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## RESEARCH ARTICLE

# Genetics of land snail *Xerolenta obvia* and related species

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**Abstract** – Land snail *Xerolenta* (*Syn.*, *Helicella*) *obvia* [MENKE, 1828] (*Eng.*, heath snail; *Hung.*, lapos kórócsiga) (1.5-2.0 cm) was analyzed here by *in silico* data mining at the DNA sequence site of *18S ribosomal RNA* gene (1801 bp; [GenBank# GU331943.1](#)) to find the most related snail species. Sequence and dendrogram analysis revealed that the pest land snail *Acusta despecta sieboldiana* [SOWERBY, 1839; PFEIFFER, 1850] shows the closest genetic distance to *X. obvia*. The ecological and medicinal impacts of sea and land snail mollusks are indicated.

**Keywords** – DNA, data mining *in silico*, *Xerolenta*, *Acusta*

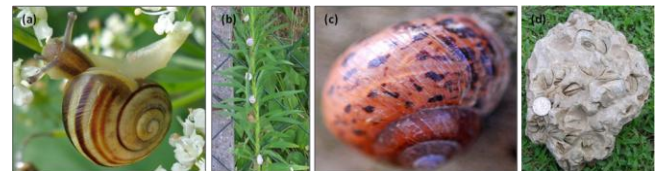
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## INTRODUCTION

The number of *Mollusca* species (*Hung.*, Puhatestűek), including the three main groups of *Gastropoda* (snails), *Bivalvia* (clams or mussels), and *Cephalopoda* (polyps) (Henderson and Henderson, 1963) (*Hung.*, csigák, kagylók, and polipok) globally is about 70.000 - 118.000 (Bitzilekis *et al.*, 2023) with the difficulties of double/triple description names (Rosenberg, 2014). The 80% of existing *Mollusca* species belongs to *Gastropoda* (Chen and Schrödl, 2022). Fossils and petrified *Mollusca* species (Fig.1.[d]) have been documented in detailed papers and books (Strausz, 1962; Báldi, 1973; Sümegei, 2008; Főzy *et al.*, 2014). New species are continuously being identified (Erőss and Petrő, 2008; Páll-Gergely *et al.*, 2021; Haraszthy, 2022; Bitzilekis *et al.*, 2023).

*Gastropods* (slugs and snails) show an evolutionary back transition from *shelled snails*; through *semi-slugs* (*Hung.*, félmeztelencsigák) with reduced small shell; to *slugs / naked mollusks* living without shell (*Hung.*, meztelencsigák). The use of term ‘back transition’ seems to be correct as mollusks phylogeny might be originated from an ancient mollusk-like? slug *Kimberella* (550 MYA) with univalve shell (Marin *et al.*, 2012). Developmental way from *snails* to *slugs* also shows steps from the transition from herbivory and detritivory, via omnivory to obligate carnivory (*e.g.*, earthworm) (Neiber *et al.*, 2020).



**Figure 1.** Image [a] of land snail *Xerolenta* (*Syn.*, *Helicella*) *obvia* (*Eng.*, heath snail; *Hung.*, lapos kórócsiga) (1.5-2.0 cm) (Source: [AfroBrazilian](#), [Latvia](#), [Wikipedia.org](#)). [b] Snails *X. obvia* resting on *Erigeron canadensis* (Soó, 1953, 1965; Greguss, 1968; Milkovits, 1972; Lehoczki *et al.*, 1992; Gulyás and Gulyás, 1993; Suba, 2002; Simoncsics, 2017), in Hungary (photo by Zs.G.Gyulai). [c] The most related species to *X. obvia* identified here is the pest land snail *Acusta despecta sieboldiana* (1-1.7 cm) (*Eng.*, Siebold's Korean round snail; in *Hung.* has not registered) (Source: Kim, Hyun-tae, <http://home.megapass.co.kr/~skua>). [d] Petrified *Mollusca* species in a crystallized lime stone rock from West Lafayette, IN, U.S.A., (collection and photo of Zs.G.Gyulai, 2103; a U.S. dollar quarter is for size scale).

The number of *snail* species in Hungary is about 302 (Soós, 1943; Krolopp, 1983 and 2014; Füköh, 1995; Domokos and Pelbárt, 2011). Of them, 201 species are of shelled snails (*i.e.*, terrestrial / land species), semi-slugs and slugs; 68 species (compared to 77 species referred to Hungary by

Cuttelod *et al.*, 2011) live in fresh waters of ponds, lakes and rivers; and 31 species belong to *Bivalvia*.

There are some unique snail species living in Hungary such as the *Bythinella hungarica* (Hung., magyar forráscsiga) [HAZAY, 1880] (described by Gy. Hazay, 1842-1887); *Helicopsis hungarica* (Hung., pusztai csiga) [SOÓS AND WAGNER, 1935] (L. SOÓS, 1879-1972; AND J. WAGNER, 1906-1948) (Varga, 2013); *Hygromia kovacsi* (Hung., dobozi pikkelyescsiga) (5 mm) [VARGA AND PINTÉR, 1972]; *Sadleriana* (Syn.: *Bythinella*) *pannonica* (Hung., pannon karsztcsga) [FRAUENFELD, 1865]; *Theodoxus danubialis* (Hung., dunai bödőncsiga) [PFEIFFER, 1828]; *Zebrina detrita sallake* (Hung., zebracsiga) [FEHÉR AND ERŐSS, 2009]; slug *Tandonia budapestensis* [HAZAY, 1880] (Eng., Budapest keeled slug) (Hazay, 1880; Reise, *et al.*, 2006; Turóci *et al.*, 2020; GBIF web source); and semi-slug *Daudebardia rufa* [DRAPARNAUD, 1805].

Here, we selected land snail *X. obvia* (Fig. 1.[a, b]) to analyze genetically (Alzohairy *et al.*, 2014; Gyulai *et al.*, 2014, 2023; Szabó *et al.*, 2023) by *in silico* data mining and find the most related species based on the sequence site at the 18S ribosomal RNA gene (1801 bp; GenBank# GU331943.1) after sequence alignment (Fig. 3), and dendrogram (Fig. 4) analysis.

## MATERIALS AND METHODS

Morphological studies were conducted in photos (Fig. 1). Total genome sizes (Fig. 2), and DNA sequence analyses of 18S ribosomal RNA gene of mollusks species were downloaded from NCBI server, and aligned by BioEdit (Hall, 1999) computer program (Fig. 3).

Genetic distances among land snail species were determined (Fig. 4) by using MEGA7 computer program (Kumar *et al.*, 2016).

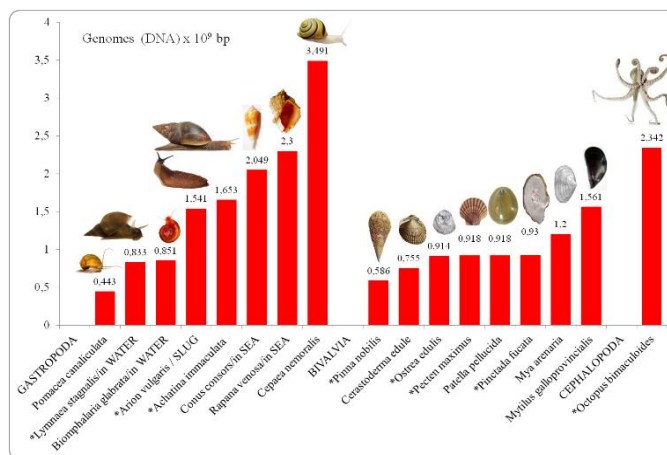
## RESULTS

### MOLLUSCA GENOM SIZES

The genome sizes of *Mollusca* species have been found to vary in wide ranges among *Gastropoda*, *Bivalvia* and *Cephalopoda* (Fig. 2). Recently, 124 *Mollusca* genome sequences are available in NCBI server. Genome sequence of *X. obvia* is not available yet.

Some well known *Mollusca* genomes are indicated in Fig. 2. such as *\*Arion vulgaris* (Spanish slug) a very invasive slug moving to West to East in Europe (Papureanu *et al.*, 2014); *\*Achatina immaculata* (Eng., giant African land snail; Hung., afrikai óriáscsiga) is a pet snail in Europe, NCBI Taxonomy ID# 2605667; *\*Lymnaea stagnalis* a great pond snail used for biological tests (Fodor *et al.*, 2020); *\*Pinna nobilis* a species of *Bivalvia* (Eng., pen shells; Hung., sonkakagyló), NCBI Taxonomy ID# 111169; *\*Ostrea edulis* (Eng., Colchester native oyster; Hung., osztriga) a

species of *Bivalvia*, Ref., xbOstEdul1.1, NCBI Taxonomy ID# 37623; *\*Pecten maximus*, Ref., xPecMax1.1. (Pennec *et al.*, 2003), NCBI Taxonomy ID# 6579; *\*Pinctada fucata* (Eng., pearl oyster; Hung., gyöngykagyló), NCBI Taxonomy ID# 50426; and *\*Octopus bimaculoides* (Eng., California two-spot octopus; Hung., polip) - coupled with *nautilus* species, NCBI Taxonomy ID# 37653.



**Figure 2.** Genome sizes (x 10<sup>9</sup> DNA bp) of indicative *Mollusca* species. Data were downloaded from NCBI server and edited by Microsoft Excel computer program. Species indicated by asterisks are discussed in the text. See *Cepaea nemoralis* (size: 2.0-2.5 cm) (Eng., lemon snail; Hung., ligeti csiga) with the largest genome.

### SEQUENCE ALIGNMENT

The longest available DNA sequence of *X. obvia* is the 18S ribosomal RNA gene (1801 bp; GenBank# GU331943.1). It was downloaded from NCBI server, and after DNA sequence alignment by BioEdit computer program (Hall, 1999) (Fig. 3), the land snail *Acusta despecta sieboldiana* (Fig. 1.[c]) (named after K.T.E. von Siebold, 1804-1885) showed the closest sequence similarity (Fig. 3), and genetic distance in dendrogram analysis (Fig. 4).

### DISCUSSION

Land snail *X. obvia* has one of the most dense snail populations in Hungary which made it useful to study the invertebrate nerve anatomy (Röhlich and Bierbauer, 1966; Vajon, 1970). *X. obvia* spread everywhere in the dry summer fields of Hungary by resting in grasses, weeds and fences (Fig. 1.[b]) being exposed to sunlight, which behavior is unique in *snails*.

However, it might correlate with the observations which reported sharp differences in survival rates (%) of snails kept at different temperatures coupled with humidity at 20 °C (72%), at 25 °C (51%), and at 30 °C (16%) (Zhang *et al.*, 2014).

*X. obvia* might be a vector of plant fungi pathogens (e.g., *Alternaria*, *Fusarium*, and *Phytophthora*), and is considered



ocean waters which causes adaptive viral immunity to mollusks. These *antiviral drugs* were found to be useful for human medications (Dang *et al.*, 2015). The observation also raises the possibility to study land snails like *X. obvia* as possible antiviral drug producers, along with protein fiber *elastin* and *epiphragmin* – the dried mucus produced to seal the snail shell production, which also has applications in human medicine (Li and Graham, 2007).

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## WEB SOURCES

GBIF - the Global Biodiversity Information Facility:

<https://www.gbif.org/>

Marine Species / The World Foraminifera Database:

<https://www.marinespecies.org>

MolluscaBase:

<https://www.molluscabase.org>

NCBI (National Center for Biotechnology Information):

<http://www.ncbi.nlm.nih.gov>

[https://en.wikipedia.org/wiki/List\\_of\\_non-marine\\_molluscs\\_of\\_Hungary](https://en.wikipedia.org/wiki/List_of_non-marine_molluscs_of_Hungary)

<https://www.invasive.org>



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