DATA NOTE

Genomic resources of two landsnail, *Aegista diversifamilia* and *Dolicheulota formosensis*, generated by Illumina paired-end sequencing [version 1; peer review: 1 approved]

Chih-Wei Huang¹, Wen-Lung Wu²

¹Department of Life Science, National Taiwan Normal University, Section 4, Taipei, 11677, Taiwan

²Biodiversity Research Center, Academia Sinica, Nankang District, Taipei, 11529, Taiwan

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Abstract

Despite the land snail harboring high biodiversity and dominance on land, just a few genetic markers are available for phylogeographic and phylogenetic research. We sequenced the partial genome of two land snail species that belong to the speciose family Bradybaenidae in East Asia: *Aegista diversifamilia* and *Dolicheulota formosensis*. The raw sequences were generated by Illumina paired-end sequencing and can be accessed in the [Sequence Read Archive](#) under the accession numbers SRR1918809 (*A. diversifamilia*) and SRR1920140 (*D. formosensis*).

Keywords

Helicoidea, Next-generation sequencing, Pulmonata, Stylommatophora

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1. **Juan Opazo**, Universidad Austral de Chile, Valdivia, Chile

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Corresponding author: Chih-Wei Huang (limnoperna@gmail.com)

Competing interests: No competing interests were disclosed.

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Introduction

Stylommatophora is the dominant gastropod clade on land. The family Bradybaenidae is mainly distributed in Asia and diversified in East Asia. However, only a handful of genetic markers are available for phylogenetic research. We selected two land snail species as representatives of Bradybaenidae: *Aegista diversifamilia* Huang *et al.*, 2014 and *Dolicheulota formosensis* (H. Adams, 1866). We subjected these species to Illumina paired-end sequencing in the hope that this will expand and provide valuable genetic resources for phylogeographic and phylogenetic research of gastropods.

Materials and methods

Genomic sequences were generated from one fresh specimen preserved at -20°C (*A. diversifamilia*) and one two-year-old ethanol-preserved specimen (*D. formosensis*), respectively. The living individual of *A. diversifamilia* was collected from leaf litter under lowland broadleaf forest in Xiulin Township, Hualien County, Taiwan in October 2013. *D. formosensis* was collected from the tree trunk of a lowland broadleaf forest in Mudan Township, Pingtung County, Taiwan in June 2012. Snails were brought back to laboratory and rinsed with ddH₂O to eliminate soil and other particles attached to the shell. The living individual of *A. diversifamilia* was preserved in a -20°C refrigerator. The individual of *D. formosensis* was relaxed under water for 12 hours and fixed by blanching with boiling water for several seconds. The specimen of *D. formosensis* was transferred to 95% ethanol solution and the ethanol was changed every 24 hours for 48 hours. The specimen of *D. formosensis* was finally preserved in 95% ethanol.

For *A. diversifamilia*, the shell was removed after the snail was crushed. Soft tissue was rinsed with TEK buffer (50 ml 1M Tris-HCl pH 7.5, 50 ml 0.2M EDTA pH 7.5, 15g KCl, pH 7.5) and then used for genomic DNA extraction with AxyPrep™ Multisource Genomic DNA Miniprep Kit (Axygen Bioscience) following the manufacturer's protocol. For *D. formosensis*, partial foot tissue was rinsed with ddH₂O several times to remove ethanol and then used

for DNA extraction through a modified phenol-chloroform method (Jiang *et al.*, 1997).

The quantity of extracted DNA solution was evaluated by Qubit® dsDNA HS Assay Kit (Life Technologies). The DNA concentration was 131 ng/μL (total mass 20.96 μg) and 52.9 ng/μL (5.92 μg) for *A. diversifamilia* and *D. formosensis*, respectively. The DNA solution was sent to BGI (Shenzhen, China) for paired-end library construction with insert size of approximately 500 base pairs using a Paired-End DNA Sample Prep Kit (Illumina). Sequencing was performed using Illumina HiSeq2000 in BGI. Raw sequences data can be accessed in Sequence Read Archive under accession number SRR1918809 for *A. diversifamilia* and SRR1920140 for *D. formosensis*.

Ethics policies

Ethical approval for the animals used was not required. Both species used in this study were common and not under list of protected species in Taiwan.

Author contributions

All authors were involved in experimental design, manuscript preparation and approval of the final version to be published.

Competing interests

No competing interests were disclosed.

Grant information

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References

- Adams H: **Descriptions of fifteen new species of land and freshwater shells from Formosa, collected by Robert Swinhoe, Esq., consul at Taiwan in that island.** *Proceedings of Zoological Society of London*. 1866; **1866**: 316–319.
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- Huang CW, Lee YC, Lin SM, *et al.*: **Taxonomic revision of *Aegista subchinensis* (Möllerndorff, 1884) (Stylommatophora, Bradybaenidae) and a description of a**

- new species of *Aegista* from eastern Taiwan based on multilocus phylogeny and comparative morphology.** *ZooKeys*. 2014; **445**: 31–55.
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- Jiang L, Wu WL, Lin YS: **Efficient methods for isolating mitochondrial DNA from fresh or fixed molluscan specimens.** *Zoological Studies*. 1997; **36**(1): 74–78.
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Juan Opazo

Instituto de Ciencias Ambientales y Evolutivas, Facultad de Ciencias, Universidad Austral de Chile, Valdivia, Chile

This data note is reporting massive amount of genetic data for two landsnail species, with the aim that this resource will serve as a platform to develop phylogenetic and phylogeographic makers. The goal of this note is well justified given that for one of the genera, *Dolicheulota*, there are no NCBI entries, whereas for the other the diversity of them is low. Samples were sequenced using standard protocols in a facility that has experience in sequencing protocols. I am convinced that this data will be useful to the scientific community, especially to those interested in the evolutionary history of gastropods.

Competing Interests: No competing interests were disclosed.

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