



## Complete mitochondrial genome of the radicine pond snail *Radix plicatula* (Gastropoda: Lymnaeidae)

Dong-Mei Qin<sup>a</sup>, Xiao-Chen Huang<sup>a</sup> , Li-Min Yang<sup>a</sup>, Xiong-Jun Liu<sup>b</sup> , Rui-Wen Wu<sup>a</sup>, Shan Ouyang<sup>a</sup>, Xiao-Ping Wu<sup>a,b,c</sup> and Shang-Hong Wang<sup>a</sup>

<sup>a</sup>School of Life Sciences, Nanchang University, Nanchang, People's Republic of China; <sup>b</sup>Poyang Lake Key Laboratory of Environment and Resource Utilization, Ministry of Education, Nanchang University, Nanchang, People's Republic of China; <sup>c</sup>School of Resource, Environment and Chemical Engineering, Nanchang University, Nanchang, People's Republic of China

### ABSTRACT

*Radix plicatula* is broadly distributed in China, as well as Russia. It is one of the intermediate hosts of *Fasciola* species which leads to the spread of fascioliasis. Here, we first described the complete mitochondrial genome of *R. plicatula*. The mitogenome is 13,751 bp in length, containing 13 protein-coding genes, 22 tRNA genes, and 2 rRNA genes. The contents of each base are 30.7% A, 39.6% T, 15.7% G, and 13.9% C. The sequence is AT rich (70.3%). Mitochondrial phylogenomic analysis showed that *R. plicatula* is close to *R. auricularia*.

### ARTICLE HISTORY

Received 27 July 2019  
Accepted 3 August 2019

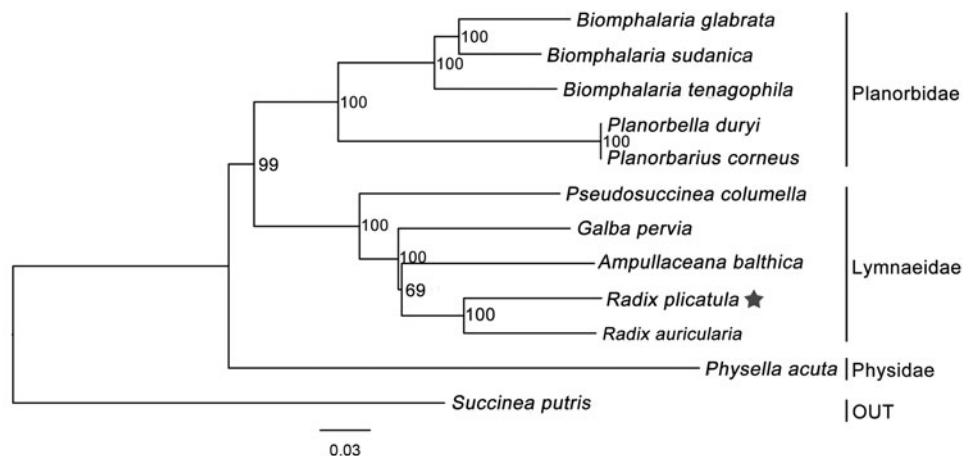
### KEYWORDS

Amphipepleinae; freshwater snail; mitochondrial genome; phylogeny; *Radix plicatula*

*Radix plicatula* is a species of aquatic pulmonate gastropod mollusk in the family Lymnaeidae, broadly distributed in China, as well as in Russia (Liu et al. 1993). *Radix* species is one of the intermediate hosts of *Fasciola* species, which play a critical role in the spread of fascioliasis in humans (Correa et al. 2010; Lawton et al. 2015). Currently, approximately 20 million people have been infected with fascioliasis worldwide (Correa et al. 2010). Due to the high plasticity of the shell shape within the *Radix* species, it is difficult to classify them only according to morphological features (Pfenninger et al.

2006; Feldmeyer et al. 2010). Recently, some studies have performed the classification and phylogenetic analysis of *Radix* species and its allies (Bargues et al. 2001; Lawton et al. 2015; Aksenova et al. 2018). So far, however, in *Radix* only one species (i.e. *R. auricularia* from Germany) had the complete mitochondrial genome.

Here, we sequenced and annotated the complete mitochondrial genome of *R. plicatula* and reconstructed the phylogenetic relationships of 12 gastropod molluscs with the focus on *Radix sensulato*. Our results provide new insights into the



**Figure 1.** Phylogenetic relationships of 12 gastropod molluscs using neighbour-Joining method. (GenBank accession numbers, *Ampullaceana balthica*: NC\_026539; *Radix plicatula*: MN175602; *Galba pervia*: NC\_018536; *Radix auricularia*: NC\_026538; *Pseudosuccinea columella*: MH614274; *Planorbarius corneus*: NC\_026708; *Biomphalaria tenagophila*: NC\_010220; *Planorbella duryi*: KY514384; *Biomphalaria sudanica*: NC\_038060; *Biomphalaria glabrata*: NC\_005439; *Physella acuta*: NC\_023253; *Succinea putris*: NC\_016190).

relationship of radicine pond snails and genetic information for controlling the spread of Fascioliasis.

Specimens were collected from ponds in Nanchang (28°39'39"N, 115°47'20"E), China, in 2019. Morphological identification was following the literature (Yen 1939; Liu et al. 1993). The voucher specimens were deposited in the Nanchang University, Nanchang, China. Foot tissue of each specimen was preserved in  $-80^{\circ}\text{C}$  and then one individual (voucher number: ncuwxp-nc-201901) was used for genomic DNA extraction, followed by the Illumina Miseq sequencing platform with the strategy of  $2 \times 250$  bp paired-ends. Complete mitochondrial genome was generated according to the previous study (Zhou et al. 2019).

Complete mtDNA sequence of *R. plicatula* is 13,751 bp in length (GenBank accession number: MN175602) and contains 13 protein-coding genes (PCGs), 22 tRNA genes, and 2 rRNA genes. The light strand includes 11 genes (four PCGs, *rnrS* gene, and six tRNA genes) and the heavy strand includes 26 genes (nine PCGs, *rnrL* gene, 16 tRNA genes). The overall base composition of the mitochondrial genome is as follows: 30.7% A, 39.6% T, 15.7% G, and 13.9% C. The sequence is AT-rich (70.3%), similar to other Panpulmonata species (Feldmeyer et al. 2010; Liu et al. 2012; Zhou et al. 2019).

Compared with *R. auricularia* mitogenome, the gene order of *R. plicatula* is identical, but different from that of *Ampullaceana balthica* because of the positional mismatch for the tRNA-Trp gene. Phylogenetic analysis based on 12 PCGs and 2 rRNA genes showed that the family Lymnaeidae is monophyletic (BS = 100), and *R. plicatula* and *R. auricularia* had a close relationship (BS = 100) (Figure 1).

## Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

## Funding

This work was supported by the National Nature Science Foundation of China [No. 31660619] and the Innovation Fund Designated for Graduate Students of Jiangxi Province [No.YC2014-S059].

## ORCID

Xiao-Chen Huang  <http://orcid.org/0000-0002-0242-3571>  
Xiong-Jun Liu  <http://orcid.org/0000-0002-5333-6670>

## References

- Aksenova OV, Bolotov IN, Gofarov MY, Kondakov AV, Vinarski MV, Bespalaya YV, Kolosova YS, Palatov DM, Sokolova SE, Spitsyn VM. 2018. Species richness, molecular taxonomy and biogeography of the radicine pond snails (Gastropoda: Lymnaeidae) in the Old World. *Sci Rep.* 8:11199.
- Bargues MD, Vigo M, Horak P, Dvorak J, Patzner RA, Pointier JP, Jackiewicz M, Meier-Brook C, Mas-Coma S. 2001. European Lymnaeidae (Mollusca:Gastropoda), intermediate hosts of trematodiasis, based on nuclear ribosomal DNA ITS-2 sequences. *Infect Genet Evol.* 1:85–107.
- Correa AC, Escobar JS, Durand P, Renaud F, David P, Jarne P, Pointier J-P, Hurtrez-Boussès S. 2010. Bridging gaps in the molecular phylogeny of the Lymnaeidae (Gastropoda: Pulmonata), vectors of Fascioliasis. *BMC Evol Biol.* 10:381–394.
- Feldmeyer B, Hoffmeier K, Pfenninger M. 2010. The complete mitochondrial genome of *Radix balthica* (Pulmonata, Basommatophora), obtained by low coverage shot gun next generation sequencing. *Mol Phylogenet Evol.* 57:1329–1333.
- Liu GH, Wang SY, Huang WY, Zhao GH, Wei SJ, Song HQ, Xu MJ, Lin RQ, Zhou DH, Zhu XQ. 2012. The complete mitochondrial genome of *Galba pervia* (Gastropoda: Mollusca), an intermediate host snail of *Fasciola* spp. *PLoS One.* 7:e42172.
- Liu YY, Zhang WZ, Wang YX. 1993. *Medical malacology*. Beijing: Ocean Press.
- Lawton SP, Lim RM, Dukes JP, Kett SM, Cook RT, Walker AJ, Kirk RS. 2015. Unravelling the riddle of *Radix*: DNA barcoding for species identification of freshwater snail intermediate hosts of zoonotic digenaeans and estimating their inter-population evolutionary relationships. *Infect Genet Evol.* 35:63–74.
- Pfenninger M, Cordellier M, Streit B. 2006. Comparing the efficacy of morphologic and DNA-based taxonomy in the freshwater gastropod genus *Radix* (Basommatophora, Pulmonata). *BMC Evol Biol.* 6:100.
- Yen TC. 1939. *Die chinensischen land-und süßwasser-gastropoden des Natur-Museums Senckenberg*. Stuttgart: Schweizerbart Science Publishers.
- Zhou YY, Liu XJ, Wu RW, Zhou CH, Ouyang S, Wu XP. 2019. The complete mitochondrial genome of invasive species *Biomphalaria straminea* (Planorbidae: *Biomphalaria*) and phylogenetic analysis. *Mitochondr DNA B Resour.* 4:937–938.