References
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References


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References


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References


References


References


References


Appendices
Appendix A - Meteorological data, readings of temperature and pH

Daily meteorological data of dipteran succession study on decomposing pig carcass.

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Readings of temperature and pH of the carcass body, larval mass as well as soil for carcass A throughout decomposition stages.

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Readings of temperature and pH of the carcass body, larval mass as well as soil for carcass B throughout decomposition stages.

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Appendix B – Phylogenetic trees

Appendix B-1

Figure: The NJ tree of Calliphoridae species was constructed on the basis of 2309bp mitochondrial COI and COII gene sequences using PAUP* 4.0b10 and rooted with Parasarcophaga albiceps (Sarcophagidae) as the outgroup. The number on the internal branches represents bootstrap values (n=10000) with 70% cut off value.
Figure: The MP tree of Calliphoridae species was constructed on the basis of 2309bp mitochondrial COI and COII gene sequences using PAUP* 4.0b10 and rooted with Parasarcophaga albicpes (Sarcophagidae) as the outgroup. The number on the internal branches represents bootstrap values (n=10000) with 70% cut off value.
Figure: Bayesian consensus phylogeny of Calliphoridae species of 2309bp mitochondrial COI and COII gene sequences using MrBayes 3.1.2 and rooted with Parasarcophaga albicpes (Sarcophagidae) as the outgroup. The number on the internal branches represents Bayesian posterior probabilities (n=1 million) with 70% cut off value.
Figure: The NJ tree of Calliphoridae species was constructed on the basis of 2172bp 28S rDNA sequences using PAUP* 4.0b10 and rooted with Parasarcophaga albipes (Sarcophagidae) as the outgroup. The number on the internal branches represents bootstrap values (n=10000) with 70% cut off value.
Appendix B-5

Figure: The MP tree of Calliphoridae species was constructed on the basis of 2172bp 28S rDNA sequences using PAUP* 4.0b10 and rooted with *Parasarcophaga albipes* (Sarcophagidae) as the outgroup. The number on the internal branches represents bootstrap values (n=10000) with 70% cut off value.
Appendix B-6

Figure: Bayesian consensus phylogeny of Calliphoridae species of 2172bp 28S rDNA sequences using MrBayes 3.1.2 and rooted with Parasarcophaga albiceps (Sarcophagidae) as the outgroup. The number on the internal branches represents Bayesian posterior probabilities (n=1 million) with 70% cut off value.
**Appendix B-7**

**Figure:** The NJ tree of Sarcophagidae species was constructed on the basis of 2308bp mitochondrial COI and COII gene sequences using PAUP® 4.0b10 and rooted with three Calliphoridae species as the outgroup. The number on the internal branches represents bootstrap values (n=10000) with 70% cut off value.
Figure: The MP tree of Sarcophagidae species was constructed on the basis of 2308bp mitochondrial COI and COII gene sequences using PAUP® 4.0b10 and rooted with three Calliphoridae species as the outgroup. The number on the internal branches represents bootstrap values (n=10000) with 70% cut off value.
Figure: Bayesian consensus phylogeny of Sarcophagidae species of 2308bp mitochondrial COI and COII gene sequences using MrBayes 3.1.2 and rooted with three Calliphoridae species as the outgroup. The number on the internal branches represents Bayesian posterior probabilities (n=1 million) with 70% cut off value.
Appendix C – Publication


# Appendix D

## List of proceedings/seminar/conference papers

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46th Annual Scientific Conference of Malaysian Society of Parasitology and Tropical Medicine, Grand Seasons Hotel, Kuala Lumpur, Malaysia (25 March 2010) |
| 2009 | Poster   | *Winner of the Honourable Mention Awards  
Tan, S.H., Mohd-Aris, E., Kurahashi, H. and Mohamed, Z.  
Genetic relationships between fifteen blow fly species (Calliphoridae) of forensic importance in Malaysia.  
The 14th Biological Science Graduate Congress, Chulalongkorn University, Bangkok, Thailand (10-12 December 2009) |
Phylogenetic analysis of some forensically important Malaysian flesh fly species (Diptera: Sarcophagidae) based on cytochrome oxidase I and II sequence.  
Applied Population Genetics In Fisheries And Aquaculture Data Clinic, 8th Residential College, University of Malaya, Kuala Lumpur, Malaysia (12 November 2009) |
Roles of forensic entomology.  
Public lecture, Sarawak Museum, Kuching, Sarawak, Malaysia (8 October 2009) |
| 2009 | Poster   | *Winner of the second prize of best poster presenter for overall category  
Tan, S.H., Mohd-Aris, E., Kurahashi, H. and Mohamed, Z.  
Genetic relationships between eight blow fly species (Calliphoridae: Chrysomya) of forensic importance in Malaysia.  
18th Malaysian Society for Molecular Biology and Biotechnology Scientific Meeting, The Saujana Kuala Lumpur Hotel, Subang Jaya, Malaysia (18-20 August 2009) |
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<td>2007</td>
<td>Oral</td>
<td>Tan, S.H.</td>
<td>DNA-based characterisation of forensically important fly species in Malaysia. Seminar, Department of Medical Entomology, National Institute of Infectious Diseases, Tokyo, Japan (8 June 2007)</td>
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<td>2006</td>
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<td>Tan, S.H., Mohd-Aris, E., and Mohamed, Z.</td>
<td>Use of PCR-RFLP assay to identify the forensically important blow fly species (Diptera: Calliphoridae) in Malaysia. 3rd Life Sciences Postgraduate Conference, University Science Malaysia, Penang, Malaysia (24-27 May 2006)</td>
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<td>Tan, S.H.</td>
<td>DNA-based characterization of forensically important fly species in Malaysia. International Networking of Young Scientists, University of Science Malaysia, Kelantan, Malaysia (13-15 February 2006)</td>
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<td>2004</td>
<td>Tan, S.H., Mohd-Aris, E., and Mohamed, Z.&lt;br&gt;&lt;br&gt;Species-specific PCR assay for two forensically important species, <em>Chrysomya megacephala</em> and <em>Chrysomya rufifacies</em> in Malaysia.&lt;br&gt;&lt;br&gt;14th Malaysian Society Molecular Biology &amp; Biotechnology Scientific Meeting. Century Mahkota Hotel, Melaka, Malaysia (19-21 July 2004)</td>
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