

# 班卡拉蝸牛（腹足綱：南亞蝸牛科）的親緣地理學

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## 摘要

屬於半樹棲性的班卡拉蝸牛群包含三個（亞）種，各族群的體型大小變異很大，左旋與右旋種的親緣關係與分類也尚未完全釐清，因此本研究藉由粒線體 DNA 的 16s rRNA 序列，來進行班卡拉蝸牛類群的親緣關係分析與遺傳隔離等議題之探討。共定序 107 隻個體，整理得到 47 個單倍型，各族群大多有自己獨有的單倍型，各族群的遺傳分化程度大致與地理距離成相關，可區分為兩大群，推論班卡拉蝸牛族群可能是由中央山脈南段比較原始的祖先族群開始向外拓展，主要有二大方向同時發生：1. 向恆春半島西南部拓殖；2. 向蘭嶼以及恆春半島其他部份拓殖。AMOVA 分析顯示（亞）種間並無分化，因此分類上建議保持 *S. bacca* 的有效種級地位，而 *S. batanica boteltobagoensis* 和 *S. b. pancala* 是 *S. batanica* 的同物異名。

關鍵詞：班卡拉蝸牛、親緣地理學、粒線體 DNA

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## 參考文獻

- 1.陳玉玲。2004。紅楠與大葉楠兩近緣種之粒線體DNA基因譜系。中國文化大學。生物科技研究所。台北，台灣。
- 2.黃重期。1995。以粒線體核酸研究南亞蝸牛屬親緣關係，國立中山大學生命科學研究所碩士論文，93 pp.
- 3.謝伯娟、黃重期、吳書平。2006。台灣蝸牛圖鑑，第二版。行政院農業委員會林務局。台北。
- 4.Avies, J. C. 2000. Phylogeography. Harvard University Press, London.
- 5.Avise, J. C., J. Arnold, R. M. Ball, E. Bermingham, T. Lamb, J. E. Neigel, C. A. Reeb and N. C. Saunders. 1987. Intraspecific phylogeography: the mitochondrial DNA bridge between population and genetics and systematics. Annual Review of Ecology and Systematic 18:489-522.
- 6.Bouchet P. and J. P. Rocroi 2005. Classification and nomenclator of gastropod families. Malacologia 47(1-2):1-397.
- 7.Brown, W. M., M. Jr. George and A. C. Wilson. 1979. Rapid evolution of animal mitochondrial DNA. Proceedings of National Academy of Science, U.S.A. 76:1967-1971.
- 8.Brown, W. M., E. W. Prager, A. Wang and A. C. Wilson. 1982. Mitochondrial DNA sequences of primates: Tempo and mode of evolution. Journal of Molecular Evolution 18:225-239.
- 9.Chang K. M. 1992. Dwarf type of *Camaena batanica pancala* (Schmacker and Boettger) from South Cape, Taiwan and its allied species (Pulmonata: Camaenidae). Bulletin of Malacology 17: 11 – 20.
- 10.Chiba, S. 1999. Accelerated evolution of land snails Mandarina in the oceanic Bonin Islands: evidence from mitochondrial DNA sequences. Evolution 53:460-471.
- 11.Cowie, R. H. 1992. Evolution and extinction of Partulidae, endemic Pacific island land snails. Philosophy Transactions of Royal Society London, Series B 335:167-191.
- 12.Davison A., S. Chiba, N. H. Barton and B. Clarke. 2005. Speciation and Gene Flow between Snails of Opposite Chirality. PLoS Biology 3:1559-1571.
- 13.Dumolin-Lapegue S, B. Demesure, S. Fineschi, V. Corre and R. J. Petit. 1997. Phylogeographic structure of white oaks throughout the European continent. Genetics, 146: 1475-1487.
- 14.Excoffier, L. G. Laval and S. Schneider. 2005. Arlequin ver. 3.0: An integrated software package for population genetics data analysis. Evolutionary Bioinformatics Online 1:47-50.
- 15.Felsenstein, J. 1985. Confidence limits on phylogenies: an approach using the bootstrap. Evolution 9(4):783-791.
- 16.Futuyma D. J. 1998. Evolutionary Biology, 3rd ed. Sinauer, Sunderland, MA.
- 17.Graur, D. and W. H. Li, 2000. Fundamentals of Molecular Evolution. 2nd ed. Sinauer Associates, Sunderland, MA
- 18.Hall, T. A. 1999.

BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series 41:95-98. 19.Hewitt, G. M. 1996. Some genetic consequences of ice ages, and their role in divergence and speciation. Biological Journal of the Linnean Society 58:247-276. 20.Hillis, D. M., C. Moritz, and B. K. Mable (eds). 1996. Molecular Systematics. Sinauer Associates, USA.

21.Hwang, C. C. 2012. Anatomy and taxonomy of *Satsuma succinata* (Adams, 1866) and *Satsuma batanica pancala* (Schmacker & Boettger, 1891) (Gastropoda: Camaenidae) from southern Taiwan . Bulletin of Malacology 35:1-11. 22.Johnson, M. S. 1982. Polymorphism for direction of coil in *Partula suturalis*: behavioural isolation and positive frequency dependent selection. Heredity 49:145-151. 23.Kameda, Y., A. Kawakita and M. Kato 2007. Cryptic genetic divergence and associated morphological differentiation in the arboreal land snail *Satsuma (Luchuhadra) largillierti* (Camaenidae) endemic to the Ryukyu Archipelago, Japan. Molecular Phylogenetics and Evolution 45:519-533. 24.Kimura M. 1980. A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. Journal of Molecular Evolution 16:111-120. 25.Kuroda T. 1941. A catalogue of molluscan shells from Taiwan (Formosa), with description of new species. Memoirs of the Faculty of Science and Agriculture Taihoku Imperial University 12: 65-216. 26.Kuroda T. 1958. Land shell fauna of Japan (4). Venus 20: 132-158.

27.Kuroda, T. 1932. Notes on the land shell fauna of Kotosyo. Bulletin of Biogeography Society, Japan 3:9-10. 28.Kuroda, T. and T. Habe. 1949. Helicacea. Saminsha, Tokyo. 29.Lai KY. 1981. Study on morphology and ecology of the land snail *Pancala batanica pancala*. Bulletin of Malacology 8: 1-10. 30.Librado, P. and J. Rozas, 2009. DnaSP v5: A software for comprehensive analysis of DNA polymorphism data. Bioinformatics 25: 1451-1452 31.Moellendorff, O. F. von. 1884. Materialien zur Fauna von China. Jahrbuch der Deutschen Malakozoologischen Gesellschaft 11:307-390. 32.Nei M., F. Tajima and Y. Tateno. 1983. Accuracy of estimated phylogenetic trees from molecular data. II. Gene frequency data. Journal of Molecular Evolution 19(2):153-70. 33.Nei, M. 1987. Molecular Evolutionary Genetics. Columbia University Press, New York. 34.Obara K. and Y. Otani. 2002. Catalogue of the Dr. Tokubei Kuroda shell collection deposited in the Nishinomiya Shell Museum. Part 1 Non-marine Gastropoda. Bulletin of the Nishinomiya Shell Museum 1: 1-139. 35.Pfeiffer, L. 1866[1865]. Description of thirteen new species of land -shells from Formosa, in the collection of the late Hugh Cuming, collected by Mr. Robert Swinhoe, Vice-Consul of that island. Proceedings of Zoological Society, London 1865:828-831. 36.Pilsbry H. A. 1895. Manual of Conchology, 2nd series (Helicidae Vol.7). Vol. 9. Academy of Natural Sciences of Philadelphia?: ?Philadelphia. 37.ruett, G. E, P. Heeger., R. L. Mynatt, A. A. Truett, J. A. Walker and J. L. Warman. 2000. Preparation of PCR Quality Mouse Genomic DNA with Hot Sodium Hydroxide and Tris (HotSHOT). BioTechniques 29: 52-54. 38.Saitou, N. and M. Nei. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Molecular Biology and Evolution 4:406-425.

39.Schmacker, B. and O. Boettger. 1891. Neue Materialien zur Charakteristik und geographischen Verbreitung chinesischer und japanischer Binnen-conchylien. II. Nachrichtsblatt der Deutschen Malakozoologischen Gesellschaft 23:145-194. 40.Shimizu Y. and R. Ueshima. 2000. Historical biogeography and interspecific mtDNA introgression in *Euhadra peliomphala* (the Japanese land snail). Heredity 85:84-96. 41.Sinakawa, K. 1979. Note on *Pancala batanica pancala* and *P. bacca*. Kainakama 13:4-6. 42.Tabe, M. 1937. Morphological study of *Coniglobus batanicus pancalus* (Schmacker and Bottger) and *C. b. boteltobagoensis* Kuroda and on the systematic position of the genus *Coniglobus*. Zoological Magazine 49:12-20. 43.Tamura K., D. Peterson, N. Peterson, G. Stecher, M. Nei and S. Kumar. 2011. MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. Molecular Biology and Evolution 28: 2731-2739.

44.Thompson, J. D., D.G.. Higgins and T. J. Gibson. 1994. CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, positions-specific gap penalties and weight matrix choice. Nucleic Acids Research 22:4673-4680. 45.Ueshima, R. and T. Asami. 2003. Single-gene speciation by left – right reversal. Nature 425: 679-679. 46.Wu, S. P., C. C. Hwang and Y. S. Lin. 2008. Systematic Revision of the Arboreal Snail *Satsuma albida* Species Complex (Mollusca: Camaenidae) with Descriptions of Fourteen New Species from Taiwan. Zoological Journal of the Linnean Society 154: 437-493. 47.Xia, X. and Z. Xie. 2001. DAMBE: Data analysis in molecular biology and evolution. Journal of Heredity 92:371-373.