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Genetic structure and new breeding populations of the garden snail *Cornu aspersum* (O. F. Müller 1774) (Mollusca: Gastropoda: Pulmonata: Helicidae) in Central Europe

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ABSTRACT

The garden snail *Cornu aspersum* is considered an invasive alien species worldwide. Despite its Mediterranean origin, its European distribution is mostly a result of man-mediated translocations. Its range is continuous in Western Europe, but Central Europe seems to be at the edge of the expansion, revealing a patchy distribution. This contribution shows new data on its distribution and genetic structure in Poland. We found two viable populations, one in northern and one in southern Poland. At both sites, juvenile individuals were present, and the southern population has persisted for several years. The genetic structure reveals relatively high divergence between localities, which suggests multiple introductions from different sources. There is no evidence that the species fulfils the invasive species definition in the studied region; however, urban heat islands in temperate areas may support source populations of this species in the future. The species may also benefit in Central Europe from climate warming.

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1. Introduction

The garden snail *Cornu aspersum* (O. F. Müller, 1774) originates from the Mediterranean region (Guiller & Madec 2010). However, recently it has been one of the most widely distributed terrestrial snails all over the world. Its occurrence has been confirmed in both Americas, Africa, Oceania, Asia and Europe (Guiller et al. 2012). Notably, the man-mediated expansion of this mollusc probably started with the Romans due to its consumption value (Guiller 1994). More recently, besides its introduction for commercial purposes, this species was spread accidentally due to transfer of vegetation (DAFF 2020). The garden snail is also kept as an ornamental pet, which may facilitate its colonization of new areas (VKM et al. 2017). Thus, episodes of introduction to new sites were numerous, and the current world distribution is a result of previous man-mediated colonization of new regions rather than dispersal from the native range of the species (Guiller et al. 2012). Despite some commercial value in many regions, the species is considered a pest (Sanderson & Sirgel 2002).

In Europe, the spread of the species in some regions is well documented, including relationships to the geologically shaped phylogeography of *C. aspersum* (Guiller & Madec 2010; Welter-Schultes 2012). Outside the Mediterranean area the species is now present in most of Western Europe, and for more than a decade new records have been obtained from Central and East European countries (Juříčková & Kapouněk 2009; Gural-Sverlova & Gural 2021) (Figure 1). In Poland, to date, there has been no widely accessible information published on the presence and breeding of the species (Wiktor 2004; Welter-Schultes 2012). However, since 2024, iNaturalist (2026) shows several records of *C. aspersum* in the state. Also, no information on either genetic structure or age structure has been published from Central Europe.

Despite its wide distribution, remarkably little is known about the genetic structure of *C. aspersum*. The BOLD (Barcode of Life Data System) database (Ratnasingham & Hebert 2007) currently contains only 148 sequences of its COI marker (mitochondrial cytochrome c oxidase subunit I), which are grouped into just six

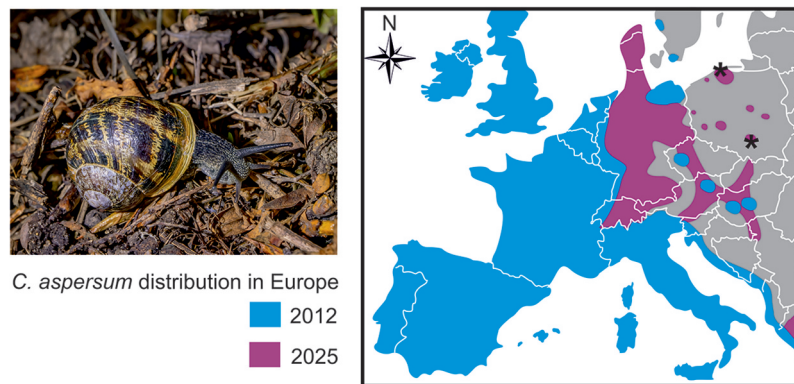


Figure 1. Distribution of *C. aspersum* in Europe in 2012 (blue, after Welter-Schultes 2012) and new sites in 2025 (purple, iNaturalist records). Asterisks indicate two populations found in Poland in Kraków (S) and Władysławowo (N).

barcode index numbers (BINs). The Kimura two-parameter (K2P) genetic distance among these BINs ranges from 3% to 19.6%, thus far exceeding typical levels of interspecific, or even higher-rank, divergence. However, drawing more profound phylogenetic and taxonomic conclusions remains unjustified, primarily due to insufficient sample sizes and inadequate geographic coverage across the species' range. For these reasons, studies employing DNA barcoding on newly identified populations of *C. aspersum* are of particular importance, as they may contribute to future studies on phylogeny. In light of the above, we describe two new breeding populations of *C. aspersum* in Poland, providing a first view of its genetic structure in the region. We also present the size structure of one population.

2. Methods

2.1. Field methods

We present first records of two *C. aspersum* populations from Poland (Figure 1). The first one was detected in the autumn of 2023 in Southern Poland, Kraków (50°02'07.7"N, 19°56'40.2"E) in a small city greenery patch of approximately 100 m² in area. It is a typical urban artificially supported gardenlike structure with mostly non-native ornamental plants. In spring 2024 (2 June 2024), we collected 85 individuals from the site for morphometric measurements. The longest axis of shells was measured using callipers with 0.05 mm accuracy.

The second site was found on 21 May 2023, in Władysławowo, northern Poland (54°47'42.0"N, 18°23'55.2"E). The specimens of *C. aspersum* were collected in an urban, synanthropic habitat within a built-up residential area, characterized by managed lawns and scattered trees. The snails were found at the boundary between a mown lawn and soil located beneath *Thuja* shrubs. From that site, four individuals were collected.

2.2. Molecular methods

For the molecular study all specimens were preserved in 80% ethanol. A small piece of tissue was taken for DNA extraction. Whole DNA was extracted using a SHERLOCK® kit (A&A Biotechnology) according to the manufacturer's procedure for fresh tissues. Extracted DNA was dissolved in 20 µL of tris-EDTA (TE) buffer and was stored at -80°C at the Department of Comparative Anatomy, Institute of Zoology and Biomedical Research, Jagiellonian University in Kraków. To determine species affiliation, we sequenced the COI marker, widely employed in animal DNA barcoding. The primers used in the study and the polymerase chain reaction (PCR) conditions are given in Hofman et al. (2022). The PCR products were purified using Exo-Sap procedure and then sequenced using BigDye Terminator v. 3.1 (Applied Biosystems). The sequencing reaction products were purified using ExTerminator Columns (A&A Biotechnology); DNA fragments were then sequenced on a 3730xl DNA Analyzer (Genomed, Warsaw, Poland). Sequences were initially aligned in the MUSCLE (Edgar 2004) program in MEGA 7 (Kumar et al. 2016) and then checked in BIOEDIT 7.1.3.0 (Hall 1999). The K2P distances were calculated in MEGA 7. The saturation test (Xia et al. 2003; Xia & Lemey 2009) was performed using DAMBE (Xia 2018). In the phylogenetic analyses, six reference sequences representing all known BINs in the BOLDSystem were used. One representative sequence per

BIN was included in order to capture the main genetic structure while avoiding overrepresentation of particular haplotypes. The sequence of *Helix pomatia* Linnaeus, 1758 was used as outgroup. The data were analysed using approaches based on Bayesian inference (BI) and maximum likelihood (ML). The best-fit model of evolution was selected by ModelTest-NG (Darriba et al. 2020) using raxmlGUI 2.0 (Edler et al. 2021). The model GTR+I+G4 was used, according to Akaike Information Criterion with a correction (AICc) and Akaike Information Criterion (AIC). The ML analysis was conducted in RAxML-NG (Kozlov et al. 2019) using raxmlGUI 2. The Bayesian analyses were run using MrBayes v. 3.2.3 (Ronquist et al. 2012) with default priors. Two simultaneous analyses were performed, each with 10,000,000 generations, with one cold chain and three heated chains, starting from random trees and sampling the trees every 1000 generations. The first 25% of the trees were discarded as burn-in. The analyses were summarized as a 50% majority-rule consensus tree. Convergence was checked in Tracer v. 1.5 (Rambaut et al. 2018). FigTree v. 1.4.4 (Rambaut 2010) was used to visualize the trees. Four species delimitation methods were performed: Poisson tree processes (PTP and bPTP) (Zhang et al. 2013), Automatic Barcode Gap Discovery (ABGD) (Puillandre et al. 2011) and Assemble Species by Automatic Partitioning (ASAP) (Puillandre et al. 2021). All these methods were used by iTaxoTools 0.1 bioinformatics platform (Vences et al. 2021).

3. Results

Species identification at both study sites was confirmed based on morphological characteristics (Figure 2) as well as by DNA barcoding.

3.1. Population structure

In Kraków, snails were observed from autumn 2023 until summer 2025. Despite some effort in seeking the snails in the nearest surroundings, *C. aspersum* has not been detected outside this patch. The only large helioid in the environs was the Roman snail *Helix pomatia*. Moreover, even during rainy and warm weather, individuals of *C. aspersum* were found no farther than 2 m from the patch on the granite pavement.

The longest axis of shells from collected snails averaged 19.79 mm (Standard Deviation (SD) ± 6.69), and the length range was from 7.3 to 31.5 mm. The data distribution was far from Gaussian (Shapiro-Wilk normality test, $d = 0.1653$; $p < .05$) and showed a bimodal shape (distribution far from bimodal according to Hartigan's dip test: $D = 0.085$, $p < .05$; Figure 3). Two shell-size classes could be distinguished: smaller than 20 mm (median = 14.5; $N = 40$), and larger than 20 mm (median = 26.9 mm; $N = 45$). In 2025, snails were still present at that site.

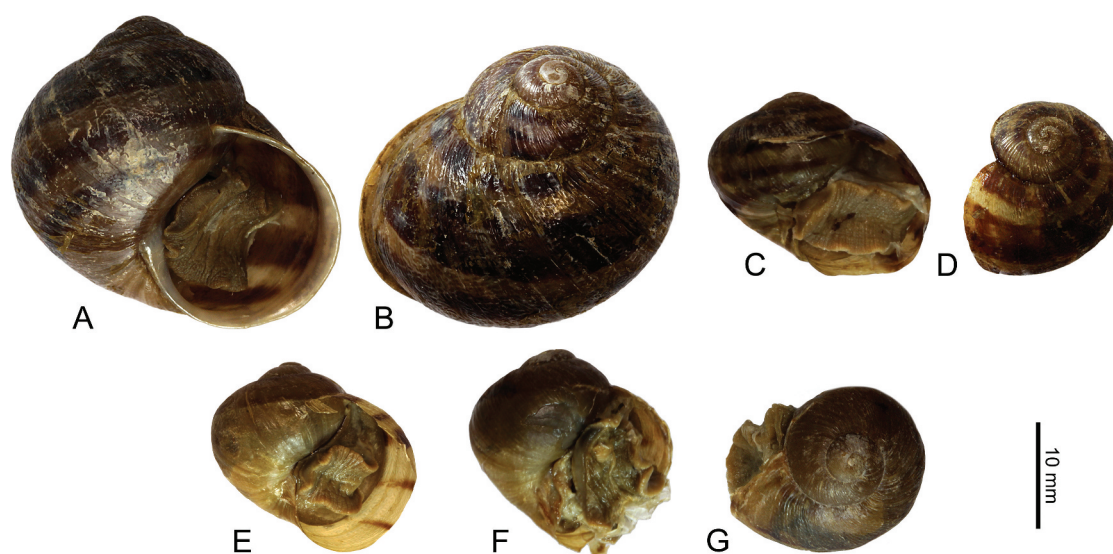


Figure 2. Shells of snails used for DNA barcoding. A–B: Kraków (3K31); C–D: Kraków (3K66); E: Władysławowo (3K67); F–G: Władysławowo (3K68). Numbers in parentheses indicate specimens and DNA extraction identifiers used for DNA barcoding (see Figure 4).

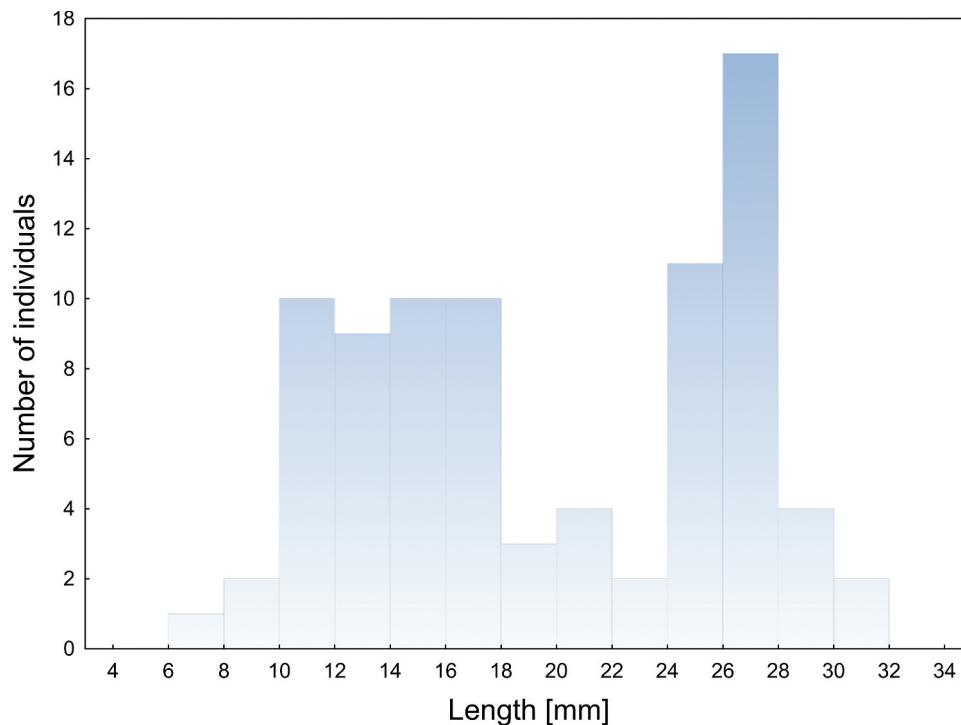


Figure 3. Distribution of shell length (mm) in 85 studied individuals of *Cornu aspersum*.

We could not analyse the population structure of individuals from Władysławowo because of the low sample size ($N = 4$). However, the sample included juvenile snails (Figure 2).

3.2. Genetic structure

For *C. aspersum*, we obtained four new sequences of COI (GenBank accession numbers PZ532586-PZ532589). All sequences were aligned to a final length of 467 bp. The alignment was checked for stop codons and none were detected. The test for the substitution saturation showed an Index of Substitution Saturation (ISS) (0.1573) significantly smaller than the critical ISS value (0.7288), indicating little saturation and that sequences are useful in phylogenetic reconstruction. In all analyses, the topologies of the resulting phylograms were identical in both the ML and BI phylogram analyses; thus, we present the phylogram computed with RAxML. The obtained sequences cluster into five distinct genetic lineages (treated here as molecular Operational Taxonomic Units (mOTUs) for convenience) (Figure 4), consistently recovered by all species

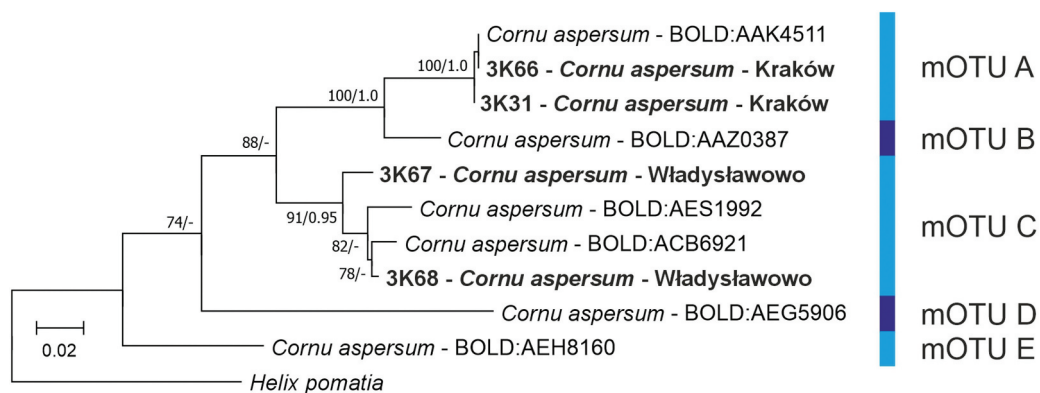


Figure 4. Maximum likelihood phylogram based on cytochrome c oxidase subunit I (COI) of the studied taxa. Bootstrap supports (if > 60%) and BP (if > 0.95) are given. Bold indicates newly obtained sequences. Results of species delimitation methods are also presented.

delimitation methods used in the analyses, although these results should be treated as preliminary. In this study, mOTUs were treated as operational genetic lineages inferred from the COI dataset and should not be interpreted as formal taxonomic units. The genetic distances among them range from 5.9% to 19.6%. The newly obtained sequences cluster into two mOTUs, with those from Kraków assigned to mOTU A and those from Władysławowo to mOTU C (with K2P distance = 10.9%). While the sequences from Kraków are nearly identical, the sequences from Władysławowo differ from each other by 2.5%, and the pairwise differences among all sequences within mOTU C range from 1% to 4%.

4. Discussion

Our contribution gives the first insight into *C. aspersum* in Poland in the context of the species' occurrence, population viability and genetic structure. To date, only grey literature contributions indicated the occurrence of this species in Poland, and records have been reported since 2024 (iNaturalist 2026). The observations presented here show that this snail may establish self-sustaining populations at least in urban climatic conditions (Kraków) and probably in mild-climate areas along the Baltic shore (site in Władysławowo). This is supported by both the size structure (numerous 1-year individuals in Kraków) and population durability (several years in Kraków). The bimodal shell-size distribution probably reflects the presence of two age cohorts, with smaller individuals representing juveniles originating from the previous breeding season and larger individuals representing older snails. Thus, the observed size structure provides additional evidence for successful reproduction and recruitment within the population. Interestingly, in 2019, dozens of *C. aspersum* specimens were detected 1 km west of the site introduced here in Kraków. However, detected individuals were removed from the environment immediately by the authors after the detection (without morphometric measurement) and to date, only several empty shells have occasionally been found in that place. Despite detection of juvenile individuals in Władysławowo, the site requires further study to obtain a larger sample size and intraseasonal observations.

Our dataset shows highly uneven sampling between the populations from Kraków and Władysławowo. This led to the conclusion that only individuals from Kraków may provide proper insights into population size structure. Also, in this population we were able to collect presence data from more than one season. However, despite finding only four specimens from Władysławowo, also there both juvenile and adults were present. Obviously, further sampling and intraseason observations should be conducted to make inferences about the viability of the population therein. However, our conclusions regarding the origin of individuals (see below), based on genetic analyses, still allow us to confirm a possible introduction into Poland from more than one source, as such inference may be drawn even from DNA sequences obtained from single individuals.

Molecular data clearly indicate how little is known about the phylogeny of the genus. The sequences obtained from both locations in Poland belong to two clearly distinct mOTUs, differing by 10.9%. Of course, our dataset is far from sufficient to draw taxonomic conclusions, given that only a single mitochondrial marker was analysed, the sample size is small, and the sampling coverage is limited. Nevertheless, this substantial divergence is noteworthy, especially since both mOTUs are strongly supported statistically in phylogenetic analyses, and their intergroup divergence far exceeds the variation observed within the most diverse group (mOTU C).

The choice of a threshold value distinguishing intra- from interspecific genetic distances is largely arbitrary, given the substantial overlap between these categories. Davison et al. (2009) found that a threshold of approximately 4% minimized false positives and negatives for a COI dataset of Stylommatophora land snails. For the superfamily Helicoidea, to which *C. aspersum* belongs, these values are relatively variable (e.g. 17.2–21.9% for *Fruticicola* (Hofman et al. 2022); 0.4–21.8% within Cretan *Xerocrassa* (Sauer and Hausdorf 2012).

It can be expected that such intergroup divergence may help explain the present-day distribution of these snails, including the origins of different lineages currently undergoing expansion; however, the available data remain fragmentary. The sequences from Kraków are nearly identical to sequences from snails collected in various regions worldwide, including the United Kingdom, France, Denmark and Croatia, as well as India, the Americas and South Africa (BOLDSystem, Ratnasingham & Hebert 2007). The sequences from Władysławowo are closely related, though not identical, to sequences from Croatia, Tunisia and Iraq. This

pattern may suggest the possibility of more than one introduction source, although this inference is tentative given the limited dataset.

The question of whether *C. aspersum* will be able to colonize the area and have some impact on local biodiversity remains unsolved. On one hand, the evidence of breeding in Poland does exist, but on the other, despite a handful of records of the species from the region (iNaturalist 2026), there are almost no records on breeding success here. Notably, despite several years of breeding in Kraków, the occupied area has not increased for several years and is delimited to a single small city greenery patch. The status (invasive or not) is unclear for Poland. To date, there are no data on rapid population growth or an impact on local biodiversity or economy. Also, due to being native to part of Europe, no international regulations on *C. aspersum* exist, which make the species of lower interest among administrations responsible for invasive alien species management (European Parliament and Council 2014). On the other hand, alien species may live in stable small populations for some time and expand due to evolutionary and environmental changes (Borden & Flory 2021). This appears to be true for an array of species previously limited to thermally polluted habitats, including plants and animals (see for example Bonk et al. 2018; Šajna et al. 2023). Adaptive changes induced by extreme conditions in the urban environment have also been revealed in native Helicidae (Kerstes et al. 2019). Although urban heat islands and climate warming may facilitate the persistence and future spread of thermophilic species, including *C. aspersum*, such effects have not yet been demonstrated for this species in Central Europe. Therefore, these considerations should be regarded as hypotheses and potential scenarios rather than evidence-based predictions. Nevertheless, continued monitoring of the species appears warranted in the context of mollusc conservation and the possible effects of ongoing climate change.

5. Conclusions

Cornu aspersum is probably able to maintain viable populations in Central Europe. We recorded two sites of the species. Breeding of the species was confirmed in one of these sites, and we suggest the possibility of its occurrence also in the other. The patchy distribution in Poland suggests that the occurrence of the species may be the result of multiple introductions rather than gradual eastward colonization; however, this hypothesis requires further verification based on broader sampling. This statement is suggested by genetic analyses revealing high genetic variation between the recorded populations. We suggest that monitoring of recorded sites of occurrence is needed for a better view of the status of the species and predictions of potentially positive trends. This is particularly important in the context of interactions with local malacofauna, including the economically important Roman snail *H. pomatia* and the legally protected *Helix lutescens* (Koralewska-Batura 1999), species of strictly delimited range at both Eurasian and national levels.

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Author contributions

CRedit: **M. Bonk:** Conceptualization, Data curation, Formal analysis, Methodology, Writing – original draft, Funding acquisition; **A. Jaszczyńska:** Conceptualization, Formal analysis, Methodology, Visualization, Writing – original draft, Writing – review & editing; **J. Kajzer-Bonk:** Conceptualization, Data curation, Formal analysis, Methodology, Visualization, Writing – original draft, Writing – review & editing; **S. Hofman:** Conceptualization, Data curation, Formal analysis, Funding acquisition, Methodology, Writing – original draft, Writing – review & editing.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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