTGCTGGAGAAGAAGATCAATATA-TTGCTTATGTAGCTTACCCCTTAGACCTTTTTG 282
rbcL-Sv5        TGTTGCTGGAGAAGAAGATCAATATA-TTGCTTAAGTAGCTTACCCCTTAGACCTTTTTG 284
rbcL-Sv4        TGTTGCTGGAGAAGAAGATCAATATA-TTGCTTAAGTAGCTTACCCCTTAGACCTTTTTG 284
rbcL-Sv2        TGTTGCTGGAGAAGAAGATCAATATAATTGCTTAAGTAGCTTACCCCTTAGACCTTTTTG 288
rbcL-Sv3        TGTTGCTGGAGAAGAAGATCAATATAATTGCTTAAGTAGCTTACCCCTTAGACCTTTTTG 287
rbcL-Sb1        TGTTGCTGGAGAAGAAGATCAATTTA-TTGCTTATGTAGCTTACCCCTTAGACCTTTTTG 283
rbcL-Sb2        TGTTGCTGGAGAAGAAGATCAATTTA-TTGCTTAAGTAGCTTACCCCTTAGACCTTTTTG 283
rbcL-Sl2        TGTTGCTGGAGAAGAAGATCAATATA-TTGCTTAAGTAGCTTACCCCTTAGACCTTTTTG 286
rbcL-Sl3        TGTTGCTGGAGAAGGAGATCAATATA-TTGCTTAAGTAGCTTACCCCTTAGACCTTTTTG 286
rbcL-Sl1        TGTTGCTGGAGAAGAAGACCAATATA-TTGCTTAAGTAGCTTACCCCTTAGACCTTTTTG 284
rbcL-St1        TGTTGCTGGAGAAGAAGACCAATAAA-TTGCTTAAGTAGCTTATCCCTTAGACCTTTTTG 285
rbcL-St4        TGTTGCTGGAGAAGAAGATCAATATA-TTGCTTATGTAGCTTATCCCTTAGACCTTTTTG 282
rbcL-St2        TGTTGCTGGAGAAGAAGATCAATATA-TTGCTTATGTAGCTTATCCCTTAGACCTTTTTG 284
rbcL-St3        TGTTGCTGGAGAAGAAGATCAATATA-TTGCTTATGTAGCTTATCCCTTAGACCTTTTTG 288
                ************** *** ****  * ******* ******** ****************

rbcL-Sb3        AAGAAGGTTCTGTTACTAACATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAG 342
rbcL-Sb4        AAGAAGGTTCTGTTACTAACATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAG 342
rbcL-Sv1        AAGAAGGTTCTGTTACTAACATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAG 342
rbcL-Sv5        AAGAAGGTTCTGTTACTAACATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAG 344
rbcL-Sv4        AAGAAGGTTCTGTTACTAACATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAG 344
rbcL-Sv2        AAGAAGGTTCTGTTACTAACATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAG 348
rbcL-Sv3        AAGAAGGTTCTGTTACTAACATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAG 347
rbcL-Sb1        AAGAAGGTTCTGTTACTAACATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAG 343
rbcL-Sb2        AAGAAGGTTCTGTTACTAACATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAG 343
rbcL-Sl2        AAGAAGGTTCTGTTACTAACATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAG 346
rbcL-Sl3        AAGAAGGTTCTGTTACTAACATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAG 346
rbcL-Sl1        AAGAAGGTTCTGTTACTAACATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAG 344
rbcL-St1        AAGAAGGTTCTGTTACTAACATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAG 345
rbcL-St4        AAGAAGGTTCTGTTACTAACATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAG 342
rbcL-St2        AAGAAGGTTCTGTTACTAACATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAG 344
rbcL-St3        AAGAAGGTTCTGTTACTAACATGTTTACTTCCATTGTAGGTAATGTATTTGGGTTCAAAG 348
                ************************************************************

rbcL-Sb3        CCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCC 402
rbcL-Sb4        CCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCC 402
rbcL-Sv1        CCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCC 402
rbcL-Sv5        CCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCC 404
rbcL-Sv4        CCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCC 404
rbcL-Sv2        CCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCC 408
rbcL-Sv3        CCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCC 407
rbcL-Sb1        CCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCC 403
rbcL-Sb2        CCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCC 403
rbcL-Sl2        CCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCC 406
rbcL-Sl3        CCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCC 406
rbcL-Sl1        CCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCC 404
rbcL-St1        CCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCC 405
rbcL-St4        CCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCC 402
rbcL-St2        CCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCC 404
rbcL-St3        CCCTACGCGCTCTACGTCTGGAAGATTTGCGAATCCCCGTTGCTTATATTAAAACCTTCC 408
                ************************************************************
```

```
rbcL-Sb3        AAGGCCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTC 462
rbcL-Sb4        AAGGCCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTC 462
rbcL-Sv1        AAGGCCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTC 462
rbcL-Sv5        AAGGCCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTC 464
rbcL-Sv4        AAGGCCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTC 464
rbcL-Sv2        AAGGCCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTC 468
rbcL-Sv3        AAGGCCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTC 467
rbcL-Sb1        AAGGCCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTC 463
rbcL-Sb2        AAGGCCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTC 463
rbcL-Sl2        AAGGCCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTC 466
rbcL-Sl3        AAGGCCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTC 466
rbcL-Sl1        AAGGCCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCTC 464
rbcL-St1        AAGGCCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCCC 465
rbcL-St4        AAGGCCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCCC 462
rbcL-St2        AAGGCCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCCC 464
rbcL-St3        AAGGCCCGCCTCATGGCATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGTCGACCCC 468
                ************************************************************ *

rbcL-Sb3        TGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGTAGGGCAG 522
rbcL-Sb4        TGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGTAGGGCAG 522
rbcL-Sv1        TGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGTAGGGCAG 522
rbcL-Sv5        TGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGTAGGGCAG 524
rbcL-Sv4        TGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGTAGGGCAG 524
rbcL-Sv2        TGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGTAGGGCAG 528
rbcL-Sv3        TGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGTAGGGCAG 527
rbcL-Sb1        TGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGTAGGGCAG 523
rbcL-Sb2        TGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGTAGGGCAG 523
rbcL-Sl2        TGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGTAGGGCAG 526
rbcL-Sl3        TGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGTAGGGCAG 526
rbcL-Sl1        TGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGTAGGGCAG 524
rbcL-St1        TGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGTAGGGCAG 525
rbcL-St4        TGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGTAGGGCAG 522
rbcL-St2        TGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGTAGGGCAG 524
rbcL-St3        TGTTGGGATGTACTATTAAACCTAAATTGGGGTTATCCGCTAAAAACTACGGTAGGGCAG 528
                ************************************************************

rbcL-Sb3        TTTATGAATGTCTTCGTGGTGGACTTGA-TTTTACCAAAGATGATGAAAACGTGAACTCC 581
rbcL-Sb4        TTTATGAATGTCTTCGTGGTGGACTTGA-TTTTACCAAAGATGATGAAAACGTGAACTCC 581
rbcL-Sv1        TTTATGAATGTCTTCGTGGTGGACTTGA-TTTTACCAAAGATGATGAAAACGTGAACTCC 581
rbcL-Sv5        TTTATGAATGTCTTCGTGGTGGACTTGA-TTTTACCAAAGATGATGAAAACGTGAACTCC 583
rbcL-Sv4        TTTATGAATGTCTTCGTGGTGGACTTGA-TTTTACCAAAGATGATGAAAACGTGAACTCC 583
rbcL-Sv2        TTTATGAATGTCTTCGTGGTGGACTTGA-TTTTACCAAAGATGATGAAAACGTGAACTCC 587
rbcL-Sv3        TTTATGAATGTCTTCGTGGTGGACTTGA-TTTTACCAAAGATGATGAAAACGTGAACTCC 586
rbcL-Sb1        TTTATGAATGTCTTCGTGGTGGACTTGA-TTTTACCAAAGATGATGAAAACGTGAACTCC 582
rbcL-Sb2        TTTATGAATGTCTTCGTGGTGGACTTGA-TTTTACCAAAGATGATGAAAACGTGAACTCC 582
rbcL-Sl2        TTTATGAATGTCTTCGTGGTGGACTTGAATTTTACCAAAGATGATGAAAACGTGAACTCC 586
rbcL-Sl3        TTTATGAATGTCTTCGTGGTGGACTTGA-TTTAACCAAAGATGATGAAAACGTGAACTCC 585
rbcL-Sl1        TTTATGAATGTCTTCGTGGTGGACTTGA-TTTTACCAAAGATGATGAAAACGTGAACTCC 583
rbcL-St1        TTTATGAATGTCTTCGTGGTGGACTTGA-TTTTACCAAAGATGATGAAAACGTGAACTCC 584
rbcL-St4        TTTATGAATGTCTTCGTGGTGGACTTGA-TTTTACCAAAGATGATGAAAACGTGAACTCC 581
rbcL-St2        TTTATGAATGTCTTCGTGGTGGACTTGA-TTTTACCAAAGATGATGAAAACGTGAACTCC 583
rbcL-St3        TTTATGAATGTCTTCGTGGTGGACTTGA-TTTTACCAAAGATGATGAAAACGTGAACTCC 587
                ***************************** *** ************************** 

rbcL-Sb3        CAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTTGTGCCGAAGCACTTTATAAAGCA 641
rbcL-Sb4        CAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTTGTGCCGAAGCACTTTATAAAGCA 641
rbcL-Sv1        CAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTTGTGCCGAAGCACTTTATAAAGCA 641
rbcL-Sv5        CAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTTGTGCCGAAGCACTTTATAAAGCA 643
rbcL-Sv4        CAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTTGTGCCGAAGCACTTTATAAAGCA 643
rbcL-Sv2        CAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTTGTGCCGAAGCACTTTATAAAGCA 647
rbcL-Sv3        CAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTTGTGCCGAAGCACTTTATAAAGCA 646
rbcL-Sb1        CAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTTGTGCCGAAGCACTTTATAAAGCA 642
rbcL-Sb2        CAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTTGTGCCGAAGCACTTTATAAAGCA 642
```

```
rbcL-Sl2        CAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTTGTGCCGAAGCACTTTATAAAGCA 646
rbcL-Sl3        CAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTTGTGCCGAAGCACTTTATAAAGCA 645
rbcL-Sl1        CAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTTGTGCCGAAGCACTTTATAAAGCA 643
rbcL-St1        CAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTTGTGCCGAAGCACTTTATAAAGCA 644
rbcL-St4        CAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTTGTGCCGAAGCACTTTATAAAGCA 641
rbcL-St2        CAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTTGTGCCGAAGCACTTTATAAAGCA 643
rbcL-St3        CAACCATTTATGCGTTGGAGAGATCGTTTCTTATTTTGTGCCGAAGCACTTTATAAAGCA 647
                ************************************************************

rbcL-Sb3        CAGGCTGAAACCGGTGAAATCAAAGGACATTACTTGAATGCTACTGCAGGTACATGCGAA 701
rbcL-Sb4        CAGGCTGAAACCGGTGAAATCAAAGGACATTACTTGAATGCTACTGCAGGTACATGCGAA 701
rbcL-Sv1        CAGACTGAAACCGGTGAAATCAAAGGGCATTACTTGAATGCTACTGCAGGTACATGCGAA 701
rbcL-Sv5        CAGACTGAAACCGGTGAAATCAAAGGGCATTACTTGAATGCTACTGCAGGTACATGCGAA 703
rbcL-Sv4        CAGACTGAAACCGGTGAAATCAAAGGGCATTACTTGAATGCTACTGCAGGTACATGCGAA 703
rbcL-Sv2        CAGACTGAAACCGGTGAAATCAAAGGGCATTACTTGAATGCTACTGCAGGTACATGCGAA 707
rbcL-Sv3        CAGACTGAAACCGGTGAAATCAAAGGGCATTACTTGAATGCTACTGCAGGTACATGCGAA 706
rbcL-Sb1        CAGGCTGAAACCGGTGAAATCAAAGGACATTACTTGAATGCTACTGCAGGTACATGCGAA 702
rbcL-Sb2        CAGGCTGAAACCGGTGAAATCAAAGGACATTACTTGAATGCTACTGCAGGTACATGCGAA 702
rbcL-Sl2        CAGGCTGAAACCGGTGAAATCAAAGGGCATTACTTGAATGCTACTGCAGGTACATGCGAA 706
rbcL-Sl3        CAGGCTGAAACCGGTGAAATCAAAGGGCATTACTTGAATGCTACTGCAGGTACATGCGAA 705
rbcL-Sl1        CAGGCTGAAACCGGTGAAATCAAAGGGCATTACTTGAATGCTACTGCAGGTACATGCGAA 703
rbcL-St1        CAGGCTGAAACCGGTGAAATCAAAGGACATTACTTGAATGCTACTGCAGGTACATGCGAA 704
rbcL-St4        CAGGCTGAAACCGGTGAAATCAAAGGACATTACTTGAATGCTACTGCAGGTACATGCGAA 701
rbcL-St2        CAGGCTGAAACCGGTGAAATCAAAGGACATTACTTGAATGCTACTGCAGGTACATGCGAA 703
rbcL-St3        CAGGCTGAAACCGGTGAAATCAAAGGACATTACTTGAATGCTACTGCAGGTACATGCGAA 707
                *** ********************** ********************************

rbcL-Sb3        GAAATGATCAAAAGAGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGAC 761
rbcL-Sb4        GAAATGATCAAAAGAGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGAC 761
rbcL-Sv1        GAAATGATCAAAAGAGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGAC 761
rbcL-Sv5        GAAATGATCAAAAGAGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGAC 763
rbcL-Sv4        GAAATGATCAAAAGAGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGAC 763
rbcL-Sv2        GAAATGATCAAAAGAGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGAC 767
rbcL-Sv3        GAAATGATCAAAAGAGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGAC 766
rbcL-Sb1        GAAATGATCAAAAGAGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGAC 762
rbcL-Sb2        GAAATGATCAAAAGAGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGAC 762
rbcL-Sl2        GAAATGATCAAAAGAGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGAC 766
rbcL-Sl3        GAAATGATCAAAAGAGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGAC 765
rbcL-Sl1        GAAATGATCAAAAGAGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGAC 763
rbcL-St1        GAAATGATGAAAAGAGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGAC 764
rbcL-St4        GAAATGATGAAAAGAGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGAC 761
rbcL-St2        GAAATGATGAAAAGAGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGAC 763
rbcL-St3        GAAATGATGAAAAGAGCTGTATTTGCTAGAGAATTGGGAGTTCCTATCGTAATGCATGAC 767
                ******** **************************************************

rbcL-Sb3        TACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGC 821
rbcL-Sb4        TACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGC 821
rbcL-Sv1        TACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGC 821
rbcL-Sv5        TACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGC 823
rbcL-Sv4        TACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGC 823
rbcL-Sv2        TACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGC 827
rbcL-Sv3        TACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGC 826
rbcL-Sb1        TACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGC 822
rbcL-Sb2        TACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGC 822
rbcL-Sl2        TACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGC 826
rbcL-Sl3        TACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGC 825
rbcL-Sl1        TACTTAACAGGGGGATTCACTGCAAATACTAGCTTAGCTCATTATTGCCGAGATAATGGC 823
rbcL-St1        TACTTAACCGGGGGATTCACTGCAAATACTACCTTAGCTCATTATTGCCGAGATAATGGC 824
rbcL-St4        TACTTAACCGGGGGATTCACTGCAAATACTACCTTAGCTCATTATTGCCGAGATAATGGC 821
rbcL-St2        TACTTAACCGGGGGATTCACTGCAAATACTACCTTAGCTCATTATTGCCGAGATAATGGC 823
rbcL-St3        TACTTAACCGGGGGATTCACTGCAAATACTACCTTAGCTCATTATTGCCGAGATAATGGC 827
                ******** ********************** ****************************
```

```
rbcL-Sb3        CTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGT 881
rbcL-Sb4        CTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGT 881
rbcL-Sv1        CTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGT 881
rbcL-Sv5        CTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGT 883
rbcL-Sv4        CTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGT 883
rbcL-Sv2        CTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGT 887
rbcL-Sv3        CTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGT 886
rbcL-Sb1        CTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGT 882
rbcL-Sb2        CTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGT 882
rbcL-Sl2        CTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGT 886
rbcL-Sl3        CTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGT 885
rbcL-Sl1        CTACTTCTTCACATTCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGT 883
rbcL-St1        CTACTTCTTCACATCCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGT 884
rbcL-St4        CTACTTCTTCACATCCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGT 881
rbcL-St2        CTACTTCTTCACATCCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGT 883
rbcL-St3        CTACTTCTTCACATCCACCGTGCAATGCATGCAGTTATTGATAGACAGAAGAATCATGGT 887
                ************** ********************************************

rbcL-Sb3        ATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAGATCATATTCACGCT 941
rbcL-Sb4        ATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAGATCATATTCACGCT 941
rbcL-Sv1        ATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAGATCATATTCACGCT 941
rbcL-Sv5        ATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAGATCATATTCACGCT 943
rbcL-Sv4        ATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAGATCATATTCACGCT 943
rbcL-Sv2        ATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAGATCATATTCACGCT 947
rbcL-Sv3        ATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAGATCATATTCACGCT 946
rbcL-Sb1        ATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAGATCATATTCACGCT 942
rbcL-Sb2        ATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAGATCATATTCACGCT 942
rbcL-Sl2        ATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAGATCATATTCACGCT 946
rbcL-Sl3        ATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAGATCATTTTCACGCT 945
rbcL-Sl1        ATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAGATCATATTCACGCT 943
rbcL-St1        ATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAGATCATGTTCACGCT 944
rbcL-St4        ATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAGATCATGTTCACGCT 941
rbcL-St2        ATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAGATCATGTTCACGCT 943
rbcL-St3        ATGCACTTCCGCGTACTAGCTAAAGCGTTACGTATGTCTGGTGGAGATCATGTTCACGCT 947
                ************************************************* ********

rbcL-Sb3        GGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAGACATCACTTTGGGCTTTGTTGATTTA 1001
rbcL-Sb4        GGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAGACATCACTTTGGGCTTTGTTGATTTA 1001
rbcL-Sv1        GGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAGACATCACTTTGGGCTTTGTTGATTTA 1001
rbcL-Sv5        GGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAGACATCACTTTGGGCTTTGTTGATTTA 1003
rbcL-Sv4        GGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTA 1003
rbcL-Sv2        GGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTA 1007
rbcL-Sv3        GGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTA 1006
rbcL-Sb1        GGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTA 1002
rbcL-Sb2        GGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTA 1002
rbcL-Sl2        GGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTA 1006
rbcL-Sl3        GGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTA 1005
rbcL-Sl1        GGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAGACATCACTTTGGGCTTTGTTGATTTA 1003
rbcL-St1        GGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTA 1004
rbcL-St4        GGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTA 1001
rbcL-St2        GGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAAACATCACTTTGGGCTTTGTTGATTTA 1003
rbcL-St3        GGTACTGTAGTAGGTAAACTTGAAGGCGAAAGAGACATCACTTTGGGCTTTGTTGATTTA 1007
                ******************************** *************************

rbcL-Sb3        CTGGCGGGATGATTTTATTGAAAAA-GATCGAAGTCCC-GGTATTTATTT-CACTCAAAG 1058
rbcL-Sb4        CTGGCGGGATGATTTTATTGAAAAA-GATCGAAGTCCC-GGTATTTATTT-CACTCAA-G 1057
rbcL-Sv1        CTGCGTG-ATGATTTTATTGAAAAA-GATCGAAGTCCC-GGTATTTATTT-CACTCAA-G 1056
rbcL-Sv5        CTGCGGGGATGATTTTATTGAAAAA-GATCGAAGTCCC-GGTATTTATTT-CACTCAA-G 1059
rbcL-Sv4        CTGGCGGGATGATTTTATTGAAAAAAGATCGAAGTCCCCGGTATTTATTTTCACTCAA-G 1062
rbcL-Sv2        CTG-CGGGATGATTTTATTGAAAAAAAATCGAAGTCCC-GGTATTTATTT-CACTCAA-G 1063
rbcL-Sv3        CTG-CGGGATGATTTTATTGAAAAAAAATCGAAGTCCC-GGTATTTATTT-CACTCAA-G 1062
rbcL-Sb1        CTGCGGGGATGATTTTATTGAAAAA-GATCGAAATCCC-GGTATTTATTT-CACTCAA-G 1058
rbcL-Sb2        CTGCGTG-ATGATTTTATTGAAAAA-GATCGAAGTCCC-GGTATTTATTT-CACTCAA-G 1057
```

```
rbcL-Sl2        CTGCCGGGATGATTTTATTGAAAAA-GATCGAAGTCCC-CGTATTTATTT-CACTCAA-G 1062
rbcL-Sl3        CTGCCGGGATGATTTTATTGAAAAA-GATCGAAGTCCC-CGTATTTATTT-CACTCAA-G 1061
rbcL-Sl1        CTGCCGTGATGATTTTATTGAAAAA-GATCGAAGTCCC-CGTATTTATTT-CACTCAA-A 1059
rbcL-St1        CTGGCGGGAGGATTTTATTGAAAAA-GATCCAAACCCGCGGTGTTTATTT-CACTCAA-G 1061
rbcL-St4        CTG-CGGGATGATTTTATTGAAAAA-GATCCAAACCCGCGGTGTTTATTT-CACTCAA-G 1057
rbcL-St2        CTGGCGTGATGATTTTATTGAAAAA-GATCGAAGCCCCCGGTGTTTATTT-CACTCAA-A 1060
rbcL-St3        CTGCCGGGATGATTTTATTGAAAAA-GATCGAAACCCCCGGTGTTTATTT-CACTCAA-G 1064
                ***     * ***************  *** **  **   ** ******* *******

rbcL-Sb3        ATTGGG-TCTCTCTACCGGGGTGTTATACCTGTGGGCTTCGGGGGGGTATTCCACGTTTT 1117
rbcL-Sb4        ATTGGG-TCTCTCTACCGGGGTGTTATACCTGGGGGCTTCAGGGGGGTATTC-ACCGTTT 1115
rbcL-Sv1        ATTGGG-TCTCTCTACCGGGGTGTTATACCTGTGGGCTTCAGGGGGGTATTC-ACG-TTT 1113
rbcL-Sv5        ATTGGGGTCTCTCTACCGGGGTGTTATACCTGTGGGCTTCAGGGGGGTATTCCACG-TTT 1118
rbcL-Sv4        ATTGGGGTCTCTCTACCGGGGTGTTATACCTGTGGGCTTCAGGGGGGTATTC-ACG-TTT 1120
rbcL-Sv2        ATTTGG-TCTCTCTACCGGGGTGTTATACCTGTAGGCTTCAGGGGGGTATTCCACG-TTT 1121
rbcL-Sv3        ATTGGG-TCTCTCTACCGGGGTGTTATACCTGTGGGCTTCAGGGGGGTATTCCACG-TTT 1120
rbcL-Sb1        ATTGGG-TCTCTCTACCGGGGTGTTATACCTGGTGGCTTCAGGGGGGTATTC-ACG-TTT 1115
rbcL-Sb2        ATTGGG-TCTCTCTACCGGG-TGTTATACCTG-TGGCTTCAGGGGG-TATTC-ACG-TTT 1111
rbcL-Sl2        ATTGGGGTCTCTCTACCGGGGGGTTATACCTGGTGGCTTCAGGGGGGTATTC-ACCGTTT 1121
rbcL-Sl3        ATTGGGGTCTCTCTACCGGGGGGTTATACCTGGTGGCTTCAGGGGGGTATTC-ACCGTTT 1120
rbcL-Sl1        GATGGGGTCTCTCTACCGGGGGGTTATACCTGGTGGCTTCAGGGGGGTATTC-ACCGTTT 1118
rbcL-St1        ATTGGGGTCTCTCTACCGGGGGGTTATACCTGGTGGCTTCAGGGGGGTATTC-ACG-TTT 1119
rbcL-St4        ATTGGGGTCTCTCTACCGGGGGGTTATACCTTGTGGCTTCAGGGGGGTATTC-ACG-TTT 1115
rbcL-St2        AATTGGGTCTCTCTACCGGGGTGTTATACCTGTGGGCTTCAGGGGGGTATTC-ACG-TTT 1118
rbcL-St3        A-TTGGGTCTCTCTACCGGGG-GTTATACCTGTGG-CTTCAGGGGG-TATTC-ACG-TTT 1118
                  * ** *************  *********   * **** ***** ***** **  ***

rbcL-Sb3        GGGCA-TATGCCTGGC-TCTGACCCAAAATTTTTGGGGGAATAAAGCCTTGTACTTACAGG 1175
rbcL-Sb4        GGGCA-TATGCCTGGC-TCTGACCCAAAATTTTTGGGGGGATAGAGGCTGGACCTAACAG- 1172
rbcL-Sv1        GGGCA-TATGCCTGGC-TCTGACCCAAGATTTTTGGGGGGATAGAGGC-TGGACCTACA-G 1169
rbcL-Sv5        GGGCA-TATGCCTGGCCTCTGACCCAAGATTTTTGGGGGGATAGATGCCTGGACCTACAAG 1177
rbcL-Sv4        GGGCA-TATGCCTTGCCTCTGACCCAAAATTTTTGGGGGGATAGATGCTT--ACTTACA-G 1176
rbcL-Sv2        TGGCAATATGCCTGGC-TCTGACCCAAAATTTTTGGGGGGATGAATGCTTGTACCTACA-G 1179
rbcL-Sv3        TGGCAATATGCCTGGC-TCTGACCCAAAATTTTTGGGGGGATGAATGCTTGTACCTACA-G 1178
rbcL-Sb1        GGCCA-TATGCCTGGCTCTTGACCCAGAATTTTTGGGGGGATGAAGGCTTGTACCTACAGG 1174
rbcL-Sb2        GGC-A-TATGCCTTGCTCT-GACCCAAGATTTTTGGGGGGATGAATCCTTGTACCTACAG- 1167
rbcL-Sl2        GGCCA-TATGCCTTGC-TCTGACCCAAAATTTTTGGGGGGATGAAGCC-TGAACTAACA-G 1177
rbcL-Sl3        GGCCA-TATGCCTTGC-TCTGACCCAAAATTTTTGGGGGGATGAAGCC-TGAACTAACA-G 1176
rbcL-Sl1        GGCCA-TATGCCTGGC-TCTGACCCAAAATTTTTGGGGGGATAGAGCC-TGTACCTACA-G 1174
rbcL-St1        GGGCA-TATGCCTGCT-CCTGACCCAGAATTTTTGGGGGGATAGAAGCTGTAACTTACA-G 1176
rbcL-St4        GGGCA-TATGCCTGGC-TCTGACCCAGAATTTTTGGGGGGATGAAGCTTGTACCTCACA-G 1172
rbcL-St2        GGGCA-TATGCCTGGC-TCTGACCCAAAATTTTTGGGGGGATGAAGCCTGAA-C-TACA-G 1173
rbcL-St3        GG-CA-TATGCCTGGC-TCTGACCCAAA-TTTTTGGGGGGATGAAGCCTGTA-CCTACA-G 1172
                 *  * *******       ******   ********* **  *        *  ***

rbcL-Sb3        TTCCGGTGGAGGGAAACTTTTAGGGACACCCTTGGGGTAATGC-GCC-----AGGTGCCG 1229
rbcL-Sb4        TTCCGGGGGGAGGAA--CTTTATGGACACCCTTGGGGTAATGC-GCC-----AGGTGCCG 1224
rbcL-Sv1        TTCCGGTGGGAGGAA-CTTTTAGGA-CACCCTTTGGGGGAAAA-GGCCCCAAGGGGCCCT 1226
rbcL-Sv5        TTCCGGTGGAAGGAA-CTTTTAGGAACACCCTTGGGGGGAAAT-GGCCCCAAGGGGCCCT 1235
rbcL-Sv4        TTTCGGTGGGAGGAA-CTTTTAAGGACACCCTTGGGGGGAAAT-GGCCCCAAGGGGGCCC 1234
rbcL-Sv2        TTCCGGTGGGAGGAA-CTTTTAGGAACACCCTTGGGGGGAAAG-CGCCCCAGGTGCCCGT 1237
rbcL-Sv3        TTCCGGTGGGAGGAA-CTTTTAGGAACACCCTTGGGGGGAAAG-CGCCCCAGGTGCCCGT 1236
rbcL-Sb1        TTCCGGTGGGAAGGAACTTTTAGGAACACCCTTGGGGGGAAAT-GCGCCCA-GGGTGCCC 1232
rbcL-Sb2        TTCCGG--GGGAGGAACCTTAAGGA-CACCCCTTGGGGGAATA-GCGCCCA-AGGGGCCC 1222
rbcL-Sl2        TTCCGGTGGAAGG-AACTTTAAGGAACACCCTTGGGGGGAAAT-GGCCCCCAAGTGGCCC 1235
rbcL-Sl3        TTCCGGTGGAAGG-AACTTTAAGGAACACCCTTGGGGGGAAAT-GGCCCCCAAGTGGCCC 1234
rbcL-Sl1        TTCCGGTGGGAGGGAACTTTAAGGACACCCCTTGGGGGGAAAT-GGCCCCCAAGGGGCCC 1233
rbcL-St1        TTTCGGGGGGAGAGAACTTTTAGGACACCCCTTGGGGGGAAAATGCGCCCAGGGTGCCGT 1236
rbcL-St4        TTC--GGGGGAAGGAAACTTTAGGACACCCTCTGGGGGAAAAG---GCCCCAGGGGCCCG 1227
rbcL-St2        TTCC-GGTGGAAGGAACTTTAAGGACACCCCTTGGGGGTAAAT-GGCGCCAAGGTGCCCT 1231
rbcL-St3        TTCC-GGTGGAGGGAACTTTAAGGACACCCCTTGGGGG-AAAT-GGCCCCA-GGTGCCCC 1228
                **   *  *     *   ** * *    **  * ***  *                *
```

```
rbcL-Sb3        TAGC--GAATC-GAGTAG--CTC-TAGAAGCAT-GTGTAAAAG----CTCGTAATGAAGG 1278
rbcL-Sb4        TAGC--GAATC-GAGTAG--CTC-TAGAAGCAT-GTGTAAAAG----CTCGTAATGAAGG 1273
rbcL-Sv1        TAAGC-GAATC-GAGTAG--CTC-TAGAAGCAT-GTGTAAAAG----CTCGTAATGAAGG 1276
rbcL-Sv5        TAACC--AATC-GAGTAG--CTC-TAGAAGCAT-GTGTAAAAG----CTCGTAATGAAGG 1284
rbcL-Sv4        TAACC-AAATC-CAGGAAAACTC-TAGAAGCAT-GTGTAAAAG----CTCGTAATGAAGG 1286
rbcL-Sv2        TACCG-AAATC-AGAGAAGCGTC-TAGAAGCAT-GTGTAAAAG----CTCGTAATGAAGG 1289
rbcL-Sv3        TACCG-AAATC-AGAGAAGCGTC-TAGAAGCAT-GTGTAAAAG----CTCGTAATGAAGG 1288
rbcL-Sb1        TAACCCGAATCCGAGTAGCCCTCATAAAACCAT-GTGTAAAAG----CTCGTAATGAAGG 1287
rbcL-Sb2        TAACCAAAACC--AGGAGCTCT---AGAAGCAT-GTGTAAAAG----CTCGTAATGAAGG 1272
rbcL-Sl2        TTTAGCAAATCGAGGTAACCTCTTAAAAAACATTGTGTAAAAAACCTCCCTTAATGAAGG 1295
rbcL-Sl3        TTTAGCAAATCGAGGTAACCTCTTAAAAAACATTGTGTAAAAAACCTCCCTTAATGAAGG 1294
rbcL-Sl1        TTAACCAAATCCAGGTAACCTCTTAAAAAACATTGTGTAAAAAACCTCCCTTAATGAAGG 1293
rbcL-St1        TAGCGAAAAACAAGGTATCTCCTAAAAAACTGT-GGTTAAAAAACCTCCTATTATGAAGG 1295
rbcL-St4        TACCCAA--TCCAGGAATCTCCTGAAAA-CCAT-GTGTTAAAAAGCTCGTA--ATGAAGG 1281
rbcL-St2        TAGCCGAAACCAGGGTATCTCCTAAAAAACCATTGTGTAAAAAACTCCCTAAATGGAAGG 1291
rbcL-St3        TTACCCAATCCAGG-TATCTCTTAAGAA-CCAT-GTGTAAAAAACTCTGTAATTGAAAGG 1285
                *         *     *          *    * *  * ***             ****

rbcL-Sb3        GC-GTGATCTT---GCTGCT-GAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGT 1333
rbcL-Sb4        GC-GTGATCTT---GCTGCT-GAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGT 1328
rbcL-Sv1        GC-GTGATCTT---GCTGCT-GAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGT 1331
rbcL-Sv5        GC-GTGATCTT---GCTGCT-GAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGT 1339
rbcL-Sv4        GC-GTGATCTT---GCTGCT-GAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGT 1341
rbcL-Sv2        GC-GTGATCTT---GCTGCT-GAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGT 1344
rbcL-Sv3        GC-GTGATCTT---GCTGCT-GAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGT 1343
rbcL-Sb1        GC-GTGATCTT---GCTGCT-GAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGT 1342
rbcL-Sb2        GC-GTGATCTT---GCTGCT-GAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGT 1327
rbcL-Sl2        GC-GTGATCTT---GCTGCT-GAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGT 1350
rbcL-Sl3        GC-GTGATCTT---GCTGCT-GAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGT 1349
rbcL-Sl1        GC-GTGATCTT---GCTGCT-GAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGT 1348
rbcL-St1        GC-GTGATCTT---GCTGCT-GAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGT 1350
rbcL-St4        GC-GTGATCTT---GCTGCT-GAGGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGT 1336
rbcL-St2        GCTGTGAACTTTGGCCCCCTAGAGGGGAAAGATATTATCCGGGAGGCTAGCAAATGGAGT 1351
rbcL-St3        GC-GTGGATCTTTTGCCGCTAAAAGGTAATGATATTATCCGTGAGGCTAGCAAATGGAGT 1344
                ** ***    *    *  **  * ** ** *********** ******************

rbcL-Sb3        CCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTTTCAAGCAGTG 1393
rbcL-Sb4        CCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTTTCAAGCAGTG 1388
rbcL-Sv1        CCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGGTTTAATTTTCAAGCAGTG 1391
rbcL-Sv5        CCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGGTTTAATTTTCAAGCAGTG 1399
rbcL-Sv4        CCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGGTTTAATTTTCAAGCAGTG 1401
rbcL-Sv2        CCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGGTTTAATTTTCAAGCAGTG 1404
rbcL-Sv3        CCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGGTTTAATTTTCAAGCAGTG 1403
rbcL-Sb1        CCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTTTCAAGCAGTG 1402
rbcL-Sb2        CCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTTTCAAGCAGTG 1387
rbcL-Sl2        CCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTTTCAAGCAGTG 1410
rbcL-Sl3        CCTGAACTTGCTGCTGCTTGTGAGGTATGGGAGGAGATCAGATTTAATTTTCAAGCAGTG 1409
rbcL-Sl1        CCTGAACTTGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTTTCAAGCAGTG 1408
rbcL-St1        CCTGAACTCGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTACCAAGCAGTG 1410
rbcL-St4        CCTGAACTCGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTACCAAGCAGTG 1396
rbcL-St2        CCTGAACTCGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTACCAAGCAGTG 1411
rbcL-St3        CCTGAACTCGCTGCTGCTTGTGAGGTATGGAAGGAGATCAGATTTAATTACCAAGCAGTG 1404
                ******** ******************** ********** *******  *********

rbcL-Sb3        GATACTTTGGATCCGCTTAAGGCTTAATTACCTTTGTCTCGTAGTGAATTAAA 1446
rbcL-Sb4        GATACTTTGGATCCGCTTAAGGCTTAATTACCTTTGTCTCGTAGTTAATTAAA 1441
rbcL-Sv1        GATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTCTCGTAGTGAATTAAA 1444
rbcL-Sv5        GATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTCTCGTAGTGAATTAAA 1452
rbcL-Sv4        GATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTCTCGTAGTGAATTAAA 1454
rbcL-Sv2        GATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTCTCGTAGTTAATTAAA 1457
rbcL-Sv3        GATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTCTCGTAGTTAATTAAA 1456
rbcL-Sb1        GATACTTTGGATCCGCTTAAGGCTTAATTACCTTTGTCTCGTAGTGAATTAAA 1455
rbcL-Sb2        GATACTTTGGATCCGCTTAAGGCTTAATTACCTTTGTCTCGTAGTGAATGAAA 1440
```

```
rbcL-Sl2        GATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTCTCGTAGTTAATTAAT 1463
rbcL-Sl3        GATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTCTCGTAGTTAATTAAT 1462
rbcL-Sl1        GATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTCTCGTAGTGAATTAAA 1461
rbcL-St1        GATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTCTCGTAGTGAATTAAA 1463
rbcL-St4        GATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTCTCGTAGTGAATTAAA 1449
rbcL-St2        GATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTCTCGTAGT-AATGAAA 1463
rbcL-St3        GATACTTTGGATCCGCTTAAGTCTTAATTACCTTTGTCTCGTAGT-AATGAAA 1456
                ******************** ********************** *** **
```

The size of the *rbc*L gene

Sequence 1: *rbc*L-St1 1463 bp

Sequence 2: *rbc*L-St2 1463 bp

Sequence 3: *rbc*L-St3 1456 bp

Sequence 4: *rbc*L-St4 1449 bp

Sequence 5: *rbc*L-Sl1 1461 bp

Sequence 6: *rbc*L-Sl2 1463 bp

Sequence 7: *rbc*L-Sl3 1462 bp

Sequence 8: *rbc*L-Sv1 1444 bp

Sequence 9: *rbc*L-Sv2 1457 bp

Sequence 10: *rbc*L-Sv3 1456 bp

Sequence 11: *rbc*L-Sv4 1454 bp

Sequence 12: *rbc*L-Sv5 1452 bp

Sequence 13: *rbc*L-Sb1 1455 bp

Sequence 14: *rbc*L-Sb2 1440 bp

Sequence 15: *rbc*L-Sb3 1446 bp

Sequence 16: *rbc*L-Sb4 1441 bp

The pairwise of similarity score

Sequences (1:2) Aligned. Score: 95	Sequences (4:6) Aligned. Score: 96	Sequences (8:11) Aligned. Score: 97
Sequences (1:3) Aligned. Score: 95	Sequences (4:7) Aligned. Score: 95	Sequences (8:12) Aligned. Score: 98
Sequences (1:4) Aligned. Score: 97	Sequences (4:8) Aligned. Score: 96	Sequences (8:13) Aligned. Score: 97
Sequences (1:5) Aligned. Score: 95	Sequences (4:9) Aligned. Score: 95	Sequences (8:14) Aligned. Score: 97
Sequences (1:6) Aligned. Score: 94	Sequences (4:10) Aligned. Score: 95	Sequences (8:15) Aligned. Score: 97
Sequences (1:7) Aligned. Score: 94	Sequences (4:11) Aligned. Score: 95	Sequences (8:16) Aligned. Score: 97
Sequences (1:8) Aligned. Score: 95	Sequences (4:12) Aligned. Score: 95	Sequences (9:10) Aligned. Score: 99
Sequences (1:9) Aligned. Score: 94	Sequences (4:13) Aligned. Score: 96	Sequences (9:11) Aligned. Score: 97
Sequences (1:10) Aligned. Score: 94	Sequences (4:14) Aligned. Score: 96	Sequences (9:12) Aligned. Score: 97
Sequences (1:11) Aligned. Score: 95	Sequences (4:15) Aligned. Score: 95	Sequences (9:13) Aligned. Score: 96
Sequences (1:12) Aligned. Score: 94	Sequences (4:16) Aligned. Score: 95	Sequences (9:14) Aligned. Score: 97
Sequences (1:13) Aligned. Score: 95	Sequences (5:6) Aligned. Score: 97	Sequences (9:15) Aligned. Score: 97
Sequences (1:14) Aligned. Score: 95	Sequences (5:7) Aligned. Score: 97	Sequences (9:16) Aligned. Score: 97
Sequences (1:15) Aligned. Score: 94	Sequences (5:8) Aligned. Score: 97	Sequences (10:11) Aligned. Score: 97
Sequences (1:16) Aligned. Score: 95	Sequences (5:9) Aligned. Score: 96	Sequences (10:12) Aligned. Score: 98
Sequences (2:3) Aligned. Score: 97	Sequences (5:10) Aligned. Score: 96	Sequences (10:13) Aligned. Score: 97
Sequences (2:4) Aligned. Score: 96	Sequences (5:11) Aligned. Score: 96	Sequences (10:14) Aligned. Score: 97
Sequences (2:5) Aligned. Score: 95	Sequences (5:12) Aligned. Score: 97	Sequences (10:15) Aligned. Score: 97
Sequences (2:6) Aligned. Score: 95	Sequences (5:13) Aligned. Score: 96	Sequences (10:16) Aligned. Score: 97
Sequences (2:7) Aligned. Score: 95	Sequences (5:14) Aligned. Score: 97	Sequences (11:12) Aligned. Score: 98
Sequences (2:8) Aligned. Score: 95	Sequences (5:15) Aligned. Score: 96	Sequences (11:13) Aligned. Score: 96
Sequences (2:9) Aligned. Score: 94	Sequences (5:16) Aligned. Score: 96	Sequences (11:14) Aligned. Score: 97
Sequences (2:10) Aligned. Score: 95	Sequences (6:7) Aligned. Score: 99	Sequences (11:15) Aligned. Score: 96
Sequences (2:11) Aligned. Score: 95	Sequences (6:8) Aligned. Score: 97	Sequences (11:16) Aligned. Score: 97
Sequences (2:12) Aligned. Score: 95	Sequences (6:9) Aligned. Score: 96	Sequences (12:13) Aligned. Score: 96
Sequences (2:13) Aligned. Score: 95	Sequences (6:10) Aligned. Score: 96	Sequences (12:14) Aligned. Score: 97
Sequences (2:14) Aligned. Score: 95	Sequences (6:11) Aligned. Score: 97	Sequences (12:15) Aligned. Score: 97
Sequences (2:15) Aligned. Score: 95	Sequences (6:12) Aligned. Score: 97	Sequences (12:16) Aligned. Score: 97
Sequences (2:16) Aligned. Score: 95	Sequences (6:13) Aligned. Score: 96	Sequences (13:14) Aligned. Score: 97
Sequences (3:4) Aligned. Score: 97	Sequences (6:14) Aligned. Score: 97	Sequences (13:15) Aligned. Score: 97
Sequences (3:5) Aligned. Score: 96	Sequences (6:15) Aligned. Score: 96	Sequences (13:16) Aligned. Score: 97
Sequences (3:6) Aligned. Score: 96	Sequences (6:16) Aligned. Score: 97	Sequences (14:15) Aligned. Score: 97
Sequences (3:7) Aligned. Score: 95	Sequences (7:8) Aligned. Score: 96	Sequences (14:16) Aligned. Score: 97
Sequences (3:8) Aligned. Score: 95	Sequences (7:9) Aligned. Score: 96	Sequences (15:16) Aligned. Score: 97
Sequences (3:9) Aligned. Score: 95	Sequences (7:10) Aligned. Score: 96	
Sequences (3:10) Aligned. Score: 95	Sequences (7:11) Aligned. Score: 96	
Sequences (3:11) Aligned. Score: 95	Sequences (7:12) Aligned. Score: 96	
Sequences (3:12) Aligned. Score: 96	Sequences (7:13) Aligned. Score: 96	
Sequences (3:13) Aligned. Score: 95	Sequences (7:14) Aligned. Score: 96	
Sequences (3:14) Aligned. Score: 96	Sequences (7:15) Aligned. Score: 95	
Sequences (3:15) Aligned. Score: 95	Sequences (7:16) Aligned. Score: 97	
Sequences (3:16) Aligned. Score: 95	Sequences (8:9) Aligned. Score: 97	
Sequences (4:5) Aligned. Score: 96	Sequences (8:10) Aligned. Score: 97	

The *mat*K sequence of *S. thorelii, S. nux-vomica, S. lucida and S. nux-blanda*

>*mat*K-St1

ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGCTTTCTATATCAACACTTCTCTTTCAAGAAGAGTATATTTTATGCACTTGCTCA
TGATCATAGCTTAAAAACCGATCTATTTTGTTGGAAGGGAAAATCCAGGTTATGATAATAAATCCAGGTTAGTAGGTACTAATTGTGAAACGTTTTCTAGGACT
GGGTAATTACTGTTTAATTACGCGAATGTATCAACAGTTAAATCATTTTTTTATGATACAAGGTTTTTCTAATAATTCTAAGCAAAATCGATTTTTATTTTTGGG
GCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATTTTCCTTTATTGTGGAAATTCGTTTTCTATACGGATTACTATCTTCTTCTATAGAAGAAGAGG
AAAGGGGTATTCAAATTACAGAATTTACATTTACGCTCAATTCATTCAATAATTCCTTTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACT
AATACCCCACCCCGTCCATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCCTCTTTGCATTTATTACGATTCTTTCTCTACGAGTATT
GTAATTATTGTAATTGGAATAATCTTATTGCTACAAAGAAACCCAGTTTTTCTTTTTTACCAAAAAGAAATAAAAGATTATTCTTCTTCTTATAAAATTCTTATG
TATGTGAATACGAATCCATTTGCCTATTACTACATAACCAATCTTCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCTATTTCTATGGAAAA
ATAGAACGTCTTGTAGAAGTCTTAGCTAAGGATTATCAAGCCAAACTACGGATGTACAAAGATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCT
GGTTTCAAAAGGGACGGCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGACCTGGGGTTTCACTCCGGGAAGGGTCTA
TATAAAGGCACTATACAAATCATTCCCCTTGACTTTATGGGGCTATCTTTCAGGAGTCTGGCGACTAAACCCCTTCAATGGTTACCGGAGTCCAAATGGAAAG
AATTAAATTCATTTCCTAATCCAATAATTCCTATTTAGGAAACAATTGGGAAACCGTTTGTTTCAAAAATTATCCCCCCCTGGGGTGGGGAAACATTGTGGGTT
AAAAGCGAAATTTTTGTGAATCCCCTTAGGGGGGTATCCAAATTAGTAAGCCGAATTTGAACTGATTTATCAGATTCGGATATTATTGGCCGGTTGGGGCGTA
TATGCAGAAATCTTTCTCATTATCATAGCGGATCTTCCAAAAAAGTGAGTTTGTATCGAATAAAGTATATACTTTGGTTTTCTTGTGCTAAAACTTTAGCTCGG
AAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTAGGGTCGGAATTTGTGGAATTCGAACTCATGTCGGAAGAAGTAGTCCTTTCTTTGAACTTCCCAA
GAGTTTCTTCTCCCTTTTGGGGGGTGTAGAGAAGTCGGTTTTAATATTGGTATTTGAATTTTATCACTGATCTGGTGAATCATCAATGATTCATATTCATTCTG
AGACCTTGTAAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTGAAATGTTGATGTAGCATGTAATAAGGGTTAAATCA
ACTGACTATTCTGCTTTCTAAATTGAGGTCTAAAAAAAAAGAAA

>*mat*K-St2

ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGCTTTCTATATCAACACTTCTCTTTCAAGAAGAGTATATTTTATGCACTTGCTCA
TGATCATAGCTTAAAAACCGATCTATTTTGTTGGAAGGGAAAATCCAGGTTATGATGGAAAATCCAGGTTAGTAGATACTAATTGTAAAACGTTTTCTAGGACT
GTGTAATTACTGTTTAATTACGCGAATGTATCAACAGTTAAATCATTTTTTTATGATACAAGGTTTTTCTAATGATTCTAAGCAAAATCGATTTTTATTTTTGGG
GCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATTTTCCTTTATTGTGGAAATTCGTTTTTTAAACGGATTACTATCTTCTTCTATAGAAGAAGAGG
AAAGGGGTATTCAAATTACAGAATTTACATTTACGCTCAATTCATTCAATATTTCCTTTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACT
AATACCCCACCCCGTCCATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCCTCTTTGCATTTATTACGATTCTTTCTCTACGAGTATT
GTAATTATTGTAATTGGAATAATCTTATTGCTACAAAGAAACCCAGTTTTTCTTTTTTACCAAAAAGAAATAAAAGATTATTCTTCTTCTTATATAATTCTTATG
TATGTGAATACGAATCCATTTTCCTCTTTCTACATAACCAATCTTCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCTATTTCTATGGAAAA
ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAAGCCAAACTACGGTTGTTCAAAGATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCT
GGTTTCAAAAGGGACGGCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGGCATTTTGACCTGGGGTTTCACTCCGGGAAGGGTCTA
TATAAAGGAATTATACCAATCATTCCCCTTGACTTTATGGGGCTATCTTTCAGAAGTGTGGCGACTAAACCCTTTCAATGGGTACGGGAGTCCAAATGGAAAG
AATTAAAACATTTCCCTAATCCAATAATGGCCTTTTAGGAAAAAATTGGGAAACCCTTTGGTCCAAAAATTATCCCCCCCTGGGGGGTGGGAACATTGGGGGT
TAAAAGCGAAATTTTTTGGAAACCCCTTAGGGGGGCATCCCATTTAGTAAGCCGGATTTGAACTGATTTATCAGATTCGGATATTATTGACCGGGTTGGGCGT
ATATGCAGAAATCTTTCTCATTATCATAGCGGATCTTCCAAAAAAGTGAGTTTGTATCGAATAAAGTATATACTTCGGTTTTCTTGTGCTAAAACTTTAGCTCG
GAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTAGGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGTCCTTTCTTTGAACTTCCCA
AGAGTTTCTTCTCCCTTTTGGGGGGTGTATAGAAGTCGGATTTAAATTTGGTATTTGGATATTATCACTGATCTGGTGAATCATCAATGATTCATATTCATTCT
GAGACCTTGTAAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTGAAATGTTGATGTAGCATGTAATAAGGGTTAAATC
AACTGACTATTCTGCTTTCTAAATTAAAGTCTAAAAAAAAAGAAA

>*mat*K-St3

ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGCTTTCTATATCAACACTTCTCTTTCAAGAAGAGTATATTTTATGCACTTGCTCA
TGATCATAGCTTAAAAACCGATCTATTTTGTTGGAAGGGAAAATCGACATAAGGGTCGCAGGTTCAGGTTAGTAGGTATCCCTACTAAATCGTTTTCTAGGAC
TGGGTAATAACTGTTTAATTACGCGAATGTATCAACAGTTAAATCATTTTTTTATGATACAAGGTTTTTCTAATGATTCTAAGCAAAATCGATTTTTATTTTTGG
GGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATTTTCCTTTATTGTGGAAATTCGTTTTCTATACGGATTACTATCTTCTTCTATAGAAGAAGAG
GAAAGGGGTATTCAAATTACAGAATTCACATTTACGCTCAATTCATTCAATATTTCCTTTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATAC

TAATACCCCACCCCGTCCATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCCTCTTTGCATTTATTACGATTCTTTCTCTACGAGTAT
TGTAATGATTGTAATTGGAATAATCTTATTGCTACAAAGAAACCCAGTTTTTCTTTTTTACCAAAAAGAAATAAAAGATTATTCTTCTTCTTAAATAATTCTTAT
GTATGTGAATACGAATCCATTTTCCTCTTTCTACATAACCAATCTTCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCTATTTCTATGGAAA
AATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAAGCCAAACTACGGTTGTTCAAAGATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTC
TGGTTTCAAAAGGGACGGCTCCTTTGATGAATAAATGGAAATCTTACCTTGGCAATTTTTGGCAATGTCATTTTGACCTGGGGTTTCACTCCGGGAAGGGTCT
ATATAAAGGAATTATACAAATCATTCCCCTTGACTTTATGGGGCTATCTTTCAGAAGTTTGGCGACTAAACCCCTTCAATGGTTACCGGAGTCCAAATGATAG
AATTAAATTCATTTCCTAATCCAATAAATGCTATTAAGGAAAAAAATGGGAAACCCTTTGTTCAAAAATTATCCCCCCCTGGGGGGGGGAACATTTGGGGGTT
AAAAGCGAAAATTTTGTGAAACCATCTAGGGGGGCATCCCATTTAGTAAGCCGGATTTGGACTGATTTATCAGATTCGGATATTATTGACCGATTTGGGCGTA
TATGCAGAAATCTTTCTCATTATCATAGCGGATCTTCCAAAAAAGTGAGTTTGTATCGAATAAAGTATATACTTCGGTTTTCTTGTGCTAAAACTTTAGCTCGG
AAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTAGGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGTCCTTTCTTTGAACTTCCCAA
GAGTTTCTTCTCCCTTTTGGGGGGTGTATAGAAGTCGGATTTAATATTGGTATTTGAATTTTATCACTGATCTGGTGAATCATCAATGATTCATATTCATTCTG
AGACCTTGTAAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTGAAATGTTGATGTAGCATGTAATAAGGGTTAAATCA
ACTGACTATTCTGCTTTCTAAATTAAAGTTTAAAAAAAAAGAAA

>*mat*K-St4

ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGCTTTCTATATCAACACTTCTCTTTCAAGAAGAGTATATTTTATGCACTTGCTCA
TGATCATAGCTTAAAAACCGATCTATTTTGTTGGAAGGGAAAATCCACCTCATGATAATAAATCCAGGTTAGTAGGTAACCCTAGTGAAACGTTTTCTAGGAG
TGGGTAATAACTGTTTAATTACGCGAATCTATCAACAGTTAAATCATTTTTTTATGATACAAGGTTTATCTAATGATTCTAAGCAAAATCGATTTTTATTTTTGG
GGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATTTTCCTTTATTGTGGAAATTCGTTTTCTATACGGATTACTATCTTCTTCTATAGAAGAAGAG
GAAAGGGGTATTCAAATTACAGAATTTACATTTACGCTCAATCCATTCAATATTTCCTTTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATAC
TAATACCCCACCCCGTCCATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCCTCTTTGCATTTATTACGATTCTTTCTCTACGAGTAT
TGTAATTATTGTAATTGGAATAATCTTATTGCTACAAAGAAACCCAGTTTTTCTTTTTTACCAAAAAGAAATAAAAGATTATTCTTCTTCTTATATAATTCTTAT
GTATGTGAATACGAATCCATTTTCCTCTTTCTACATAACCAATCTTCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCTATTTCTATGGAAA
AATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAAGCCAAACTACGGTTGTTCAAAGATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTC
TGGTTTCAAAAGGGACGGCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGACCTGGGGTTTCACTCCGGGAAGGGTCT
ATATAAAGGAATTATACAAACCATTCCCCTGGACTTTATGGGGCTATCTTTCAGAAGTGTGGCGACTAAACCCTTTCAATGGGTACCGGAGTCCAAATGGAAA
AAATTAAATTCATTTTCTAACCCAATAATGCCTATTTAGGAAGAAATTGGGATACCCTTGGGTCCAAAAATTATCCCCCTCTGGGTTGGATCAACATTGGGGG
TTAAAAGCGAAATTTTTGTGAATCCATTTAGGGGGGCATCCCATTTAGTAAGCCGGATTTGGACTGATTTATCAGATTCGGATATTATTGACCGATTTGGGCG
TATATGCAGAAATCTTTCTCATTATCATAGCGGATCTTCCAAAAAAGTGAGTTTGTATCGAATAAAGTATATACTTCGGTTTTCTTGTGCTAAAACTTTAGCTC
GGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTAGGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGTCCTTTCTTTGAACTTCCC
AAGAGTTTCTTCTCCCTTTTGGGGGGTGTATAGAAGTCGGATTTAATATTGGTATTTGAATTTTATCACTGATCTGGTGAATCATCAATGATTCATATTCATTC
TGAGACCTTGTAAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTGAAATGTTGATGTAGCATGTAATAAGGGTTAAAT
CAACTGACTATTCTGCTTTCTAAATTAAAGTTTAAAAAAAAAGAAA

>*mat*K-sl1

ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGCTTTCTATATCAACACTTCTCTTTCAAGAAGAGTATATTTATGCATTTGCTCAT
GATCATAGCTTAAAAACCGATCTATTTTGTTGGAAGGGAAAATCCAGGTTTTGTTGGACAATCCAGGTTAGTTGATAATAAATCCAAAACGTTTTCTAGGATTG
TGAAACTACTTTTTAATTACTCGAATGTATCAACAGTTAAATCATTTTTTTATGATACAAGGTTTTTCTAATGATTCTAAACAAAATCGATTTTTATTTTTGGGG
CACAGCAAGAATTTGTATTATCAAATGATATCAGAGGGATTTTCCTTTATTGTGGAAATTCGTTTTCTAAACGGATTACTATCTTCTTCTAGAGAAGAAGAGGA
AAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCTTTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTA
ATACCCCACCCCGTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTGCATTTATTACGATTCTTTCTCTACGAGTATTG
TAATTATTGTAATTGGAATAATCTTATTTCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTCTTAAATAATTCTTAAGT
ATGTGAATACGAATCCATTTTCGTCTTTCTACATAACCAATCTTCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATGGAAAAA
TAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAAGATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTG
GTTTCAAAAGGGACGGCTCCTTTGATGAATAAATGGAAATCTTACCTTGGCAATTTTTGGCAATGGCATTTTGACCTGGGGTTTCACTCCGGGAAGGGTCTAT
ATAAAGGAATTATACCAATCATTCCCTTTGACTTTATGGGGCTATCTTTCAGAAGGGGTCCGACTAAACCTTTTCAATGGGTACGGGAGTCCAAATGGAAAGA
ATTTAAACATTTCCCAAACCAAATAATGGCTATTAGGAAAAAAATGGGAAACCCCTTGGTCCAAAAATTATTCCCTCCTGGGGGGTGGGAACATTGGTGGTTA
AAAGCCAAAAGTTTGTGAACCCACTTTAAGGGGCATCCCATTTAGTAAAGCCGGTTTGGACTGATTTATCAGATTCGGATATTATTGACCGATTTGGGCGTAT

ATGCAGAAATCTTTCTCATTATCATAGCGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCTTGTGCTAAAATTTTAGCTCGGA
AACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTAGGGTCGGAATTTTTGGAATTTAAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTCCCAAGA
GTTTCTTCGCCCTTTTGGGGGGGTGTATAGAAGTCGGATTTGGATTTTGGTATTTGGAATATTATCACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTG
AGACCTTGTAAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTGAAATGTTGATGTAGCATGTAATAAGGGTTAAATCA
ACTGACTATTCTGCTTTCTAAACTAAAGTCTAGATGAGTTATCA

>*mat*K-Sl2

ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGCTTTCTATATCAACACTTCTCTTTCAAGAAGAGTAGATTTATGCATTTGCTCAT
GATCATAGCTTAAAAACGGATCTATATTGTTGGACGGGAATTTCCAGATTTTGTTGGACAACCCAGGTTAGTTGATAATAAATCCAAAACGTTTTCTAAGATTG
TGAAAATCCGTGTTAATTACTCGAATGTATCAACAGTTAAATCATTTCTTTATGATACAAGGTTTTTCTAATGATTCTAAACAAAATCGATTTTTATTTTTGGGC
CACAGCAAGAATTGGTATTACCAAATGATATCAAAGGGATTTTCCCTTATTGTGGAAATTCGTTTTCTAAACGGATTACTATCTTCTTCTAGAGAAGAAGAGGA
AAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCTTTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTA
ATACCCCACCCCGTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTGCATTTATTACGATTCTTTCTCTACGAGTATTG
TAATTATTGTAATTGGAATAATCTTATTTCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTCTTAAATAATTCTTAAGT
ATGTGAATACGAATCCATTTTCGTCTTTCTACATAACCAATCTTCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATGGAAAAA
TAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAAGATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTG
GTTTCAAAGGGGACGGCTCCTTTGATGAATAAATGGAAATCTTACCTTGGCAATTTTTGGCAATGTCATTTTGACCTGGGGTTTCACTCCGGGAAGGGTCTAT
ATAAAGGAATTATACCAATCATTCCCCTGGACTTTATGGGGCTATCTTTCAGAAGGGGTCCGACTAAACCTTTTCAATGGGTACGGGAGTCCAAATGGAAAGA
ATTTAAACATTTCCTAAACCAAATAATGCCCATTAGGAAAAAAATGGGAAACCCCTTGGTCCAAAAATTATTCCCTCCTGGGGGGTGGGACCATTGGTGGTTA
AAACCCAAAAGTTTGTGAACCCACCTTAAGGGGCATCCCATTAGTTAAAGCCGGTTTGGACTGATTTATCAGATTCGGATATTATTGACCGATTTGGGCGTAT
ATGCAGAAATCTTTCTCATTATCATAGCGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCTTGTGCTAAAATTTTAGCTCGGA
AACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTAGGGTCGGAATTTTTGGAATTTAAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTCCCAAGA
GTTTCTTCGCCCTTTTGGGGGGGTGTATAGAAGTCGGATTTGGATTTTGATATTTGGAATTGTATCACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTG
AGACCTTGTAAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTGAAATGTTGATGTAGCATGTAATAAGGGTTAAATCA
ACTGACTATTCTGCTTTCTAAACTAAAGTTTAAATGAGTTATCA

>*mat*K-Sl3

ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGCTTTCTATATCAACACTTCTCTTTCAAGAAGAGTAGATTTATGCATTTGCTCAT
GATCATAGCTTAAAAACGGATCTATATTGTTGGACGGGAATTTCCAGATTTTGTTGGACAACCCAGGTTAGTTGATAATAAATCCAAAACGTTTTCTAAGATTG
TGAAAATCCGTGTTAATTACTCGAATGTATCAACAGTTAAATCATTTTTTTATGATACAAGGTTTTTCTAATGATTCTAAACAAAATCGATTTTTATTTTTGGGC
CACAGCAAGAATTTGTATTACCAAATGATATCAAAGGGATTTTCCCTTATTGTGGAAATTCGTTTTCTAAACGGATTACTATCTTCTTCTAGAGAAGAAGAGGA
AAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCTTTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTA
ATACCCCACCCCGTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTGCATTTATTACGATTCTTTCTCTACGAGTATTG
TAATTATTGTAATTGGAATAATCTTATTTCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTCTTAAATAATTCTTAAGT
ATGTGAATACGAATCCATTTTCGTCTTTCTACATAACCAATCTTCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATGGAAAAA
TAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAAGATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTG
GTTTCAAAAGGGACGGCTCCTTTGATGAATAAATGGAAATCTTACCTTGGCAATTTTTGGCAATGTCATTTTGACCTGGGGTTTCACTCCGGGAAGGGTCTAT
ATAAAGGAATTATACCAATCATTCCCCTGGACTTTATGGGGCTATCTTTCAGAAGGGGTCCGACTAAACCTTTTCAATGGGTACGGGAGTCCAAATGGAAAGA
ATTTAAACATTTCCTAAACCAAATAATGCCCATTAGGAAAAAAATGGGAAACCCCTTGGTCCAAAAATTATTCCCTCCTGGGGGGTGGGACCATTGGTGGTTA
AAACCCAAAAGTTTGTGAACCCACCTTAAGGGGCATCCCATTAGTTAAAGCCGGTTTGGACTGATTTATCAGATTCGGATATTATTGACCGATTTGGGCGTAT
ATGCAGAAATCTTTCTCATTATCATAGCGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCTTGTGCTAAAATTTTAGCTCGGA
AACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTAGGGTCGGAATTTTTGGAATTTAAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTCCCAAGA
GTTTCTTCGCCCTTTTGGGGGGGTGTATAGAAGTCGGATTTGGATTTTGATATTTGGAATTGTATCACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTG
AGACCTTGTAAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTGAAATGTTGATGTAGCATGTAATAAGGGTTAAATCA
ACTGACTATTCTGCTTTCTAAACTAAAGTTTTAATGAGTTATCC

>*mat*K-Sv1

ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGGCTTTCTATATCAACACTTCTCTTTCAAGAAGAGTATATTTATGCATTTGCTCA
TGATCATAGCTTAAAAACCGATCTATTTTGTTGGAAGGGAAAATCCAGGTTTTGTTGGACAATCCAGGGTAGTCGATAATAAGATCAAAACGTTATCTAAGGT
GGTGAAACTACTTTTTAATTACTCAAATGTAAAAACAGTTAAGTCAAGTTTACATGATTTTTTTGATTTTTCTAATGATTCTAAACAAAATCGATTTTTATTTTT
GGGGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATTTTCCTTTATTGTGGAAATGTCGTTTTCTAAAAGGATTACTATCTTCTTCTAGAGAAGGA
GGGGAAAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCTTTCTTAGAGGACAACTTTTCACATCTCAATTATGTGTTAGATA
TACTAATACCCCACCCCGTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTGCATTTATTACGATTCTTTCTCTACGAG
TATTGTAATTATTGTAATTGGAATAATCTTATTTCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTCTTAAATAATTCT
TAAGTAGGTCAATACGAATCCATTTTCGTCTTTCTACATAACCAATCTTCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATGG
AAAAATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAAGATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCA
TTCTGGTTTCAAAAGGGACGGCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGACCTGGGGTTTCACTCCGGGAAGGG
TCTATATAAAGGAATTATACCAATCATTCCCTTTGACTTTATGGGGCTATCTTTTAGAAGTGGCGCGTCTAAACCCTTTCAATGGGTACGGGAGTCCAAATGA
AAAGAATTAAAACATTTCCTAACCCAAAAAAGGGCTATTATAGGAAAATTGGAAACCCCCTTGGTCCAAAATTATTTCCCCTCTGGGTGTGGGAAACATATGG
GGTTATAAGCAAAAAGTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAAGCCGGTTTGGACTGATTTATCAGATTCGGATATTATTGACCGATTTGGG
CGTATATGCAGAAATCTTTCTCATTATCATAGTGGATCTTCCAAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCTTGTGCTAAAACTTTAGC
TCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTAGGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTC
CCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTGGTATTTTGGTATTTGGAATATTATCACTGATCTGGTGAATCAGCAATGATTCATATT
CATTCTGAGACCTTGTAAATGGATTTAAACCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTGAAATGTTGATGTAGCATGTAATAAGGGT
TAAATCAACTGACTATTCTGCTTTTCTAAATAAAGTCTAAAAAAGGAAAAA

>*mat*K-Sv2

ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGGCTTTCTATATCAACACTTCTCTTTCAAGAAGAGTATATTTATGCATTTGCTCA
TGATCATAGATTAAAAACCGATCTATTTTGTTGGAATGGAAAACCCATGCTTTTTTGGACAATCCAGGGTAATCGATAATAAGATCAAAACGTTATCTAAGGTG
GTGAAACTACTTTTTAATTACTCAAATGTAAAAACAGTTAAGTCAAGTTTACATGATTTTTTTGATTTTTCTAATGATTCTAAACAAAATCGATTTTTATTTTTG
GGGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATTTTCCTTTATTGTGGAAATGTCGTTTTCTAGAAGGATTACTATCTTCTGCTAGAGAAGAAA
GGGAAAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCTTTCTTAGAGGACAACTTTTCACATCTCAATTATGTGTTAGATAT
ACTAATACCCCACCCCGTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTGCATTTATTACGATTCTTTCTCTACGAGT
ATTGTAATTATTGTAATTGGAATAATCTTATTTCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTCTTAAATAATTCTT
AAGTAGGTCAATACGAATCCATTTTCGTCTTTCTACATAACCAATCTTCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATGGA
AAAATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAAGATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCAT
TCTGGTTTCAAAAGGGACGGCTCCTTTGATGAATAAATGGAAATCTTACCTTGGCAATTTTTGGCAATGTCATTTTGACCTGGGGTTTCACTCCGGGAAGGGT
CTATATAAAGGAATTATACCAATCATTCCCTTTGACTTTATGGGGCTATCTTTTAGAAGTGGCGCGTCTAAACCCTTTCAATGGGTACGGAAGTCCAAATGAA
AAGAATTAATTCATTTTCTAATCCAAATAAGGGCTATTATAGGAAAATTGGGAAACCCCTTGGTCCAAAATTATTTCCCCTCTGGGTGTGGGAAACATATGGG
GTTATAAGCGAAAAGTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAACCCGGTTTGGACTGATTTATCAGATTCGGATATTATTGACCGATTTGGGC
GTATATGCAGAAATCTTTCTCATTATCATAGTGGATCTTCCAAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCTTGTGCTAAAACTTTAGCT
CGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTAGGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTCC
CAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTGGTATTTTGGTATTTGGAATATTATCACTGATCTGGTGAATCAGCAATGATTCATATTC
ATTCTGAGACCTTGTAAATGGATTTAAACCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTGAAATGTTGATGTAGCATGTAATAAGGGTT
AAATCAACTGACTATTCTGCTTTTCTAAATAAAGTCTAAAAAAGGAAAAA

>*mat*K-Sv3

ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGGCTTTCTATATCAACACTTCTCTTTCAAGAAGAGTATATTTATGCATTTACTCA
TGATCATAGTTTAAAAACCGATCTATTTTGTTGGGAAGGAAAAGCCAGGCTTTTTTGGAAAATCCAGGGTAATCGATAATAAGATCAAAACGTTATCTAAGGT
GGTGAAACTAGTTTTTAATTACTCAAATGTAAAAACATTTAAGTCAAGTTTACAAGATTTTTTTGATTTTTCTAATGATTCTAAACAAAATCGATTTTTATTTTT
GGGGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATTTTCCTTTATTGTGGAAATGTCGTTTTCTAGAAGGATTACTATCTTCTGCTAGAGAAGA
AAGGGAAAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCTTTCTTAGAGGACAACTTTTCACATCTCAATTATGTGTTAGAT
ATACTAATACCCCACCCCGTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTGCATTTATTACGATTCTTTCTCTACGA
GTATTGTAATTATTGTAATTGGAATAATCTTATTTCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTCTTAAATAATTC

TTAATAAGGTCAATACGAATCCATTTTCGTCTTTCTACATAACCAATCTTCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATG
GAAAAATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAAGATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTC
ATTCTGGTTTCAAAAGGGACGGCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGACCTGGGGTTTCACTCCGGGAAGG
GTCTATATAAAGGAATTATACCAATCATTCCCTTTGACTTTATGGGGCTATCTTTTAGAAGTGGCGCGTCTAAACCCTTTCAATGGGTACGGAAGTCCAAATG
AAAAGAATTAATTCATTTTCTAATCCAAATAAGGGCTATTATAGGAAAATTGGGAAACCCCTTGGTCCAAAATTATTTCCCCTCTGGGTGTGGGAAACATATG
GGGTTATAAGCGAAAAGTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAAGCCGGTTTGGACTGATTTATCAGATTCGGATATTATTGACCGATTTGG
GCGTATATGCAGAAATCTTTCTCATTATCATAGTGGATCTTCCAAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCTTGTGCTAAAACTTTAG
CTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTAGGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTT
CCCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTGGTATTTTGGTATTTGGAATATTATCACTGATCTGGTGAATCAGCAATGATTCATAT
TCATTCTGAGACCTTGTAAATGGATTTAAACCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTGAAATGTTGATGTAGCATGTAATAAGGG
TTAAATCAACTGACTATTCTGCTTTTCTAAATAAAGTCTAAAAAAGGAAAAA

>*mat*K-Sv4

ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGGCTTTCTATATCAACACTTCTCTTTCAAGAAGAGTATATTTATGCATTTGCTCA
TGATCATAGTTTAAAAACCGGTCTATTTTGTTGGAATGGAAAATCCATGGTTTTTTGGACAATCCAGGGTAATCGATAATAAGATCAAAACGTTATCTAAGGTG
GTGAAACTAGTTTTTAATTACTCAAATGTAAAAACAGTTAAGTCAAGTTTACATGATTTTTTTGATTTTACTAATGATTCTAAACAAAATCGATTTTTATTTTTG
GGGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATTTTCCTTTATTGTGGAAATGTCGTTTTCTAGAAGGATTACTATCTTCTGCTAGAGAAGAAA
GGGAAAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCTTTCTTAGAGGACAACTTTTCACATCTCAATTATGTGTTAGATAT
ACTAATACCCCACCCCGTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTGCATTTATTACGATTCTTTCTCTACGAGT
ATTGTAATTATTGTAATTGGAATAATCTTATTTCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTCTTAAATAATTCTT
AAGTAGGTCAATACGAATCCATTTTCGTCTTTCTACATAACCAATCTTCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATGGA
AAAATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAAGATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCAT
TCTGGTTTCAAAAGGGACGGCTCCTTTGATGAATAAATGGAAATCTTACCTTGGCAATTTTTGGCAATGTCATTTTGACCTGGGGTTTCACTCCGGGAAGGGT
CTATATAAAGGAATTATACCAATCATTCCCTTTGACTTTATGGGGCTATCTTTTAGAAGTGGCGCGTCTAAACCCTTTCAATGGGTACGGAAGTCCAAATGAA
AAGAATTAATTCATTTTCTAATCCAAATAAGGGCTATTATAGGAAAATTGGGAAACCCCTTGGTCCAAAATTATTTCCCCTCTGGGTGTGGGAAACATATGGG
GTTATAAGCGAAAAGTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAAGCCGGTTTGGACTGATTTATCAGATTCGGATATTATTGACCGATTTGGGC
GTATATGCAGAAATCTTTCTCATTATCATAGTGGATCTTCCAAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCTTGTGCTAAAACTTTAGCT
CGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTAGGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTCC
CAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTGGTATTTTGGTATTTGGAATATTATCACTGATCTGGTGAATCAGCAATGATTCATATTC
ATTCTGAGACCTTGTAAATGGATTTAAACCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTGAAATGTTGATGTAGCATGTAATAAGGGTT
AAATCAACTGACTATTCTGCTTTTCTAAATAAAGTCTAAAAAAGGAAAAA

>*mat*K-Sv5

ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGGCTTTCTATATCAACACTTCTCTTTCAAGAAGAGTATATTTATGCATTTGCTCA
TGATCATAGTTTAAAAACCGGTCTATTTTGTTGGAAAGGAAAATCCAAGGTTTTTTGGAAAATCCAGGGTAATCGATAAAAAGATCAAAACGTTATCTAAGGT
GGTGAAACTAGTTTTTAATTACTCAAATGTAAAAACATTTAAGTCAAGTTTAACAGATTTTTTTGATTTTTATAATGATTCTAAACAAAATCGATTTTTATTTTT
GGGGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATTTTCCTTTATTGTGGAAATGTCGTTTTCTAGAAGGATTACTATCTTCTGCTAGAGAAGA
AAGGGAAAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCTTTCTTAGAGGACAACTTTTCACATCTCAATTATGTGTTAGAT
ATACTAATACCCCACCCCGTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTGCATTTATTACGATTCTTTCTCTACGA
GTATTGTAATTATTGTAATTGGAATAATCTTATTTCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTCTTAAATAATTC
TTAAGTAGGTCAATACGAATCCATTTTCGTCTTTCTACATAACCAATCTTCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATG
GAAAAATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAAGATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTC
ATTCTGGTTTCAAAAGGGACGGCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGACCTGGGGTTTCACTCCGGGAAGG
GTCTATATAAAGGAATTATACAAAACATTCCCTTTGACTTTATGGGGCTATCTTTTAGAAGTGGCGCGTCTAAACCCTTTCAATGGGTACCGAAGTCCAAATG
AAAAGAATTAATTCATTTTCTAATCCAAACAAGGACTTATATAGGAAAATTGGGAAACCCCTTGGTCCAAAATTATTTCCCCTCTGGGTGTGGGAAACATATG
GGGTTATAAGCGAAAAGTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAAGCCGGTTTGGACTGATTTATCAGATTCGGATATTATTGACCGATTTGG
GCGTATATGCAGAAATCTTTCTCATTATCATAGTGGATCTTCCAAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCTTGTGCTAAAACTTTAG
CTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTAGGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTT

CCCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTGGTATTTTGGTATTTGGAATATTATCACTGATCTGGTGAATCAGCAATGATTCATAT
TCATTCTGAGACCTTGTAAATGGATTTAAACCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTGAAATGTTGATGTAGCATGTAATAAGGG
TTAAATCAACTGACTATTCTGCTTTTCTAAATAAAGTCTAAAAAAGGAAAAA

>*mat*K-Sb1

ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGCTTTCTATATCAACTTCCTCTTCTAACAAAGAGTATATTTATCCACTAACTCAT
GATCATAGCTTAAAAAGCGATCTATTTTGGTGAAACCGAAAATCCCGGTGTCTGAGAAAATCTCAGGTTAAATGATAATAAATCCAAAACGTTTTCTAGGATT
GTGAAACTACTGTTTAATTACGCGAATGTATCAACAGTTAAATCATTTTTTTATGATACAAGGTTTTTCTAATGATTCTAAACAAAATCGATTTTTATTTTTGGG
CCACACCAAGAATTTGTATTCCCAAATGATATCCGAGGGATTTTCCTTTATTGTGGAAATTCGTTTTTTAAACGGATTACTATCTTCTTCTAGAGAAGAAGAGG
ATAGGGGAAATTCAAATCCCAAATTCACATTTACGCCCAATTCATTCAATATTTCCTTTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACT
AATACCCCAACCCGTCCATCTGGAAATCCTGGTTCAAACCCTTCGCTAATGGGTAAAAGATGCCTCTTCTTTGCATTTATTACGATTCTTTTTCTACGAGTATT
GTAATTATTGTAATTGGAATAATCTTATTTCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAACGAAATAAAAGATTATTCTTCTTCTTAAAAAATCCTTAAG
TATGTGAATACGAATCCATTTTCGTCTTTCTACATAACCAATCTTCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCCATTTCTATGGAAAA
ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAAGATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCT
GGTTTCAAAAGGGACGGCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGACCTGGGGTTTCACTCCGGGAAGGGTCTA
TATAAAGGAATTATACCAATCATTCCCCTGGACTTTATGGGGCTATCTTTCAGAGGGGGGCGAACTAAACCCCTTCAATGGGTACCGGAGTCCAAATGGAAAG
AATTAAAACCTTTTCCTAAACCAAAAAAGGCCTATTAGAAGAAAATTGGGATACCCCTTGGTCCAAAAATTATTCCCCCCTGGGGTTTGGGAACATTGGGGGT
TAAAAGCGAAAATTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAGCCGGGTTTGGACTGATTTATCAGATTCGGATATTATTGACCGATTTGGGCGT
ATATGCAGAAATCTTTCTCATTATCATAGCGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCTTGTGCTAAAACTTTAGCTCG
GAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTAGGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTCCCA
AGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTAAATTTGGTATTTGGTTATTATCACTGATCTGGTGAATCAGCAATGATTCATATTCATTCT
GAGACCTTGTAAATGGATTTAAGCCTTAAATGAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTGAAATGTTGATGTAGCATGTAATAAGGGTTAAATC
AACTGACTATTCTGCTTTTTAAATTAAAGTCTTTAAAAGGAAACA

>*mat*K-Sb2

ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGCTTTCTATATCAACTTCCTCTTCTAACAAAGAGTATATTTATCCACTAACTCAT
GATCATAGCTTAAAAAGCGATCTATTTTGGTGAAACCGAAAATCCCGGTGTCTGAGAAAATCTCAGGTTAAATGATAATAAATCCAAAACGTTTTCTAGGATT
GTGAAACTACTGTTTAATTACGCGAATGTATCAACAGTTAAATCATTTTTTTATGATACAAGGTTTTTCTAATGATTCTAAACAAAATCGATTTTTATTTTTGGG
CCACAGCAAGAATTTGTATTCTCAAATGATATCCGAGGGATTTTCCTTTATTGTGGAAATTCGTTTTTTAAACGGATTACTATCTTCTTCTAGAGAAGAAGAGG
AAAGGGGAATCCAAATTCCAGAATTCACATTTACGCCAAATTCATTCAATATTTCCTTTCTTAGAGGACAAATTTTCACATCTAAATTATGTGTTAGATATACT
AATACCCCACCCCGTCCATCTGGAAATCCTGGTTCAAACCCTTCGCTAATGGGTAAAAGATGCCTCTTCTTTGCATTTATTACGATTCTTTTTCTACGAGTATT
GTAATTATTGTAATTGGAATAATCTTATTTCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAACGAAATAAAAGATTATTCTTCTTCTTAAATAATCCTTAAG
TATGTGAATACGAATCCATTTTCGTCTTTCTACATAACCAATCTTCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCCATTTCTATGGAAAA
ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAAGATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCT
GGTTTCAAAAGGGACGGCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGACCTGGGGTTTCACTCCGGGAAGGGTCTA
TATAAAGGAATTATACCAATCATTCCCCTTGACTTTATGGGGCTATCTTTCAGAGGGGGGCCAACTAAACCCCTTCAATGGGTACCGGAGTCCAAATGGATAA
AATTAAAACATTTTCCTAAACCAAAAAAGCCCTATTAGAGAAAATTTGGGAAACCCCTTGGTCCAAAAATTATTCCCCCCTGGGGTTTGGGAACATTGGGGGT
TAAAAACGAAAATTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAGCCGGGTTTGGACTGATTTATCAGATTCGGATATTATTGACCGATTTGGGCGT
ATATGCAGAAATCTTTCTCATTATCATAGCGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCTTGTGCTAAAACTTTAGCTCG
GAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTAGGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTCCCA
AGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTAAATTTGGTATTTGGTTATTATCACTGATCTGGTGAATCAGCAATGATTCATATTCATTCT
GAGACCTTGTAAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTGAAATGTTGATGTAGCATGTAATAAGGGTTAAATC
AACTGACTATTCTGCTTTTTAAACTAAAGTCTTTAAAAGGAAACA

>*mat*K-Sb3

ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGCTTTCTATACCAACTTCCTCTTCTAACAAAGAGTATATTTATCCACTAACTCAT
GATCATAGCTTAAAAATCGATCTATTTTGGTGAAAGGGAAAATCCCGGTTAACCTAGGTGAAACCGGTTAGTTGATAATAAATCCAAAACGTTTTCTAGGATT
GTGAAACTACTGTTTAATTACGCGAATGTATCAACAGTTAAATCATTTTTTTATGATACAAGGTTTTTCTAATGATTCTAAACAAAATCGATTTTTATTTTTGGG

CCACAGCAAGAATTTGTATTCCCAAATGATATCCGAGGGATTTTCCCTTATTGTGGAAATTCGTTTTTTAAACGGATTACTATCTTCTTCTAGAGAAGAAGAGG
AAAGGGGAATTCAAATTCCAGAATTCACATTTACGCCCAATTCATTCAATATTTCCTTTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACT
AATACCCCACCCCGTCCATCTGGAAATCCTGGTCCAAACCCTTCGCTAATGGGTAAAAGATGCCTCTTCTTTGCATTTATTACGATTCTTTTTCTACGAGTATT
GTAATTATTGTAATTGGAATAATCTTATTTCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAACGAAATAAAAGATTATTCTTCTTCTTAAATAATCCTTAAG
TATGTGAATACGAATCCATTTTCGTCTTTCTACATAACCAATCTTCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCCATTTCTATGGAAAA
ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAAGATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCT
GGTTTCAAAAGGGACGGCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGACCTGGGGTTTCACTCCGGGAAGGGTCTA
TATAAAGGAATTATACCCATCATTCCCCTTGACTTTATGGGGCTATCTTTCAGAAGGGGGCCAACTAAACCCCTTCAATGGGTACCGGAGTCCAAATGGATAA
AATTAAAACATTTTCCTAAACCAAAAAAGGCCTATTAGGGAAAAATTGGGAAACCCCTTGGTCCAAAAATTATTCCCCCCTGGGGTTTGGGAACATTGGGGGT
TAAAAGCGAAAATTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAGCCGGGTTTGGACTGATTTATCAGATTCGGATATTATTGACCGATTTGGGCGT
ATATGCAGAAATCTTTCTCATTATCATAGCGGATCTTCCAAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCTTGTGCTAAAACTTTAGCTCG
GAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTAGGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTCCCA
AGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTAAATTTGGTATTTGGTTATTATCACTGATCTGGTGAATCAGCAATGATTCATATTCATTCT
GAGACCTTGTAAATGGATTTAAGCCTAAACTAAAATGATGAAGATGAAGAAAAAGTTTTCTACTATTCTGAAATGTTGATGTAGCATGTAATAAGGGTTAAATC
AACTGACTATTCTGCTTTTTAAATTAAAATCTTTAAAAGGAAACA

>*mat*K-Sb4

ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGCTTTCTATATCAACACGTTTCTCTAAAGAAGAGTATATTTATGCATTTGCTCAT
GATCATAGCTTAAAAACCGATCTATTTTGTTGAAAGGGAAAATCCCGGTTTTGTTGGAAAATCCAGGTTAGTTGATAATAAATCCAAAACGTTTTCTAGGATTG
TGAAACTACTGTTTAATTACGCGAATGTATCAACAGTTAAATCATTTTTTTATGATACAAGGTTTTTCTAATGATTCTAAACAAAATCGATTTTTATTTTTGGGC
CACAGCAAGAATTTGTATTCCCAAATGATATCCGAGGGATTTCCCTTTATTGTGGAAATTCGTTTTTTAAACGGATTACTATCTTCTTCTAGAGAAGAAGAGGA
AAGGGGTATTCAAATTCCAGAATTCACATTCACGCCCAATTCATTCAATATTTCCTTTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTA
ATACCCCACCCCGTCCATCTGGAAATCCTGGTTCAAACCCTTCGCTAATGGGTAAAAGATGCCTCTTCTTTGCATTTATTACGATTCTTTTTCTACGAGTATTG
TAATTATTGTAATTGGAATAATCTTATTTCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAACGAAATAAAAGATTATTCTTCTTCTTAAAAAATCCTTAAGT
ATGTGAATACGAATCCATTTTCGTCTTTCTACATAACCAATCTTCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCCATTTCTATGGAAAAA
TAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAAGATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTG
GTTTCAAAAGGGACGGCTCCTTTGATGAATAAATGGAAATCTTACCTTGGCAATTTTTGGCAATGTCATTTTGACCTGGGGTTTCACTCCGGGAAGGGTCTAT
ATAAAGGAATTATACCAATCATTCCCCTTGACTTTATGGGGCTATCTTTCAGAAGGGGGGCGACTAAACCCCTTCAATGGGTACCGGAGTCCAAATGGAAAGA
ATTAAAACATTTTCCCAAACCAAAAAAGGCCTATTAGGAGAAAATTGGGAAACCCCTTGGTCCAAAAATTATTCCCCCCTGGGGGGTGGGAACATTGGGGGTT
AAAAGCGAAAATTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAGCCGGGTTTGGACTGATTTATCAGATTCGGATATTATTGACCGATTTGGGCGTA
TATGCAGAAATCTTTCTCATTATCATAGCGGATCTTCCAAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCTTGTGCTAAAACTTTAGCTCGG
AAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTAGGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTCCCAA
GAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTAAATTTGGTATTTGGATATTATCACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTG
AGACCTTGTAAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTGAAATGTTGATGTAGCATGTAATAAGGGTTAAATCA
ACTGACTATTCTGCTTTTTGAAATAAAGTCTTAAAAAGGAAACA

The multiple sequence alignment of *mat*K gene

```
matK-Sv3        ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGGCTTTCTATA 60
matK-Sv5        ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGGCTTTCTATA 60
matK-Sv2        ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGGCTTTCTATA 60
matK-Sv4        ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGGCTTTCTATA 60
matK-Sv1        ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGGGCTTTCTATA 60
matK-Sl2        ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGG-CTTTCTATA 59
matK-Sl3        ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGG-CTTTCTATA 59
matK-sl1        ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGG-CTTTCTATA 59
matK-Sb1        ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGG-CTTTCTATA 59
matK-Sb2        ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGG-CTTTCTATA 59
matK-Sb3        ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGG-CTTTCTATA 59
matK-Sb4        ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGG-CTTTCTATA 59
matK-St1        ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGG-CTTTCTATA 59
matK-St4        ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGG-CTTTCTATA 59
matK-St3        ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGG-CTTTCTATA 59
matK-St2        ATGGAGGAAATCCAAAGATATTTACAGCTTGATAGATCTCAACAACACGG-CTTTCTATA 59
                ************************************************* *********

matK-Sv3        TCAACACTTCTCTTTCAAGAAGAGTATATTT-ATGCATTTACTCATGATCATAGTTTAAA 119
matK-Sv5        TCAACACTTCTCTTTCAAGAAGAGTATATTT-ATGCATTTGCTCATGATCATAGTTTAAA 119
matK-Sv2        TCAACACTTCTCTTTCAAGAAGAGTATATTT-ATGCATTTGCTCATGATCATAGATTAAA 119
matK-Sv4        TCAACACTTCTCTTTCAAGAAGAGTATATTT-ATGCATTTGCTCATGATCATAGTTTAAA 119
matK-Sv1        TCAACACTTCTCTTTCAAGAAGAGTATATTT-ATGCATTTGCTCATGATCATAGCTTAAA 119
matK-Sl2        TCAACACTTCTCTTTCAAGAAGAGTAGATTT-ATGCATTTGCTCATGATCATAGCTTAAA 118
matK-Sl3        TCAACACTTCTCTTTCAAGAAGAGTAGATTT-ATGCATTTGCTCATGATCATAGCTTAAA 118
matK-sl1        TCAACACTTCTCTTTCAAGAAGAGTATATTT-ATGCATTTGCTCATGATCATAGCTTAAA 118
matK-Sb1        TCAACTTCCTCTTCTAACAAAGAGTATATTT-ATCCACTAACTCATGATCATAGCTTAAA 118
matK-Sb2        TCAACTTCCTCTTCTAACAAAGAGTATATTT-ATCCACTAACTCATGATCATAGCTTAAA 118
matK-Sb3        CCAACTTCCTCTTCTAACAAAGAGTATATTT-ATCCACTAACTCATGATCATAGCTTAAA 118
matK-Sb4        TCAACACGTTTCTCTAAAGAAGAGTATATTT-ATGCATTTGCTCATGATCATAGCTTAAA 118
matK-St1        TCAACACTTCTCTTTCAAGAAGAGTATATTTTATGCACTTGCTCATGATCATAGCTTAAA 119
matK-St4        TCAACACTTCTCTTTCAAGAAGAGTATATTTTATGCACTTGCTCATGATCATAGCTTAAA 119
matK-St3        TCAACACTTCTCTTTCAAGAAGAGTATATTTTATGCACTTGCTCATGATCATAGCTTAAA 119
matK-St2        TCAACACTTCTCTTTCAAGAAGAGTATATTTTATGCACTTGCTCATGATCATAGCTTAAA 119
                 ****       * * *  ******* **** ** ** *  ************* *****

matK-Sv3        AACCGATCTATTTTGTTGGGAAGGAAAAGCCAGGCT-TTTTTGGAAAATCC-AGGGTAAT 177
matK-Sv5        AACCGGTCTATTTTGTTGGAAAGGAAAATCCAAGGT-TTTTTGGAAAATCC-AGGGTAAT 177
matK-Sv2        AACCGATCTATTTTGTTGGAATGGAAAACCCATGCT-TTTTTGGACAATCC-AGGGTAAT 177
matK-Sv4        AACCGGTCTATTTTGTTGGAATGGAAAATCCATGGT-TTTTTGGACAATCC-AGGGTAAT 177
matK-Sv1        AACCGATCTATTTTGTTGGAAGGGAAAATCCAGGTT-TTGTTGGACAATCC-AGGGTAGT 177
matK-Sl2        AACGGATCTATATTGTTGGACGGGAATTTCCAGATT-TTGTTGGACAACCC-AGGTTAGT 176
matK-Sl3        AACGGATCTATATTGTTGGACGGGAATTTCCAGATT-TTGTTGGACAACCC-AGGTTAGT 176
matK-sl1        AACCGATCTATTTTGTTGGAAGGGAAAATCCAGGTT-TTGTTGGACAATCC-AGGTTAGT 176
matK-Sb1        AAGCGATCTATTTTGGTGAAACCGAAAATCCCGGT--GTCTGAGAAAATCTCAGGTTAAA 176
matK-Sb2        AAGCGATCTATTTTGGTGAAACCGAAAATCCCGGT--GTCTGAGAAAATCTCAGGTTAAA 176
matK-Sb3        AATCGATCTATTTTGGTGAAAGGGAAAATCCCGGTTAACCTAGGTGAAACC--GGTTAGT 176
matK-Sb4        AACCGATCTATTTTGTTGAAAGGGAAAATCCCGGTT-TTGTTGGAAAATCC-AGGTTAGT 176
matK-St1        AACCGATCTATTTTGTTGGAAGGGAAAATCCAGGTT-ATGATAATAAATCC-AGGTTAGT 177
matK-St4        AACCGATCTATTTTGTTGGAAGGGAAAATCCACCTC-ATGATAATAAATCC-AGGTTAGT 177
matK-St3        AACCGATCTATTTTGTTGGAAGGGAAAATCGACATA-AGGGTCGCAGGTTC-AGGTTAGT 177
matK-St2        AACCGATCTATTTTGTTGGAAGGGAAAATCCAGGTT-ATGATGGAAAATCC-AGGTTAGT 177
                **  * ***** *** **     ***   *                      ** **

matK-Sv3        CGATAATAAGATCAAAACGTTATCTAAGGTGGTGAAACTAGTTTTTAATTACTCAAATGT 237
matK-Sv5        CGATAAAAAGATCAAAACGTTATCTAAGGTGGTGAAACTAGTTTTTAATTACTCAAATGT 237
matK-Sv2        CGATAATAAGATCAAAACGTTATCTAAGGTGGTGAAACTACTTTTTAATTACTCAAATGT 237
matK-Sv4        CGATAATAAGATCAAAACGTTATCTAAGGTGGTGAAACTAGTTTTTAATTACTCAAATGT 237
matK-Sv1        CGATAATAAGATCAAAACGTTATCTAAGGTGGTGAAACTACTTTTTAATTACTCAAATGT 237
matK-Sl2        TGATAATAAATCCAAAACGTTTTCTAAGATTGTGAAAATCCGTGTTAATTACTCGAATGT 236
matK-Sl3        TGATAATAAATCCAAAACGTTTTCTAAGATTGTGAAAATCCGTGTTAATTACTCGAATGT 236
matK-sl1        TGATAATAAATCCAAAACGTTTTCTAGGATTGTGAAACTACTTTTTAATTACTCGAATGT 236
matK-Sb1        TGATAATAAATCCAAAACGTTTTCTAGGATTGTGAAACTACTGTTTAATTACGCGAATGT 236
matK-Sb2        TGATAATAAATCCAAAACGTTTTCTAGGATTGTGAAACTACTGTTTAATTACGCGAATGT 236
matK-Sb3        TGATAATAAATCCAAAACGTTTTCTAGGATTGTGAAACTACTGTTTAATTACGCGAATGT 236
matK-Sb4        TGATAATAAATCCAAAACGTTTTCTAGGATTGTGAAACTACTGTTTAATTACGCGAATGT 236
matK-St1        AGGTACTAATTGTGAAACGTTTTCTAGGACTGGGTAATTACTGTTTAATTACGCGAATGT 237
matK-St4        AGGTAACCCTAGTGAAACGTTTTCTAGGAGTGGGTAATAACTGTTTAATTACGCGAATCT 237
matK-St3        AGGTATCCCTACTAAATCGTTTTCTAGGACTGGGTAATAACTGTTTAATTACGCGAATGT 237
matK-St2        AGATACTAATTGTAAAACGTTTTCTAGGACTGTGTAATTACTGTTTAATTACGCGAATGT 237
                 * **         ** **** **** *   * * **       ******** * *** *
```

```
matK-Sv3        AAAAACATTTAAGTCAAGTTTACAAGATTTTTTTGATTTTTCTAATGATTCTAAACAAAA 297
matK-Sv5        AAAAACATTTAAGTCAAGTTTAACAGATTTTTTTGATTTTTATAATGATTCTAAACAAAA 297
matK-Sv2        AAAAACAGTTAAGTCAAGTTTACATGATTTTTTTGATTTTTCTAATGATTCTAAACAAAA 297
matK-Sv4        AAAAACAGTTAAGTCAAGTTTACATGATTTTTTTGATTTTACTAATGATTCTAAACAAAA 297
matK-Sv1        AAAAACAGTTAAGTCAAGTTTACATGATTTTTTTGATTTTTCTAATGATTCTAAACAAAA 297
matK-Sl2        ATCAACAGTTAAATCATTTCTTTATGATACAA--GGTTTTTCTAATGATTCTAAACAAAA 294
matK-Sl3        ATCAACAGTTAAATCATTTTTTTATGATACAA--GGTTTTTCTAATGATTCTAAACAAAA 294
matK-sl1        ATCAACAGTTAAATCATTTTTTTATGATACAA--GGTTTTTCTAATGATTCTAAACAAAA 294
matK-Sb1        ATCAACAGTTAAATCATTTTTTTATGATACAA--GGTTTTTCTAATGATTCTAAACAAAA 294
matK-Sb2        ATCAACAGTTAAATCATTTTTTTATGATACAA--GGTTTTTCTAATGATTCTAAACAAAA 294
matK-Sb3        ATCAACAGTTAAATCATTTTTTTATGATACAA--GGTTTTTCTAATGATTCTAAACAAAA 294
matK-Sb4        ATCAACAGTTAAATCATTTTTTTATGATACAA--GGTTTTTCTAATGATTCTAAACAAAA 294
matK-St1        ATCAACAGTTAAATCATTTTTTTATGATACAA--GGTTTTTCTAATAATTCTAAGCAAAA 295
matK-St4        ATCAACAGTTAAATCATTTTTTTATGATACAA--GGTTTATCTAATGATTCTAAGCAAAA 295
matK-St3        ATCAACAGTTAAATCATTTTTTTATGATACAA--GGTTTTTCTAATGATTCTAAGCAAAA 295
matK-St2        ATCAACAGTTAAATCATTTTTTTATGATACAA--GGTTTTTCTAATGATTCTAAGCAAAA 295
                *  **** **** ***  * *    ***      * ***   **** ******* *****

matK-Sv3        TCGATTTTTATTTTTGGGGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATT 357
matK-Sv5        TCGATTTTTATTTTTGGGGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATT 357
matK-Sv2        TCGATTTTTATTTTTGGGGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATT 357
matK-Sv4        TCGATTTTTATTTTTGGGGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATT 357
matK-Sv1        TCGATTTTTATTTTTGGGGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATT 357
matK-Sl2        TCGATTTTTATTTTTGGGCCACAGCAAGAATTGGTATTACCAAATGATATCAAAGGGATT 354
matK-Sl3        TCGATTTTTATTTTTGGGCCACAGCAAGAATTTGTATTACCAAATGATATCAAAGGGATT 354
matK-sl1        TCGATTTTTATTTTTGGGGCACAGCAAGAATTTGTATTATCAAATGATATCAGAGGGATT 354
matK-Sb1        TCGATTTTTATTTTTGGGCCACACCAAGAATTTGTATTCCCAAATGATATCCGAGGGATT 354
matK-Sb2        TCGATTTTTATTTTTGGGCCACAGCAAGAATTTGTATTCTCAAATGATATCCGAGGGATT 354
matK-Sb3        TCGATTTTTATTTTTGGGCCACAGCAAGAATTTGTATTCCCAAATGATATCCGAGGGATT 354
matK-Sb4        TCGATTTTTATTTTTGGGCCACAGCAAGAATTTGTATTCCCAAATGATATCCGAGGGATT 354
matK-St1        TCGATTTTTATTTTTGGGGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATT 355
matK-St4        TCGATTTTTATTTTTGGGGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATT 355
matK-St3        TCGATTTTTATTTTTGGGGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATT 355
matK-St2        TCGATTTTTATTTTTGGGGCACAGCAAGAATTTGTATTCTCAAATGATATCAGAGGGATT 355
                ****************** **** ******** *****  ***********  *******

matK-Sv3        TTCCTTTATTGTGGAAATGTCGTTTTCTAGAAGGATTACTATCTTCTTCTAGAGAAGAAA 417
matK-Sv5        TTCCTTTATTGTGGAAATGTCGTTTTCTAGAAGGATTACTATCTTCTTCTAGAGAAGAAA 417
matK-Sv2        TTCCTTTATTGTGGAAATGTCGTTTTCTAGAAGGATTACTATCTTCTTCTAGAGAAGAAA 417
matK-Sv4        TTCCTTTATTGTGGAAATGTCGTTTTCTAGAAGGATTACTATCTTCTTCTAGAGAAGAAA 417
matK-Sv1        TTCCTTTATTGTGGAAATGTCGTTTTCTAAAAGGATTACTATCTTCTTCTAGAGAAGGAG 417
matK-Sl2        TTCCCTTATTGTGGAAAT-TCGTTTTCTAAACGGATTACTATCTTCTTCTAGAGAAGAAG 413
matK-Sl3        TTCCCTTATTGTGGAAAT-TCGTTTTCTAAACGGATTACTATCTTCTTCTAGAGAAGAAG 413
matK-sl1        TTCCTTTATTGTGGAAAT-TCGTTTTCTAAACGGATTACTATCTTCTTCTAGAGAAGAAG 413
matK-Sb1        TTCCTTTATTGTGGAAAT-TCGTTTTTTAAACGGATTACTATCTTCTTCTAGAGAAGAAG 413
matK-Sb2        TTCCTTTATTGTGGAAAT-TCGTTTTTTAAACGGATTACTATCTTCTTCTAGAGAAGAAG 413
matK-Sb3        TTCCCTTATTGTGGAAAT-TCGTTTTTTAAACGGATTACTATCTTCTTCTAGAGAAGAAG 413
matK-Sb4        TCCCTTTATTGTGGAAAT-TCGTTTTTTAAACGGATTACTATCTTCTTCTAGAGAAGAAG 413
matK-St1        TTCCTTTATTGTGGAAAT-TCGTTTTTTAAACGGATTACTATCTTCTTCTATAGAAGAAG 414
matK-St4        TTCCTTTATTGTGGAAAT-TCGTTTTTTAAACGGATTACTATCTTCTTCTATAGAAGAAG 414
matK-St3        TTCCTTTATTGTGGAAAT-TCGTTTTTTAAACGGATTACTATCTTCTTCTATAGAAGAAG 414
matK-St2        TTCCTTTATTGTGGAAAT-TCGTTTTTTAAACGGATTACTATCTTCTTCTATAGAAGAAG 414
                * ** ************* ******* ** * ******************** ***** *

matK-Sv3        GGGAAAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCT 477
matK-Sv5        GGGAAAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCT 477
matK-Sv2        GGGAAAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCT 477
matK-Sv4        GGGAAAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCT 477
matK-Sv1        GGGAAAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCT 477
matK-Sl2        AGGAAAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCT 473
matK-Sl3        AGGAAAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCT 473
matK_sl1        AGGAAAGGGGTATTCAAATTACAGAATTCACATTTATGCTCAATTCATTCAATATTTCCT 473
matK-Sb1        AGGATAGGGGAAATTCAAATCCCAAATTCACATTTACGCCCAATTCATTCAATATTTCCT 473
matK-Sb2        AGGAAAGGGGAATCCAAATTCCAGAATTCACATTTACGCCAAATTCATTCAATATTTCCT 473
matK-Sb3        AGGAAAGGGGAATTCAAATTCCAGAATTCACATTTACGCCCAATTCATTCAATATTTCCT 473
matK-Sb4        AGGAAAGGGGTATTCAAATTCCAGAATTCACATTCACGCCCAATTCATTCAATATTTCCT 473
matK-St1        AGGAAAGGGGTATTCAAATTACAGAATTTACATTTACGCTCAATTCATTCAATAATTCCT 474
matK-St4        AGGAAAGGGGTATTCAAATTACAGAATTTACATTTACGCTCAATCCATTCAATATTTCCT 474
matK-St3        AGGAAAGGGGTATTCAAATTACAGAATTCACATTTACGCTCAATTCATTCAATATTTCCT 474
matK-St2        AGGAAAGGGGTATTCAAATTACAGAATTTACATTTACGCTCAATTCATTCAATATTTCCT 474
                 *** ***** *    ** * *  **** ***** * **  *** ********* *****
```

```
matK-Sv3        TTCTTAGAGGACAACTTTTCACATCTCAATTATGTGTTAGATATACTAATACCCCACCCC 537
matK-Sv5        TTCTTAGAGGACAACTTTTCACATCTCAATTATGTGTTAGATATACTAATACCCCACCCC 537
matK-Sv2        TTCTTAGAGGACAACTTTTCACATCTCAATTATGTGTTAGATATACTAATACCCCACCCC 537
matK-Sv4        TTCTTAGAGGACAACTTTTCACATCTCAATTATGTGTTAGATATACTAATACCCCACCCC 537
matK-Sv1        TTCTTAGAGGACAACTTTTCACATCTCAATTATGTGTTAGATATACTAATACCCCACCCC 537
matK-Sl2        TTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTAATACCCCACCCC 533
matK-Sl3        TTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTAATACCCCACCCC 533
matK_sl1        TTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTAATACCCCACCCC 533
matK-Sb1        TTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTAATACCCCAACCC 533
matK-Sb2        TTCTTAGAGGACAAATTTTCACATCTAAATTATGTGTTAGATATACTAATACCCCACCCC 533
matK-Sb3        TTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTAATACCCCACCCC 533
matK-Sb4        TTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTAATACCCCACCCC 533
matK-St1        TTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTAATACCCCACCCC 534
matK-St4        TTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTAATACCCCACCCC 534
matK-St3        TTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTAATACCCCACCCC 534
matK-St2        TTCTTAGAGGACAACTTTTCACATCTAAATTATGTGTTAGATATACTAATACCCCACCCC 534
                ************** *********** ***************************** ***

matK-Sv3        GTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTG 597
matK-Sv5        GTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTG 597
matK-Sv2        GTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTG 597
matK-Sv4        GTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTG 597
matK-Sv1        GTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTG 597
matK-Sl2        GTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTG 593
matK-Sl3        GTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTG 593
matK_sl1        GTACATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCTTCTTTG 593
matK-Sb1        GTCCATCTGGAAATCCTGGTTCAAACCCTTCGCTAATGGGTAAAAGATGCCTCTTCTTTG 593
matK-Sb2        GTCCATCTGGAAATCCTGGTTCAAACCCTTCGCTAATGGGTAAAAGATGCCTCTTCTTTG 593
matK-Sb3        GTCCATCTGGAAATCCTGGTCCAAACCCTTCGCTAATGGGTAAAAGATGCCTCTTCTTTG 593
matK-Sb4        GTCCATCTGGAAATCCTGGTTCAAACCCTTCGCTAATGGGTAAAAGATGCCTCTTCTTTG 593
matK-St1        GTCCATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCCTCTTTG 594
matK-St4        GTCCATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCCTCTTTG 594
matK-St3        GTCCATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCCTCTTTG 594
matK-St2        GTCCATCTGGAAATCCTGGTTCAAACCCTTCGCTATTGGGTAAAAGATGCCTCCTCTTTG 594
                ** ***************** ************** ***************** ******

matK-Sv3        CATTTATTACGATTCTTTCTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 657
matK-Sv5        CATTTATTACGATTCTTTCTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 657
matK-Sv2        CATTTATTACGATTCTTTCTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 657
matK-Sv4        CATTTATTACGATTCTTTCTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 657
matK-Sv1        CATTTATTACGATTCTTTCTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 657
matK-Sl2        CATTTATTACGATTCTTTCTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 653
matK-Sl3        CATTTATTACGATTCTTTCTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 653
matK_sl1        CATTTATTACGATTCTTTCTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 653
matK-Sb1        CATTTATTACGATTCTTTTTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 653
matK-Sb2        CATTTATTACGATTCTTTTTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 653
matK-Sb3        CATTTATTACGATTCTTTTTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 653
matK-Sb4        CATTTATTACGATTCTTTTTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 653
matK-St1        CATTTATTACGATTCTTTCTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 654
matK-St4        CATTTATTACGATTCTTTCTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 654
matK-St3        CATTTATTACGATTCTTTCTCTACGAGTATTGTAATGATTGTAATTGGAATAATCTTATT 654
matK-St2        CATTTATTACGATTCTTTCTCTACGAGTATTGTAATTATTGTAATTGGAATAATCTTATT 654
                ****************** ***************** ************************

matK-Sv3        TCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTC 717
matK-Sv5        TCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTC 717
matK-Sv2        TCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTC 717
matK-Sv4        TCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTC 717
matK-Sv1        TCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTC 717
matK-Sl2        TCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTC 713
matK-Sl3        TCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTC 713
matK_sl1        TCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAAAGAAATAAAAGATTATTCTTCTTC 713
matK-Sb1        TCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAACGAAATAAAAGATTATTCTTCTTC 713
matK-Sb2        TCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAACGAAATAAAAGATTATTCTTCTTC 713
matK-Sb3        TCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAACGAAATAAAAGATTATTCTTCTTC 713
matK-Sb4        TCTACAAAGAAACCCAGTTTTTCTTTTTTAACAAAACGAAATAAAAGATTATTCTTCTTC 713
matK-St1        GCTACAAAGAAACCCAGTTTTTCTTTTTTACCAAAAAGAAATAAAAGATTATTCTTCTTC 714
matK-St4        GCTACAAAGAAACCCAGTTTTTCTTTTTTACCAAAAAGAAATAAAAGATTATTCTTCTTC 714
matK-St3        GCTACAAAGAAACCCAGTTTTTCTTTTTTACCAAAAAGAAATAAAAGATTATTCTTCTTC 714
matK-St2        GCTACAAAGAAACCCAGTTTTTCTTTTTTACCAAAAAGAAATAAAAGATTATTCTTCTTC 714
                 **************************** ***** ************************
```

```
matK-Sv3        TTAAATAATTCTTAATAAGGTCAATACGAATCCATTTTCGTCTTTCTACATAACCAATCT 777
matK-Sv5        TTAAATAATTCTTAAGTAGGTCAATACGAATCCATTTTCGTCTTTCTACATAACCAATCT 777
matK-Sv2        TTAAATAATTCTTAAGTAGGTCAATACGAATCCATTTTCGTCTTTCTACATAACCAATCT 777
matK-Sv4        TTAAATAATTCTTAAGTAGGTCAATACGAATCCATTTTCGTCTTTCTACATAACCAATCT 777
matK-Sv1        TTAAATAATTCTTAAGTAGGTCAATACGAATCCATTTTCGTCTTTCTACATAACCAATCT 777
matK-Sl2        TTAAATAATTCTTAAGTATGTGAATACGAATCCATTTTCGTCTTTCTACATAACCAATCT 773
matK-Sl3        TTAAATAATTCTTAAGTATGTGAATACGAATCCATTTTCGTCTTTCTACATAACCAATCT 773
matK_sl1        TTAAATAATTCTTAAGTATGTGAATACGAATCCATTTTCGTCTTTCTACATAACCAATCT 773
matK-Sb1        TTAAAAAATCCTTAAGTATGTGAATACGAATCCATTTTCGTCTTTCTACATAACCAATCT 773
matK-Sb2        TTAAATAATCCTTAAGTATGTGAATACGAATCCATTTTCGTCTTTCTACATAACCAATCT 773
matK-Sb3        TTAAATAATCCTTAAGTATGTGAATACGAATCCATTTTCGTCTTTCTACATAACCAATCT 773
matK-Sb4        TTAAAAAATCCTTAAGTATGTGAATACGAATCCATTTTCGTCTTTCTACATAACCAATCT 773
matK-St1        TTATAAAATTCTTATGTATGTGAATACGAATCCATTTGCCTATTACTACATAACCAATCT 774
matK-St4        TTATATAATTCTTATGTATGTGAATACGAATCCATTTTCCTCTTTCTACATAACCAATCT 774
matK-St3        TTAAATAATTCTTATGTATGTGAATACGAATCCATTTTCCTCTTTCTACATAACCAATCT 774
matK-St2        TTATATAATTCTTATGTATGTGAATACGAATCCATTTTCCTCTTTCTACATAACCAATCT 774
                *** * *** ****   * ** *************** * * ** ***************

matK-Sv3        TCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATGGAAAA 837
matK-Sv5        TCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATGGAAAA 837
matK-Sv2        TCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATGGAAAA 837
matK-Sv4        TCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATGGAAAA 837
matK-Sv1        TCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATGGAAAA 837
matK-Sl2        TCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATGGAAAA 833
matK-Sl3        TCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATGGAAAA 833
matK_sl1        TCTCATTTACGATCAACATCCTTTGAGGCCCTTCTTGAACGAATCCATTTCTATGGAAAA 833
matK-Sb1        TCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCCATTTCTATGGAAAA 833
matK-Sb2        TCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCCATTTCTATGGAAAA 833
matK-Sb3        TCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCCATTTCTATGGAAAA 833
matK-Sb4        TCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCCATTTCTATGGAAAA 833
matK-St1        TCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCTATTTCTATGGAAAA 834
matK-St4        TCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCTATTTCTATGGAAAA 834
matK-St3        TCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCTATTTCTATGGAAAA 834
matK-St2        TCTCATTTACGATCAACATCCTTTGAGGTCCTTCTTGAACGAATCTATTTCTATGGAAAA 834
                **************************** ***************** **************

matK-Sv3        ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAA 897
matK-Sv5        ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAA 897
matK-Sv2        ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAA 897
matK-Sv4        ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAA 897
matK-Sv1        ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAA 897
matK-Sl2        ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAA 893
matK-Sl3        ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAA 893
matK_sl1        ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAA 893
matK-Sb1        ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAA 893
matK-Sb2        ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAA 893
matK-Sb3        ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAA 893
matK-Sb4        ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAGGCCAAACTATGGTTGTTCAAA 893
matK-St1        ATAGAACGTCTTGTAGAAGTCTTAGCTAAGGATTATCAAGCCAAACTACGGATGTACAAA 894
matK-St4        ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAAGCCAAACTACGGTTGTTCAAA 894
matK-St3        ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAAGCCAAACTACGGTTGTTCAAA 894
matK-St2        ATAGAACGTCTTGTAGAAGTCTTTGCTAAGGATTATCAAGCCAAACTACGGTTGTTCAAA 894
                ********************** ************** ********* ** *** ****

matK-Sv3        GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 957
matK-Sv5        GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 957
matK-Sv2        GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 957
matK-Sv4        GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 957
matK-Sv1        GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 957
matK-Sl2        GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAGGGGACG 953
matK-Sl3        GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 953
matK_sl1        GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 953
matK-Sb1        GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 953
matK-Sb2        GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 953
matK-Sb3        GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 953
matK-Sb4        GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 953
matK-St1        GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 954
matK-St4        GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 954
matK-St3        GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 954
matK-St2        GATCCTTTCATACATTATGTTAGGTATCAAGGAAAATTCATTCTGGTTTCAAAAGGGACG 954
                ************************************************** ******
```

```
matK-Sv3        GCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGAC 1017
matK-Sv5        GCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGAC 1017
matK-Sv2        GCTCCTTTGATGAATAAATGGAAATCTTACCTTGGCAATTTTTGGCAATGTCATTTTGAC 1017
matK-Sv4        GCTCCTTTGATGAATAAATGGAAATCTTACCTTGGCAATTTTTGGCAATGTCATTTTGAC 1017
matK-Sv1        GCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGAC 1017
matK-Sl2        GCTCCTTTGATGAATAAATGGAAATCTTACCTTGGCAATTTTTGGCAATGTCATTTTGAC 1013
matK-Sl3        GCTCCTTTGATGAATAAATGGAAATCTTACCTTGGCAATTTTTGGCAATGTCATTTTGAC 1013
matK-sl1        GCTCCTTTGATGAATAAATGGAAATCTTACCTTGGCAATTTTTGGCAATGGCATTTTGAC 1013
matK-Sb1        GCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGAC 1013
matK-Sb2        GCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGAC 1013
matK-Sb3        GCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGAC 1013
matK-Sb4        GCTCCTTTGATGAATAAATGGAAATCTTACCTTGGCAATTTTTGGCAATGTCATTTTGAC 1013
matK-St1        GCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGAC 1014
matK-St4        GCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGTCATTTTGAC 1014
matK-St3        GCTCCTTTGATGAATAAATGGAAATCTTACCTTGGCAATTTTTGGCAATGTCATTTTGAC 1014
matK-St2        GCTCCTTTGATGAATAAATGGAAATCTTACCTTGTCAATTTTTGGCAATGGCATTTTGAC 1014
                ********************************** *************** *********

matK-Sv3        CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACCAATCATTCCCTTTGAC 1077
matK-Sv5        CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACAAAACATTCCCTTTGAC 1077
matK-Sv2        CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACCAATCATTCCCTTTGAC 1077
matK-Sv4        CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACCAATCATTCCCTTTGAC 1077
matK-Sv1        CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACCAATCATTCCCTTTGAC 1077
matK-Sl2        CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACCAATCATTCCCCTGGAC 1073
matK-Sl3        CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACCAATCATTCCCCTGGAC 1073
matK-sl1        CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACCAATCATTCCCTTTGAC 1073
matK-Sb1        CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACCAATCATTCCCCTGGAC 1073
matK-Sb2        CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACCAATCATTCCCCTTGAC 1073
matK-Sb3        CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACCCATCATTCCCCTTGAC 1073
matK-Sb4        CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACCAATCATTCCCCTTGAC 1073
matK-St1        CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGCACTATACAAATCATTCCCCTTGAC 1074
matK-St4        CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACAAACCATTCCCCTGGAC 1074
matK-St3        CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACAAATCATTCCCCTTGAC 1074
matK-St2        CTGGGGTTTCACTCCGGGAAGGGTCTATATAAAGGAATTATACCAATCATTCCCCTTGAC 1074
                ********************************** * *****  * ******* * ***

matK-Sv3        TTTATGGGGCTATCTTTTAGAAGTGGCGCGTCTAAACCCTTTCAATGGGTACGGAAGTCC 1137
matK-Sv5        TTTATGGGGCTATCTTTTAGAAGTGGCGCGTCTAAACCCTTTCAATGGGTACCGAAGTCC 1137
matK-Sv2        TTTATGGGGCTATCTTTTAGAAGTGGCGCGTCTAAACCCTTTCAATGGGTACGGAAGTCC 1137
matK-Sv4        TTTATGGGGCTATCTTTTAGAAGTGGCGCGTCTAAACCCTTTCAATGGGTACGGAAGTCC 1137
matK-Sv1        TTTATGGGGCTATCTTTTAGAAGTGGCGCGTCTAAACCCTTTCAATGGGTACGGGAGTCC 1137
matK-Sl2        TTTATGGGGCTATCTTTCAGAAGGGGTCCGACTAAACCTTTTCAATGGGTACGGGAGTCC 1133
matK-Sl3        TTTATGGGGCTATCTTTCAGAAGGGGTCCGACTAAACCTTTTCAATGGGTACGGGAGTCC 1133
matK-sl1        TTTATGGGGCTATCTTTCAGAAGGGGTCCGACTAAACCTTTTCAATGGGTACGGGAGTCC 1133
matK-Sb1        TTTATGGGGCTATCTTTCAGAGGGGGGGCGAACTAAACCCCTTCAATGGGTACCGGAGTCC 1133
matK-Sb2        TTTATGGGGCTATCTTTCAGAGGGGGGGCCAACTAAACCCCTTCAATGGGTACCGGAGTCC 1133
matK-Sb3        TTTATGGGGCTATCTTTCAGAAGGGGGGCCAACTAAACCCCTTCAATGGGTACCGGAGTCC 1133
matK-Sb4        TTTATGGGGCTATCTTTCAGAAGGGGGGCGACTAAACCCCTTCAATGGGTACCGGAGTCC 1133
matK-St1        TTTATGGGGCTATCTTTCAGGAGTCTGGCGACTAAACCCCTTCAATGGTTACCGGAGTCC 1134
matK-St4        TTTATGGGGCTATCTTTCAGAAGTGTGGCGACTAAACCCTTTCAATGGGTACCGGAGTCC 1134
matK-St3        TTTATGGGGCTATCTTTCAGAAGTTTGGCGACTAAACCCCTTCAATGGTTACCGGAGTCC 1134
matK-St2        TTTATGGGGCTATCTTTCAGAAGTGTGGCGACTAAACCCTTTCAATGGGTACGGGAGTCC 1134
                ***************** **  *        *******  ******** *** * *****

matK-Sv3        AAATGAAAAGAATTAATTCATTTTC-TAATCCAAATAAGGGCTATTATAGGAAAATTGGG 1196
matK-Sv5        AAATGAAAAGAATTAATTCATTTTC-TAATCCAAACAAGGACTTATATAGGAAAATTGGG 1196
matK-Sv2        AAATGAAAAGAATTAATTCATTTTC-TAATCCAAATAAGGGCTATTATAGGAAAATTGGG 1196
matK-Sv4        AAATGAAAAGAATTAATTCATTTTC-TAATCCAAATAAGGGCTATTATAGGAAAATTGGG 1196
matK-Sv1        AAATGAAAAGAATTAAAACATTTCC-TAACCCAAAAAAGGGCTATTATAGGAAAATTGGA 1196
matK-Sl2        AAATGGAAAGAATTTAAACATTTCC-TAAACCAAATAATGCCCATTAGGAAAAAAATGGG 1192
matK-Sl3        AAATGGAAAGAATTTAAACATTTCC-TAAACCAAATAATGCCCATTAGGAAAAAAATGGG 1192
matK-sl1        AAATGGAAAGAATTTAAACATTTCC-CAAACCAAATAATGGCTATTAGGAAAAAAATGGG 1192
matK-Sb1        AAATGGAAAGAATTAAAACCTTTTCCTAAACCAAAAAAGGCCTATTAGAAGAAAATTGGG 1193
matK-Sb2        AAATGGATAAAATTAAAACATTTTCCTAAACCAAAAAAGCCCTATTAGAGAAAATTTGGG 1193
matK-Sb3        AAATGGATAAAATTAAAACATTTTCCTAAACCAAAAAAGGCCTATTAGGGAAAAATTGGG 1193
matK-Sb4        AAATGGAAAGAATTAAAACATTTTCCCAAACCAAAAAAGGCCTATTAGGAGAAAATTGGG 1193
matK-St1        AAATGGAAAGAATTAAATTCATTTCCTAATCCAATAATTCCTATTTAGGAAACAATTGGG 1194
matK-St4        AAATGGAAAAAATTAAATTCATTTTCTAACCCAATAATGCCTATTTAGGAAGAAATTGGG 1194
matK-St3        AAATG-ATAGAATTAAATTCATTTCCTAATCCAATAAATGCTATTAAGGAAAAAAATGGG 1193
matK-St2        AAATGGAAAGAATTAAAACATTTCCCTAATCCAATAATGGCCTTTTAGGAAAAAATTGGG 1194
                ***** * * **** *     **    ** ****  *         *      *  ***
```

```
matK-Sv3        AAACCCCTTGGTCCAAAATTATTTCCCCTCTGGGTGTGGGAAACATATGGGGTTATAAGC 1256
matK-Sv5        AAACCCCTTGGTCCAAAATTATTTCCCCTCTGGGTGTGGGAAACATATGGGGTTATAAGC 1256
matK-Sv2        AAACCCCTTGGTCCAAAATTATTTCCCCTCTGGGTGTGGGAAACATATGGGGTTATAAGC 1256
matK-Sv4        AAACCCCTTGGTCCAAAATTATTTCCCCTCTGGGTGTGGGAAACATATGGGGTTATAAGC 1256
matK-Sv1        AACCCCCTTGGTCCAAAATTATTTCCCCTCTGGGTGTGGGAAACATATGGGGTTATAAGC 1256
matK-Sl2        AAACCCCTTGGTCCAAAAATTATTCCCTCCTGGGGGGTGGGACCATTGGTGGTTAAAACC 1252
matK-Sl3        AAACCCCTTGGTCCAAAAATTATTCCCTCCTGGGGGGTGGGACCATTGGTGGTTAAAACC 1252
matK-sl1        AAACCCCTTGGTCCAAAAATTATTCCCTCCTGGGGGGTGGGAACATTGGTGGTTAAAAGC 1252
matK-Sb1        ATACCCCTTGGTCCAAAAATTATTCCCCCCTGGGGTTTGGGAACATTGGGGGTTAAAAGC 1253
matK-Sb2        AAACCCCTTGGTCCAAAAATTATTCCCCCCTGGGGTTTGGGAACATTGGGGGTTAAAAAC 1253
matK-Sb3        AAACCCCTTGGTCCAAAAATTATTCCCCCCTGGGGTTTGGGAACATTGGGGGTTAAAAGC 1253
matK-Sb4        AAACCCCTTGGTCCAAAAATTATTCCCCCCTGGGGGGTGGGAACATTGGGGGTTAAAAGC 1253
matK-St1        AAACCGTTTGTTTCAAAAATTATCCCCCCCTGGGGTGGGGAAACATTGTGGGTTAAAAGC 1254
matK-St4        ATACCCTTGGGTCCAAAAATTATCCCCCTCTGGGTTGGATCAACATTGGGGGTTAAAAGC 1254
matK-St3        AAACCCTTTG-TTCAAAAATTATCCCCCCCTGGGGGGGGGAACATTTGGGGGTTAAAAGC 1252
matK-St2        AAACCCTTTGGTCCAAAAATTATCCCCCCCTGGGGGGTGGGAACATTGGGGGTTAAAAGC 1254
                *  **  * * * ***** *  * ***  *****       *   *    ***** ** *

matK-Sv3        GAAAAGTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAAGCCGGTTTGGACTGAT 1316
matK-Sv5        GAAAAGTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAAGCCGGTTTGGACTGAT 1316
matK-Sv2        GAAAAGTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAACCCGGTTTGGACTGAT 1316
matK-Sv4        GAAAAGTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAAGCCGGTTTGGACTGAT 1316
matK-Sv1        AAAAAGTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAAGCCGGTTTGGACTGAT 1316
matK-Sl2        CAAAAGTTTGTGAACCCACCTTAAGGGGCATCCCATTAGTTAAAGCCGGTTTGGACTGAT 1312
matK-Sl3        CAAAAGTTTGTGAACCCACCTTAAGGGGCATCCCATTAGTTAAAGCCGGTTTGGACTGAT 1312
matK sl1        CAAAAGTTTGTGAACCCACTTTAAGGGGCATCCCATTTAGTAAAGCCGGTTTGGACTGAT 1312
matK-Sb1        GAAAATTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAGCCGGGTTTGGACTGAT 1313
matK-Sb2        GAAAATTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAGCCGGGTTTGGACTGAT 1313
matK-Sb3        GAAAATTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAGCCGGGTTTGGACTGAT 1313
matK-Sb4        GAAAATTTTTGGTAACCCATTAGGGGGGCATCCCATTTAGTAAGCCGGGTTTGGACTGAT 1313
matK-St1        GAAATTTTTGTGAATCCCCTTAGGGGGGTATCCAAATTAGTAAGCCGAATTTGAACTGAT 1314
matK-St4        GAAATTTTTGTGAATCCATTTAGGGGGGCATCCCATTTAGTAAGCCGGATTTGGACTGAT 1314
matK-St3        GAAAATTTTGTGAAACCATCTAGGGGGGCATCCCATTTAGTAAGCCGGATTTGGACTGAT 1312
matK-St2        GAAATTTTTTGGAAACCCCTTAGGGGGGCATCCCATTTAGTAAGCCGGATTTGAACTGAT 1314
                 ***  ***  * * **   *   **** **** * *   ***  *   **** ******

matK-Sv3        TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1376
matK-Sv5        TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1376
matK-Sv2        TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1376
matK-Sv4        TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1376
matK-Sv1        TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1376
matK-Sl2        TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1372
matK-Sl3        TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1372
matK-sl1        TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1372
matK-Sb1        TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1373
matK-Sb2        TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1373
matK-Sb3        TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1373
matK-Sb4        TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1373
matK-St1        TTATCAGATTCGGATATTATTGGCCGGTTGGGGCGTATATGCAGAAATCTTTCTCATTAT 1374
matK-St4        TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1374
matK-St3        TTATCAGATTCGGATATTATTGACCGATTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1372
matK-St2        TTATCAGATTCGGATATTATTGACCGGGTTGGGCGTATATGCAGAAATCTTTCTCATTAT 1374
                ********************** ***  * ******************************

matK-Sv3        CATAGTGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCT 1436
matK-Sv5        CATAGTGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCT 1436
matK-Sv2        CATAGTGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCT 1436
matK-Sv4        CATAGTGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCT 1436
matK-Sv1        CATAGTGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCT 1436
matK-Sl2        CATAGCGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCT 1432
matK-Sl3        CATAGCGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCT 1432
matK-sl1        CATAGCGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCT 1432
matK-Sb1        CATAGCGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCT 1433
matK-Sb2        CATAGCGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCT 1433
matK-Sb3        CATAGCGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCT 1433
matK-Sb4        CATAGCGGATCTTCCAAAAAAAAGAGTTTGTATCGAATAAAGTATATACTTCGGCTTTCT 1433
matK-St1        CATAGCGGATCTTCCAAAAAAGTGAGTTTGTATCGAATAAAGTATATACTTTGGTTTTCT 1434
matK-St4        CATAGCGGATCTTCCAAAAAAGTGAGTTTGTATCGAATAAAGTATATACTTCGGTTTTCT 1434
matK-St3        CATAGCGGATCTTCCAAAAAAGTGAGTTTGTATCGAATAAAGTATATACTTCGGTTTTCT 1432
matK-St2        CATAGCGGATCTTCCAAAAAAGTGAGTTTGTATCGAATAAAGTATATACTTCGGTTTTCT 1434
                ***** ***************  **************************** ** *****
```

```
matK-Sv3        TGTGCTAAAACTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1496
matK-Sv5        TGTGCTAAAACTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1496
matK-Sv2        TGTGCTAAAACTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1496
matK-Sv4        TGTGCTAAAACTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1496
matK-Sv1        TGTGCTAAAACTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1496
matK-Sl2        TGTGCTAAAATTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1492
matK-Sl3        TGTGCTAAAATTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1492
matK-sl1        TGTGCTAAAATTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1492
matK-Sb1        TGTGCTAAAACTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1493
matK-Sb2        TGTGCTAAAACTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1493
matK-Sb3        TGTGCTAAAACTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1493
matK-Sb4        TGTGCTAAAACTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1493
matK-St1        TGTGCTAAAACTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1494
matK-St4        TGTGCTAAAACTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1494
matK-St3        TGTGCTAAAACTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1492
matK-St2        TGTGCTAAAACTTTAGCTCGGAAACACAAAAGTACTGTACGTGCTTTTTTGAAAAGATTA 1494
                ********** ************************************************

matK-Sv3        GGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTC 1556
matK-Sv5        GGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTC 1556
matK-Sv2        GGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTC 1556
matK-Sv4        GGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTC 1556
matK-Sv1        GGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTC 1556
matK-Sl2        GGGTCGGAATTTTTGGAATTTAAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTC 1552
matK-Sl3        GGGTCGGAATTTTTGGAATTTAAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTC 1552
matK-sl1        GGGTCGGAATTTTTGGAATTTAAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTC 1552
matK-Sb1        GGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTC 1553
matK-Sb2        GGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTC 1553
matK-Sb3        GGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTC 1553
matK-Sb4        GGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGCCCTTTCTTTGAACTTC 1553
matK-St1        GGGTCGGAATTTGTGGAATTCGAACTCATGTCGGAAGAAGTAGTCCTTTCTTTGAACTTC 1554
matK-St4        GGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGTCCTTTCTTTGAACTTC 1554
matK-St3        GGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGTCCTTTCTTTGAACTTC 1552
matK-St2        GGGTCGGAATTTTTGGAATTCGAACTCATGTCGGAAGAAGTAGTCCTTTCTTTGAACTTC 1554
                ************ *******  ********************** *****************

matK-Sv3        CCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTGGTATTTTGGTATT 1616
matK-Sv5        CCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTGGTATTTTGGTATT 1616
matK-Sv2        CCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTGGTATTTTGGTATT 1616
matK-Sv4        CCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTGGTATTTTGGTATT 1616
matK-Sv1        CCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTGGTATTTTGGTATT 1616
matK-Sl2        CCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTGG-ATTTTGATATT 1611
matK-Sl3        CCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTGG-ATTTTGATATT 1611
matK-sl1        CCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTGG-ATTTTGGTATT 1611
matK-Sb1        CCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTA--AATTTGGTATT 1611
matK-Sb2        CCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTA--AATTTGGTATT 1611
matK-Sb3        CCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTA--AATTTGGTATT 1611
matK-Sb4        CCAAGAGTTTCTTCGCCCTTTTGGGGGGTGTATAGAAGTCGGATTTA--AATTTGGTATT 1611
matK-St1        CCAAGAGTTTCTTCTCCCTTTTGGGGGGTGTAGAGAAGTCGGTTTTA--AATTTGGTATT 1612
matK-St4        CCAAGAGTTTCTTCTCCCTTTTGGGGGGTGTATAGAAGTCGGATTTA--AATTTGGTATT 1612
matK-St3        CCAAGAGTTTCTTCTCCCTTTTGGGGGGTGTATAGAAGTCGGATTTA--AATTTGGTATT 1610
matK-St2        CCAAGAGTTTCTTCTCCCTTTTGGGGGGTGTATAGAAGTCGGATTTA--AATTTGGTATT 1612
                ************** ***************** ********* ***   *  *** ****

matK-Sv3        TGGAATATTTAAACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTGAGACCTTGT 1676
matK-Sv5        TGGAATATTTAAACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTGAGACCTTGT 1676
matK-Sv2        TGGAATATTTAAACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTGAGACCTTGT 1676
matK-Sv4        TGGAATATTTAAACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTGAGACCTTGT 1676
matK-Sv1        TGGAATATTTAAACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTGAGACCTTGT 1676
matK-Sl2        TGGAATTGTATAACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTGAGACCTTGT 1671
matK-Sl3        TGGAATTGTATAACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTGAGACCTTGT 1671
matK-sl1        TGGAATATTATAACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTGAGACCTTGT 1671
matK-Sb1        TGGT-TATTATAACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTGAGACCTTGT 1670
matK-Sb2        TGGT-TATTATAACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTGAGACCTTGT 1670
matK-Sb3        TGGT-TATTATAACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTGAGACCTTGT 1670
matK-Sb4        TGGA-TATTATAACTGATCTGGTGAATCAGCAATGATTCATATTCATTCTGAGACCTTGT 1670
matK-St1        TGGA-TTTTATAACTGATCTGGTGAATCATCAATGATTCATATTCATTCTGAGACCTTGT 1671
matK-St4        TGGA-TTTTATAACTGATCTGGTGAATCATCAATGATTCATATTCATTCTGAGACCTTGT 1671
matK-St3        TGGA-TTTTATAACTGATCTGGTGAATCATCAATGATTCATATTCATTCTGAGACCTTGT 1669
matK-St2        TGGA-TATTATAACTGATCTGGTGAATCATCAATGATTCATATTCATTCTGAGACCTTGT 1671
                ***  *  *  ***************** ******************************
```

```
matK-Sv3        AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1736
matK-Sv5        AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1736
matK-Sv2        AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1736
matK-Sv4        AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1736
matK-Sv1        AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1736
matK-Sl2        AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1731
matK-Sl3        AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1731
matK-sl1        AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1731
matK-Sb1        AAATGGATTTAAGCCTTAAATGAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1730
matK-Sb2        AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1730
matK-Sb3        AAATGGATTTAAGCCTAAACTAAAATGATGAAGATGAAGAAAAAGTTTTCTACTATTCTG 1730
matK-Sb4        AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1730
matK-St1        AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1731
matK-St4        AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1731
matK-St3        AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1729
matK-St2        AAATGGATTTAAGCCTAAATGAAAATGATGAAGAGATAACAAAAGTTTTCTACTATTCTG 1731
                ********************  **   ************   *  ********************

matK-Sv3        AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTTCTAAATA 1796
matK-Sv5        AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTTCTAAATA 1796
matK-Sv2        AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTTCTAAATA 1796
matK-Sv4        AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTTCTAAATA 1796
matK-Sv1        AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTTCTAAATA 1796
matK-Sl2        AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTCTAAACTA 1791
matK-Sl3        AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTCTAAACTA 1791
matK-sl1        AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTCTAAACTA 1791
matK-Sb1        AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTTTAAATTA 1790
matK-Sb2        AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTTTAAACTA 1790
matK-Sb3        AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTTTAAATTA 1790
matK-Sb4        AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTTTGAAATA 1790
matK-St1        AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTCTAAATTG 1791
matK-St4        AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTCTAAATTA 1791
matK-St3        AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTCTAAATTA 1789
matK-St2        AAATGTTGATGTAGCATGTAATAAGGGTTAAATCAACTGACTATTCTGCTTTCTAAATTA 1791
                **************************************************   ** *

matK-Sv3        AAGTCTAAAAAAGGAAAAA 1815
matK-Sv5        AAGTCTAAAAAAGGAAAAA 1815
matK-Sv2        AAGTCTAAAAAAGGAAAAA 1815
matK-Sv4        AAGTCTAAAAAAGGAAAAA 1815
matK-Sv1        AAGTCTAAAAAAGGAAAAA 1815
matK-Sl2        AAGTTTAAATGAGTTATCA 1810
matK-Sl3        AAGTTTTAATGAGTTATCC 1810
matK-sl1        AAGTCTAGATGAGTTATCA 1810
matK-Sb1        AAGTCTTTAAAAGGAAACA 1809
matK-Sb2        AAGTCTTTAAAAGGAAACA 1809
matK-Sb3        AAATCTTTAAAAGGAAACA 1809
matK-Sb4        AAGTCTTAAAAAGGAAACA 1809
matK-St1        AGGTCTAAAAAAAAAGAAA 1810
matK-St4        AAGTTTAAAAAAAAAGAAA 1810
matK-St3        AAGTTTAAAAAAAAAGAAA 1808
matK-St2        AAGTCTAAAAAAAAAGAAA 1810
                *  * *  *  *
```

The size of the *mat*K gene

Sequence 1: *mat*K-St1 1810 bp

Sequence 2: *mat*K-St2 1810 bp

Sequence 3: *mat*K-St3 1808 bp

Sequence 4: *mat*K-St4 1810 bp

Sequence 5: *mat*K-sl1 1810 bp

Sequence 6: *mat*K-Sl2 1810 bp

Sequence 7: *mat*K-Sl3 1810 bp

Sequence 8: *mat*K-Sv1 1815 bp

Sequence 9: *mat*K-Sv2 1815 bp

Sequence 10: *mat*K-Sv3 1815 bp

Sequence 11: *mat*K-Sv4 1815 bp

Sequence 12: *mat*K-Sv5 1815 bp

Sequence 13: *mat*K-Sb1 1809 bp

Sequence 14: *mat*K-Sb2 1809 bp

Sequence 15: *mat*K-Sb3 1809 bp

Sequence 16: *mat*K-Sb4 1809 bp

The pairwise of similarity score

Sequences (1:2) Aligned. Score: 96	Sequences (4:7) Aligned. Score: 92	Sequences (8:13) Aligned. Score: 92
Sequences (1:3) Aligned. Score: 96	Sequences (4:8) Aligned. Score: 92	Sequences (8:14) Aligned. Score: 93
Sequences (1:4) Aligned. Score: 96	Sequences (4:9) Aligned. Score: 92	Sequences (8:15) Aligned. Score: 92
Sequences (1:5) Aligned. Score: 92	Sequences (4:10) Aligned. Score: 91	Sequences (8:16) Aligned. Score: 94
Sequences (1:6) Aligned. Score: 91	Sequences (4:11) Aligned. Score: 92	Sequences (9:10) Aligned. Score: 99
Sequences (1:7) Aligned. Score: 91	Sequences (4:12) Aligned. Score: 91	Sequences (9:11) Aligned. Score: 99
Sequences (1:8) Aligned. Score: 91	Sequences (4:13) Aligned. Score: 92	Sequences (9:12) Aligned. Score: 98
Sequences (1:9) Aligned. Score: 91	Sequences (4:14) Aligned. Score: 92	Sequences (9:13) Aligned. Score: 92
Sequences (1:10) Aligned. Score: 90	Sequences (4:15) Aligned. Score: 92	Sequences (9:14) Aligned. Score: 93
Sequences (1:11) Aligned. Score: 90	Sequences (4:16) Aligned. Score: 93	Sequences (9:15) Aligned. Score: 92
Sequences (1:12) Aligned. Score: 90	Sequences (5:6) Aligned. Score: 97	Sequences (9:16) Aligned. Score: 94
Sequences (1:13) Aligned. Score: 91	Sequences (5:7) Aligned. Score: 98	Sequences (10:11) Aligned. Score: 99
Sequences (1:14) Aligned. Score: 91	Sequences (5:8) Aligned. Score: 94	Sequences (10:12) Aligned. Score: 98
Sequences (1:15) Aligned. Score: 91	Sequences (5:9) Aligned. Score: 94	Sequences (10:13) Aligned. Score: 92
Sequences (1:16) Aligned. Score: 92	Sequences (5:10) Aligned. Score: 94	Sequences (10:14) Aligned. Score: 92
Sequences (2:3) Aligned. Score: 96	Sequences (5:11) Aligned. Score: 94	Sequences (10:15) Aligned. Score: 92
Sequences (2:4) Aligned. Score: 96	Sequences (5:12) Aligned. Score: 93	Sequences (10:16) Aligned. Score: 93
Sequences (2:5) Aligned. Score: 95	Sequences (5:13) Aligned. Score: 93	Sequences (11:12) Aligned. Score: 99
Sequences (2:6) Aligned. Score: 93	Sequences (5:14) Aligned. Score: 94	Sequences (11:13) Aligned. Score: 92
Sequences (2:7) Aligned. Score: 93	Sequences (5:15) Aligned. Score: 93	Sequences (11:14) Aligned. Score: 92
Sequences (2:8) Aligned. Score: 93	Sequences (5:16) Aligned. Score: 95	Sequences (11:15) Aligned. Score: 92
Sequences (2:9) Aligned. Score: 92	Sequences (6:7) Aligned. Score: 99	Sequences (11:16) Aligned. Score: 94
Sequences (2:10) Aligned. Score: 92	Sequences (6:8) Aligned. Score: 93	Sequences (12:13) Aligned. Score: 92
Sequences (2:11) Aligned. Score: 92	Sequences (6:9) Aligned. Score: 92	Sequences (12:14) Aligned. Score: 92
Sequences (2:12) Aligned. Score: 92	Sequences (6:10) Aligned. Score: 92	Sequences (12:15) Aligned. Score: 91
Sequences (2:13) Aligned. Score: 94	Sequences (6:11) Aligned. Score: 92	Sequences (12:16) Aligned. Score: 93
Sequences (2:14) Aligned. Score: 94	Sequences (6:12) Aligned. Score: 92	Sequences (13:14) Aligned. Score: 98
Sequences (2:15) Aligned. Score: 94	Sequences (6:13) Aligned. Score: 92	Sequences (13:15) Aligned. Score: 97
Sequences (2:16) Aligned. Score: 95	Sequences (6:14) Aligned. Score: 93	Sequences (13:16) Aligned. Score: 97
Sequences (3:4) Aligned. Score: 97	Sequences (6:15) Aligned. Score: 92	Sequences (14:15) Aligned. Score: 98
Sequences (3:5) Aligned. Score: 93	Sequences (6:16) Aligned. Score: 94	Sequences (14:16) Aligned. Score: 97
Sequences (3:6) Aligned. Score: 92	Sequences (7:8) Aligned. Score: 93	Sequences (15:16) Aligned. Score: 96
Sequences (3:7) Aligned. Score: 92	Sequences (7:9) Aligned. Score: 92	
Sequences (3:8) Aligned. Score: 92	Sequences (7:10) Aligned. Score: 92	
Sequences (3:9) Aligned. Score: 92	Sequences (7:11) Aligned. Score: 92	
Sequences (3:10) Aligned. Score: 91	Sequences (7:12) Aligned. Score: 92	
Sequences (3:11) Aligned. Score: 91	Sequences (7:13) Aligned. Score: 92	
Sequences (3:12) Aligned. Score: 91	Sequences (7:14) Aligned. Score: 93	
Sequences (3:13) Aligned. Score: 92	Sequences (7:15) Aligned. Score: 93	
Sequences (3:14) Aligned. Score: 92	Sequences (7:16) Aligned. Score: 94	
Sequences (3:15) Aligned. Score: 92	Sequences (8:9) Aligned. Score: 98	
Sequences (3:16) Aligned. Score: 93	Sequences (8:10) Aligned. Score: 98	
Sequences (4:5) Aligned. Score: 93	Sequences (8:11) Aligned. Score: 98	
Sequences (4:6) Aligned. Score: 92	Sequences (8:12) Aligned. Score: 98	

VITA

Miss Kanittha Nakkliang was born on August 11, 1990 in Suratthani, Thailand. She got a Bachelor's degree of Applied Thai Traditional Medicine with first class honor from Faculty of Rajamangala University of Technology Thanyaburi, Thailand in 2013.

Publication

Nakkiang, K., Palanuvej, C., and Ruangrungsi, R. Microscopic analysis of Selected Strychnos species in Thailand. Proceedings of the 2nd International Conference on Advanced Pharmaceutical Research Strategies and Innovation in Pharmaceutical Research: Safety, Efficacy and Quality, pp. 164-169, Pathumthani, 2015.