

การปรับปรุงอนุกรรมวิชานและการวิเคราะห์ความสัมพันธ์ทางสายวิ世พนากาражของหอยตันไม้
สกุล *Amphidromus* Albers และการแสดงนัยทางชีวภูมิศาสตร์ของสปีชีส์
ที่พบในประเทศไทย

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ศูนย์วิทยทรัพยากร
จุฬาลงกรณ์มหาวิทยาลัย
วิทยานิพนธ์นี้เป็นส่วนหนึ่งของการศึกษาตามหลักสูตรวิทยาศาสตรดุษฎีบัณฑิต
สาขาวิทยาศาสตร์ชีวภาพ
คณะวิทยาศาสตร์ จุฬาลงกรณ์มหาวิทยาลัย
ปีการศึกษา 2547
ISBN 974-17-6559-2
ลิขสิทธิ์ของจุฬาลงกรณ์มหาวิทยาลัย

**TAXONOMIC REVISION AND PHYLOGENETIC ANALYSIS OF
THE TREE SNAIL GENUS *Amphidromus* Albers
AND IMPLICATION FOR BIOGEOGRAPHY OF THAI SPECIES**

Mr. Chirasak Sutcharit

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**A Dissertation Submitted in Partial Fulfillment of the Requirements
for the Degree of Doctoral of Philosophy in Biological Sciences**

**Faculty of Science
Chulalongkorn University
Academic Year 2004
ISBN 974-17-6559-2**

Thesis Title	Taxonomic Revision and Phylogenetic Analysis of the tree snail genus <i>Amphidromus</i> Albers and Implication for Biogeography of Thai Species
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จิรศักดิ์ สุจิริต: การปรับปรุงอนุกรมวิธานและการวิเคราะห์ความสัมพันธ์ทางสายวิวัฒนาการของหอยตื้นไม้สกุล *Amphidromus* Albers และการแสดงนัยทางชีวภูมิศาสตร์ของสปีชีส์ที่พบในประเทศไทย (TAXONOMIC REVISION AND PHYLOGENETIC ANALYSIS OF THE TREE SNAIL GENUS *Amphidromus* Albers AND IMPLICATION FOR BIOGEOGRAPHY OF THAI SPECIES) อาจารย์ที่ปรึกษา: รศ. ดร. สมศักดิ์ ปัญหา อาจารย์ที่ปรึกษาร่วม: Assoc. Prof. Dr. Takahiro Asami. จำนวน 169 หน้า. ISBN 974-17-6559-2

หอยตื้นไม้สกุล *Amphidromus* เป็นทากนกที่มีความสวยงามและมีการกระจายพันธุ์จำกัดอยู่ในแถบเอเชียตะวันออกเฉียงใต้ จัดได้ว่าเป็นหอยที่มีรูปแบบจำเพาะทางชีววิทยา เพราะมีความสามารถในการปรับตัวให้สามารถอาศัยอยู่บนดินไม่ได้เป็นอย่างเดียว ซึ่งในปัจจุบันกำลังอยู่ในสภาวะที่เสี่ยงต่อการสูญพันธุ์เนื่องจากการทำลายลินที่อยู่อาศัย แม้ว่าหอยตื้นไม้สกุล *Amphidromus* จะเป็นที่ดึงดูดความสนใจของนักวิทยาศาสตร์ แต่โดยพื้นฐานแล้วการศึกษาขั้งขาดความถูกต้องในด้านการจัดจำแนกและการศึกษาทางวิวัฒนาการ เป็นอย่างมาก การศึกษาครั้งนี้ได้นำเสนอทางอนุกรมวิธานและความสัมพันธ์ทางวิวัฒนาการของหอยในสกุลย่อย *Amphidromus* และสกุลย่อย *Syndromus*

ทำการศึกษาความสามารถที่ห้องลักษณะทางสัณฐานวิทยา และความสัมพันธ์ของสัณฐานวิทยาและชีวโมเลกุล เพื่อนำใช้ในการประเมินความถูกต้องของการจัดจำแนกหอยสกุลนี้ในประเทศไทย สำหรับการศึกษาทางอนุกรมวิธานนี้ใช้ลักษณะเปลือกร่วนทั้งระบบสืบพันธุ์ และฟันในหอย 10 ชนิด พบร่องรอยสกุลย่อย *Amphidromus* มีขนาดของเปลือกที่ใหญ่กว่าและมี epiphilic caecum ยาวกว่าหอยสกุลย่อย *Syndromus* นอกจากนี้ส่วนปลายของระบบสืบพันธุ์เพศ ตลาดข้ามภายในของอวัยวะสืบพันธุ์ของทั้งสองเพศ และสัณฐานวิทยาของฟันสามารถใช้ในการจำแนกหอยในทั้งสองสกุลย่อยได้เป็นอย่างดี ผลการศึกษาในครั้งนี้สอดคล้องกับระบบการจัดจำแนกแบบเดิมที่อาศัยเปลือกเพียงอย่างเดียว นอกจากนี้ยังสามารถอุดมด้วยความหลากหลายในสายพันธุ์หอยตื้นไม่ที่มีความสัมพันธ์ซ้อนต่อการจัดจำแนกได้ เช่น *A. inversus*, *A. atricallosus* และ *A. glaucolarynx*

จากการศึกษาความสัมพันธ์ทางวิวัฒนาการของหอยจำนวน 17 ชนิด โดยอาศัยทั้งลักษณะทางสัณฐานวิทยา และลำดับเบสที่อยู่บนในโตกอนเดรีช 16S rDNA พบว่าห้องลูกทั้งสองส่วนนี้มีความสอดคล้องกันแสดงความสัมพันธ์แบบวิวัฒนาการบรรพนຽมเดียว ในหอยทั้งสกุลนี้และในสกุลย่อย *Amphidromus* แต่จากการข้อมูลทางสัณฐานวิทยาไม่สามารถบ่งชี้ถึงความสัมพันธ์ในระดับชนิดได้ในขณะที่ผลจากการศึกษาลำดับเบสบนในโตกอนเดรีชเดิมเชื่อของหอยในสกุลย่อย *Syndromus* ซึ่งให้เห็นถึงความสัมพันธ์แบบวิวัฒนาการขนาด โตกอนเดรีชมี *A. glaucolarynx* แยกออกมาเป็นสกุลของตนเอง แต่หอยตื้นไม้ชนิดอื่นๆ ในสกุลย่อย *Syndromus* ที่เหลือจะมีความสัมพันธ์เป็นแบบวิวัฒนาการบรรพนຽมเดียว นอกจากนี้แล้วความสัมพันธ์แบบวิวัฒนาการหลานบรรพนຽมของไม้โตกอนเดรีชเดิมเชื่อของหอยตื้นไม้ชนิดเดียวทั้งหมดทั้งสองสกุลย่อย

จากการศึกษาดังกล่าวบ่งชี้ให้เห็นว่า ยังมีความจำเป็นที่จะต้องปรับปรุงแก้ไขอนุกรมวิธานของหอยตื้นไม้ในหลายกรณี เช่น *A. glaucolarynx* ควรที่แยกออกจากสกุลย่อย การปรับปรุงอนุกรมวิธานในสกุลย่อย *Syndromus* โดยอาศัยหลักการการแบ่งแยกทางการสืบพันธุ์ระหว่างประชารัฐ อาจจะบ่งชี้ว่าชั้นเมสปีชีส์ที่ซ้อนเร็น ซึ่งมีลักษณะตลาดข้ามสั้นของเปลือกคล้ายคลึงกันอยู่ อาทิ เช่นในหอยตื้นไม้ชนิด *A. (S.) xiengensis* เป็นต้น นอกจากนี้ยังแสดงหลักฐานลักษณะกำหนดทางวิวัฒนาการของความของเปลือกแบบเวียนซ้ำและเวียนขวาในหอยสกุลนี้ได้เป็นครั้งแรก และจากการคำนวณอายุโดยอาศัยตัวการเปลี่ยนแปลงทางวิวัฒนาการของลำดับเบสบนไม้โตกอนเดรีชเดิมเชื่อของหอยตื้นไม้สกุลนี้อาจจะถือกำเนิดมาในยุคโอลิโภเซน (ประมาณ 35 ล้านปี) หรือในยุคไพลอยอเซน (ประมาณ 3.5 ล้านปี) โดยใช้เป็นตัวการเปลี่ยนแปลงสูงสุดและต่ำสุดที่เกย์มีรายงานในหอยทากบก

สาขาวิชา	วิทยาศาสตร์ชีวภาพ	ลายมือชื่อนิสิต	<i>Chirasak Sutcharit</i>
ปีการศึกษา	2547	ลายมือชื่ออาจารย์ที่ปรึกษา	
		ลายมือชื่ออาจารย์ที่ปรึกษาร่วม	

##4273855623 MAJOR : Biological Science

KEY WORDS: Land Snail/ *Amphidromus*/ Camaenidae/ Phylogeny/ Taxonomy/
Systematic

CHIRASAK SUTCHARIT: TAXONOMIC REVISION AND PHYLOGENETIC ANALYSIS OF THE TREE SNAIL GENUS *AMPHIDROMUS* Albers AND IMPLICATION FOR BIOGEOGRAPHY OF THAI SPECIES. THESIS ADVISOR: ASSOC. PROF. Dr. SOMSAK PANHA, THESIS CO-ADVISOR: ASSOC. PROF. Dr. TAKAHIRO ASAMI, 169 pp. ISBN 974-17-6559-2

The genus *Amphidromus* is the colourful land snail occupying the arboreal habitat and extensive distribution over Southeast Asia. The snails exhibit various peculiar biological features which apparently represent adaptive specializations, and it is presently under severe extinction pressure due to forest destruction. Although *Amphidromus* have consistently attracted the attention of biologist, these studies have generally lacked an accurate taxonomy and evolutionary perspective. This thesis addresses this shortcoming by concerning systematic studies focusing on the two subgenera, *Amphidromus* and *Syndromus*.

A combined approach of morphology and molecular phylogeny were used in effort to test previously proposed conventional shell taxonomy. Taxonomic studies using genitalia, radula and shell of 10 species from Thailand. The result revealed that the subgenus *Amphidromus* has a longer epiphalllic caecum and larger shell size than the subgenus *Syndromus*. The terminal portion of male organ, the sculpture of both sex organs and radula morphology are also significant for classification of the two subgenera. The anatomy of genitalia and radula characteristic are congruent with the conventional shell taxonomy. It should be noted that, at least as far as the close relations within the complicated species of *A. atricallosus*, *A. inversus* and *A. glaucolarynx* are concerned.

The phylogenies of 17 *Amphidromus* species were examined based on morphological characters and mt16S rDNA sequences. Both results perform monophyly of the genus and subgenus *Amphidromus*, but the morphological cladogram could not reflect the relationship among species level. While, the mtDNA phylogeny exhibits a paraphyletic of the subgenus *Syndromus*. *Amphidromus glaucolarynx* was arranged into the most basal clade in the genus. The rest members of *Syndromus* s. str. were clustered monophyletic. Intraspecific polyphyly of mtDNA haplotypes was detected in several taxa of both subgenera.

The results indicate that taxonomic relations in many cases have to reviewed, for example *A. glaucolarynx* should be classified separately from the two subgenera. The revision of the subgenus *Syndromus* based on reproductive isolation between populations seems to discover the existence of multiple cryptic species with similar shell-color patterns for example in *A. (Syndromus) xiengensis*. In addition, the present study is the first hand information providing the evidence of phylogenetic constraint of chiral dimorphism of the genus *Amphidromus*. The substitution rates available for pulmonate mitochondrial rDNA suggest that the ancestral dimorphism originated in the Oligocene (35 Mya) based on the most conservative estimate of the substitution rate, or in the Pliocene (3.5 Mya) at the youngest age of divergence.

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Acknowledgements

I am extremely grateful to my advisors Associate Professor Dr. Somsak Panha and co-advisor Associate Professor Dr. Takahiro Asami for their continual advice, support and encouragement during my study both in Thailand and Japan, particularly Dr. Somsak Panha for his kind selecting me as a TRF RGJ fellow. I would like to thank my other committee members Professor Dr. Siriwat Wongsiri, Professer Dr. Visut Baimai and Dr. Tosak Seelanan for their consistent interest in my research. I have been fortunate to have invaluable contributions from many people, while investigating molecular research at Department of Biology, Shinshu University, Matsumoto, Japan. Firstly, Dr. Keichi Seiki supported me through teaching, training and all kind assistants, Dr. Masanao Honda kindly provided software, which I frequently used in most of my molecular phylogenetic analyses. I would like to thank Dr. Menno Schilthuisen, University of Malaysia, Sabah and Mr. Fred Naggs, The Natural History Museum, London, that obtainable the tissues samples from Malaysia and Sri Lanka, respectively. Throughout my study, I have spent a great time with the following persons like Mr. Surakit Polkoksung, Mrs. Chanidaporn Tumpeesuwan, Ms. Bang-on Kong-im, Ms. Pongpan Prasankok, Mr. Sakbowon Tumpeesuwan and Mr. Wachira Srikoom who I am grateful for their friendship and wonderful field collecting. I also greatly indebted to Dr. Noppadon Kitana, Dr. Wichae Khonsue, Dr. Piyoros Tongkerd and Mr. Suriya Natsupakphong for their kindly photocopy of the valuable literatures. Financial support from the Thailand Research Fund through the Royal Golden Jubilee Ph.D. Program (No. PHD/0125/2543). And all parts of my research can be done completely by additional enormous supports from various sources of funding from The Biodiversity Research and Training Program (BRT 139035 for Dr. Somsak Panha), The Thailand Research Fund (R_144026 for Dr. Somsak Panha), The Hitachi Scholarship Foundation, Tokyo, Japan and Chulalongkorn University for parts of international presentation grant. Finally, I express my final gratitude to my parents for their support. I would have never been able to finish this work without their help, encouragement and endless patience.

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