

## REFERENCES

- Altschul, S.F. Gish, W., Miller, W., Myers, E.W., and Lipman, D.J. 1990. Basic Local Alignment Search Tool. J. Mol. Biol. 215 : 403-410.
- Apples, J.B., and Honeycutt, R.L. 1986. rDNA : Evolution over billion years. In DNA systematics. Vol. 2. Dutta., S.K. (ed.). CRC Press, Boca Raton, Fla. pp. 81-135.
- Black, W.C., IV, McLain, D.K. and Rai, K.S. 1989. Patterns of variation in the rDNA cistron within and among World populations of a mosquito, *Aedes albopictus* (Skuse). Genetics 121 : 539-550.
- Borror, D.J., Delong, D.M., and Triplehorn, C.A. 1976. An introduction to the study Of insects. New York : Rinehart and Winston. pp. 690 – 699.
- Cano, R.J., Poinar, H.N., Pieniazek, N.J., Acra, A., and Poinar JR, G.O. 1993. Amplification and sequencing of DNA from a 120-135. Million-year-old weevil. Nature 363 : 536-538.
- Cavalier-Smith, T. (editor) 1985. The evolution of genome size. Wiley, NY. pp. 313.
- Cavalli-Sforza, L.L., and Edwards, A.W.F. 1967. Phylogenetic analysis : Models and estimation procedures. Evolution 21 : 550-570.
- Chen, W., Hoy, J.W., and Schneider, R.W. 1992. Species-specific polymorphisms in transcribed ribosomal DNA of five *Pythium* species. Exp. Mycol. 16 : 22-34.
- Collins, F.H., Porter, C.H. and Cope, S.E. 1990. Comparison of rDNA and mtDNA in the sibling species *Anopheles freeborni* and *A. hermsi*. Am. J. Trop. Med. Hyg. 42 : 417-423.
- Estoup, A., Solignac, M., Harry, M., and Cornuet, J.-M. 1993. Characterization of (GT)<sub>n</sub> and (CT)<sub>n</sub> microsatellites in two insect species : *Apis mellifera* and *Bombus terrestris*. Nucleic Acids Res 21 : 1427-1438.
- Estoup, A., Solignac, M., and Cornuet, J.-M. 1994. Precise assessment of the number of patriline and of genetic relatedness in honeybee colonies. Proc. R. Soc. Lond. B 258 : 1-7.

- Estoup, A., Garnery, L., Solignac, M., and Cornuet, J.-M. 1995. Microsatellite Variation in honey bee (*Apis mellifera* L.) population : Hierarchical genetic structure and test of the infinite allele and stepwise mutation models. Genetic 140 : 679-695.
- Estoup, A., Solignac, M., Cornuet, J.-M., Gouget, J., and Scholls, A. 1996. Genetic differentiation of continental and island populations of *Bombus terrestris* (Hymenoptera : Apidae) in Europe. Mol. Ecol. 5 : 19-31.
- Felsenstein, J. 1993. PHYLIP : phylogeny inference package (version 3.56 C) University of Washington Seattle, USA.
- Garnery, L., Cornuet, J.-M., and Solignac, M. 1992. Evolutionary history of the honeybee *Apis mellifera* inferred from mitochondrial DNA analysis. Mol. Ecol. 1 : 145-154.
- Garza, J.C., Slatkin, M., and Freimer, N.B. 1995. Microsatellite allele frequencies in humans and chimpanzees with implications for constraints on allele size. Mol. Biol. Evol. 12 : 594-603.
- Gojmerac, W.L. 1980. Bee, Beekeeping, Honey and Pollination. Westport : The AVJP publishing company. pp. 27 – 55.
- Gutell, R.R., Larsen, N., and Woese, C.R. 1994. Lessons from evolving rRNA : 16S and 23S rRNA structures from a comparative perspective. Microbiol. Rev. 58 : 10-26.
- Hall, H.G., and Smith, D.R. 1991. Distinguishing African and European honeybee matrilineages using amplified mitochondrial DNA. Proc. Natl. Acad. Sci. USA. 88 : 4548 – 4552.
- Higgins, D.G., and Sharp, P.M. 1988. CLUSTAL : a package for performing multiple sequence alignment on a microcomputer. Gene 73 : 237-244.
- Hillis, D.M., and Davis, S.K. 1986. Evolution of ribosomal DNA : fifty million years of recorded history in the frog genus *Rana*. Evolution 40 : 1275-1288.
- Hillis, D.M., and Dixon, M.T. 1991. Ribosomal DNA : molecular evolution and phylogenetic inference. Quarterly Review of Biology 66 : 411-453.

- Hsiao, C., Chatterton, N.J., Asay, K.H., and Jensen, K.B. 1994. Phylogenetic relationships of 10 grass species : an assessment of phylogenetic utility of the internal transcribed spacer region in nuclear ribosomal DNA in monocots. Genome 37(1) : 112-120.
- Karl, S.A., Bowen, B.W., and Avise, J.C. 1992. Global population genetic structure and male-mediated gene flow in the green turtle (*Chelonia mydas*) : RFLP analysis of anonymous nuclear loci. Genetics 131 : 163-173.
- Karl, S.A., and Avise, J.C. 1993. PCR-based assays of Mendelian polymorphisms from anonymous single-copy nuclear DNA : techniques and applications for population genetics. Mol. Biol. Evol. 10 : 342-361.
- Li, W.H., Luo, C.C., and Wu, C.I. 1985. Evolution of DNA sequences. MacIntyre, R.J. (ed.), Molecular evolutionary genetics. Plenum, New York. New York, USA.
- Limbipichai, K. 1990. Morphometric studies on the eastern honey bee (*Apis cerana* Fabricius) in Thailand and the Malaysian peninsula. Master's Thesis. Department of Biology, Chulalongkorn University.
- Mindell, D.P., and Honeycutt, R.L. 1990. Ribosomal RNA in vertebrates : evolution and phylogenetic applications. Annu. Rev. Ecol. Syst. 21 : 541-566.
- Moritz, R.F.A., Kryger, P., Koeniger, N., Estoup, A., and Tingek, S. 1995. High degree of polyandry in *Apis dorsata* queens detected by DNA microsatellite variability. Behav. Ecol. Sociobiol. 37 : 357-363.
- Nakamura, J., Wongsiri, S., and Sasaki, M. 1991. *Apis cerana* on Samui Island and its beekeeping. Honeybee Science. 12(1) : 27 : 30.
- Oldroyd, B.P., Smolenski, A., Cornuet, J.M., Wongsiri, S., Estoup, A., Rinderer, T., and Crozier, R.H. 1995. Levels of polyandry and intracolony genetic relationships in *Apis florea*. Behav. Ecol. Sociobiol. 37 : 329-335.
- Oldroyd, B.P., Clifton, M.J., Wongsiri, S., Rinderer, T., Sylvester, H.A., and Crozier, R.H. 1997. Polyandry in genus *Apis*, particularly *Apis andreniformis*. Behav. Ecol. Sociobiol. 40 : 17-26.

- Oldroyd, B.P., Clifton, M.J., Parker, K., Wongsiri, S., Rinderer, T.E., and Crozier, R.H. 1998. Evolution of mating behavior in the Genus *Apis* and an estimate of mating frequency in *Apis cerana* (Hymenoptera : Apidae). Ann. Entomo. Soc. Am. 91 (5) : 700-709.
- Packer, L., and Owen, R.E. 1992. Variable enzyme systems in the Hymenoptera. Biochem. Syst. Ecol. 20 : 1-7.
- Pamilo, P.S.L., Varvic-Aho, and Pekkarinen, A. 1978. Low enzyme gene variability in Hymenoptera as a consequence of haplodiploidy. Hereditas 88 : 93-99.
- Pamilo, P.S.L., and Crozier, R.H. 1981. Genetic Variation in male haploids under deterministic selection. Genetics 98 : 190-214.
- Paskewitz, S.M., Wesson, D.M., and Collines, F.H. 1993. The internal transcribed spacers of ribosomal DNA in five members of the *Anopheles gambiae* species complex. Insect Mol. Biol. 2(4) : 247-257.
- Pramual, C. 1994. DNA analysis of Genetic Diversity of *Apis cerana* Fabricius in Thailand. Master's Thesis. Department of Biology, ChulalongKorn University.
- Promega, 1996. Technical manual for OmniBase DNA cycle sequencing system. Promega : Medison.
- Pootong, S. 1999. Investigation of genetic variation among Thai honeybee *A. cerana* using mitochondrial DNA control region. Master's Thesis. Department of Biochemistry, ChulalongKorn University.
- Queller, D.C., Strassmann, J.E., and Hughes, C.R. 1993. Microsatellites and Kinship. Trends Ecol. Evol. 8 : 285-288.
- Raymond, M., and Rousset. 1995. GENEPOP (Version 1.2) : a population genetics software for extract tests and ecumenicism. J. Heredity 86 : 248-249.
- Rinderer, T.E., Wongsiri, S., Kuang, B., Liu, J., Oldroyd, B.P., Sylvester, H.A., De Guzman, L., Kuang, H., Dong, X., and Zhai, W. 1996. Comparative nest architecture of the dwarf honey bees. J. Apicultural Res. 35(1) : 19-26.

- Rubinsztein, D.C., Amos, W., Leggo, J., Goodburn, S., Jain, S., Li, S.H., Margolis, L., Ross, A.A., and Ferguson-Smith, M.A. 1995. Microsatellite evolution-evidence for directionality and variation in rate between species. Nat. Genet. 10 : 337-343.
- Ruttner, F. 1988. Biogeography and Taxonomy of Honey Bee. Springer-Verlag : Berlin. pp. 120 – 166.
- Saitou, N., and Nei, M. 1987. The neighbor-joining method : a new method for reconstructing phylogenetic trees. Mol. Biol. Evol. 4 : 406-425.
- Sappal, N.P., Jeng, R.S., Hubbes, M., and Liu, F. 1995. Restriction fragment length polymorphisms in polymerase chain reaction amplified ribosomal DNAs of three *Trichogramma* (Hymenoptera : Trichogrammatidae) species. Genome 38 : 419-425.
- Sheppard, W.S., and McPheron, B.A. 1991. Ribosomal DNA diversity in Apidae. In D.R. Smith (ed.), Diversity in the Genus *Apis*. Oxford : Westview Press. pp.89 – 102.
- Sihanuntavong, D. 1997. Genetic variation in mitochondrial genes of honey bee *Apis cerana* in Thailand. Master's Thesis. Department of Biotechnology, Chulalongkorn University.
- Sites, J.W., Jr., and Davis, S.K., 1989. Phylogenetic relationships and molecular variability within and among six chromosome races of *Sceloporus grammucus* (Sauria, Iguanidae), based on nuclear and mitochondrial markers. Evolution 43 : 296-317.
- Smith, D.R. 1991. African bees in the Americas : insights from biogeography and genetics. Trans Ecol. Evol. 6 : 17-21.
- Songram, O. 1997. Genetic variation of *Apis cerana* in Thailand inferred by PCR-RFLP analysis of the mitochondrial ATPase6-ATPase8 gene. Master's Thesis. Department of Biochemistry, Chulalongkorn University.

- Tang, T., Toe, L., Back, C., and Unnasch, T.R. 1996. Intra – specific heterogeneity of the rDNA internal transcribed spacer in the *Simulium damnosum* (Diptera : Simuliidae) complex. Mol. Biol. Evol. 13(1) : 244-252.
- Tangjingjai, W. 1998. Sequence variation in internal transcribed spacer region of ribosomal DNA from *Tropilaelaps clareae*. Master's Thesis. Department of Biotechnology, Chulalongkorn University.
- Tautz, D. 1989. Hypervariability of Simple sequences as a general source for polymorphic DNA markers. Nucl. Acids Res. 17 : 6463 – 6471.
- Tingek, S., Mardan, M., Rinderer, T.E., Koeniger, N., And Koeniger, G. 1988. Rediscovery of *Apis vechti* (Maa, 1953) : the Saban honey bee. Apidologie. 19 (1) : 97 – 102.
- Turbeville, J.M., Pfeifer, D.M., Field, K.G., and Raft, R.A. 1991. The phylogenetic status of arthropods as inferred from 18S rRNA sequences. Mol. Biol. Evol. 8 : 669-686.
- Uthaisang, W. 1994. Preparation of DNA probe for the analysis of genetic variation in *Apis cerana*. Master's Thesis. Department of Biochemistry, Chulalongkorn University.
- Valdes, A.M., Slatkin, M., and Freimer, M.B. 1993. Allele frequencies at microsatellite loci : stepwise mutation model revisited. Genetics. 133: 737 – 749.
- Verma, L.R. 1992. Species and genetic diversity in Himalayan honeybee. In L.R. varma (ed.), Honeybees in mountain agriculture. Boulder : Westview Press. pp. 39 – 49.
- Vogler, A.P., and DeSalle, R. 1994. Evolution and Phylogenetic information content of the ITS-1 Region in the Tiger Beetle *Cicindela dorsalis*. Mol. Biol. Evol. 11(3) : 393-405.
- Weber, A. O. M., and Wong, C. 1993. Mutation of human short tandem repeats. Hum. Mol. Genet. 2 : 1123-1128.

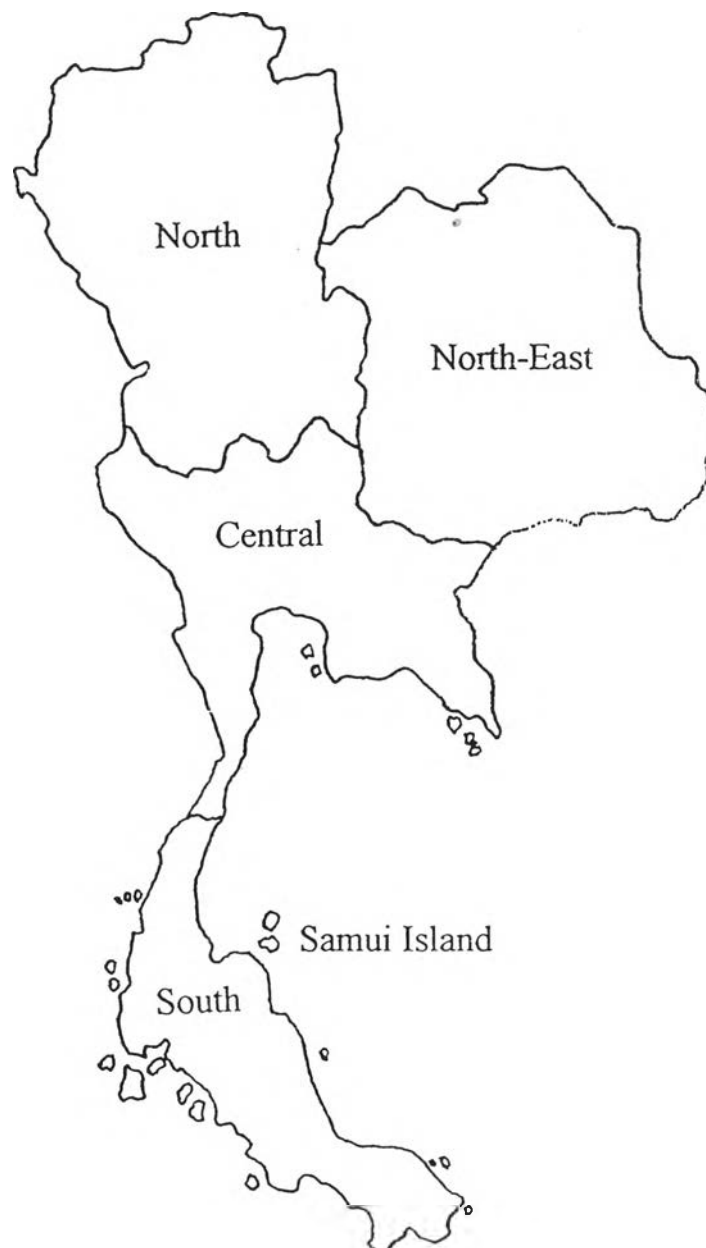
- Weissenbach, J., Gyapay, G., Dib, C. Vignal, A., Marisette, J., Millasseau, p., Vaysseix, G., and Lathrop, M. 1992. A second generation linkage map of the human genome. Nature 359 : 794-801.
- Wetton, J.H., Carter, R.E., Parkin, D.T., and Walters, D. 1987. Demographic study of a wild house sparrow population by DNA fingerprinting. Nature 327 : 147-149.
- White, T.J., Bruns, T., Lee, S., and Taylor, J. 1990. Amplification and direct sequencing Of fungal ribosomal RNA genes for phylogenetics. In Innis, M.A., Gelfand, D.H., Sninsky, J.J., and White.T.J. (eds), PCR protocols : a guid to methods and applications. Academic Press, San Diego. pp. 315 – 322.
- Wongsiri, S., and Tangkanasing, P. 1987. Mites, Pests and Beekeeping with *Apis cerana* and *Apis mellifera* in Thailand. American Bee J. 117 : 500-503.
- Wongsiri, S., Limbipichai, K., and Tangkanasing, P. 1990. Evidence of reproductive isolation confirms that *Apis andreniformis* Smith(1958) is a separate species from sympatic *Apis florea* (Fabricius, 1787). Apidologie 21 : 47-52.
- Wongsiri, S. 1992. Beekeeping problems in developing countries of South East Asia. In Varma, L.R. (ed.), Honeybees in mountain agriculture. Boulder : Westview Press. pp. 239 - 247.
- Wongsiri, S., and Chen, P.P. 1995. Effects of agricultural development on honey bees in Thailand. Bee world. 76 (1) : 3 - 5.
- Wright, J.M. 1993. DNA fingerprinting of fishes. In Hochachka, P.W., and Mommsen, T., (ed.), Biochemistry and Molecular biology of Fishes. New York : Elsevier. pp. 57-91.
- Zhen-Ming, J., Guanhuang, Y., Shuangxiu, H., Shikui, L., And Zaijin, R. 1992. The advancement of agricultural science and technology in China. In Varma, L.R (ed.), Honeybees in mountain agriculture. Boulder: Westview Press. pp.133-141.
- Zhuo, L., Sajdak, S.L, and Phillips, R.B. 1994. Minimal intraspecific variation in the sequence of the transcribed spacer regions of the ribosomal DNA of lack trout (*Salvelinus namaycush*). Genome 37(4) : 664-671.

## **APPENDICES**



## APPENDIX 1

Thailand Map indicate sampling locations of *A. cerana*



## APPENDIX 2

BLAST result of ITS region of nuclear ribosomal RNA gene of *A. cerana*

Sequences producing significant alignments:	Score	P
	(bits)	Value
<a href="#">emb Y15966 CTY15966</a> <i>Cladosporium tenuissimum</i> 5.8S rRNA gene and...	844	0.0
<a href="#">qb L25429 CLSRGA</a> <i>Cladosporium cladosporioides</i> ribosomal RNA gen...	833	0.0
<a href="#">emb AJ222808 CSPA808</a> <i>Cladosporium</i> sp. DNA for internal transcri...	801	0.0
<a href="#">qb AF035674 AF035674</a> <i>Loboa lobo</i> internal transcribed spacer 1,...	735	0.0
<a href="#">qb L25431 CLSRGC</a> <i>Cladosporium herbarum</i> ribosomal RNA gene fragment	726	0.0
<a href="#">qb L25432 CLSRGD</a> <i>Cladosporium oxysporum</i> ribosomal RNA gene frag...	724	0.0
<a href="#">qb L25433 CLSRGE</a> <i>Cladosporium sphaerospermum</i> ribosomal RNA gene..	718	0.0
<a href="#">emb AJ222807 CSPA807</a> <i>Cladosporium</i> sp. DNA for internal transcri...	333	2e-89
<a href="#">qb AF013228 </a> <i>Hormonema dematioides</i> 18S ribosomal RNA gene, part...	327	1e-87
<a href="#">qb L25430 CLSRGB</a> <i>Cladosporium fulvum</i> ribosomal RNA gene fragment	317	1e-84
<a href="#">qb AF013226 </a> <i>Kabatina thujae</i> 18S ribosomal RNA gene, partial se...	315	5e-84
<a href="#">qb AF027763 </a> <i>Dothidea hippophaeos</i> CBS 186.58 18S ribosomal RNA ...	315	5e-84
<a href="#">qb AF027764 AF027764</a> <i>Dothidea insculpta</i> CBS 189.58 18S ribosoma...	315	5e-84

[emb|Y15966|CTY15966](#) *Cladosporium tenuissimum* 5.8S rRNA gene and partial  
internal transcribed spacers 1 and 2  
Length = 573

Score = 844 bits (426), Expect = 0.0  
Identities = 497/513 (96%), Gaps = 7/513 (1%)  
Strand = Plus / Plus

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Query: 4   gtgaacctgCGGagggatcattacaagtGacccCGGCTaaccaccGGGatgttcataac 63
          |||
Sbjct: 22  gtgaacctgCGGagggatcattacaagtGacccCGGCTaaccaccGGGatgttcataac 81

Query: 64   cctttgtgtCGactctgttgCctcCGGG-cGaccctGcctcGGGCGGGGctccgg 122
          |||
Sbjct: 82   cctttgtgtCGactctgttgCctcCGGGGCGaccctGcctcGGGCGGGGctccgg 141

Query: 123  gtggacacttcaaaactcttgCgtaactttGcagtctgagtaaacttaattaataaattaa 182
          |||
Sbjct: 142  gtggacacttcaaaactcttgCgtaactttGgagtctgagtaaacttaattaataaattaa 201

Query: 183  aactttcaacaacGGatctcttgGttctGcatcgatgaagaacGcagcGaaatGcgata 242
          |||
Sbjct: 202  aacttttaacaacGGatctcttgGttctGgcatcgatgaagaacGcagcGaaatGcgata 261

Query: 243  agtaatgtgaattGcagaattcagTcaatcatcgaatcttt-aacGcacattGcgcccc 301
          |||
Sbjct: 262  agtaatgtgaattGgagaattcagTgaatcatcgaatctttgaacGcacattGcgcccc 321

Query: 302  tggattccGGGGGGcatGcctgttcGagcGtcatttcaccactcaagcctcGcttgGta 361
          |||
Sbjct: 322  tggattccGGGGGGcatGcctgttcGagcGtcatttcaccactcaagcctcGcttgGta 381

Query: 362  ttgggcaacGcggTccGccGcgtGcctcaaatcGaccGgctgggtcttctGtcccct-cg 420
          |||
Sbjct: 382  ttgggcaacGcggTccGccG-cgtGcctcaaatcGaccGgctgggtcttctGtcccctaag 440

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## APPENDIX 3

Collection of *A. cerana* from the North of Thailand

Code of Colonies	Sampling area	Size of allele (bp)			Composite haplotype		
		LocusA28	LocusA107	LocusA113	I	II	III
N1	Muang, Lamphun	118/125	167/167	186/186	ND	AAA	ND
N2	Muang, Uttaradit	118/118	167/167	186/186	AAA	AAA	ND
N3	Muang, Uttaradit	ND	167/167	186/196	ND	ND	ND
N5	Muang, Lamphun	115/115	165/167	186/186	AAA	ND	AAC
N6	Muang, Lamphun	125/125	167/167	186/186	AAA	AAA	ND
N7	San pa tong, Chiang mai	118/118	167/167	186/196	AAA	AAA	ND
N9	San pa tong, Chiang mai	118/118	167/167	186/186	AAA	AAA	AAC
N12	San pa tong, Chiang mai	115/118	167/167	186/196	ND	AAA	ND
N13	Hang dong, Chiang mai	118/121	167/167	186/186	AAA	AAA	AAC
N14	Muang, Uttaradit	ND	167/167	186/186	BAA	AAA	ND
N15	Muang, Phitsanulok	115/120	167/167	182/186	AAA	AAA	AAB
N16*	Muang, Phitsanulok	118/125	167/167	186/196	ADA	AAA	AAC
N17	Muang, Phitsanulok	108/118	167/167	186/186	AAA	AAA	ND
N18	Phayuha khiri, Nakhon sawan	115/118	165/165	186/186	ND	ND	ND
N19	Phayuha khiri, Nakhon sawan	115/121	167/167	186/196	AAA	AAA	ND
N20	Manorom, Chai nat	113/120	167/167	186/186	AAA	AAA	ND
N21	Wat sing, Chai nat	116/116	ND	186/186	AAG	AAA	ND
N22	Muang, Chai nat	118/118	167/167	182/186	AAA	AAA	AAC
N23	Banphot phisai, Nakhon sawan	120/120	167/167	186/186	AAA	AAA	ND
N24*	Banphot phisai, Nakhon sawan	118/118	167/167	186/186	ND	AAA	AAD
N25	Banphot phisai, Nakhon sawan	118/118	167/167	ND	AAA	AAA	ND
N26	Muang, Kamphaeng phet	117/120	167/167	186/196	AAA	AAA	ND
N27	Ban tak, Tak	118/118	167/167	186/196	AAA	AAA	AAC
N28*	Ban tak, Tak	117/120	167/167	186/186	AAA	ND	ND
N29	Sam ngao, Tak	114/118	169/169	186/196	AAA	ACA	ND
N30	Sam ngao, Tak	118/120	158/161	182/196	AAA	ND	AAD

Code of Colonies	Sampling area	Size of allele (bp)			Composite haplotype		
		LocusA28	LocusA107	LocusA113	I	II	III
N31	Sam ngao, Tak	132/132	167/167	186/196	ND	ND	ND
N32	Thoen, Lampang	110/120	156/167	186/196	AAA	AAA	AAC
N33	Thoen, Lampang	117/119	ND	186/186	ND	ND	ND
N35	Mae tha, Lampang	112/120	167/167	186/186	ND	ND	AAE
N36	Mae tha, Lampang	121/121	167/167	186/196	AAA	AAA	ND
N37	Doi saket, Chiang mai	118/126	167/167	ND	AAA	AAA	AAC
N38	Doi saket, Chiang mai	119/119	167/167	186/186	ND	AAA	ND
N39	Doi saket, Chiang mai	121/129	157/167	186/186	AAA	AAA	ND
N40	Doi saket, Chiang mai	118/124	167/167	186/196	ND	ND	AAC
N41	Wiang pa pao, Chiang mai	118/120	167/167	186/196	AAA	ACA	AAC
N42	Wiang pa pao, Chiang mai	115/115	167/167	186/186	AAA	AAA	ND
N43	Wiang pa pao, Chiang mai	118/118	ND	ND	AAA	AAA	AAB
N44	Ngao, Lampang	114/119	158/167	186/186	AAA	AAA	AAC
N45	Sungmen, Phrae	112/117	157/167	186/196	AAA	AAA	AAB
N46	Sungmen, Phrae	119/119	167/167	186/186	AAA	AAA	ND
N47	Sungmen, Phrae	120/120	167/167	186/196	ND	AAA	AAB
N48	Sungmen, Phrae	114/119	159/167	186/186	AAA	AAA	ND
N49	Chom thong, Chiang mai	115/121	157/157	186/196	ND	ND	ND
N50	Chom thong, Chiang mai	118/118	157/157	186/196	ND	ND	ND
N51	Bang rakam, Chiang mai	118/124	167/167	186/196	ND	ND	ND
N52	Bang rakam, Chiang mai	118/124	ND	186/186	ND	ND	ND

I = Composite haplotype of ATPase6-ATPase8 gene of mtDNA digested with *TaqI*, *SspI* and *VspI* (Songram, 1997)

II = Composite haplotype of rRNA gene, lrRNA gene and inter COI-COII of mtDNA digested with *DraI* (Sihanuntavong, 1997)

III = Composite haplotype of mtDNA control region digested with *TaqI*, *RsaI* and *HinfI* (Pootong, 1999)

ND = non determined

\* = ITS amplified product of 580 bp was sequenced

### Collection of *A. cerana* from the Central of Thailand

Code of Colonies	Sampling area	Size of allele (bp)			Composite haplotype		
		LocusA28	LocusA107	LocusA113	I	II	III
C1	Phrapradaeng, Samut prakan	118/118	167/167	186/196	ADA	AAA	ND
C2	Kamphaengsan, Nakhorn pathom	115/115	165/167	ND	AAA	AAA	ND
C3	Dan chang, Suphan buri	118/121	167/167	182/186	AAA	ADA	ND
C4	Muang, Samut songkhram	115/115	158/167	182/186	AAA	AAA	ND
C5	Muang, Samut songkhram	118/118	167/167	186/186	AAA	AAA	ND
C6	Muang, Samut songkhram	120/120	158/158	186/196	AAH	AAA	ND
C7*	Phrapradaeng, Samut phakan	118/118	167/167	186/186	ADA	AAA	ND
C8	Dcn tum, Nakhorn pathom	118/118	167/167	186/196	AAA	AAA	AAD
C9	Dan chang, Suphan buri	113/113	167/167	186/196	AAA	AAA	AAC
C10	Dan chang, Suphan buri	118/126	167/167	196/196	ADA	AAA	AAD
C11	Pong nam ron, Chanthaburi	117/117	167/167	196/196	AAA	AAA	ND
C12*	Makham, Chanthaburi	118/118	167/167	182/196	AAA	AAA	AAC
C13	Makham, Chanthaburi	115/118	167/167	186/186	AAA	AAA	ND
C14	Makham, Chanthaburi	116/116	167/167	196/196	AAA	AAA	ND
C15*	Muang, Trat	118/120	167/167	186/196	AAA	AAA	ND
C16*	Khao saming, Trat	120/120	167/167	186/196	ND	AAA	AAC
C17	Khao saming, Trat	113/118	167/167	186/196	ND	AAA	ND
C18	Muang, Trat	115/121	161/166	186/186	AAA	AAA	AAD
C20	Sam roi yod, Prachuap khiri khan	120/124	157/157	186/196	ND	AAA	AAB
C21*	Sam roi yod, Prachuap khiri khan	110/118	156/156	186/186	ND	AAA	ND
C25	Mae krong, Samut songkhram	118/122	167/167	182/186	ND	AAA	AAB
C26	Mae krong, Samut songkhram	114/114	167/167	196/196	ND	AAA	ND
C27	Mae krong, Samut songkhram	118/118	167/167	186/196	ND	AAA	AAC
C28	Mae krong, Samut songkhram	115/120	167/167	186/196	ND	AAA	AAB
C29	Mae krong, Samut songkhram	118/118	167/167	186/186	ND	AAA	ND
C30	Muang, Samut sakhorn	115/120	167/167	182/186	ND	AAA	ND
C33	Cha-am, Phetchaburi	118/118	167/167	186/186	ND	ND	AAB
C34	Hua hin, Prachuap khiri khan	122/122	157/167	186/186	ND	ND	AAD
C35	Hua hin, Prachuap khiri khan	116/119	167/167	186/186	ND	ND	ND
C36	Pran buri, Prachuap khiri khan	121/121	167/167	186/186	ND	ND	AAD

Code of Colonies	Sampling area	Size of allele (bp)			Composite haplotype		
		LocusA28	LocusA107	LocusA113	I	II	III
C37	Kui buri, Prachuap khiri khan	121/121	167/167	186/186	ND	ND	AAD
C38	Muang, Prachuap khiri khan	114/120	167/167	186/186	ND	ND	AAB
C39	Thap sakae, Prachuap khiri khan	119/125	157/167	186/196	ND	ND	AAB
C40	Thap sakae, Prachuap khiri khan	121/125	167/167	182/186	ND	ND	ND
C41	Bang saphan, Prachuap khiri khan	109/121	167/167	186/196	ND	ND	AAB
C42	Bang saphan, Prachuap khiri khan	119/119	167/167	186/196	ND	ND	ND
C43	Bang saphan, Prachuap khiri khan	ND	167/167	ND	ND	ND	AAB
C44	Bang saphan, Prachuap khiri khan	121/125	167/167	186/186	ND	ND	ND
C45	Bang saphan, Prachuap khiri khan	116/119	167/167	196/196	ND	ND	AAD
C46	Thap sakae, Prachuap khiri khan	115/117	167/167	182/186	ND	ND	AAB
C47	Muang, Samut songkhram	117/123	167/167	182/182	ND	ND	ND
C48	Muang, Samut songkhram	119/123	159/167	182/186	ND	ND	ND
C49	Muang, Samut songkhram	116/118	159/167	182/186	ND	ND	ND
C50	Muang, Samut songkhram	119/122	167/167	186/186	ND	ND	ND
C51	Muang, Samut songkhram	123/127	167/167	182/196	ND	ND	ND
C52	Muang, Samut songkhram	118/121	167/167	186/186	ND	ND	ND
C53	Muang, Samut songkhram	115/120	167/167	186/186	ND	ND	ND
C54	Muang, Samut songkhram	121/121	167/167	186/186	ND	ND	ND
C55	Muang, Samut songkhram	116/116	167/167	186/196	ND	ND	ND
C56	Muang, Samut songkhram	ND	159/167	186/186	ND	ND	ND
C57	Muang, Samut songkhram	120/120	159/159	182/186	ND	ND	ND
C58	Muang, Samut songkhram	123/126	156/159	186/186	ND	ND	ND
C59	Muang, Samut songkhram	116/119	167/167	182/186	ND	ND	ND
C60	Muang, Samut songkhram	116/127	167/167	182/186	ND	ND	ND

I = Composite haplotype of ATPase6-ATPase8 gene of mtDNA digested with *TaqI*, *SspI* and *VspI* (Songram, 1997)

II = Composite haplotype of sRNA gene, lrRNA gene and inter COI-COII of mtDNA digested with *DraI* (Sihanuntavong, 1997)

III = Composite haplotype of mtDNA control region digested with *TaqI*, *RsaI* and *HinfI* (Pootong, 1999)

ND = non determined

\* = ITS amplified product of 580 bp was sequenced

### Collection of *A. cerana* from the North-East of Thailand

Code of Colonies	Sampling area	Size of allele (bp)			Composite haplotype		
		LocusA28	LocusA107	LocusA113	I	II	III
NE1	Na haeo, Loai	112/119	167/167	186/186	ND	ND	ND
NE2	Na haeo, Loai	115/115	167/167	186/196	ND	AAA	ND
NE3	Na haeo, Loai	119/119	167/167	186/196	AAA	AAA	ND
NE14	Muang, Khonkaen	115/123	167/167	186/186	AAA	AAA	ND
NE15	Muang, Khonkaen	118/118	167/167	186/186	ADA	AAA	AAE
NE16	Chum phae, Khonkaen	119/119	167/167	186/186	AAA	AAA	ND
NE17	Chum phae, Khonkaen	120/126	156/167	186/186	AAA	AAA	ND
NE18	Chum phae, Khonkaen	108/112	167/167	186/196	AAH	AAD	ND
NE19	Chum phae, Khonkaen	114/119	167/167	196/196	AAH	ND	ND
NE20	Ubol ratana, Khonkaen	121/121	167/167	186/186	AAA	ACA	ND
NE21	Non sang, Nong bua lamphu	118/120	167/167	186/186	AAA	AAA	AAF
NE22	Non sang, Nong bua lamphu	115/120	167/169	186/196	AAA	AAA	ND
NE23	Non sang, Nong bua lamphu	120/127	167/169	182/186	AAA	AAA	AAB
NE24*	Nong wua so, Udon thani	119/123	159/167	196/196	AAA	AAA	ND
NE25	Muang, Udon thani	119/119	156/167	196/196	AAA	AAA	ND
NE26*	Muang, Udon thani	119/127	158/167	186/186	AAA	AAA	ND
NE27	Muang, Udon thani	116/116	167/167	186/186	AAA	AAA	ND
NE28	Muang, Nong khai	121/121	156/159	186/186	AAA	AAA	ND
NE29	Muang, Nong khai	120/123	165/165	186/196	AAA	AAA	ND
NE30*	Nong han, Udon thani	122/127	157/167	186/186	AAA	AAA	ND
NE31	Phang khon, Sakon nakhon	119/119	167/167	ND	AAA	AAA	ND
NE32	Nong bun nak, Nakhon ratchasima	114/127	167/167	ND	AAA	AAA	ND
NE33	Nong bun nak, Nakhon ratchasima	119/119	167/167	186/186	AAA	AAA	ND
NE34	Nong bun nak, Nakhon ratchasima	121/127	167/167	186/186	AAA	ND	ND
NE35*	Nong bun nak, Nakhon ratchasima	108/125	167/167	196/196	ND	ND	ND
NE36	Kranuan, Khonkean	121/121	159/166	186/196	ND	ND	ND
NE39	Kranuan, Khonkean	117/121	159/167	186/186	ND	ND	ND
NE40	Kranuan, Khonkean	115/117	167/167	186/186	ND	ND	ND
NE41	Kranuan, Khonkean	118/122	167/167	186/186	ND	ND	ND
NE42	Prakhon chai, Buriram	120/120	167/167	186/186	ND	ND	ND



Code of Colonies	Sampling area	Size of allele (bp)			Composite haplotype		
		LocusA28	LocusA107	LocusA113	I	II	III
NE43	Prakhon chai, Buriram	114/118	167/167	186/196	ND	ND	AAC
NE44	Prakhon chai, Buriram	118/126	167/167	196/196	ND	ND	ND
NE45	Prakhon chai, Buriram	114/118	167/167	196/196	ND	ND	ND
NE46	Prakhon chai, Buriram	114/114	167/167	196/196	ND	ND	ND
NE47	Prakhon chai, Buriram	119/119	167/167	186/196	ND	ND	AAD
NE52	Rattanakaburi, Surin	118/125	167/167	186/196	ND	ND	AAD
NE55	Prasat, Surin	119/120	167/167	186/186	ND	ND	AAB
NE56	Prasat, Surin	120/126	167/167	186/186	ND	ND	AAB
NE57	Prasat, Surin	126/126	167/167	186/186	ND	ND	ND
NE59	Prasat, Surin	126/126	167/167	186/196	ND	ND	ND
NE60	Prasat, Surin	126/126	167/167	186/186	ND	ND	ND
NE61	Nong bun nak, Nakhon ratchasima	118/120	159/167	186/186	ND	ND	AAB
NE62	Nong bun nak, Nakhon ratchasima	120/122	159/167	186/186	ND	ND	AAB
NE63	Nong bun nak, Nakhon ratchasima	116/120	159/167	186/186	ND	ND	AAD
NE64	Nong bun nak, Nakhon ratchasima	121/122	167/167	186/186	ND	ND	AAB
NE65	Nong bun nak, Nakhon ratchasima	117/122	167/167	186/196	ND	ND	ND
NE66	Nong bun nak, Nakhon ratchasima	117/118	167/167	186/186	ND	ND	AAD
NE70	Thawatchaburi, Roiet	126/126	167/167	186/196	ND	ND	AAB
NE71	Thawatchaburi, Roiet	122/126	167/167	186/186	ND	ND	ND
NE72	Warin chamrab, Ubon ratchathani	115/126	167/167	196/196	ND	ND	AAB
NE73	Muang, Si sa ket	118/120	167/167	186/196	ND	ND	ND
NE74	Muang, Kalasin	115/120	159/167	196/196	ND	ND	ND
NE75	Muang, Khonkaen	119/120	167/167	186/186	ND	ND	AAB
NE76	Muang, Khonkaen	120/126	167/167	186/186	ND	ND	ND

I = Composite haplotype of ATPase6-ATPase8 gene of mtDNA digested with *TaqI*, *SspI* and *VspI* (Songram, 1997)

II = Composite haplotype of rRNA gene, lrRNA gene and inter COI-COII of mtDNA digested with *DraI* (Sihanuntavong, 1997)

III = Composite haplotype of mtDNA control region digested with *TaqI*, *RsaI* and *HinfI* (Pootong, 1999)

ND = non determined

\* = ITS amplified product of 580 bp was sequenced

**Collection of *A. cerana* from the South of Thailand.**

Code of Colonies	Sampling area	Size of allele (bp)			Composite haplotype		
		LocusA28	LocusA107	LocusA113	I	II	III
S1	Thalang, Phuket	116/120	167/167	186/196	BBB	ND	ND
S2	Muang, Chumphon	121/125	167/167	196/196	CED	AEF	ND
S3	Muang, Chumphon	117/123	167/167	186/196	BBB	ND	ND
S4	Tha chana, Suratthani	123/128	169/169	196/196	ND	ND	BBA
S5	Muang, Chumphon	120/120	167/167	186/186	ND	ND	ND
S6	Tha chana, Suratthani	114/122	167/169	186/196	BBB	ND	BBA
S8	Tha chana, Suratthani	118/124	167/167	196/196	ND	ND	BBA
S9	Tha chana, Suratthani	118/121	167/169	186/186	ND	ND	BBA
S10	Tha chana, Suratthani	ND	159/169	196/196	BBB	ND	BBA
S11	Muang, Phuket	121/121	167/167	ND	ND	BBB	ND
S13	Muang, Phuket	116/126	166/167	186/196	BBB	ND	BBA
S14	Thalang, Phuket	117/119	167/169	196/196	BBB	ND	ND
S15	Thalang, Phuket	ND	167/167	186/186	BBB	ND	ND
S16	Muang, Phuket	126/130	167/167	196/196	BBB	ND	BBA
S17	Sawi, Chumphon	115/117	167/167	186/186	BBB	ND	BBA
S18	Sawi, Chumphon	118/118	167/167	186/196	BBB	BBB	ND
S19	Sawi, Chumphon	119/119	167/167	186/186	ND	ND	ND
S20	Sawi, Chumphon	ND	167/169	186/186	BBB	ND	ND
S21	Muang, Chumphon	114/114	161/169	186/196	BBB	ND	ND
S22*	Muang, Chumphon	114/119	167/167	186/186	BBB	ND	BBA
S23	Muang, Chumphon	114/118	155/167	186/196	BBB	BBB	ND
S24	Muang, Chumphon	124/128	167/169	186/196	ND	BBB	ND
S25	Kra buri, Ranong	116/126	167/167	196/196	BBB	ND	ND
S26	Kra buri, Ranong	117/123	167/169	186/196	ND	ND	ND
S27	Kapoe, Ranong	114/118	167/167	186/196	ND	ND	BBA
S28	Kapoe, Ranong	121/121	167/167	186/196	BBB	BBB	ND
S29	Kapoe, Ranong	121/125	169/169	196/196	BBB	ND	BBJ
S30	Kapoe, Ranong	119/124	167/167	186/196	BBB	BBB	ND
S31	Muang, Ranong	118/121	155/167	186/186	BBB	BBB	BBA
S32	Muang, Ranong	117/125	167/169	186/196	ND	BBB	BBA

Code of Colonies	Sampling area	Size of allele (bp)			Composite haplotype		
		LocusA28	LocusA107	LocusA113	I	II	III
S33	Khuraburi, Phang nga	125/125	167/167	186/196	BBB	BBB	ND
S34	Khuraburi, Phang nga	117/128	167/169	186/196	BBB	BBB	BBA
S35	Phanom, Suratthani	114/117	167/169	186/186	BBB	BBB	BBA
S36	Ao luk, Krabi	109/123	167/167	186/186	BBB	BBB	BBA
S37	Ao luk, Krabi	116/119	ND	186/186	BBB	BBB	ND
S38	Ao luk, Krabi	114/122	167/167	186/186	BBE	BBB	BBA
S39	Ao luk, Krabi	114/118	167/167	186/186	ND	BBB	ND
S40	Ao luk, Krabi	121/124	167/167	ND	BBB	BBB	ND
S41	Muang, Krabi	125/125	167/167	186/186	ND	BBB	ND
S42	Muang, Krabi	114/119	167/167	186/196	BBB	BBB	BBA
S43	Muang, Krabi	118/123	167/167	186/186	BBB	BBB	ND
S44	Muang, Krabi	119/119	167/167	186/186	ND	BBB	BBA
S45	Muang, Krabi	119/124	167/167	186/196	ND	BBB	BBA
S46	Nua khlohng, Krabi	124/124	167/167	186/196	ND	BBB	ND
S47	Nua khlohng, Krabi	116/116	167/167	186/186	BBB	BBB	BBA
S48	Nua khlohng, Krabi	116/125	167/167	186/196	BBB	BBB	BBA
S49	Nua khlohng, Krabi	111/124	167/167	186/186	ND	BBB	BBA
S50	Khao phanom, Krabi	118/127	167/167	186/196	BBB	BBB	ND
S51	Thung yai, Nakhon sri thammarat	124/127	167/167	196/196	BBC	BBB	BBG
S52	Thung yai, Nakhon sri thammarat	118/118	ND	ND	BBB	BBB	ND
S53	Thung yai, Nakhon sri thammarat	125/125	167/169	186/186	BBC	BBB	BBG
S54	Sikao, Trang	120/127	167/167	186/186	BBB	BBB	BBA
S55	Huai yot, Trang	118/126	167/167	186/196	ND	BBB	ND
S56	Huai yot, Trang	124/127	167/167	186/186	BBB	BBB	ND
S57	Huai yot, Trang	121/125	167/169	196/196	BBB	BBB	BBA
S58	Huai yot, Trang	124/127	167/167	196/196	ND	BBB	ND
S59*	Sri banphot, Phatthalung	118/118	167/167	186/196	BBF	BBB	ND
S60	Sri banphot, Phatthalung	109/126	ND	196/196	CED	AEE	ND
S61	Sri banphot, Phatthalung	127/127	167/169	186/186	ND	BBB	BBA
S62	Pa bon, Phatthalung	120/124	167/167	186/196	BBB	BBB	BBA
S63	Hat yai, Songkhla	113/121	167/169	186/186	BBB	BBB	BBA
S64	Muang, Songkhla	109/121	167/167	196/196	BBB	BBB	ND
S65*	Muang, Songkhla	119/119	167/167	186/186	BBE	BBB	ND

Code of Colonies	Sampling area	Size of allele (bp)			Composite haplotype		
		LocusA28	LocusA107	LocusA113	I	II	III
S66*	Muang, Songkhla	125/125	167/167	186/196	BBC	BBB	BBA
S67	Muang, Songkhla	121/121	167/167	196/196	ND	BBB	ND
S68	Muang, Songkhla	121/125	167/167	186/186	BBB	BBB	BBA
S69	Nakhon sri thammarat	117/121	167/167	186/196	BBB	BBB	BBA
S70	Nakhon sri thammarat	125/125	167/167	ND	BBB	BBB	BBA
S71	Tha sala, Nakhon sri thammarat	119/119	167/167	186/196	BBB	BBB	BBA
S72	Tha sala, Nakhon sri thammarat	117/117	167/169	186/196	ND	BBB	BBA
S73	Tha sala, Nakhon sri thammarat	118/118	167/167	186/196	ND	ND	BBA

I = Composite haplotype of ATPase6-ATPase8 gene of mtDNA digested with *TaqI*, *SspI* and *VspI* (Songram, 1997)

II = Composite haplotype of rRNA gene, lrRNA gene and inter COI-COII of mtDNA digested with *DraI* (Sihanuntavong, 1997)

III = Composite haplotype of mtDNA control region digested with *TaqI*, *RsaI* and *HinfI* (Pootong, 1999)

ND = non determined

\* = ITS amplified product of 580 bp was sequenced

**Collection of *A. cerana* from the Samui Island of Thailand.**

Code of Colonies	Sampling area	Size of allele (bp)			Composite haplotype		
		LocusA28	LocusA107	LocusA113	I	II	III
I4	Tham Bon Aungthong	118/124	167/167	196/196	ND	BBB	BBA
I5	Tham Bon Aungthong	124/124	167/167	196/196	ND	ND	ND
I6	Tham Bon Aungthong	118/124	167/167	196/196	ND	BBB	BCA
I9	Tham Bon Bophut	118/124	167/167	196/196	BBB	BBB	BCA
I10	Tham Bon Maret	118/118	167/167	196/196	BBB	BBB	BBA
I12	Tham Bon Maret	118/121	167/167	196/196	BBB	BBB	BBA
I14	Tham Bon Lipanoi	118/118	167/167	196/196	BBB	BBB	BBA
I16	Tham Bon Maenam	118/118	167/167	196/196	BCB	BBC	ND
I17	Tham Bon Maenam	124/124	167/167	196/196	BBB	BBB	BBA
I19	Tham Bon Maenam	118/126	167/167	196/196	BBB	BBB	BBA
I20	Tham Bon Maenam	119/119	167/167	196/196	BBB	BBB	BBA
I21*	Tham Bon Maenam	118/124	167/167	196/196	BCB	BBC	BCH
I22	Tham Bon Maenam	116/124	167/167	196/196	BCB	BBC	BCI
I23	Tham Bon Maenam	124/124	167/167	196/196	BCC	BBC	ND
I24	Tham Bon Maenam	118/118	167/167	196/196	BCB	BBC	ND
I25	Tham Bon Bophut	124/124	167/167	196/196	BBB	BBB	BBA
I26	Tham Bon Bophut	118/124	167/167	196/196	BBB	BBB	BBA
I27	Tham Bon Bophut	114/124	167/167	196/196	BCC	BBC	BCA
I28	Tham Bon Bophut	124/124	167/167	196/196	BBB	BBB	BBA
I29*	Tham Bon Maret	114/119	167/167	196/196	BCC	BBC	BCA
I30	Tham Bon Maret	124/124	167/167	196/196	BCC	BBC	BBA
I31	Tham Bon Maret	116/124	167/167	196/196	BCC	BBC	BBA
I32	Tham Bon Maret	118/126	167/167	196/196	BCC	BBC	BCH
I33*	Tham Bon Maret	118/118	167/167	196/196	BCC	BBC	ND
I34	Tham Bon Maret	118/118	167/167	196/196	ND	BBB	BBA
I35*	Tham Bon Maret	124/124	167/167	196/196	BBB	BBB	ND
I36	Tham Bon Maret	118/124	167/167	196/196	BCC	BBC	BBA
I37	Tham Bon Bophut	118/124	167/167	196/196	BBB	BBB	BBA
I38	Tham Bon Aungthong	113/121	167/167	196/196	ND	ND	ND
I39	Tham Bon Maret	ND	167/167	196/196	ND	ND	ND

Code of Colonies	Sampling area	size of allele (bp)			Composite haplotype		
		LocusA28	LocusA107	LocusA113	I	II	III
I40	Tham Bon Thalingngam	110/126	167/167	196/196	ND	ND	ND
I41	Tham Bon Lipanoi	122/126	167/167	196/196	ND	ND	ND
I42	Tham Bon Bophut	121/121	167/167	196/196	ND	ND	ND
I43	Tham Bon Maret	116/116	ND	ND	ND	ND	ND
I44	Tham Bon Talingngam	119/119	167/167	186/196	ND	ND	ND
I45	Tham Bon Lipanoi	126/126	167/167	196/196	ND	ND	ND
I47	Tham Bon Talingngam	116/120	167/167	196/196	ND	ND	ND
I48	Tham Bon Maret	116/122	167/167	196/196	ND	ND	ND

I = Composite haplotype of ATPase6-ATPase8 gene of mtDNA digested with *TaqI*, *SspI* and *VspI* (Songram, 1997)

II = Composite haplotype of sRNA gene , lrRNA gene and inter COI-COII of mtDNA digested with *DraI* (Sihanuntavong, 1997)

III = Composite haplotype of mtDNA control region digested with *TaqI*, *RsaI* and *HinfI* (Pootong,1999)

ND = non determined

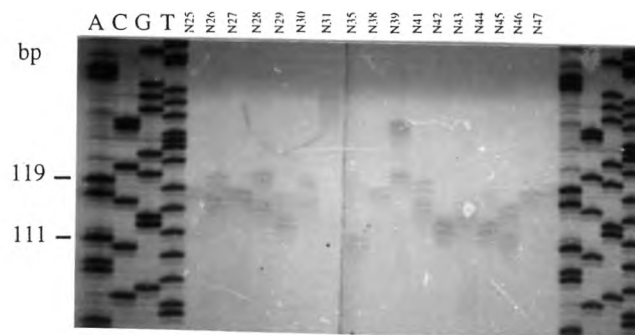
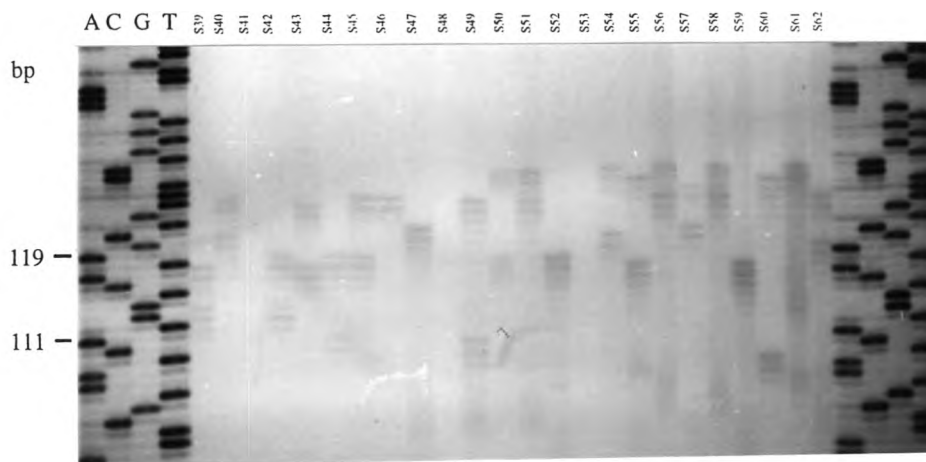
\* = ITS amplified product of 580 bp was sequenced



## APPENDIX 4

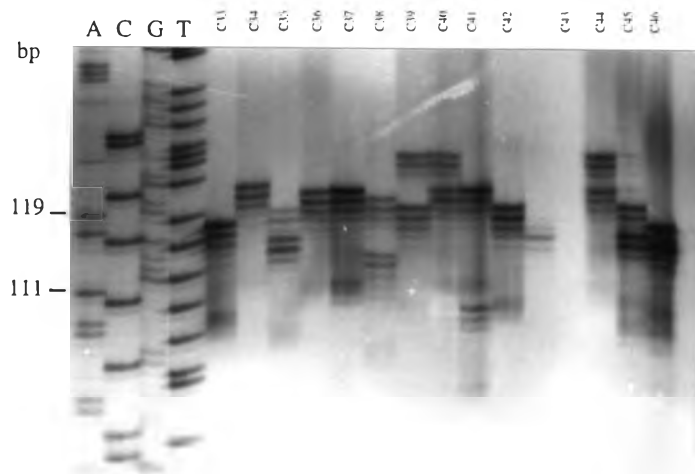
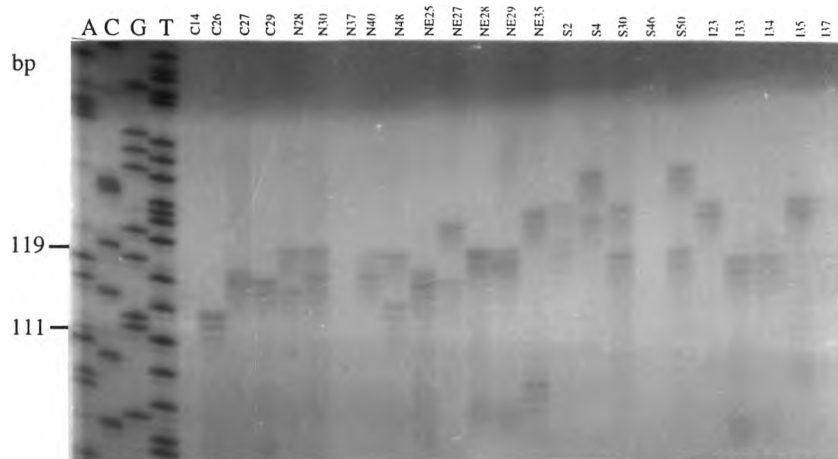
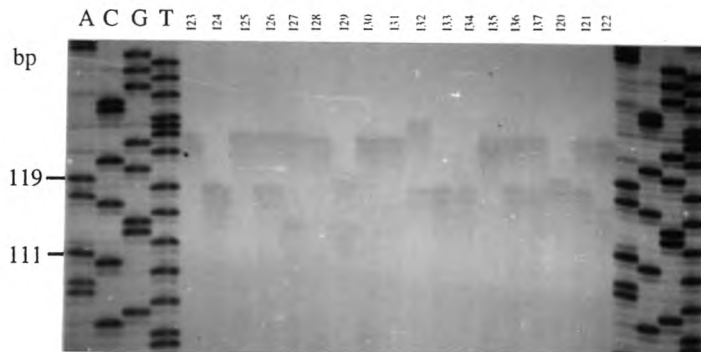
**PCR amplification patterns of the three microsatellite loci (A28, A107 and A113) for 266 *A. cerana* individuals collected from five geographic locations in Thailand.**

### Microsatellite locus A28



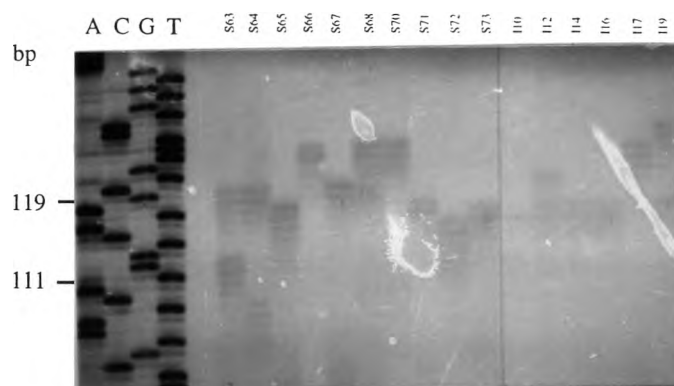
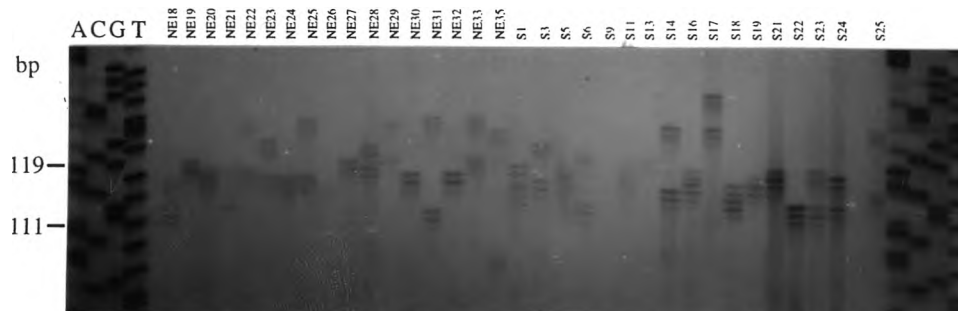
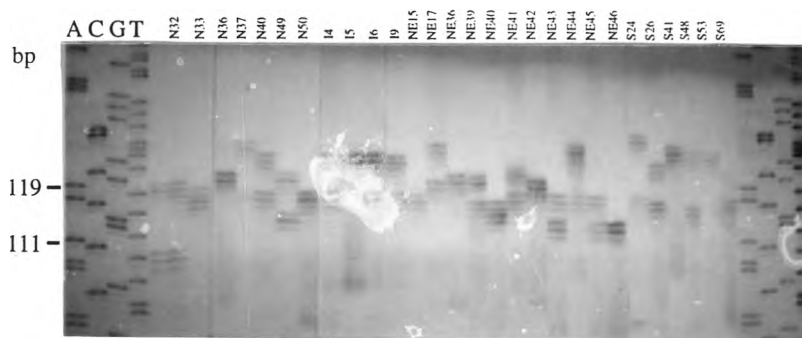


Microsatellite locus A28 (continued)

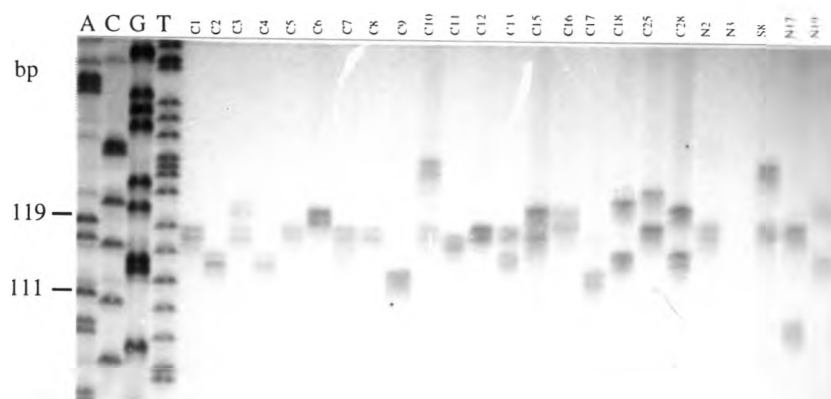
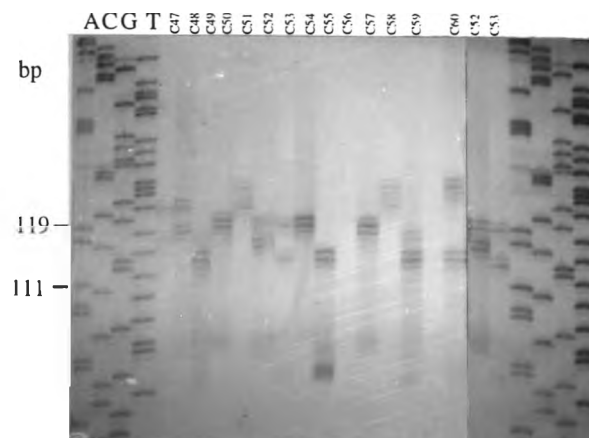
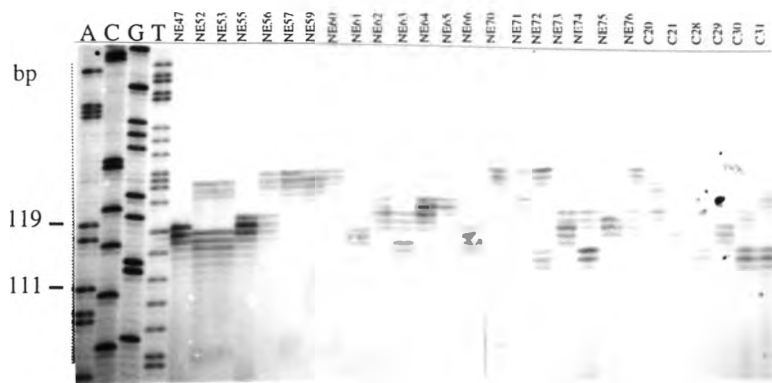




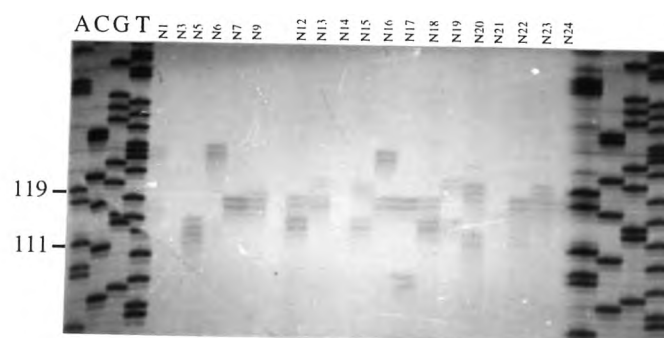
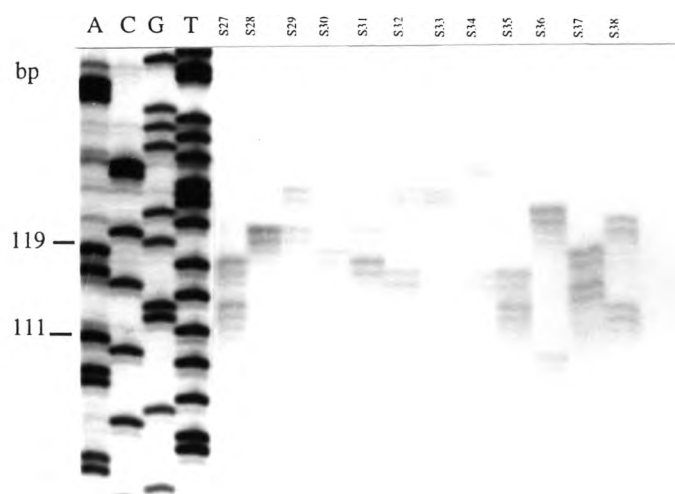
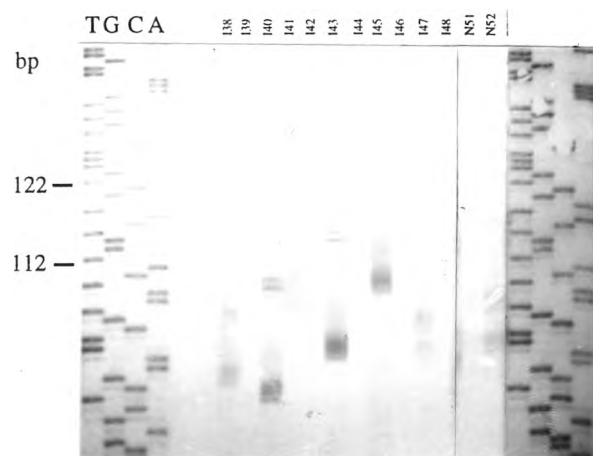
Microsatellite locus A28 (continued)



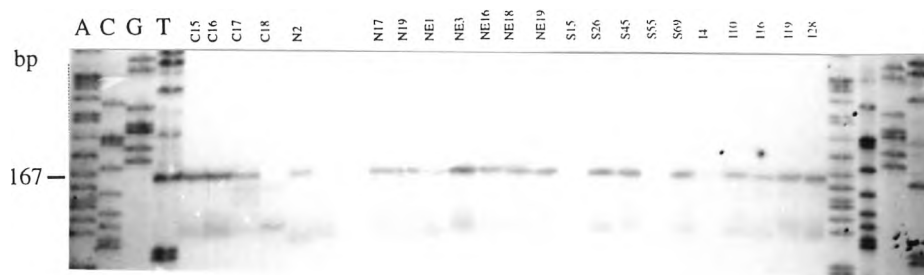
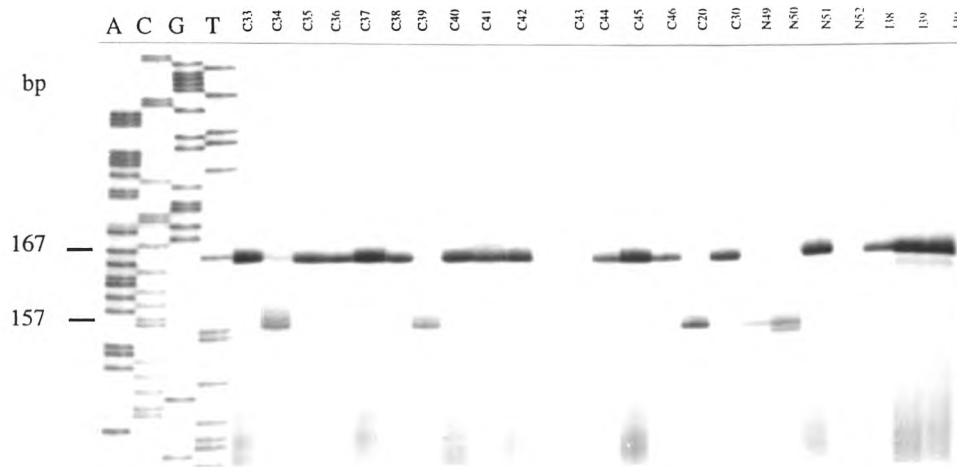
Microsatellite locus A28 (continued)



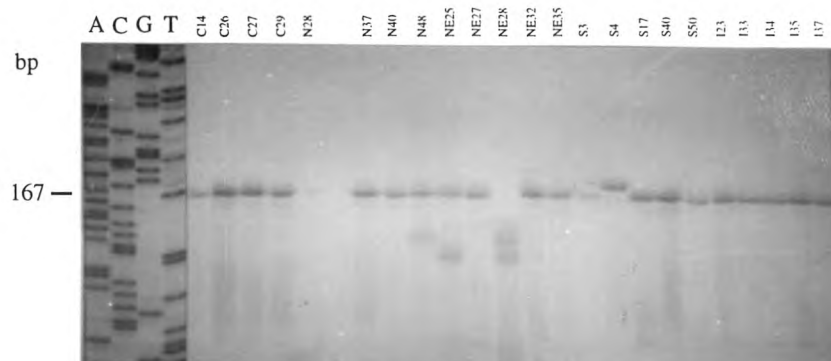
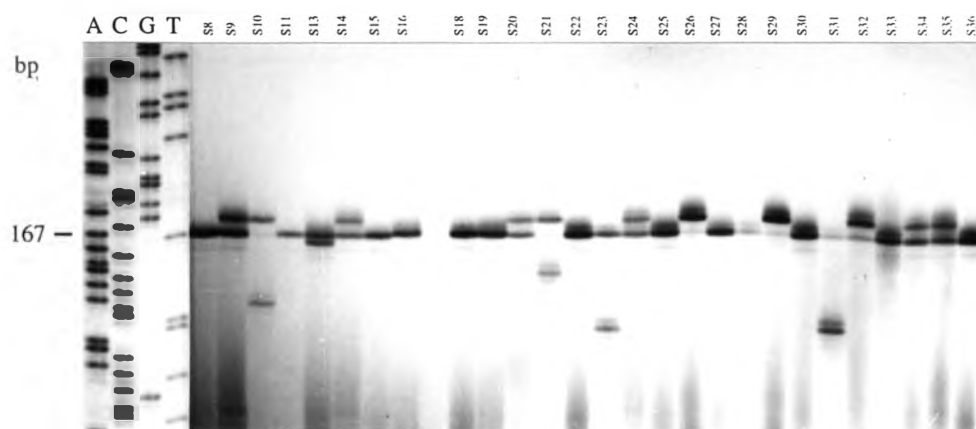
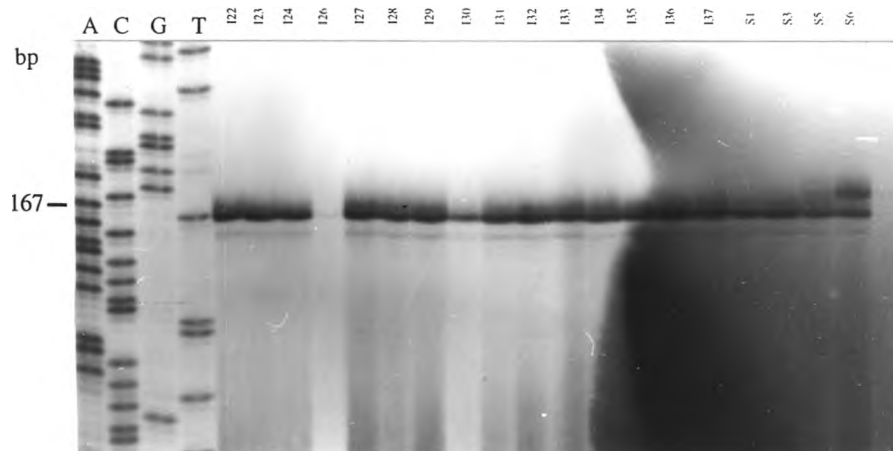
Microsatellite locus A28 (continued)



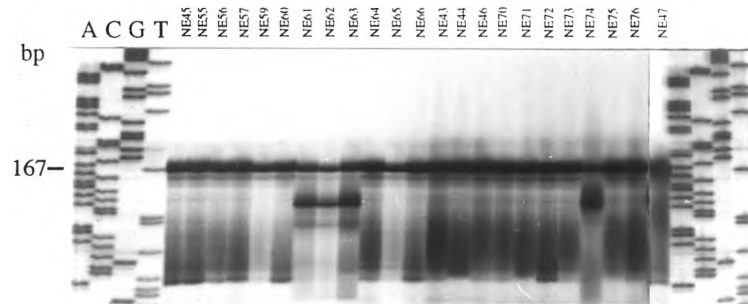
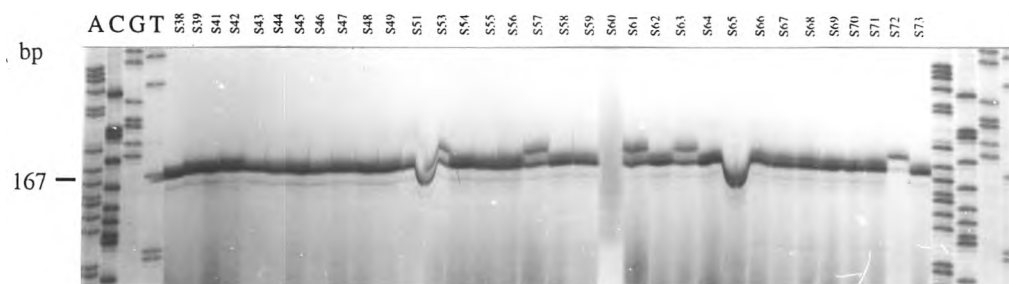
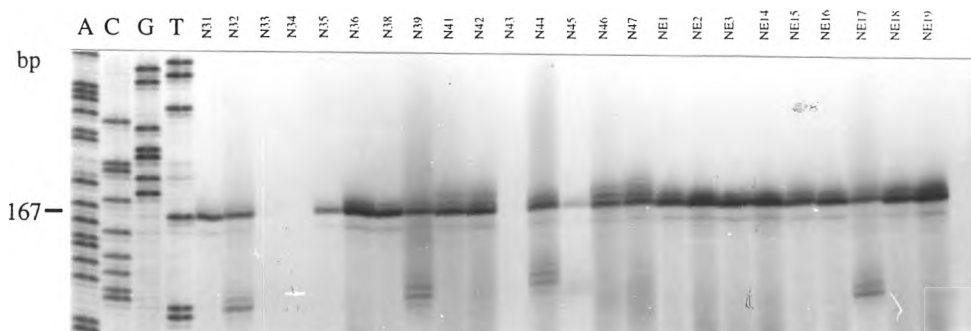
Microsatellite locus A107 (continued)



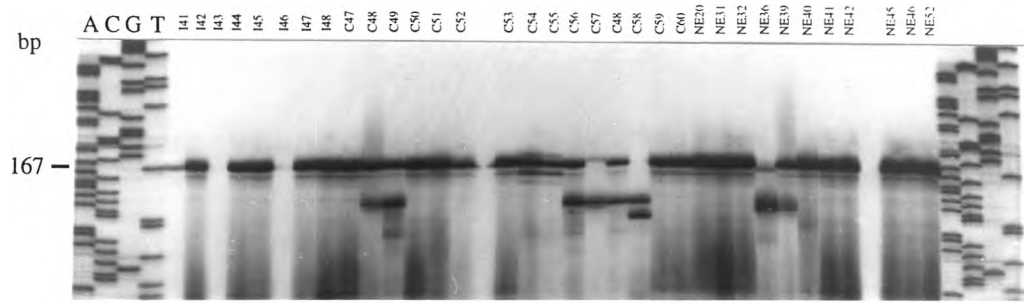
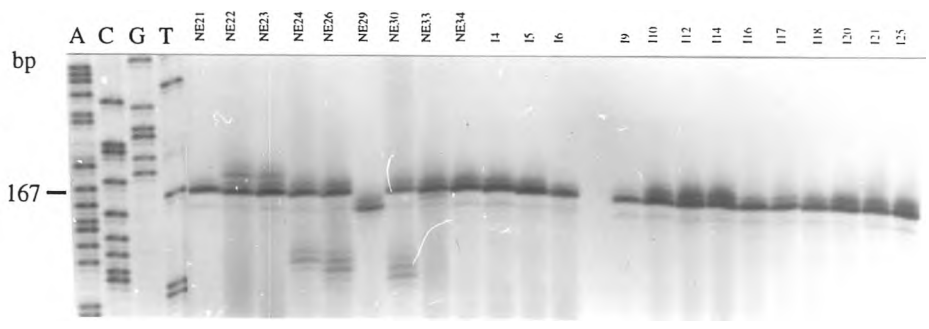
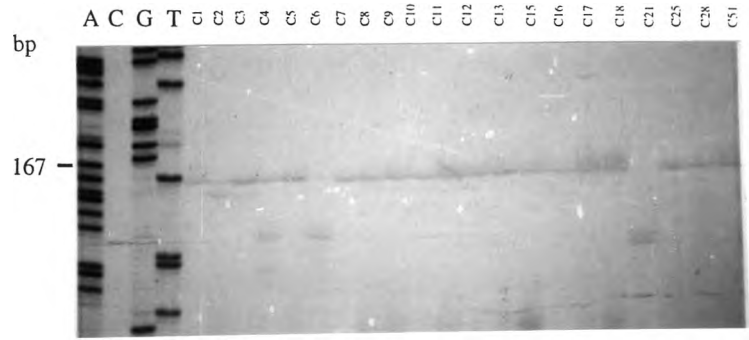
Microsatellite locus A107 (continued)



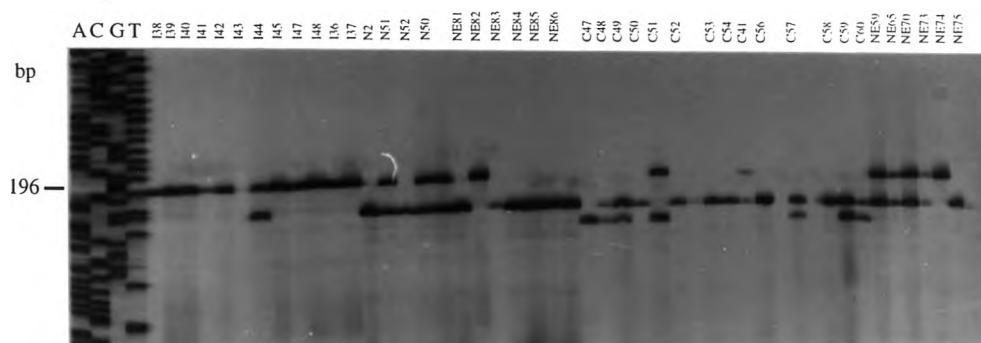
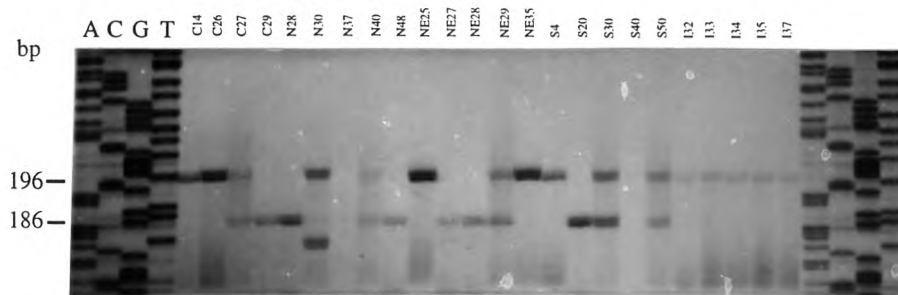
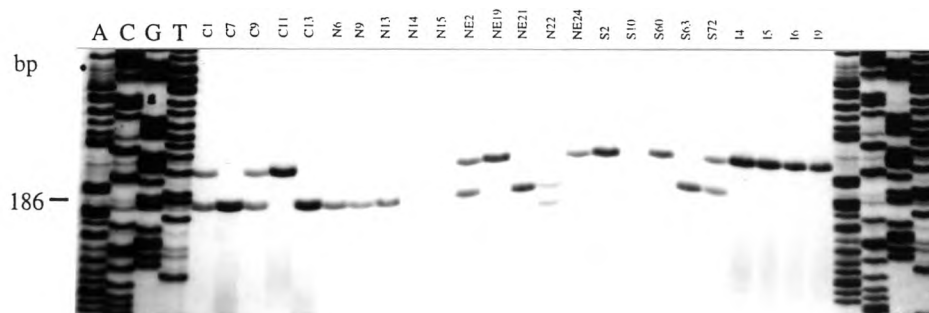
Microsatellite locus A107 (continued)



Microsatellite locus A107 (continued)

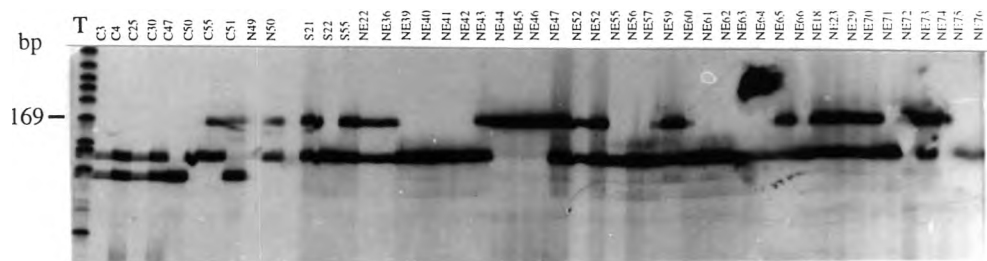
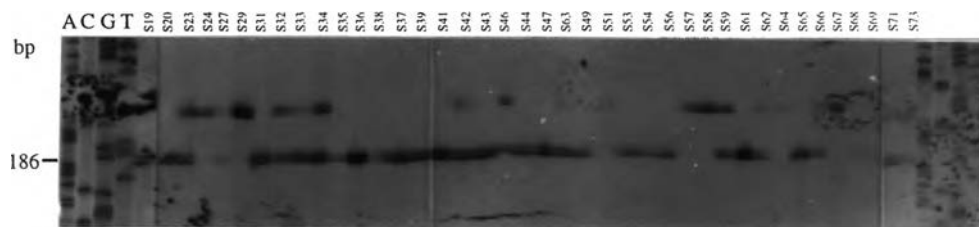
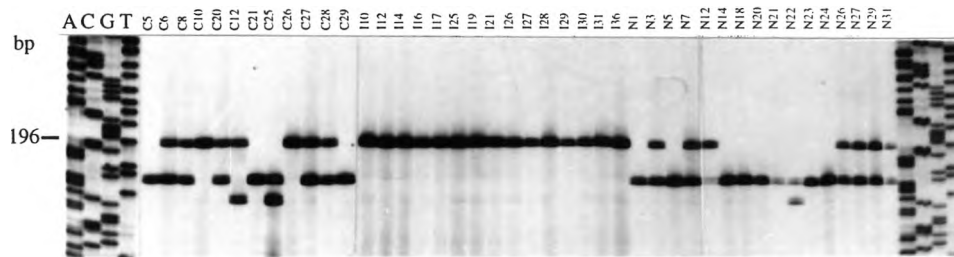


Microsatellite locus A113 (continued)

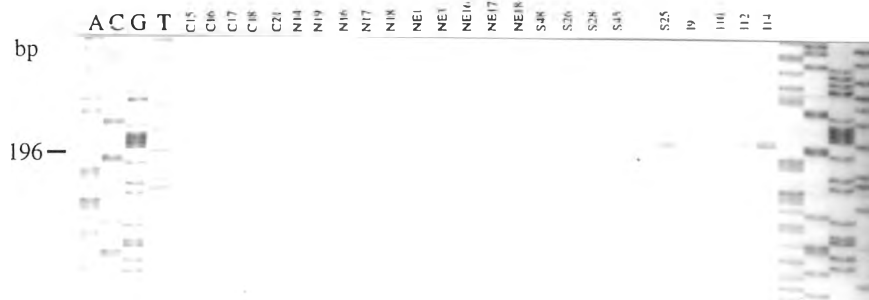
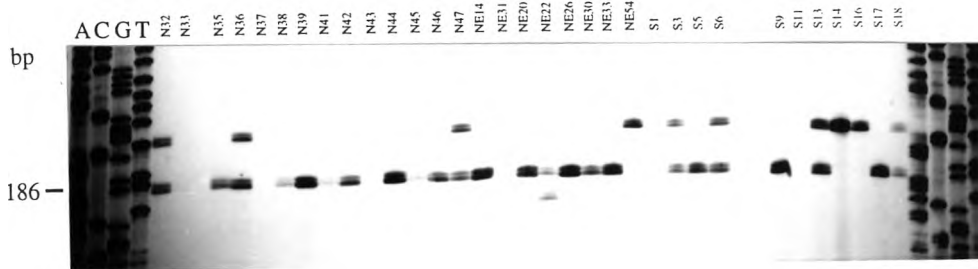
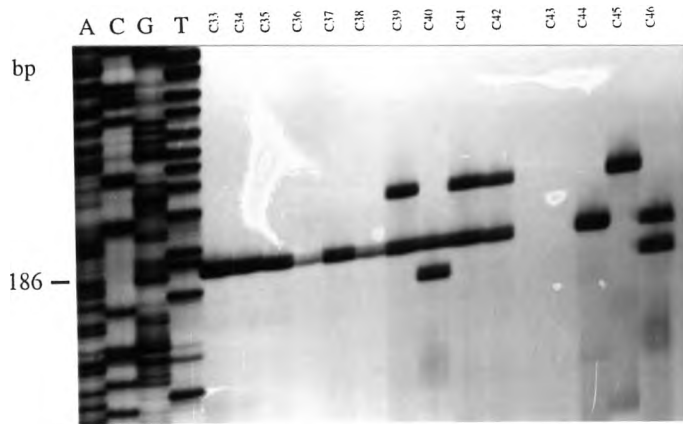




Microsatellite locus A113 (continued)



Microsatellite locus A113 (continued)



## **BIOGRAPHY**

Miss Supak Lararoon was born on March 8, 1974. She graduated with the Bachelor degree of Science in Biochemistry from chulalongkorn University in 1994.