



Short Note

Assessing beaver origins in North-Western Italy: a mitochondrial DNA comparison with Swiss and French populations

Andrea MOSINI¹, Lorenzo ATTILI^{2,*}, Antonella PIZZARELLI², Rita LORENZINI², Andrea VIVIANO³, Leonardo ANCILLOTTO^{3,4}, Elias PESENTI⁵, Emiliano MORI^{3,4}

¹Valgrande Società Cooperativa, Via alla Cartiera 41, 28923 Verbania (VCO), Italy

²Istituto Zooprofilattico Sperimentale del Lazio e della Toscana "M. Aleandri", Centro di Referenza Nazionale per la Medicina Forense Veterinaria, 58100 Grosseto, Italy

³Istituto di Ricerca sugli Ecosistemi Terrestri IRET, Consiglio Nazionale delle Ricerche, Via Madonna del Piano 10, 50019 Sesto Fiorentino (FI), Italy

⁴National Biodiversity Future Center (NBFC), 90133 Palermo, Italy

⁵Service des Forêts et de la Nature, Direction des Institutions de l'Agriculture et des Forêts, Ruelle de Notre-Dame 2, 1700 Fribourg, Switzerland

Keywords:

Castor fiber
mtDNA
molecular identification
range expansion
North-Western Italy.

Article history:

Received: 12 December 2024

Accepted: 11 April 2025

Acknowledgements

We would like to thank all volunteers who helped us in this research. We also thank Emanuele Lubian (Ospedale Veterinario Universitario di Lodi, Università di Milano), LIPU Wildlife Recovery Center "La Fagiana" and the Ticino park for providing the beaver sample from Ticino river. We are grateful to an anonymous reviewer and the Editor who kindly provided us with useful comments on the first draft of the manuscript. This research was funded by WWF Italia (Prot. 0261766708092023 UOR: 532). EM and LAN were also funded by the National Recovery and Resilience Plan (NRRP), Mission 4 Component 2 Investment 1.4 - Call for tender No. 3138 of 16 December 2021, rectified by Decree n. 3175 of 18 December 2021 of Italian Ministry of University and Research funded by the European Union - NextGenerationEU; Project code CN_00000033, Concession Decree No. 1034 of 17 June 2022 adopted by the Italian Ministry of University and Research, CUP B83C22002930006, Project title "National Biodiversity Future Center - NBFC". As the Editor-in-Chief is exceptionally an author of this work, to avoid any conflict of interest the Editor-in-Chief role for this manuscript was exceptionally handled by Romolo Caniglia.

Abstract

Mitochondrial DNA sequences can be used to infer haplotype diversity in range-expanding species. The Eurasian beaver *Castor fiber* is experiencing a remarkable recovery in Europe following centuries of exploitation and local extinctions. The species has recently recolonized also Central Italy, likely due to unauthorized releases, whereas the first individuals occurring in North-Eastern Italy may be the results of natural range expansion from neighboring countries. Since the last months of 2023, presence signs were also observed in North-Western Italy, near the border with Switzerland. To assess the genetic diversity and origin of Italian beaver populations, we conducted mitochondrial DNA analysis on samples from this newly colonized area, revealing the occurrence of two mtDNA haplotypes belonging to the western mitochondrial lineage of the Eurasian beaver. Molecular sexing also confirmed the occurrence of both males and females. Therefore, monitoring this population should be urgently established following European laws. Future genetic investigations using nuclear DNA markers will be crucial for understanding the origin of these new populations and informing effective conservation strategies.

Genetic monitoring plays a key role in understanding population dynamics of species undergoing range expansions, especially those with complex life histories and distribution patterns (Excoffier et al., 2009). For instance, genetic data can reveal the source populations from which individuals originated, the dispersal routes they followed, and the factors influencing their colonization success or failure (Ibrahim et al., 1996; Ramos et al., 2016; Swan et al., 2022). Ultimately, genetic monitoring provides insights into the dynamics of species range expansion, aiding in the development of effective conservation and management strategies (Schwartz et al., 2007; Fabbri et al., 2014).

The Eurasian beaver *Castor fiber*, a once ubiquitous species across Eurasia, has experienced a dramatic decline due to centuries of human exploitation, including overhunting and habitat destruction (Halley and Rosell, 2003; Wróbel, 2020; Halley et al., 2021). Despite this historical population bottleneck, beavers have successfully recolonized much of their former range through reintroduction programs and legal protection (Kodzhabashev et al., 2021; Pucci et al., 2021; Bouroş et al., 2022).

Reintroduction programs have been crucial for the survival of Eurasian beavers in Europe, though at the same time fostering genetic confusion, as animals from diverse geographical origins have been used in reintroduction efforts, resulting in deeply admixed populations (Ducroz et al., 2005; Durka et al., 2005; Biedrzycka et al., 2014; Frosch et al., 2014).

Molecular techniques have been used to unravel the genetic origins of recolonizing beavers by tracing the ancestry of newly observed beaver populations (Kropf et al., 2013; Minnig et al., 2016). Previous phylogeographic studies (Durka et al., 2005) identified two mitochondrial lineages in the Eurasian beaver, which corresponded to eastern and western populations, separated from one another in Central-Eastern Europe.

In Italy, the species was first re-observed in 2018, after about 500 years of absence, in the northeast of the country, as a result of natural spreading from the reintroduced populations in Austria (Attili et al., 2023; Mori et al., 2024). Furthermore, beaver occurrence has been recorded since 2021 in Central and Southern Italy as well, most likely as the result of unauthorized releases (Pucci et al., 2021; Capobianco et al., 2023). Currently, the Italian population counts for at least 40-50 individuals, sharing the same mitochondrial DNA haplotypes occurring

*Corresponding author

Email address: lorenzo.attili@izslt.it (Lorenzo ATTILI)

Table 1 – List of *Castor fiber* samples analyzed in this study. H = hair, B = blood T = tissue. CR haplotype nomenclature follows Munclinger et al. (2022). – = not identified.

| Sample ID | Locality (Country) | Biological material | CR haplotype | Sex |
|-----------|---|---------------------|--------------|-----|
| PIE1 | Fondotoce, Verbania Province (Italy) | H | – | – |
| PIE2 | Fondotoce, Verbania Province (Italy) | H | ga1 | M |
| LOM1 | Lake Maggiore, Varese Province (Italy) | H | JF7 | F |
| LOM2 | Ticino Park, Milano Province (Italy) | B | JF7 | M |
| S1 | Canton of Fribourg (Switzerland) | T | ga1 | – |
| S2 | Canton of Neuchâtel (Switzerland) | T | ga1 | – |
| S3 | Canton of Valais (Switzerland) | T | ga1 | – |
| SWISS 1 | Canton of Fribourg (Switzerland) | T | ga1 | – |
| SWISS 2 | Canton of Fribourg (Switzerland) | T | fi1 | – |
| SW6 | Canton of Obwalden (Switzerland) | T | fi1 | – |
| SW7 | Canton of Fribourg (Switzerland) | T | ga1 | – |
| FR1 | Le Bourget-du-Lac, Savoie department (France) | T | ga1 | – |
| FR2 | Arenthon, Haute-Savoie department (France) | T | ga1 | – |

in populations of Switzerland, Austria and the Balkan Peninsula (Attili et al., 2023).

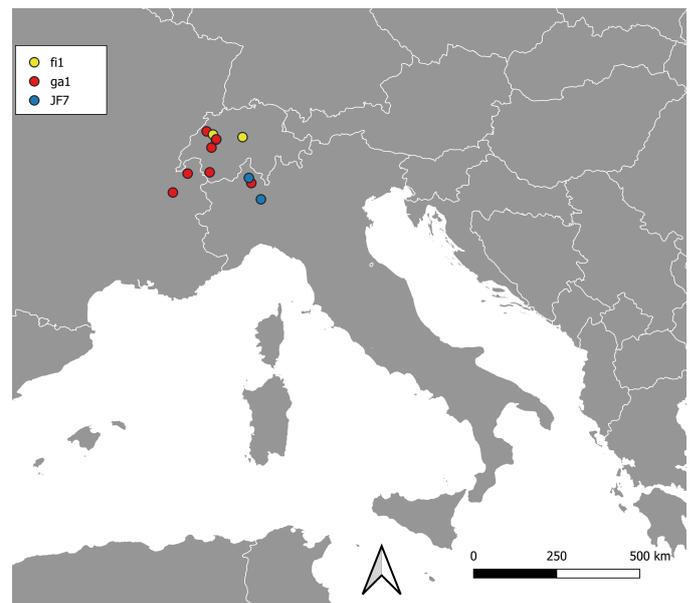
In late 2023 and 2024, at least four more individuals have been recorded in North-Western Italy (provinces of Verbano-Cusio-Ossola, Varese, Novara and Milano), on Lake Maggiore, Toce and Ticino riverbanks, about 50 km south to the southernmost known Swiss records (Mori et al., 2024). Given this geographic distance from the northern areas of beaver occurrence and the lack of signs of presence between these areas, natural spreading might be controversial. Furthermore, in the vicinity of the newly colonized sites, a zoo that formerly housed North American beavers *Castor canadensis* is still active, raising questions about the specific identity of the individuals currently present in the wild. Therefore, we aimed at assessing the origins of these beavers by sequencing mitochondrial DNA from noninvasive samples (hairs) and tissues from beavers collected in North-Western Italy and neighboring countries (Switzerland and France). We predicted that 1) individuals from North-Western Italy belong to *C. fiber* and 2) are genetically close to those occurring in Switzerland and France.

Three hair samples were collected in 2024 from North-Western Italy, at two different sites along Toce river (Verbano-Cusio-Ossola province, PIE1, PIE2) and Lake Maggiore (Varese province, LOM1), supplemented by a blood sample from a live beaver rescued along Ticino river (Milano province, LOM2).

Nine muscle tissue samples were also gathered from Switzerland ($n = 7$, from deceased individuals due to natural causes or car accidents, in Canton of Fribourg, Canton of Valais, Canton of Obwalden and Canton of Neuchâtel) and South-Western France, Rhone river basin in Savoie Department ($n = 2$) (Tab. 1, Fig. 1). DNA was isolated from approximately 15 mg of muscle, 5–10 hairs and 200 μ l of whole blood in EDTA using the Maxwell16 Instrument (Promega, Madison, USA) and following the producer's handbook.

A fragment of 330 base pairs (bp) in a highly variable section of the mtDNA Control Region (CR) was amplified and sequenced using the beaver-specific primers CR_Castor F and R (Attili et al., 2023). PCR reactions contained 2.5 μ l of 10X Gold buffer (Thermo Fisher Scientific, Waltham, MA, USA), 200 μ M of each dNTP, 2.5 mM MgCl₂, 10 pmol of each primer, 1U of AmpliTaqGold polymerase (Thermo Fisher Scientific), 3 μ l template DNA (10–50 ng) and PCR grade H₂O in a final volume of 25 μ l. PCR tubes were loaded onto an ABI Veriti® 96-Well Thermal Cycler (Thermo Fisher Scientific) under the following conditions: an initial activation step at 94 °C for 3 min; 38 cycles of 94 °C for 30 s, 56 °C for 30 s, 72 °C for 30 s, followed by a final extension of 5 min at 72 °C. Negative and positive controls were included to check success of amplifications and monitor contaminations.

PCR products were cleaned up with the QIAquick PCR purification kit (QIAGEN) and sequenced bidirectionally using the BigDye Terminator Cycle Sequencing Kit (Applied Biosystems). Unincorporated dyes and contaminants were removed with the Agencourt® CleanSEQ solu-

**Figure 1** – Map of sampling sites. Localities are described in detail in Tab. 1. Made with QGIS using Natural Earth Data.

tion (Beckman Coulter, Beverly, MA, USA), then loaded on ABI 3130 Genetic Analyzer (Applied Biosystems).

CR sequences were edited and aligned with 31 sequences downloaded from GenBank, covering the current Eurasian range of *C. fiber* (Ducroz et al., 2005; Durka et al., 2005; Horn et al., 2011; Kropf et al., 2013; Frosch et al., 2014; Senn et al., 2014) using MEGA11 (Tamura et al., 2021). The final alignment was trimmed to the common 330 bp fragment. The software DnaSP 6.0 (Rozas et al., 2017) was used to determine the number of haplotypes and a median-joining network (Bandelt et al., 1999) was constructed using the software PopArt (Leigh and Bryant, 2015) to visualize their relationships.

Given the lack of sexual size dimorphism in Eurasian beavers, sex of individuals from North-Western Italy was molecularly determined following the protocol of Goldberg et al. (2011).

Sequencing of mitochondrial partial CR from all Eurasian beaver samples collected in this study produced three different haplotypes: ga1, JF7 and fi1, following the nomenclature in Munclinger et al. (2022) (Tab. 1; Fig. 1). One hair sample from North-Western Italy (PIE1) yielded only a partial fragment of 150 bp that matched *Castor fiber* sequences (100% of identity in BLAST NCBI <http://www.ncbi.nlm.nih.gov/blast>), but it was not possible to identify the haplotype and we excluded it from subsequent analyses. No evidence of *C. canadensis* was found in our beaver samples. In North-Western Italy we found ga1 and JF7 haplotypes only. These haplotypes were first described as native to

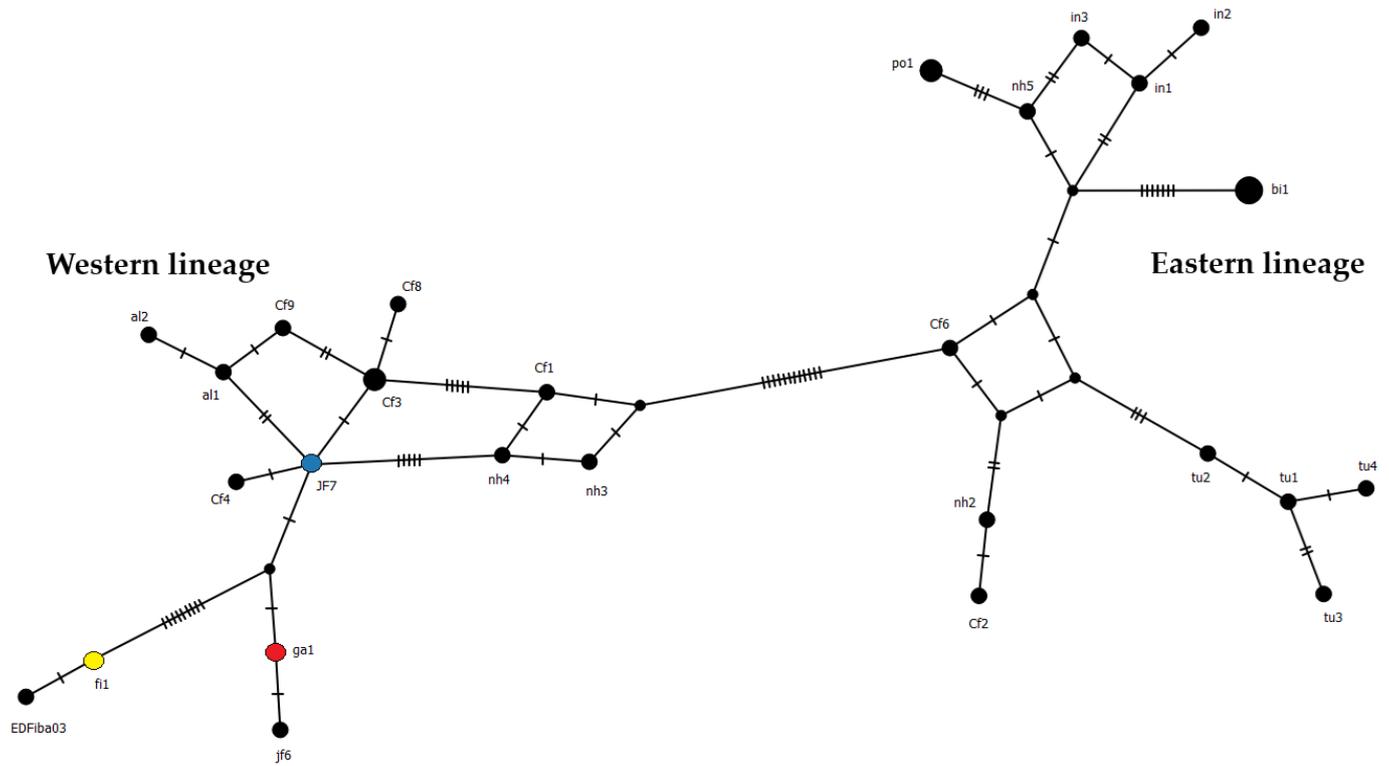


Figure 2 – Median-joining network of mitochondrial CR haplotypes in Eurasian beavers. Eastern lineage and Western lineage are shown according to Durka et al. (2005). The haplotypes found in this study are marked in blue (JF7), red (ga1) and yellow (fi1).

the relict populations in France (Durka et al., 2005) and Russia (Voronezh) (Senn et al., 2014) respectively, but currently they are widespread across Europe (Biedrzycka et al., 2014; Frosch et al., 2014; Minnig et al., 2016; Kropf et al., 2013; Horn et al., 2011; Munclinger et al., 2022). Molecular sexing suggested that a male and a female at least occur in the study area.

Among beavers from Switzerland, we identified ga1 and fi1 haplotypes, while in France only ga1 was found, in agreement with the literature ((Durka et al., 2005; Senn et al., 2014; Minnig et al., 2016; Attili et al., 2023): Fig. 1). In regions near the Alps, the ga1 haplotype was identified, while in the Swiss Plateau (northeast), the fi1 haplotype was observed.

When the sequences from this study were added to published sequences, two clades were visible in the median-joining network (Figure 2), consistent with previous phylogeographic studies (Durka et al., 2005).

All beavers analyzed in the present survey were grouped into the alleged Western lineage, although it is currently recognized that there is not clear correspondence between mtDNA clades and geographic populations (Senn et al., 2014; Munclinger et al., 2022). A mixture of haplotypes currently occurs in most beaver populations in Europe, following reintroduction events both legal and unofficial (Senn et al., 2014). In North-Western Italy we detected two haplotypes, which are very widespread in neighboring countries (Durka et al., 2005; Minnig et al., 2016; Attili et al., 2023). Therefore, our findings are consistent with the hypothesis that at least two individuals may have spontaneously dispersed from the Swiss population following ecological corridors linking Switzerland to Northern Piedmont and Lombardy (Treves et al., 2020; Falaschi et al., 2024). However, the possibility of unauthorized releases of individuals descending from a genetically mixed stock, as the case of Central Italy, cannot be discarded (Attili et al., 2023; Bertolino et al., 2023).

The recent arrival of Eurasian beavers in North-Western Italy, following their expansion from Switzerland, may represent an opportunity for ecological restoration and biodiversity enhancement. However, it is also possible that the beavers found in this region originate from Central Europe, sharing the same haplotype with populations from that

area (see (Attili et al., 2023)). This raises the hypothesis that some individuals may have been introduced from Central Europe rather than arriving solely through natural expansion. None of these hypotheses could be actually ruled out.

The Eurasian beaver is listed in Annex II of the Habitats Directive (92/43/EEC); thus, Piedmont and Lombardy should actively contribute to the recovery of a keystone species that is naturally returning after centuries of local extinction (Treves et al., 2020). Furthermore, Eurasian beavers, as ecosystem engineers, play a crucial role in shaping aquatic environments; their dam-building activities create wetland habitats that support a multitude of plant and animal species (Viviano et al., 2022) and provide essential ecosystem services such as flood mitigation, water filtration, and carbon sequestration. By protecting and promoting beaver populations, Piedmont and Lombardy can not only restore natural processes but also contribute to climate change mitigation and adaptation strategies (Treves et al., 2022). Additionally, the presence of beavers can attract eco-tourism, generating economic benefits for local communities (Treves and Comino, 2024). While potential conflicts with human activities may arise, careful management and public education can mitigate these issues and foster coexistence between humans and beavers (Falaschi et al., 2024). 🐾

References

- Attili L., Pizzarelli A., Viviano A., Mori E., Cirovic D., Kropf M., Lorenzini R., 2023. First molecular evidence on the puzzling origin of beavers in central Italy. *Hystrix* 34: 139–142. 10.4404/hystrix-00623-2023
- Bandelt H.J., Forster P., Röhl A., 1999. Median-joining networks for inferring intraspecific phylogenies. *Mol. Biol. Evol.* 16(1): 37–48. 10.1093/oxfordjournals.molbev.a026036
- Bertolino S., Bartolommei P., Ferri M., Gasperini S., Grignolio S., Lapini L., Scandura M., Scillitani L., Monaco A., Genovesi P., Amori G., Apollonio M., Loy A., Martinoli A., Cerri J., 2023. The strange case of beaver return in Italy: origins and management. *Hystrix* 34: 84–91. 10.4404/hystrix-00654-2023
- Biedrzycka A., Konior M., Babik W., Świsłocka M., Ratkiewicz M., 2014. Admixture of two phylogeographic lineages of the Eurasian beaver in Poland. *Mamm. Biol.* 79: 287–296. 10.1016/j.mambio.2014.04.005
- Bouros G., Paladi V., Cassir P., 2022. First report of Eurasian beaver (*Castor fiber* Linnaeus 1758) in the Republic of Moldova. *North-West. J. Zool.* 18: 71–76.
- Capobianco G., Viviano A., Mazza G., Cimorelli G., Casciano A., Lagrotteria A., Fusillo R., Marcelli M., Mori E., 2023. “Oops... a beaver again!” Eurasian beaver *Castor fiber* recorded by citizen-science in new areas of Central and Southern Italy. *Animals* 13: 1699. 10.3390/ani13101699

- Ducroz J.F., Stubbe M., Saveljev A.P., Heidecke D., Samjaa R., Ulevičius A., Stubbe A., Durka W., 2005. Genetic variation and population structure of the Eurasian beaver *Castor fiber* in Eastern Europe and Asia. *J. Mammal.* 86(6): 1059–1067. 10.1644/1545-1542(2005)86[1059:GVAPSO]2.0.CO;2
- Durka W., Babik W., Ducroz J.F., Heidecke D., Rosell F., Samjaa R., Saveljev A.P., Stubbe A., Ulevičius A., Stubbe M., 2005. Mitochondrial phylogeography of the Eurasian beaver *Castor fiber* L. *Mol. Ecol.* 14(12): 3843–3856. 10.1111/j.1365-294X.2005.02704.x
- Excoffier L., Foll M., Petit R.J., 2009. Genetic consequences of range expansions. *Annu. Rev. Ecol. Syst.* 40: 481–501. 10.1146/annurev.ecolsys.39.110707.173414
- Fabbri E., Caniglia R., Galov A., Arbanasić H., Lapini L., Bošković I., Florijancić T., Vlasseva A., Ahmed A., Mirchev R.L., Randi E., 2014. Genetic structure and expansion of golden jackals (*Canis aureus*) in the north-western distribution range (Croatia and eastern Italian Alps). *Conserv. Gen.* 15: 187–199. 10.1007/s10592-013-0530-7
- Falasci M., Ficotola G.F., Viviano A., Mazza G., Mori E., 2024. Environmental suitability and potential range expansion of the Eurasian beaver in Italy. *Anim. Conserv.* 27: 324–337. 10.1111/acv.12910
- Frosch C., Kraus R.H., Angst C., Allgöwer R., Michaux J., Teubner J., Nowak C., 2014. The genetic legacy of multiple beaver reintroductions in Central Europe. *PLoS ONE* 9(5): e97619. 10.1371/journal.pone.0097619
- Goldberg C.S., Woodruff K., Toldness R., Waits L.P., 2011. Robust molecular sex identification of beaver (*Castor canadensis*) from non-destructive samples. *Conserv. Genet. Resour.* 3: 729–731. 10.1007/s12686-011-9443-2
- Halley D.J., Rosell F., 2003. Population and distribution of Eurasian beavers (*Castor fiber*). *Lutra* 46: 91–101.
- Halley D.J., Saveljev A.P., Rosell F., 2021. Population and distribution of beavers *Castor fiber* and *Castor canadensis* in Eurasia. *Mamm. Rev.* 51(1): 1–24. 10.1111/mam.12216
- Horn S., Durka W., Wolf R., Ermala A., Stubbe A., Stubbe M., Hofreiter M., 2011. Mitochondrial Genomes Reveal Slow Rates of Molecular Evolution and the Timing of Speciation in Beavers (*Castor*), One of the Largest Rodent Species. *PLoS ONE* 6(1): e14622. 10.1371/journal.pone.0014622
- Ibrahim K.M., Nichols R.A., Hewitt G.M., 1996. Spatial patterns of genetic variation generated by different forms of dispersal during range expansion. *Heredity* 77: 282–291. 10.1038/hdy.1996.142
- Kodzhbashchev N.D., Tsvyatkov D.D., Krastev K.V., Ignatov M.M., Teofilova T.M., 2021. The Eurasian Beaver *Castor fiber* Linnaeus, 1758 (Rodentia: Castoridae) is returning to Bulgaria. *Acta Zool. Bulg.* 73: 587–595.
- Kropf M., Hölzler G., Parz-Gollner R., 2013. Genetic evidence on the origin of the current beaver (*Castor fiber*) population in Lower Austria. *Šumar. List* 137: 591–596.
- Leigh J.W., Bryant D., 2015. POPART: full-feature software for haplotype network construction. *Methods Ecol. Evol.* 6: 1110–1116. 10.1111/2041-210X.12410
- Minnig S., Angst C., Jacob G., 2016. Genetic monitoring of Eurasian beaver (*Castor fiber*) in Switzerland and implications for the management of the species. *Russian J. Theriol.* 15: 20–27.
- Mori E., Puttock A., Viviano A., Mosini A., Campbell-Palmer R., Ancillotto L., Trentanovi G., Scarfò M., Leoncini F., Pontarini R., Mazza G., Needham R., 2024. How many beavers activity is there in Italy? Using field signs to monitor and map a returned species. *Mamm. Res.* 69: 519–532. 10.1007/s13364-024-00763-0
- Munclinger P., Syrůčková A., Náhlavský J., Durka W., Saveljev A.P., Rosell F., Stubbe A., Stubbe M., Ulevičius A., Samiya R., Yanuta G., Vorel A., 2022. Recovery in the meltingpot: complex origins and restored genetic diversity in newly established Eurasian beaver (Rodentia: Castoridae) populations. *Biol. J. Linn. Soc.* 135: 793–811. <https://doi.org/10.1093/biolinnean/blac003>
- Pucci C., Senserini D., Mazza G., Mori E., 2021. Reappearance of the Eurasian beaver *Castor fiber* L. in Tuscany (Central Italy): the success of unauthorised releases? *Hystrix* 32: 1–4. 10.4404/hystrix-00445-2021
- Ramos R., Song G., Navarro J., Zhang R., Symes C.T., Forero M.G., Lei F., 2016. Population genetic structure and long-distance dispersal of a recently expanding migratory bird. *Mol. Phyl. Evol.* 99: 194–203. 10.1016/j.ympev.2016.03.015
- Rozas J., Ferrer-Mata A., Sánchez-DelBarrio J.C., Guirao-Rico S., Librado P., Ramos-Onsins S.E., Sánchez-Gracia A., 2017. DnaSP 6: DNA sequence polymorphism analysis of large data sets. *Mol. Biol. Evol.* 34: 3299–3302. 10.1093/molbev/msx248
- Senn H., Ogden R., Frosch C., Syrůčková A., Campbell-Palmer R., Munclinger P., Durka W., Kraus R.H.S., Saveljev A., Nowak C., Stubbe A., Stubbe M., Michaux J., Lavrov V., Samiya R., Ulevičius A., Rosell F., 2014. Nuclear and mitochondrial genetic structure in the Eurasian beaver (*Castor fiber*)—implications for future reintroductions. *Evol. Appl.* 7: 645–662. 10.1111/eva.12162
- Schwartz M.K., Luikart G., Waples R.S., 2007. Genetic monitoring as a promising tool for conservation and management. *Trends Ecol. Evol.* 22: 25–33. 10.1016/j.tree.2006.08.009
- Swan T., Russell T.L., Staunton K.M., Field M.A., Ritchie S.A., Burkot T.R., 2022. A literature review of dispersal pathways of *Aedes albopictus* across different spatial scales: implications for vector surveillance. *Parasites & Vectors* 15: 303. 10.1186/s13071-022-05413-5
- Tamura K., Stecher G., Kumar S., 2021. MEGA11: molecular evolutionary genetics analysis version 11. *Mol. Biol. Evol.* 38: 3022–3027. 10.1093/molbev/msab120
- Treves A., Bottero M., Caprioli C., Comino E., 2020. The reintroduction of *Castor fiber* in Piedmont (Italy): An integrated SWOT-spatial multicriteria based approach for the analysis of suitability scenarios. *Ecol. Indic.* 118: 106748. 10.1016/j.ecolind.2020.106748
- Treves A., Terenziani A., Angst C., Comino E., 2022. Predicting habitat suitability for *Castor fiber* reintroduction: MaxEnt vs SWOT-Spatial multicriteria approach. *Ecol. Inform.* 72: 101895. 10.1016/j.ecoinf.2022.101895
- Treves A., Comino E., 2024. A bibliometric literature review in beaver management: when does the beaver become a resource? *Mammal Rev.* 54: 213–228. 10.1111/mam.12338
- Viviano A., Mazza G., Di Lorenzo T., Mori E., 2022. Housed in a lodge: occurrence of animal species within Eurasian beaver constructions in Central Italy. *Eur. J. Wildl. Res.* 68: 75. 10.1007/s10344-022-01625-3
- Wróbel M., 2020. Population of Eurasian beaver (*Castor fiber*) in Europe. *Glob. Ecol. Conserv.* 23: e01046. 10.1016/j.gecco.2020.e01046

Associate Editor: Romolo Caniglia