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Source: Zoological Science, 16(1): 175-184

Published By: Zoological Society of Japan

URL: https://doi.org/10.2108/zsj.16.175

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Molecular Phylogeny of Orthopteroid Insects based on the Mitochondrial Cytochrome Oxidase II Gene

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ABSTRACT—Phylogenetic relationships among 18 species of orthopteroid insects (Blattaria: cockroaches, Isoptera: termites, Mantodea: mantids, Grylloblattodea: grylloblattids, Phasmatodea: stick-insects, Orthoptera-Caerifera: locusts, Orthoptera-Ensifera: crickets, and Dermaptera: earwigs), were estimated based on DNA sequencing of the mitochondrial cytochrome oxidase II gene. Our results drew attention to the need for caution in using third codon positions for tree construction, since it was likely that base pair substitutions of third codon positions in the COII gene were saturated among taxa used in the present study. We also detected that there were many phylogenetically informative sites in first codon positions. Phylogenetic trees using first and second codon positions based on both the neighbor-joining method and parsimony analysis indicated that the topology was nearly identical to each other. The phylogenetic relationships among these taxa differ from the current classification based on morphological characters. The inferred trees showed that grylloblattids were not a primitive group, but closely related to the Dictyoptera. Stick-insects were closely related to the Dictyoptera and grylloblattids, not to crickets. Locusts and crickets formed a monophyletic group. Earwigs were only distantly related to the Dictyoptera. Within the Dictyoptera, cockroaches and termites constituted a monophyletic group, with mantids as a sister group to that complex.

INTRODUCTION

Several phylogenetic hypotheses based on morphological characters have been proposed for orthopteroid insects (reviewed in Kristensen, 1995). Hennig (1969, 1981) suggested that the "lower Neoptera" might have two entities, Embioptera (web-spinners) and the "Orthopteromorpha", which includes Grylloblattodea (grylloblattids), Dermaptera (earwigs), Mantodea (mantids), Blattodea (cockroaches), Isoptera (termites), Orthoptera-Ensifera (crickets), Orthoptera-Caelifera (locusts) and Phasmatodea (stick-insects). Furthermore, he suggested that the Orthopteromorpha might be represented as (Grylloblattodea + (Dermaptera + (Mantodea + (Blattodea + Isoptera))) + (Orthoptera-Ensifera + (Orthoptera-Caelifera + Phasmatodea))). The relationships among the monophyletic subgroups of the Orthopteromorpha, however, are still unresolved (Boudreaux, 1979; Hennig, 1969, 1981). Kukalová-Peck and Brauckmann (1992) and Kukalová-Peck and Peck (1993) has advocated the monophyly of a lineage comprising the Embioptera + (Isoptera + Orthoptera-Caelifera) + Phasmatodea, and that comprising the Zoraptera + Grylloblattodea + Dermaptera + (Blattodea + Mantodea). There were also suggestions that stick-insects were more closely

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related to the cockroach-like insects rather than to the Orthoptera (Ragge, 1955; Ross, 1955). Additionally, it is possible that crickets and locusts may not be monophyletic group (Hennig, 1969, 1981; Kristensen, 1995), and were each given ordinal status by Kevan (1986). The systematic position of grylloblattids is also controversial. In general, based on anatomical data, grylloblattids are considered to be a relic species and an intermediate form between cockroaches and the Orthoptera, and one of the primitive groups among orthopteroid insects (Walker, 1914, 1933, 1938; Crampton, 1915, 1935; Imms, 1945). Nagashima (1982) studied grylloblattid head anatomy in detail in comparison with other orthopteroid insects and indicated that grylloblattids were not a primitive group among these insects. The precise topology of the tree that includes cockroaches, termites and mantids also remains a topic of active discussion. Kristensen (1975) suggested the same relationships as Hennig (1969, 1981), but later Kristensen (1981) grouped all three taxa into the same order "Dictyoptera" and waited for further work to resolve the phylogeny. In this study, we use Dictyoptera as this meaning. Another phylogenetic hypothesis based on morphological characters is (termite + (cockroach + mantid)) proposed by Boudreaux (1979). Thorne and Carpenter (1992) recently did a parsimony analysis using 70 morphological and ecological characters, and found a single most parsimonious tree which supported the hypothesis of Boudreaux. Kukalová-Peck and

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Peck's (1993) analysis of wing structures also supported this relationship. Kambhampati (1995) constructed a phylogeny of cockroaches and related insects based on mitochondrial 16S and 12S rRNA genes, and found that termites were the sister group to a clade consisting of cockroaches and mantids. The primary goal of his study, however, was not to investigate the phylogeny of the Dictyoptera. Therefore, the relationships of these groups were only briefly discussed in his study.

In this study, we investigated the phylogenetic relationships among the Orthopteromorpha based on the complete nucleotide sequence of the mitochondrial cytochrome oxidase subunit II (COII). We chose this system for analysis because the lengths of COII genes of each group are nearly identical, thus facilitating the alignment and comparison of the sequences, and because a phylogenetic analysis of the Orthopteromorpha using modern methodology and based on sufficient numbers of characters is lacking.

MATERIALS AND METHODS

Insects

The species investigated are listed in Table 1. The sequences of termite (*Zootermopsis angusticollis*), locust (*Schistocerca gregaria*), cricket (*Acheta domesticus*) and milkweed bug (*Oncopeltus fasciatus*) genes were obtained from GenBank Data Libraries (Accession nos. M83968, M83966, M83961 and M83959, respectively; Liu and Beckenbach, 1992). The phylogeny of insect orders based on morphology (Kristensen, 1991) and of the holometabolous insect orders inferred from 18S and 28S ribosomal DNA sequences and morphology (Fig. 9 and Fig. 10 in Whiting *et al.*, 1997) showed that the Hemiptera was the sister group of the orthopteroid insects. Consequently,

we used milkweed bugs as an outgroup.

DNA extraction

For termites, total genomic DNA was extracted from a total body with the hindgut removed; in all other insect leg tissue was used. Fresh or frozen materials, or samples preserved in acetone were used for DNA extraction. The procedure of the extraction was modified from Laird *et al.* (1991). Tissue was homogenized with a pair of dissecting scissors in a 1.5 ml microcentrifuge tube containing 500 μ l of lysis buffer (100 mM Tris-HCl, 5 mM EDTA, 0.2% SDS, 200 mM NaCl) and 50 μ g of Proteinase K (Wako Chemicals). The mixture was incubated overnight at 56°C. 10 μ g of RNase A (Boeringer Mannheim) was added to the mixture, and incubated at 37°C for 30 min. Following a series of phenol-chloroform and chloroform extractions, DNA was precipitated with an equal volume of isopropanol. Pellets were rinsed with 70% ethanol, dried under vacuum and dissolved in 40 μ l of TE buffer (10 mM Tris-HCl, 1 mM EDTA).

DNA amplification

The COII region of mitochondrial DNA was amplified using polymerase chain reaction (PCR; Saiki et al., 1985). Two pairs of primers were used for the amplification. The primer sequences are shown in Table 2. A-tLEU and B-tLYS, and C1-J-2773 followed Liu and Beckenbach (1992) and Miura et. al. (1998), respectively. Another internal primer (A-COII) was chosen in regions of sequence conservation between Drosophila yakuba and other insects and were based on partial sequences as they were obtained. The reaction was performed in an ASTEC PC-700 programmable temperature control system or GeneAmp 2400 thermal cycler (Perkin-Elmer) under the following conditions: 35 cycles of denaturing at 94°C for 1min, annealing at 50°C for 1min and extending at 70°C for 2 min (Liu and Beckenbach, 1992). The reaction mix was performed in a final volume of 40 μ l of the following solution: 30 μ l of distilled water, 4 μ l of 10 × PCR buffer (Takara, TaKaRa Taq: containing 100 mM Tris-HCl (pH8.3), 500 mM KCl, 15 mM MgCl_2, 0.01% (w/v) gelatin), 4 μl of dNTP mix (1 mM of each dNTP), 0.2 µl of each primer (100 pM), 0.7

Table 1.	List of the	e species	used i	n this	studv
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Таха	Order	Family	Species
Cockroach	Blattaria	Blaberidae Blattellidae Blattidae	Salganea taiwanensis Lobopterella dimidiatipes Periplaneta fulginosa
Termite	Isoptera	Rhinotermitidae Termitidae Termopsidae	Reticulitermes speratus Longipeditermes longipes Zootermopsis angusticollis*
Mantid	Mantodea	Mantidae Manidae	Tenodera angustipennis Statilia maculata
Grylloblattid	Grylloblattodea	Grylloblattidae	Galloisiana nipponensis
Stick-insect	Phasmatodea	Phasmatidae Phasmatidae Phasmatidae	Trigonophasma rubescens Neohirasea japonica Baculum irregulariterdentatum
Locust	Orthoptera	Pyrgomorphidae Acrididae Acrididae	Atractomorpha lata Mecostethus alliaceus Schistocerca gregaria*
Cricket		Gryllidae Gryllidae	Teleogryllus emma Acheta domesticus*
Earwig	Dermaptera	Carcinophoridae	Anisolabis maritima
Milkweed-bug	Hemiptera	Lygaeidae	Oncopeltus fasciatus*

The COII sequences of species with stars were obtained from GenBank Data Libraries.

Table 2. Primer sequences used in this study

Primer Name	Primer Sequences	Position spannned
A-tLEU	5'-ATGGCAGATTAGTGCAATGG-3'	3018-3038
B-tLYS	5'-GTTTAAGAGACCAGTACTTG-3'	3804-3784
C1-J-2773	5'-ATACCTCGACG(AT)TATTCAGA-3'	2773-2792
A-COII	5'-TGAAGTTATGAATATTCAGA-3'	3398-3417

Brackets show degenerated positions. The position of each primer refers to the complete *Drosophila yakuba* sequences (Clary and Wolstenholme, 1985).

U of Taq polymelase (Takara, TaKaRa Taq) and 2 μl of template DNA.

DNA purification and sequencing

PCR products were electrophoresed in a 1% agarose gel, and purified using Prep-A-Gene DNA Purification Kit (BIO RAD). The purified products were used as a template for the sequencing reaction. The sequencing reaction was performed using a Dye-Terminator Cycle Sequencing Kit (Perkin-Elmer) and GeneAmp 2400 thermal cycler. Electrophoresis and data collection were performed using an automatic DNA sequencer (Perkin-Elmer, model 373S) with 6% polyacrylamide gel (TOYOBO, Super Reading DNA Sequence Solution), following the recommended procedure. Both strands of the amplified PCR product were sequenced.

Phylogenetic analysis

Sequences were aligned using the Clustal W program package (Thompson et al., 1994), and confirmed with aligned sequences of 10 orders of insects (Liu and Beckenbach, 1992). The number of nucleotide substitutions were estimated according to Kimura's two-parameter methods (Kimura, 1980). Distance matrices were analyzed by the neighbor-joining method (Saitou and Nei, 1987) to construct phylogenetic trees using Clustal W. All alignment positions where there was a gap in any sequence were included in the distance analysis. A bootstrap analysis (Felsenstein, 1985) of 1000 replications was carried out . We also used PAUP 3. 1. 1. program package (Swofford, 1993) to carry out non-weighted parsimony analysis using the heuristic search option with tree bisection-reconnection. In the parsimony analyses, gaps were treated as a fifth base. The data set was also bootstrapped for 1000 replications with five random addition sequence replicates for each bootstrap replicate using PAUP. The numbers of base pair substitution in pairwise comparisons of each codon position were counted. We performed our analyses using (1) the complete data set, and restricted subsets of the data, namely (2) first codon positions, (3) second codon positions and (4) first and second codon positions.

The nucleotide sequence data reported in this paper will appear in the DDBJ, EMBL and GenBank nucleotide sequence databases with the following accession nos: AB005459, AB005461, AB005463-AB005470, AB005905, AB006435, AB006436, AB011233 and AB011234.

RESULTS

Nucleotide sequences

The COII genes ranged from 670 bp in stick-insects to 690 bp in milkweed bugs. The aligned sequences are shown in the Appendix. The sequences of *Salganea taiwanensis* and *O. fasciatus* have TAG and TAA at the 3' end, potentially encoding the entire terminator. All of other sequences end in T. The transcripts of such mitochondrial genes that have incomplete stop codons contain a stop codon created by posttranscriptional polyadenylation (Wolstenholme, 1992).

Several internal insertion/deletion events could be seen. In the sequences of crickets, an insertion of three nucleotides appeared at positions 349-351, and a deletion of two codons occured at positions 394-399. In the stick-insect sequences, a deletion of two codons also occured at positions 373-378 (see Appendix). A total of 549 of the 693 nucleotide sites were variable, including 225 first, 101 second and 223 third codon positions. It was shown that the numbers of variable sites in the first codon position were as many as those in the third codon position. Average numbers of nucleotide substitution counted based on pairwise comparisons of each codon position are shown in Fig. 1. On the first, second and third codon positions, 5.6-36.4% (average 27.3%), 1.3-22.1% (average 15.6%) and 24.7-61.0% (average 44.8%) were variable, respectively. Average transition (Ti) and transversion (Tv) rates at each codon position are 12.8 and 15.0% (first position), 8.8 and 7.0% (second position) and 16.3 and 29.8% (third position).

Phylogenetic inference

Firstly, phylogenetic trees were inferred based on the neighbor-joining method and on parsimony analysis using



Fig. 1. The average numbers and S. E. of base pair substitution of the first, second and third codon positions of mitochondrial cytochrome oxidase II gene among 19 species used in this study. The numbers of different characters of each codon position were counted in pairwise comparisons of all species.

complete nucleotide sequences, first codon positions and second codon positions (trees not shown). In the bootstrap parsimony trees, tree length, consistency index, rescaled consistency index and retention index are as follows; 2160 steps, 0.40, 0.14 and 0.34 (complete nucleotide), 584 steps, 0.46, 0.22 and 0.49 (first position), 302 steps, 0.52, 0.31 and 0.59 (second position). In all trees, monophyly of each order excluding cockroaches and termites was supported in 50% or more of the bootstrap replicates. Monophyly of cockroaches and termites was not supported in the parsimony trees using all data sets and first codon positions, and using second codon positions, respectively. Although some monophyletic groups (cockroach + termite in the trees using first codon position, and cockroach + termite + mantid + grylloblattid in the trees using second codon positions) were supported, phylogenetic relationships among the other orders were supported in less than 50% bootstrap replicates.

Secondly, bootstrap trees were inferred based on the first and second codon positions (Fig. 2). Fig. 2A is the neighborjoining tree, while Fig. 2B is the parsimony tree. Monophyly of each order was supported in both trees. Monophyly of the cockroach + termite clade was also supported. Earwig was shown to be the basal taxon. Grylloblattids were shown to be more closely related to the Dictyoptera. Monophyly of the clade consisting of cockroaches, termites, mantids and grylloblattids, however, was supported in less than 50% bootstrap replicates in the neighbor-joining tree. Monophyly of the Dictyoptera was supported in Fig. 2A, but relationships among the cockroach-



Fig. 2. Bootstrap trees using first and second codon positions based on the neighbor-joining method (A), and on parsimony analysis (B). Both trees were done using 1000 replications of bootstrapping. In the parsimony tree, italic numerals above the branches are branch lengths, while numerals below the branches indicate bootstrap values. Tree length: 858 steps, consistency index: 0.49, rescaled consistency index: 0.27, retention index: 0.55. See Table 1 for complete names of taxa.

termite, mantids and grylloblattids clade were not resolved in Fig. 2B. Stick-insects were shown to be more closely related to the monophyletic group consisting of the Dictyoptera and grylloblattids in the neighbor-joining tree. The phylogenetic position of stick-insects, however, is not clear in the parsimony tree.

DISCUSSION

This study is the first comprehensive study focused on the phylogeny among orthopteroid insects based on the molecular chracters. Especially, molecular phylogenetic relationships between grylloblattids and other orthopteroid insects have not been studied until the present study. Although Liu and Beckenbach (1992) discussed about the evolution and characteristics of COII genes of 10 orders of insects, they used only 4 species belonging to 3 orders for orthopteroid insects.

We analyzed phylogenetic relationships using the following data sets; all nucleotide sites, first codon positions, second codon positions (trees not shown), and first and second codon positions (Fig. 2). Not surprisingly, there were many variable sites in the third codon positions (96.5%). By contrast, there were more variable sites in the first codon positions (97.4%). These high values in the first codon positions are noteworthy, because percentages of variable sites in the first and third codon positions of COII genes among 10 orders of insects are 70.0 and 91.3%, respectively (Liu and Beckenbach, 1992). The average numbers of nucleotide substitutions of the first codon positions were, however, shown to be much less than those of the third codon positions (Fig. 1). When the first codon positions were used for the phylogenetic analysis, monophyly of all orders (excluding cockroaches in the parsimony tree) was supported. Phylogenetic trees using only third codon positions did not support the monophyly of these groups (trees not shown). Furthermore, the ratio of Ti to Tv at the third codon positions (0.55) were shown to be much smaller than those of the first (0.85) and second codon positions (1.23). The ratio of Ti to Tv can decrease as a result of multiple substitutions at a sites within a gene (Simon et al., 1994). It is clear that nucleotide substitutions of the third codon positions of COII gene are saturated in pairwise comparisons between orders. Edwards et al. (1991) and Irwin et al. (1991) found that the inclusions of third position changes can obscure relationships in deep phylogenies. Moreover, we thought that there were many informative sites for phylogenetic analyses in the first codon positions. When only second codon positions were used for analyses, there were only 101 variable characters. Consequently, we used the first + second codon positions to construct phylogenetic trees.

Our phylogenetic trees using the first and second codon positions indicate that stick-insects are not closely related to locusts or crickets. More likely, they are more closely related to the Dictyoptera and grylloblattids. There was a relatively high genetic difference between locusts and crickets, but it was shown that they were a monophyletic group. Earwigs were the most phylogenetically distant from the Dictyoptera, suggesting that they are basal among the Orthopteromorpha used in the present study. The above-mentioned relationships are different from relationships presently accepted based on morphological characters (Hennig, 1969, 1981; Boudreaux, 1979; Kristensen, 1981, 1995; Kukalová-Peck and Brauckmann, 1992; Kukalová-Peck and Peck, 1993). Ross (1955), however, suggested that stick-insects were more closely related to cockroaches and mantids, based on egg morphology. A monophyly of locusts and crickets also has been suggested (Boudreaux, 1979; Kukalová-Peck and Brauckmann, 1992; Kukalová-Peck and Peck, 1993). However, earwigs were always thought to be closely related to the Dictyoptera until the present study (Hennig, 1969, 1981; Boudreaux, 1979; Kukalová-Peck and Brauckmann, 1992; Kukalová-Peck and Peck, 1993; Kristensen, 1995).

Grylloblattids were shown not to be a basal taxon among orders used in this study, but to be more closely related to the Dictyoptera. Nagashima (1982) pointed out that the extrinsic muscles of the antenna of grylloblattids were like those of mantids and web-spinners, and that those of the mandible resembled those of cockroaches, termites, mantids and stickinsects. He also showed that the muscles of the maxilla resembled those of earwigs. However, Ando and Nagashima (1982) pointed out that the pattern of embryonic development in *Galloisiana nipponensis* differed from that of earwigs. These morphological data were in agreement with the results of our present study. Unfortunately, we could not use webspinners in this study, so phylogenetic relationships among grylloblattids, Dictyoptera and web-spinners still remains ambiguous.

In the trees using the first and second codon positions, cockroaches were shown to be more closely related to termites than mantids, although bootstrap confidence is not high (64% in the neighbor-joining tree, 57% in the parsimony tree). There has not hitherto been molecular data which supports this relationship. *Cryptocercus* spp. and *Mastotermes darwiniensis*, which are generally recognized to be most primitive cockroaches and termites, as well as mantid species belonging to other families than the Mantidae need to be included in further molecular studies of the Dictyoptera to resolve relationships within this group.

Although COII gene is a relatively conserved gene in the mitochondrial DNA (Clary and Wolstenholme, 1985; Liu and Bechenbach, 1992), this gene is probably not the best gene for revealing robust phylogenetic relationships among orthopteroid insects. However, COII gene is clearly useful for the phylogeny to some extent, and this study is the first step to analyze molecular phylogenetic relationships among orthopteroid insects. It is clear that the phylogenetic analyses of numerous taxa, including web-spinners and based on not only molecular data of other genes but also morphological data are needed to determine precise relationships among these groups.

ACKNOWLEDGMENTS

We thank Dr. M. Maryati for her support in the field sampling, and Dr. T. Nagashima for providing *Galloisiana nipponensis*. Dr. R. Ueshima taught us the sequencing technique. We are also grateful to Drs. C. A. Nalepa, C. Bandi, M. Terayama and Mr. N. Lo, who gave us valuable comments on the manuscript. Mr. T. Miura helped and supported us at our field sampling and sequencing. This study was supported by Research Fellowships of the Japan Society for the Promotion of Science for Young Scientists for K. M., and in part by a Grant-in-Aid from the International Scientific Research Program (No. 08041136) and a Scientific Research Grant (no. 07454211, 10440231) from the Ministry of Education, Science, Sports and Culture of Japan.

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(Received March 2, 1998 / Accepted October 21, 1998)

APPENDIX

Aligned sequence of the mitochondrial cytochrome oxidase II gene of 18 species of orthopteroid insects and milkweed-bugs used as an outgroup. Dots indicate identity to the *S. taiwanensis* sequences. Gaps are indicated by dashes. See Table 1 for complete names of taxa.

							60
s.	taiwanensis	ATGACAACAT	GATCTAATAT	ΑΑΑCTTACAA	GATAGTGCGT	CACCTATTAT	AGAACAATTA
L.	dimidiatipes		G.A		AT.	A	
Ρ.	fulginosa	• • • • • • • • • • •	G	T	AA.		
<i>R</i> .	speratus	• • • • • • • • • • •	IAC	GAC	CG.AA.	.(((
L.	longipes		IAAI.	CAC	AA.	.6	• • • • • • • • • •
۲. ۲	angusticollis	·····			CAA.	.GA	• • • • • • • • • • •
1.	angustipennis	····G·I····			····A··I·	CT.A	• • • • • • • • • • •
з. с	maculata	····G·I····			······	CI.A	· · · · · · · · · · · · · · · · · · ·
и. Т	rubescens	Λ T		тт		ΔC Δ	
N.	iaponica	Δ		тт	СТ.Т.	.CAT.A	
R.	irreaulariterdentatum	Δ		Т. Т.	ΑΤ.Α.	T.A	C
Α.	lata	G.T	AC.A	тт.тс.т	AT.	T.A	
Μ.	alliaceus	G		.TCA	G.AC.	AT.A	
s.	gregaria	G	A T.	.TCTA.T	G.AT.	AT.A	GG
Τ.	emma	G.T	Ст.	T	AAT.A.	.CAC.A	C.T
Α.	domesticus	G.C	T.	T	AAT.A.	.TC.A	C.C
Α.	maritima	TGT.	GT.	GTT	AG.ATA	T.A	
0.	fasciatus	AG	ATA	ТТС.Т	CGCAAAT.	T.A.CA	GC.T
~	,					TTTTATCACT	120
5.	taiwanensis		AIGAICAIGC				AGITACITAT
L.	aimiaiatipes	•••••		· · · · A · · · · ·	····	A	A
Р. р	ruiginosa			.CAC	CA.I		· · · A I · A · · ·
к. 1	longines	с.т	····CA.	AA	••••••••••••••••••••••••••••••••••••••		
7	angusticollis	тт т	C	ΛΑ ((Λ	G AC		ΔΤΤΔ
T.	anaustinennis		сд.		Δ((ΔΟΤΔΤΘΔΟ	C. AGG C
s.	maculata	ATT .	Т.	ΔΔΤ.Τ	ΑCT	G.TA.TAC	AGGA
G.	nipponensis	T		AC.C	T.AACT.C.	GGCTC.	AC
Τ.	rubescens	T	CCAT	.AAC	Τ.ΑΑ	G.TAAC	AA
Ν.	japonica	TT.	AT	.AA	Τ.ΑΑ	GA.CAC	AT.A
Β.	irregulariterdentatum	.AC.T	.CAT	.AT	Τ.ΑΑ	GAAC	GA
A.	lata	TCA.TTT.	A.	AA.GA	C.AA.T	AC.ATCA.	TAGG
М.	alliaceus	TCA.TT.	A.	.AG.TG.A	T.ATT	AC.GTTA.	TGGAC
s.	gregaria	TCA.TT.	CGCA	.ACTA.GG.C	G.ATT	AC.GT.A.	TAGG
Τ.	emma	c.ttt.	CCA.	СТ	T.AT	ACTGTTC.	CAT.A
Α.	domesticus	<u></u> T <u>T</u> .	A.	· · · · <u>A</u> · <u>-</u> · · · ·	C.AC	ACTGTTT.	G.A
Α.	maritima		A.		I.AA.IG.	ACCATIA.	.AGG
0.	fasciatus	.CAAIAI.	CA.	AA	I.AACI	ACA.	IAI.
							180
ς	taiwanensis	ΔΤΛΑΤΛΑΤCA	CATTAATTTA	ΤΛΛΟΛΛΤΤΤΤ	ΛΟΟΛΑΤΟΘΑΤ	ΤΟΟΤΤΤΤΛΟΛ	ACCACAACTT
J.	dimidiatines	T G TC					
Ρ.	fulainosa		A T				
R.	speratus	C		A			A
L.	longipes	.CT	T.A.TCC.	A	GA	.TA.AC	A.A
Ζ.	angusticollis	T.TCAT	ACCAT	GAAC	GAGC	ATA.AC	CACA
Τ.	angustipennis	T.AT	AAC	ATA	.TGGTC	ATG.CA	СТТ
S.	maculata	TT.AT	.TCAAC	ATA.A.	.TAGTC	ATG.AA	CTTA.
G.	nipponensis	TGGA.	GTGTT	CTTCAC	.TTCTA	ATT.A	.AACC
Τ.	rubescens	.CTT.	TAAT	ATA.A.	AG.CTA	A.C.AC	TA.A
Ν.	japoniça	.CTT.	\underline{T} \underline{T}	<u>T</u> ACAA	.T.AATTT.A	ATA.AC	A.A
В.	ırregularıterdentatum	.CG.A.	1T	TAAA.	AGA	ATT.A	TA.A
A.	ιατα		ACA.CAT	IIAC	.AAA	A.A.AAC.	A. <u>TA</u> .A
м. с	anogania		AIAIA.		.GA.GAA	AIA.AC.	1
э. т	gregaria omma						1II.A
1.	domesticus				· · · · · · · · · · · · · · · · · · ·		AC.
н. Л	maritima				······································	. T T . A C . C	AC.
0	fasciatus		Δ ΓΛΛΓ	Δ Τ Λ Λ	. IA I . TT		ΑC. Τ ΛΟ
<u> </u>		1 A . D U . A I		A		AII.4C.1	AC.

182	
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							240
S.	taiwanensis	ATTGAAGTAA	CTTGAACTAT	TGCACCCGCA	ΑΤCΑΤCΤΤΑΑ	TTTTTATTGC	TATCCCATCT
L.	dimidiatipes	G	A	C	TTC.T.	.CC	СТ.АА
Ρ.	fulginosa	G	• • • • • • • • • • •	TA	G.ATCG		AG.A
R.	speratus	ACT.	.AA	G	G	.A	AAC
L.	longipes	GAC.C	TGA	CA	TTCG	.A	Α
Ζ.	angusticollis	CT	ΤΑ	AT	G.ACG	.ACA.	CTC
Τ.	angustipennis	T.AA.CC	ΤΑ	.TTGT	G.AG.T		AT.AT
S.	maculata	T.GA.CC	TCA	.CTTTT	G.AG.T		AC.T
G.	nipponensis	A	Τ	.AAT	G.ACT	.CCC	AC
Τ.	rubescens	T	TAG.	.A.GT	T.A.CAT	C	A.CA
N.	japonica	T	TAG.	AAA	A.CAT		A.CATC
Β.	irregulariterdentatum	T	TG	.ATT	A.C.CT	.A	A.CAA
Α.	lata	AC	ΤCC.	.ATTTA.T	T.CA	.C	AC.AA
М.	alliaceus	ACT.	ТС.С	ATTA	T.CAC	.CC	ΑΤ.ΑΑ
S.	gregaria	AC	TCAGC	.TTA	T.CA		CC.TA
Τ.	emma	A.T.	Τ	.TTTT	CA		.T.AT
Α.	domesticus	A.T.	ΤC	.TT			ΑΤ.ΑΑ
Α.	maritima	T.	TG		G.T.CT.	Δ	ΤΟΤΔ
0.	fasciatus		Τ	ΔΑΤΤΔΤ	ТСА	с	
							CC.A
							300
s.	taiwanensis	TTACGATTAT	TATATTTAAT	AGATGAAATT	ΑΑΤΑΑΤCCCA	CTATCACTTT	ΑΑΑΑΑ
L.	dimidiatipes	CC			A.	.CT.AA	
Ρ.	fulginosa	с.т.		C	A.	.AG.TA	A
R.	speratus	CGC.TC	C	C	C.CCAG	.AACC.	G.AG.A
L.	longipes	сссс	C	CGC	C.CCAG	ΤΑΑΑC.	((G
Ζ.	angusticollis	CC	CC.T		C.CCA.		(((
Τ.	angustipennis	C.TTA.T.		ΤΑC	ΤCΑ		
s.	maculata	C.TCA.T.	· · · · · · · · · · · · · · · · · · ·	Τ	ТСС		
G.	nipponensis	T.G. TC	.T			۲۸۰۰ ۲	Δ
Τ.	rubescens	C	.T	C	CA.	ΤΑΑΑ(GG.A
Ν.	japonica	Τ			T.	ΤΑς.ΑΑΑ.	Τ
Β.	irregulariterdentatum	СТСС	.C		GAG.	.ΑΑΑC	GG AG G
A.	lata	СС.ТС		TTC	G ΔG ΔΤ	ΤΔ Τ Δ	Τ Δ
М.	alliaceus		CC.		GCAG. G.AT	ΤΔΤΔΔ.	Т
s.	gregaria	C			GTAG. G.A.	ΤΔΤΔΔ.	ТС
Τ.	emma	T		ТС.	TAG	ΤΔΤΔΔ	Δ
Α.	domesticus			ТС	TAG	ΤΔ ΔΔ	Δ
Α.	maritima		GT	G T G	тс		д
0.	fasciatus	CATC.T.		Т	СТС		ТСТ
		ci i Arci i i	••••			AAACC.	1
							360
S.	taiwanensis	GGTCATCAAT	GATATTGAAG	CTATGAATAT	TCAGATTTTC	TAAAAGTT	-GAATTTGAT
L.	dimidiatipes	A					-
Ρ.	fulginosa	G.		Τ		C	-
R.	speratus	A	C	Α	Δ	C C Δ	- ((
L.	longipes	AC			С А	C C C	- (
Ζ.	angusticollis	A C		Т		T A	_
Τ.	angustipennis	A		Т		$CTC T \Lambda_{}$	
s.	maculata			Т	····C	G A	
G.	nipponensis			·····		((A	
Τ.	rubescens	Α	· · · · · · · · · · · · · · · · · · ·	Δ			- · · · · · · · · · · · · · · · · · · ·
N.	iaponica		····· · · · · · · · · · · · · · · · ·	Τ	T A		
Β.	irreaulariterdentatum		·····	т.	••••••••••••••••••••••••••••••••••••••	ATC CA A	
A.	lata			, т	•••••A	TA	
Μ.	alliaceus		•••••	т с	•••••A	····IA··	C
S.	areaaria	Δ. GA	· · · · · · · · · · · · · · · · · · ·	Λ	····A		
Τ.	emma	Δ.	тс	Λ	••••C••CΑ ΔΤ Δ	u.cA	 T
À.	domesticus	Δ	тс	π	ΛΙ····Α ΛΤ Α		1 C
Α.	maritima		·····	~···· T	міА т	ΑΙΑ.(ΑΙ Τ Γ	
ο.	fasciatus	A		Δ	····ι Τ CΛ	Δ ΤΛ	
	-	· · · · · · · · · · · · ·			· · · · · · · · · · · · · · · · · · ·	~ • • • • • • • •	

S. taiwanensis TCATACATA TCCACAAAA TCAAATAGT AATGAACAT TTCCATACT TGATGAGT J. dimidiatipes T T								420
L dimidiatipes .T. T. T. T	S.	taiwanensis	ΤCΑΤΑCΑΤΑΑ	TCCCACAAAA	TGAAATAAGT	AATGAAACAT	TTCGACTACT	TGATGTAGAT
P. Fulginosa	L.	dimidiatipes	T	.TT	AA	.TAA.T.AT.	.CT.	Α
R. speratus	Ρ.	fulginosa	TT	.TC	CGAA	A.T.T	TT	A
L. longipes	R.	speratus	T	.TGG.	GACCAA	CCAAGC.	T.	GCACC
2. angusticollis	L.	longipes	G	.A.AG.	ACCA.CCA	.T.A.TG		AAC
7. angustipennis G.TT T.T	Ζ.	angusticollis		CAT.TG.	AGAT.AC	GAT		AAACCC
S. maculata	Τ.	angustipennis	G.TT	.TT	A.	CCCT.T.ATA	TT.	AAT
G. nipponensis .T	S.	maculata	T	.TT	C.T.AC	TTAT.T.ATA	CT	AT
1. rubescens	G.	nipponensis	T	CACC.T	CGGAA	.CAAGG	.CT.	A
M. japonica T.I	1.	rubescens	•• <u>T</u> •• <u>T</u> ••••	. <u>T</u>	.A.TGAA.	A.TGAT.	.AT	A
B: Irregulariterdentatum I.T. I. AATGG, G. A. CC. T. A. TAA, CG. C	N.	japonica	· · T · · <u>T</u> · · · ·	·T	.CGAA.	GT.A.TGATA	.ATT.	A
A. lata A. T. J AAATG. GG. ACC. T.AA TAA. C. G. C	в.	irregulariterdentatum	··· <u>·</u> ·· <u>T</u> ··· <u>·</u>	.A	.A.TGA.TCA	AA.T.GT.	GT <u>.</u> .	A
M. altraceus A.TT CAG. CA. C.C. GAA T.GGCT C.TT. CAG., CA. A.C.C., GAA T.GG. A.C.TT. CAG.TTI.G. A.G. A.C. T.G. A A A T.G. A C.T. T.G. A.C. C.G. A.C. C.C. C.G. A.C. C.C. C.G. A.C. C.C. C.G. A.A. A.C. C.C. C.G. A.A. C.G. A.A. C.C. C.G. A.A. C.C. C.G. A.A. C.C. T.T. A.A. C.C. C.C. A.A. C.G. A.A. C.G. A.A. C.G. A.A. C.G. C.G. A.A. C.G. A.G. C.C. T.T. A.G. T.T. C.G.	Α.	lata	A.III	.AAAIG.GG.	ACC.T.AA	.TAA.C.G.C	· · · · · · · · · T ·	AC
S. pregaria A. 1 CAG. L. A. C.C A. C.C	м.	alliaceus	A.II	CAGG	A	TGG	.CT	· · · · · · T · · ·
1. emma	5.	gregaria	A.TT	CAGC.	ACCGAA	TGG	· · · · <u>·</u> · · <u>·</u> · ·	A
A. domesticus	1.	emma	<u>C</u> <u>I</u> <u>I</u>	CAG.III.G.	.A.GA	TCA	· · · · <u>I</u> · · <u>I</u> · ·	AG
A. maritima	Α.	domesticus	· · I · · <u>I</u> · · · I	CAG.C.I.G.	.ATA	ТСА	.ctt <u>.</u> .	ACC
0. Tasciatus AAAC CIIA AA.IGA 480 S. taiwanensis AACCGAGCCA GATTACCAAT AAATTCTTTT ATTCGAATTA TTATTACAGC AACTGATGTC L. dimidiatipes T. T. A.C.CC A.A G.A G.A G.A G.A G.A G.A G.G TAT. T TT TT TT TT G.C.C.T.T AAA	Α.	maritima	· · · · · <u> </u> · · · ·	. I I I C I G .	GIC.I.TA	.TAAGTGGG.	$\cdots \overline{1}$	G.GGI
480 S. taiwanensis AACCGAGCCA GATTACCAAT AAATTCTTT ATTCGAATTA TTATTACAGC AACTGATGTC J. dimidiatipes .T. T. AC CCC. T. T	0.	fasciatus	••••	AAAC	CTTA	A.TGA	T.	AACC
5. taiwanensis AACCGAGCCA GATTACCAAT AAATTCTTT ATTCGAATTA TTATTACAGC AACTGATGTC 1. dimidiatipes								100
S. Cummensis AACCGAUCA GATTACGAT GAAT AGATICTTT ATTGAATTA THATTACAGE AACTGATGT 1. dimidiatipes	c	taiwananaia		CATTACCAAT	AAATTCTTT		TTATTACACC	480
L. diminifiant press 1.1.1.1.AC CCCC.1.1. A.A. 1.1.1.1.AC CCCC.1.1. A.A. P. fulginosa 1.1.1.7G C.CT. A.A. G.A. G.A. G.A. G.A. G.A. G.A. C.A. G.A. G.A. <td>5.</td> <td>dimidiatinos</td> <td></td> <td>GATTACCAAT</td> <td>AAATICITTI</td> <td>ATTCGAATTA</td> <td>TIATIACAGC</td> <td></td>	5.	dimidiatinos		GATTACCAAT	AAATICITTI	ATTCGAATTA	TIATIACAGC	
<i>n</i> . Ingrinsia IIIIIII C.C. IIIIIIIIIIIIIIIIIIIIIIIIII		fulginger			• • • • • • • • • • • • • • • • • • •	• • • • • • • • • •		· · · IA · · · · · I
A. Sperduss ALCA ALCA ALCA ALCA	г. D	ruiginosa	·······		· · · · A · A · · ·		G.A	
L. Iongupes I. A. C. A. I. C. A. I. C. A. I. C. A. C. M. C. A. C. M. 2. angusticellis I. A. C. A. C. C	κ.	speratus	AI.G	$\frac{1}{T}$	ACCA	CC.AG	.AG.A	.G.ACA
2. angustipennis	L. 7	angusticallia			CACCA	• • • • • • • • • •	.CG.A	.G.ACA
A. angust lipemits	Ζ. Τ	angustipoppis		C	CA	·····	.CG.A	CGA
3. midululu CA.A. CI	ι. ς	maculata	····.A.A.	C	· · · · A · · · · A	.CA1	.AI.	.GAA A
G. mipponents	з. с	nippopopoio	CA.A.	CII	····A··C·A		.AI.	. GAA A
1. Japonica	и. Т	rubascans	AII. T ATA		LALAL	CGG.A.		.G.A
M. japonica International Internatedinternatinal International International Internation	N .	ianonica			A.A	· · · · · · · · · A ·	G.AI.	AI
B. Inregulariter dentatum III. AIAG AIAGA AIAGA G.G.A. A.G.G.A.A.G.G.A.A.G.G.G.G.A.A.G.G.G.G	D.	japonica			IGIA		G.AI.	IACA
A. Idua GA.A. T.A.C	D.	lata			A.A	A.		A
M. diffuedus A.H. TCC	А. М	alliacous	·····GA.A.	T.A.C	A.AGAA	GAC	.AA	
3. gregulitu	M.	areania	••••••••••••••••••••••••••••••••••••••		A.CGAA	GGG.AC	.A.CC.G	.I.ACA
7. emma 1.1.1.1.A.A. 111	з. т	omma	····A.A.	TT		G.AG.AI	.A.CA.G	. I . A I
A. domesticus	1.	domosticus	••••••••••••••••••••••••••••••••••••••			CAT	.AG	
A. maritima AAC.IGG IGC.I.I.I. ITAA.CAA G.CG.A.I.GIG	А. Л	aomitima	A			CAT	.AG.A	
5. taiwanensis CTACATTCTT GAACTGTTCC AAGATTAGGA GTAAAAGCAG ATGCAACCCC TGGTCGATTA L. dimidiatipes A. P. fulginosa A. TC. A. AA. CT. R. speratus TC. TC. AA. J. longipes TC. A.T. A.A. J. longipes TC.A. A.T. A.G. J. angusticollis C.A. A.T. A.C. J. angustipennis A.T. A.T. A.A. S. maculata A.T. A.T. A.C. J. poponensis A.C. A.C. A.T. J. japonica A.T. A.T. A.T. A.T. A.T. A. lata A.T. A.T. G.A.	л. О	facciatus				G.CGA	•	
5. taiwanensis CTACATTCTT GAACTGTTCC AAGATTAGGA GTAAAAGCAG ATGCAACCCC TGGTCGATTA 1. dimidiatipes A. A.A.A. C	υ.	rusciulus	•••••••	1	AAGCAA	· · · · · · · · · · · · · · · · · · ·	.A	.G.ACI
S. taiwanensisCTACATTCTT GAACTGTTCC AAGATTAGGA GTAAAAGCAG ATGCAACCCC TGGTGATTAL. dimidiatipesA.P. fulginosa.TA.R. speratusTC.TCA.L. longipesTC.A.MagusticollisA.T. angustipennisA.T.A.T.A.A.S. maculataA.T.A.T.A.A.C. C. A.AA.C.C. IpponensisA.T.A.T.A.A.C. C. A.A.A.S. maculataA.T.A.T.A.A.A.T.A.A.C. C. A.A.A.C. C. C. A.A.A.A.T.A.T.A.T.A.A.C. C. C. C.A.T. <t< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td>540</td></t<>								540
DescriptionCharacteristicCharacteristicCharacteristicCharacteristicCharacteristic1. dimidiatipesAACCTCGC.P. fulginosaAACCT.A.C.G.TA.R. speratusTC.AA.GT.A.C.G.TA.L. longipesTC.AA.GT.A.C.G.A.A.A.C.J. angusticollisTC.AA.GT.A.C.A.A.A.J. angustipennisA.T.A.A.C.CA.A.T.A.G.S. maculataA.T.A.CAA.TC.A.A.A.G. nipponensisAA.CA.T.TCA.N. japonicaA.C.C.AAA.TCACAT.CATT.GT.A.A. lataA.T.A.T.A.T.A.T.A.T.A.A.B. irregulariterdentatumA.T.A.T.G.A.GCC.A.T.A.A.A. lataA.T.A.AGA.GCC.A.T.A.A.A.A.S. gregariaG.AGCL.GT.A.A.A.A.A.A.A.A. domesticusA.T.A.AGA.GCCL.A.T.A.A.A.A. domesticusA.T.G.AGCCL.A.T.A.A.A.A.A.JaponicaA.T.A.T.A.AAA.A.T.A.A.A.A. <td>ς.</td> <td>taiwanensis</td> <td>CTACATTCTT</td> <td>GAACTGTTCC</td> <td>AAGATTAGGA</td> <td>GTAAAAGCAG</td> <td>ΑΤΩΓΑΛΩΓΟΟ</td> <td>TCCTCCATTA</td>	ς.	taiwanensis	CTACATTCTT	GAACTGTTCC	AAGATTAGGA	GTAAAAGCAG	ΑΤΩΓΑΛΩΓΟΟ	TCCTCCATTA
P. fulginosa TA.	Ĩ.	dimidiatines	Δ			T C	TGT	G C
R. speratus TC AA G. G. G. A C. C. A. A. AC. L. longipes TC. A. AA G. G. G. A C. C. A. A. AC. L. longipes TC. A. AAG. TA. A.GC.T Z. angusticollis TC. A. AA.C. CA. A.GC.T J. angustipennis A.TA. AA.C. CA. A.A. S. maculata A.TA. AA.C. TC. TA.T.T. TA. G. nipponensis A.TA. AA.C. TC.T. A.A. Japonica A.CA. ATA. TC.AC. A.T. N. japonica A.TA. TC.AG. AT. GC. A. lata A.TC.G. AA.C. TCACT. GAT. GC. M. alliaceus T.CG.A. GCC. A.T. GC. GC. G.A. G.A. J. emma A.TC. G.A. GCC. A.T. G.A. G.A. G.A. G.A. A. domesticus A.TC. G.A. GCC. G.A. G.A. G.A. G.G. </td <td>Ρ.</td> <td>fulainosa</td> <td>Τ Λ</td> <td>Λ</td> <td>тстт</td> <td></td> <td>· · · · · · · · · · · · · · · · · · ·</td> <td>Λ</td>	Ρ.	fulainosa	Τ Λ	Λ	тстт		· · · · · · · · · · · · · · · · · · ·	Λ
L. longipes TC.A. AG. TC.A. AC. TC.A. AC. TC.A. AC. TC. AA. AC. TC. AA. A A AA. A AA. A AA. A A AA. A AA. A AA. A	R.	speratus	т с	۸۸		G A	C C A	Λ Λ C
Z. angusticollisC.AAA.C. CAA.C. CA.TCA.A.A.T. angustipennisA.TAAA.CAA.TTTT. A.A.S. maculataA.TAAA.CAA.TTTT. A.A.G. nipponensisAA.CAA.CAA.TTTTT. A.A.T. rubescensA.C.C.AAA.CAA.CAA.TTG.TCC.TC.N. japonicaA.TAAA.CATATC.ACATTGTA. A.A.B. irregulariterdentatumA.TATA. TTC.AGATTGTAA.A.A. lataA.TC.GAA.C. TGCTA.T A.TGAA.M. alliaceusC.AGAA.AGCCC AAT. A.TCG. AA.S. gregariaC.AGAAGCTCATTG. AA.T. C. AGAAGCCCA.T. ATTG. AG.A.T. C. AGAAGCCCA.T. ATTG. AG.A.T. C. AGAAGCCCA.T. ATTG. AG.A.T. C. AGAAGCCCA.T. ATTG. AG.A. domesticusA.TCAG.A. maritimaCAG.AA.C. TTCTATTAA.A. maritimaCAGAA.CATTATTATTGG.	Ï.	lonaines	Т С А	Λ G	т	۰	т	Λ.Α
T. angustipennisA.TA.A.CTA.T.TA.TT.A.A.A.S. maculataA.TAA.CT.T.T.A.A.A.G. nipponensisAA.CG.TTG.TT.T. rubescensA.CC.AATATC.AC.A.TT.N. japonicaA.TATA.T.GATTGT.B. irregulariterdentatumA.TCGAT.GATAATA.A. lataA.TCGAT.GATAATA.M. alliaceusC.AAA.C.TGCTA.TA.TCC.S. gregariaC.AGAGCC.A.TAA.A. domesticusA.TCAAGCC.A.TAA.A. maritimaG.AGAGCCC.A.T.A. maritimaG.AGAGCCC.A.T.A. maritimaG.AGAGCCC.A.T.A. maritimaG.AGAGCCC.A.T.A. maritimaG.AGAGCCCATA. MaritimaG.AGCCCATATA. MaritimaG.AGCCCATATA. MaritimaG.AGAGCCCATA. MaritimaG.AGAATATA. MaritimaG.AATATATA. MaritimaATATATATA. M	7.	anausticollis	Γ····C··Α·	ΛΛ (·····	Λ Τ C	C A	A
S. maculataA.TA.A.A.C.A.TT.TT.C.T.A.A.A.A.G. nipponensisA.TA.CA.C.CC.G.TT.C.T.A.A.A.T. rubescensA.C.C.A.ATA.A.TC.AC.ATT.GTA.T.N. japonicaA.TA.T.A.TTC.AG.ATT.GT.A.A.A.B. irregulariterdentatumA.T.CG.ATG.T.A.TCTACTGG.ATT.GT.A.A.A.A. lataA.T.C.G.AAA.C.TGCTA.TA.TC.TAA.A.A.S. gregariaT.C.A.GA.A.GCCCA.T.A.A.G.A.T. emmaA.T.CC.A.A.GCTC.A.T.G.A.G.C.A. domesticusA.TC.G.A.TTCT.T.G.A.T.G.A.GCCC.A. maritimaTG.A.GA.C.TTCT.G.A.T.GT.T.G.A.CA.G.A.C.TTCT.T.G.A.T.GT.C.A.	Τ.	anaustinennis	Δ Τ Δ	Λ (д. тс. Т	тт	Λ
G. nipponensisA.TA.CA.C.C. A.CG.TT.CG.TT.CC.TC.T. rubescensA.CC.A.A.T.A.TC.AC.ATT.GT.A.T.N. japonicaA.TA.T.A.TTC.AG.ATT.GT.A.A.B. irregulariterdentatumA.TCG.ATG.TCTACTGG.ATT.GT.A.A.A. lataA.TCG.AA.C.TGCT.A.T.TC.AC.A.A.M. alliaceus.T.CCGA.GCCCA.T.A.A.S. gregariaC.A.GA.GCCCA.T.G. A.T. emmaA.TCCA.A.GCTC.A.T.A. domesticusA.TCG.A.TTCT.G.A.T.A. maritimaTG.A.TTCT.T.ATT.GT.T.O. fasciatusGAA.C.TCTC.ATT.	s.	maculata	Δ Τ	ΔΔ (Λ Τ	т т		Λ
T. rubescensA.CCA.ATT. C.A.TC.ACATTGTA.TN. japonicaA.TA.TT.A.TTC.AGATTGTA.A.A.B. irregulariterdentatumA.TCGAT.G.TCTACTGG.ATT.G.T.CCAA. lataA.TC.G.AA.C.TGCTA.TA.TT.CTACTAM. alliaceusCA.GAA.GCCCA.TA.A.A.S. gregariaC.A.GATGCGA.T.A.A.T. emmaA.TCA.A.GCTCA.T.G.A.A. domesticusA.TCC.A.GATCGCCTG.A.T.A. maritimaTG.AGATTCTTA.T.GT.T.O. fasciatusCAGAA.C.TCTCATT.GT.T.	G.	nipponensis	Δ	۲۵	с с	с тт	С	с тс
N. japonica A.TA. TTC.AGATT. ATT. GTA. A.A. B. irregulariterdentatum A.TCGAT.G. TCTACTG .GATT. .GT. .CAA. A. lata A.TCG. AA.C. TGCTA.T A.TT. .CTA. M. alliaceus C.A. GTAA. .GCCCATT. CTA. S. gregaria C.A. GAATGCG ATT. GAA. T. emma A.TC. AAGCTC A.TG. A.TG. A. domesticus A.TC. C.A. .GCCCT .G.A.T. A. maritima TG.A. GAA TTCTT ATT. O. fasciatus AGAA.C. ATGATT. A.A.	Τ.	rubescens	A.CCA.	ΔΤΔ		ΔΤΤ	с бт	Δ Τ
B. irregulariterdentatum A.TCG A.T.G TCTACTG GATT. GT. A. lata A.TC.G. AA.C. TGCTA.T A.TT. GT. GT. M. alliaceus CA. GAA. .GCCC A.TATT. G. A.A. S. gregaria CA. GAA. .GCCC A.TATT. G. A.A. T. emma A.TC A.A. .GCTC A.T. AG. A. domesticus A.TC. G.A. AI. ATT. G. A. maritima TG. G.A. GA TCTC A.A. GT. O. fasciatus G. AI.G. GTC AIT. G.	Ν.	japonica	Α.ΤΔ	ΤΔ	TTC.AG	ΔΤΤ	GT A	ΑΑ
A. lata A.TCG. AA.C TGCTA.T A.TT CTA M. alliaceus CA. GAA. .GCCC A.TATT. T.A. S. gregaria CA. GA TGCTG. T.ATT. G.A. T. emma A.TC AA. GCCC A.TG. AG. A. domesticus A.TC. AA. GCCCT A.T. G. A. maritima TG. GA. TTCTT A. A.TG. O. fasciatus G. GAA.C. ATC. ATT. GAA.C.	Β.	irregulariterdentatum	A.TCG.	AT.G.	TCTACT	G ATT	G. T	
M. alliaceus TCG.AAGCCCA.TATT. S. gregaria CAG.ATGCG.TATT. T. emma A.TCAG.ATGCGA.T. A. domesticus A.TCAG.ATGCCT. A. maritima TG.AG.ATTCTT. O. fasciatus G.AG.ATCTC	Α.	lata	A.TCG		TGCT. A T	Δ.ΤΤ	τΔ	
S. gregaria C.AG.A TGCGTATTG. AG T. emma A.TCAAGCTC A.TA.T. AA A. domesticus A.TCG.A TGC.CTGA.TA.T. AA A. maritima TG.AG.A TTCTTATTGTTGG O. fasciatus G.AG.AA.CTCTC ATTA.AATC.T	М.	alliaceus		G.AA	GCCC	Α.Τ. ΔΤΤ	ΤΔ	ΔΔ
T. emma A.TCAAGCTCA.TA.T. AAA. A. domesticus A.TCCT. CGCCCTGA.TCA. A. maritima TG.AGA TTCTTATTGTTGG O. fasciatus CAG.AA.C TCTC ATTA.AAAA.	s.	gregaria	A	G.A	TGC	Τ ΔΤΤ	G	Δ G
A. domesticus A.TC. CT. CGCCCT CGCCCCT CGCCCCT CGCCCCT CGCCCCT CGCCCCT CGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	Τ.	emma	A.TC	ΔΔ	GCTC	Δ.Τ	Τ Δ	Α
A. maritima TG.A TTCTT GTT. GG 0. fasciatus A. G.AA.C. CTCTATT. GTT. GG	A.	domesticus	Α.Τ		CGCCC	G. Δ T		Δ
0. fasciatusCAG.AA.CTCTC ATTT.A AATC.T	A.	maritima	Τ	G.A	TTCT	ΔΤΤ	GT T	
	0.	fasciatus	CA.	G.AA.C	.тстс	ATT.	TA	AATC.T

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							600
S.	taiwanensis	ΑΑΤCΑΑΑCAA	GTTTCCTAAT	TACCCGACCA	GGAGTATTTT	ATGGTCAATG	TTCAGAAATC
L.	dimidiatipes	• • • • • • • • • • •	.AT	C.AT	A.TC.	Τ	T
Ρ.	fulginosa	CTT.	.ATT	ATT	TTA.	A	СТ
R.	speratus	C	.ATC	C.AT.ACT	TA.CC.A.	A	C
L.	longipes	T	.ATTC	AT	CTC.A.	.CA	T
Ζ.	angusticollis	T	.ATA	ACC	CC.C.		C
Τ.	angustipennis	G	CATTG.T.	ATTT	C.	.CAG	T
s.	maculata	G	CATTG.T.	ATTT	TC.		
G.	nipponensis	CT.G	.GA.AT	AG	C.AC.	.CA	С
Т.	rubescens	CG	.AGAT.	A.ATAAT	TA.A.		TT
Ν.	japonica	G.T.	.AAAT.	A.ATTAAT	TA		ССТ
Β.	irregulariterdentatum	G	.AA.AAT.	A.AAAT	GTA.A.	TG	
A.	lata	CG	ΤΑΑΑ	AT	TA	ΤG	СТ
М.	alliaceus	GG	CATAC	ATTT	TTC.	ΤС	TT
s.	gregaria	GG	CAAC	A.ATT	C.	ΤΑ	C
Τ.	emma	TT.	ACTA	ATT	T	A	
A.	domesticus	G.TT.	AA	C.AT	T	A	C
Α.	maritima	GGTT.	.ATTATT.	A.ATGG.T	GT	G	TT
0.	fasciatus	GG	.AA.TAA	AC	A.TA.	TCG	T
							660
s.	taiwanensis	TGTGGAGCAA	ATCATAGATT	ΤΑΤΑCCAATC	GTTATTGAAA	GAATTTCAAT	ΤΑΑΤΑΑΤΤΤΟ
L.	dimidiatipes	T.		T		C.T	C.GA
Ρ.	fulainosa	G	C	TT		C	A
R.	speratus		C	СТ	ACA C	G.AGGC	AC.C
L.	lonaipes	C		CG		G.AGC	Α
Ζ.	anausticollis		(Δ	G A C	ΔΔΤ
Τ.	anaustinennis			Т	Δ		Δ
s.	maculata	G	C	C T	Δ		
G.	nipponensis	G T	сс	с			(
T.	rubescens	Δ		с тт		G AC	СТ
N.	iaponica	Δ	• • • • • • • • • • •	т			
В.	irreaulariterdentatum	ΤΔ Τ	• • • • • • • • • • •	т	G		
Δ.	lata	•••••	·····	с тт	ΛC Λ		ΔΟΤΔ
М.	alliaceus	••••			6	C G	
S.	areaaria	т	·····	т	Λ	C G	Λ ΤΤΛ Τ
Τ.	emma	тт	с т	•••••	Λ	G AAATT	
Δ.	domesticus	Т	····c··	тт	Λ (G AAATTC	Λ Λ
A.	maritima	Т	•••••	·····	· · · · · · · · · · · · · · · · · · ·		
0	fasciatus	•••••	·····	с тт	· · · · · · · · · · · · · · · · · · ·		••••••••••••••••••••••••••••••••••••••
۰.	, ascrutus	• • • • • • • • • • •		C	• • • • • • • • • • •		· · · A · · C · · ·
					693		
S.	taiwanensis	ΔΤΤΔΔΟΤGΔΔ	ΤΓΓΑΤΑΛΑΤ	AAATTAG			
Ĩ.	dimidiatines	Δ			T		
Р.	fulainosa	т	ΤΔ	G AT			
R.	speratus	G		GAG AT			
ï.	lonaines	т.		GAG AT			
7.	anausticollis	G A					
T.	angustinennis	Т Л Т					
s.	maculata	Т Л Т					
G.	ninnonensis						
т.	rubescens	Λ		G.GAAGCI			
N.	ianonica	····Α···· Λ					
R	irregulariterdentatum	Α					
Δ.	lata	АG л т	ATTA	т			
л.	alliacous	·····A···I	.AAGAII.	····			
ς.	areaaria	······································		···IC·			
у. Т	omma	····/		····			
1.	domesticus						
Δ.	maritima		. IA.A IIA	CICA.CAI			
0	fasciatus			TTAACTACC	 TA A		
0.	I USCIULUS	I.AA	• IA. C IC	. I TAAGTAGC	IAA		