

New tardigrade records from Monviso (Cottian Alps, Italy) with sequencing of the *Acanthechiniscus victor* (Ehrenberg, 1853) mitogenome

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The Alps are recognised as a hotspot of biodiversity and have historically been extensively studied. However, despite the number of studies devoted to the biodiversity of the Alps, large knowledge gaps are still present. The Southwestern Alps are a biodiverse region known for hosting many endemic animals and plants. To increase the faunistic knowledge of the Southwestern Alps, we have produced the first survey of the tardigrades from Monviso. Notably, we sequenced the mitogenome of the rarely found Arctic-alpine *Acanthechiniscus victor* (Ehrenberg, 1853), which is an important addition to the existing knowledge as it is the second mitogenome to be sequenced for the tardigrade superfamily Echiniscoidea. The findings of this study highlight how continued explorations of the European mountain ecosystem are still needed to fill in the knowledge gaps regarding its biodiversity.

Key words: NGS sequencing, Echiniscidae, Southwestern Alps, mitochondrial genome, whole genome amplification, taxonomy.

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The Southwestern Alps are a very biodiverse region (one of the most species-rich in Europe; Médail 2004) due to their role as an ice refugia during the Pleistocene glaciations (Schönswetter *et al.* 2005; Smyčka *et al.* 2017) with many endemic plant and animal species residing there (Aeschmann *et al.* 2011; Minelli *et al.* 2005). In the Southwestern Alps, the Cottian Alps are known in particular for their outstanding naturalistic value, with some notable endemism such as the Lanza's Salamander – *Salamandra*

lanzai Nascetti, Andreone, Capula and Bullini 1988 (Andreone *et al.* 2004), as well as the beetle *Carabus cychroides* Baudi di Selve 1864 (Anselmo & Rizzioli 2022).

Tardigrades are a group of ecdysozoan microinvertebrates known for the ability of some species to survive an almost complete loss of body water (Schill 2018). Despite the older belief that due to their small size and stress-tolerance abilities, tardigrades can easily disperse over long distances, recent studies



have painted a different picture, with many geographically restricted and endemic species being found (Gąsiorek 2024). Tardigrade researchers have historically been more abundant in Europe, which has resulted in the continent becoming the most well-characterised continent regarding tardigrade fauna (McInnes 1994). However, many European localities are still not well explored. For example, studies on the tardigrade fauna in the Southwestern Alps are absent, except for an isolated description of *Claxtonia pardalis* (Degma & Schill 2015) from the Maritime Alps.

With this study, we aim to provide a faunistic account of tardigrades from the Monviso massif (Cottian Alps) from 30 moss samples collected *ad hoc* along an altitudinal range. The faunistic survey was conducted with standard morphological identification methods, and we additionally sequenced the mitogenome of *Acanthechiniscus victor* (Ehrenberg 1853), a rarely-found Arctic-alpine species.

Materials and Methods

Sampling and tardigrades extraction

Samples of moss growing on rock (30 in total) were collected in August 2023 by M.C.L. on the Monviso Massif (Italy), in an area between 44°39'14"-44°43'14" N and 7°4'4"-7°6'33" E (DMS) and at altitudes between 1790-2840 m above sea level (a.s.l.) The complete sampling data is available in Table 1. Sampling was done under sampling permit Prot. 0001492 of 17/04/2023 issued by Parco del Monviso (Cuneo, Italy).

Immediately after collection, the samples were stored in paper bags where they were left to be desiccated at room temperature and kept dry until processing. To extract the tardigrades from their substrates, fragments of all samples (1-3 g of dry samples) were placed in distilled water for ca. 30 minutes. After soaking, the samples were sieved (sieves meshes: 500 and 32 µm) to separate the tardigrades and eggs from the substrate; the animals and eggs were then isolated using a needle and a glass pipette under a stereomicroscope. The remaining sieved mosses containing tardigrades were stored frozen at -20°C the Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Kraków, Poland. Taxonomic identifications were done by comparing the specimens with their original descriptions (for references, see the *Taxonomic account* section below). When a positive determination was not possible,

Table 1

Sampling data and presence of tardigrades

Sample code	Sampling date	Coordinates	elevation (m a.s.l.)	Tardigrades present
IT.248	20-Aug-2023	44°41'26"N 7°6'23"E	2030	Yes
IT.249	20-Aug-2023	44°41'23"N 7°6'21"E	2070	Yes
IT.250	20-Aug-2023	44°39'59"N 7°6'33"E	2640	No
IT.251	20-Aug-2023	44°40'4"N 7°6'21"E	2640	No
IT.252	20-Aug-2023	44°40'46"N 7°6'12"E	2520	Yes
IT.253	20-Aug-2023	44°40'47"N 7°6'9"E	2480	No
IT.254	20-Aug-2023	44°40'51"N 7°6'4"E	2430	No
IT.255	20-Aug-2023	44°40'56"N 7°5'38"E	2350	No
IT.256	20-Aug-2023	44°41'26"N 7°5'51"E	2240	No
IT.257	21-Aug-2023	44°42'9"N 7°5'29"E	2100	Yes
IT.258	21-Aug-2023	44°42'9"N 7°5'29"E	2110	Yes
IT.259	21-Aug-2023	44°42'15"N 7°5'38"E	2110	Yes
IT.260	21-Aug-2023	44°42'36"N 7°6'2"E	2360	No
IT.261	21-Aug-2023	44°42'56"N 7°5'55"E	2360	No
IT.262	21-Aug-2023	44°43'14"N 7°6'14"E	2470	Yes
IT.263	21-Aug-2023	44°42'47"N 7°6'8"E	2280	No
IT.264	21-Aug-2023	44°42'35"N 7°6'27"E	2180	Yes
IT.265	21-Aug-2023	44°42'30"N 7°6'31"E	2100	Yes
IT.266	21-Aug-2023	44°42'5"N 7°6'46"E	1790	No
IT.267	22-Aug-2023	44°42'11"N 7°5'10"E	2190	Yes
IT.268	22-Aug-2023	44°42'31"N 7°4'51"E	2430	No
IT.269	22-Aug-2023	44°42'44"N 7°4'4"E	2840	No
IT.270	22-Aug-2023	44°42'44"N 7°4'2"E	2870	No
IT.271	22-Aug-2023	44°42'28"N 7°4'20"E	2630	Yes
IT.272	22-Aug-2023	44°42'27"N 7°4'26"E	2540	No
IT.273	22-Aug-2023	44°42'35"N 7°4'53"E	2460	Yes
IT.274	22-Aug-2023	44°42'31"N 7°4'51"E	2430	No
IT.275	22-Aug-2023	44°42'18"N 7°4'59"E	2290	No
IT.276	22-Aug-2023	44°42'13"N 7°5'6"E	2210	Yes
IT.277	22-Aug-2023	44°42'9"N 7°5'17"E	2160	No

specimens were assigned only to the genus level or were marked as *confer* (cf.) to the most similar species.

Microscopy and imaging

For the light microscopy, specimens were mounted on microscope slides in a small drop of Hoyer's medium, secured with a cover slip and dried at 50 °C for a week. The slides were examined under a Leica

DMLB light microscope with phase contrast (PCM), associated with a digital camera. All the figures were assembled in Figure J (Mutterer & Zinck 2013).

Whole genome amplification, sequencing and mitogenome assembly

The mitochondrial genome of one *Acanthechiniscus victor* individual was sequenced. One individual from sample IT.271 was subjected to Whole Genome Amplification (WGA) following the protocol of Vecchi and Stec (2024), but with the REPLI-g Advanced DNA Single Cell Kit (Qiagen) instead of the REPLI-g Mini Kit (Qiagen). The Celero™ DNA-Seq Library Preparation kit (Tecan Genomics, Redwood City, CA) was used for the library preparation following the manufacturer's instructions. Both the input and final library were quantified by the Qubit 2.0 Fluorometer (Invitrogen, Carlsbad, CA) and were quality tested by an Agilent 2100 Bioanalyzer High Sensitivity DNA assay (Agilent technologies, Santa Clara, CA). The libraries were then prepared for sequencing and were sequenced on NovaSeq X in the paired-end 150 bp mode. The library preparation and sequencing were performed by a commercial provider (IGA Technology, Udine, Italy). The reads were trimmed and quality filtered with the fastp software (options: -q 15 -u 50 -l 100 -correction --detect_adapter_for_pe; Chen *et al.* 2018), then the mitogenome was assembled with NOVOPlasty v.4.3.5 with the k-mer size 33 (Dierckxsens *et al.* 2016), using a COI sequence from *Acanthechiniscus goedeni* (Grigarick, Mihelčič and Schuster, 1964) as bait (GenBank OP729912; Vecchi *et al.* 2023). The mitogenome annotation and visualisation was performed as in Vecchi and Stec (2024). The raw reads are deposited in NCBI SRA under Bioproject PRJNA1368705.

Results

Tardigrades were present in 13 of the 30 samples examined. A total of 23 tardigrade morphospecies were identified, with more details provided in the *Taxonomic account* below. Only the photographs of three species are presented herein, whereas more comprehensive photographic documentation is available at Vecchi *et al.* (2026).

The sequencing of *A. victor* produced a circularised mitogenome of 14443 bp (Figure 1; GenBank PX698838; SM.01). In the mitogenome, 12 protein-coding genes, 20 tRNA and 2 rRNA genes were annotated. The nad4l gene was missing; however,

more than a true absence it was most probably not identified by the annotation software (an unannotated region is present between nad4 and trnT, where the gene is found in other taxa; Arakawa 2018). trnF and trnH were not annotated, but as in the precedent case, this was probably a lack of annotation rather than a true absence.

Taxonomic account

Phylum: Tardigrada Doyère, 1840

Class: Heterotardigrada Marcus, 1936

Order: Echiniscoidea Richters, 1926

Family: Echiniscidae Thulin, 1928

Acanthechiniscus victor (Ehrenberg 1853)

Figure 2A-C

Material examined: 16 individuals from sample IT.271.

Notes: This species has a Boreal-alpine distribution (McInnes 1994). A complete mitochondrial genome has been sequenced for an individual of this population, which is available in GenBank under accession number PX698838. Genomic reads are available for this species in NCBI SRA under project PRJNA1368705.

Claxtonia sp.

Figure 2D-F

Material examined: 27 individuals from sample IT.259, 1 individual from sample IT.265.

Notes: Based on the morphology of the ornamentation of the plates (Figures 2E, F), the individuals probably belong to the same species as *Claxtonia* sp.3 from Gąsiorek *et al.* (2023), which was found in Vallone di Brocan (Maritime Alps, about 60 km in distance from the samples analysed in this study). Further studies are required to shed light on the exact attribution of the individuals found in this study.

Echiniscus merokensis Richters 1904

Material examined: 5 individuals from sample IT.264

Echiniscus blumi Richters 1903

Material examined: 13 individuals from sample IT.258, 10 individuals from sample IT.264, 2 individuals from sample IT.265.

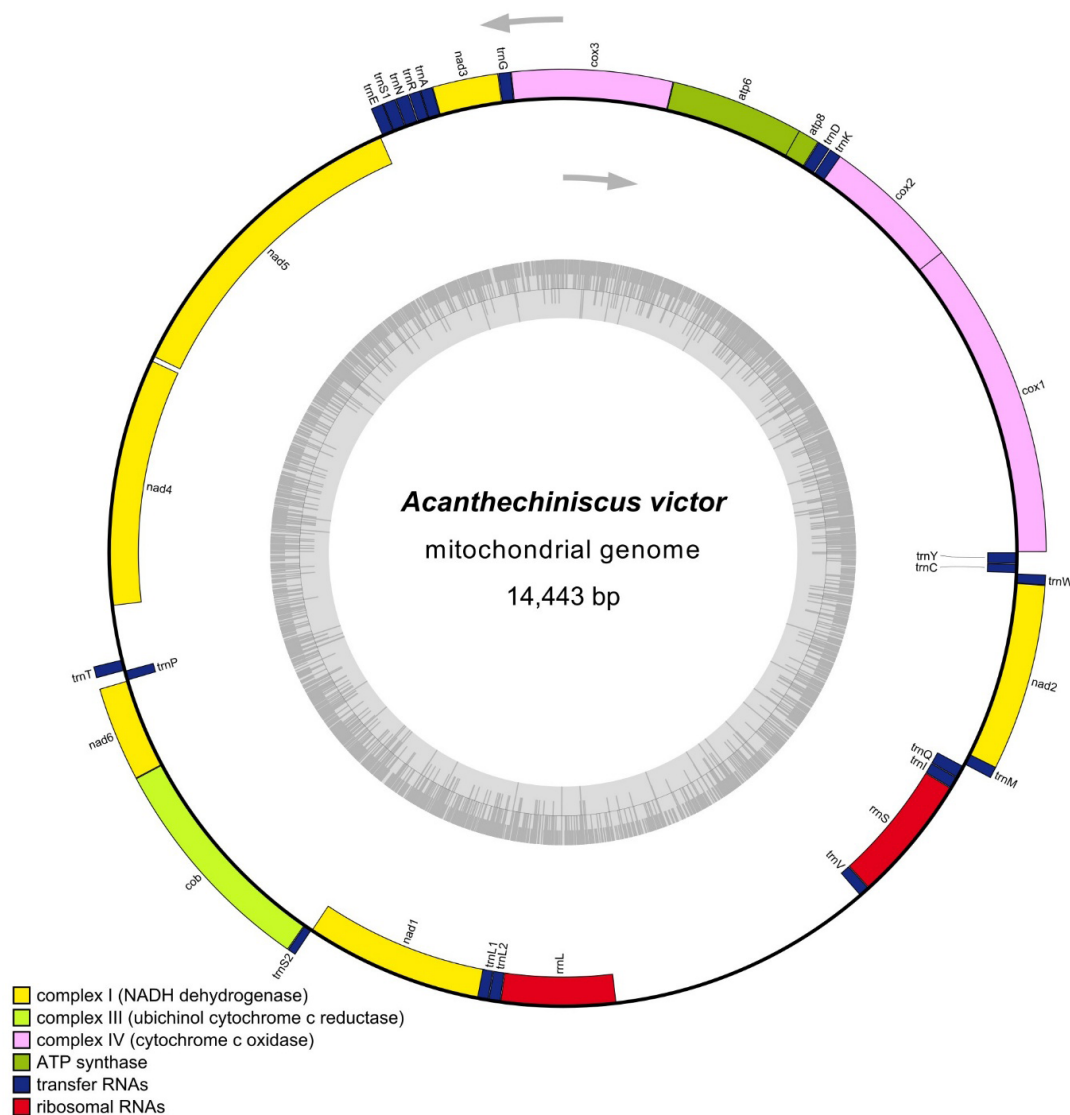


Fig. 1. *Acanthechiniscus victor* mitogenome visualization: inner circle represents GC content. Grey arrows indicate the direction of transcription.

Pseudechiniscus (Pseudechiniscus) sp.

Material examined: 3 individuals from sample IT.264.

Notes: *Pseudechiniscus* with a well-developed ventral ornamentation.

Class: Eutardigrada Richters 1926

Order: Apochela Schuster, Nelson, Grigarick and Christenberry 1980

Family: Milnesiidae Ramazzotti 1962

Milnesium sp.

Material examined: 8 individuals + 1 exuvia with eggs from sample IT.257, 6 individuals from sample IT.258, 8 individuals from sample IT.259, 6 individuals + 1 exuvia with eggs from sample IT.264.

Notes: the individuals resemble *Milnesium alpigenum* Ehrenberg, 1853 and *Milnesium inceptum* Morek, Suzuki, Schill, Georgiev, Yankova, Marley and Michalczyk, 2019; however, it was not possible to discriminate between these two species morphologically.

Order: Parachela Schuster, Nelson, Grigarick and Christenberry 1980

Superfamily: Isohypsibioidea Sands, McInnes, Marley, Goodal-Copestake, Convey and Linse 2008

Isohypsibius schaudinni (Richters 1909)

Material examined: 7 individuals from sample IT.256.

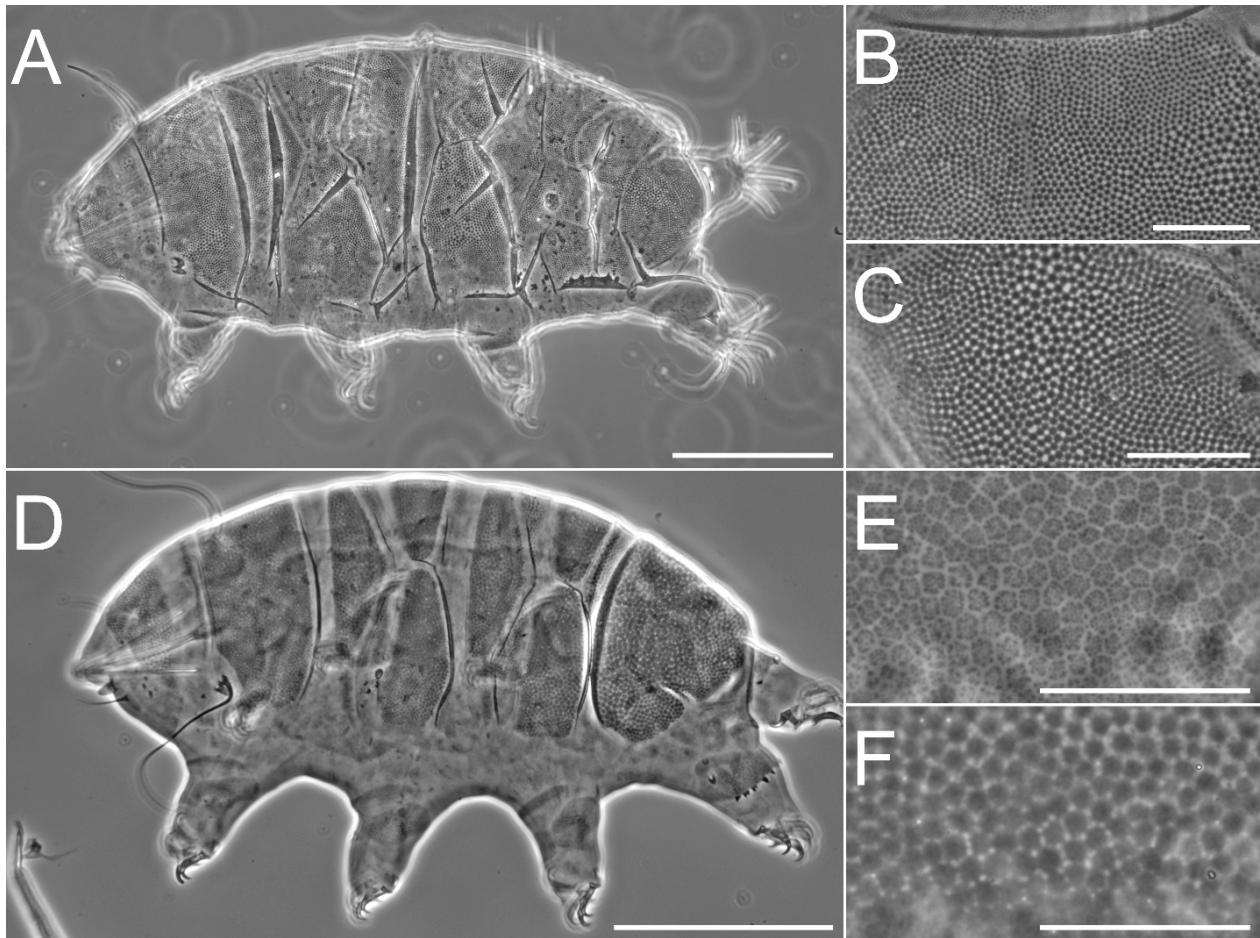


Fig. 2. *Acanthechiniscus victor* and *Claxtonia* sp. A) *A. victor* in toto; B-C) *A. victor* scapular and caudal plates ornamentation, respectively; D) *Claxtonia* sp. in toto; E-F) *Claxtonia* sp. caudal plate ornamentation in two different focal planes. Scale bars: A, D 100 µm; B, C, E, F 20 µm.

Superfamily: Hypsibioidea Pilato 1969
in Marley *et al.* (2011)

Ramazzottius sp. A

Material examined: 11 individuals + 5 eggs from sample IT.273.

Notes: The individuals and eggs (Figure 3) did not match any described species, indicating it is probably a new taxon.

Ramazzottius sp. B

Material examined: 2 individuals from sample IT.258.

Notes: Due to the lack of eggs, it was not possible to classify those individuals below the genus level.

Guidettion prorsirostre (Thulin 1928)

Material examined: 1 individual from sample IT.248.

Diphascon cf. *faialense*

Material examined: 4 individuals + 1 exuvia with eggs from sample IT.248.

Notes: The closest match to the examined individuals is *Diphascon faialense* Fontoura and Pilato 2007; however, it differs from this species by longer claws (II-III ext. *pt* 44.8-43.5 in *D. faialense*, 54.6-63.5 in the examined individuals) and the % buccal tube/buccal-pharyngeal tube (37% in *D. faialense*, 31-38% in the examined individuals).

Hypsibius microps Thulin 1928

Material examined: 4 individuals from sample IT.276.

Hypsibius sp.

Material examined: 1 individual from sample IT.252.

Notes: Unidentified *Hypsibius* with 2 macroplacoids and no microplacoid.

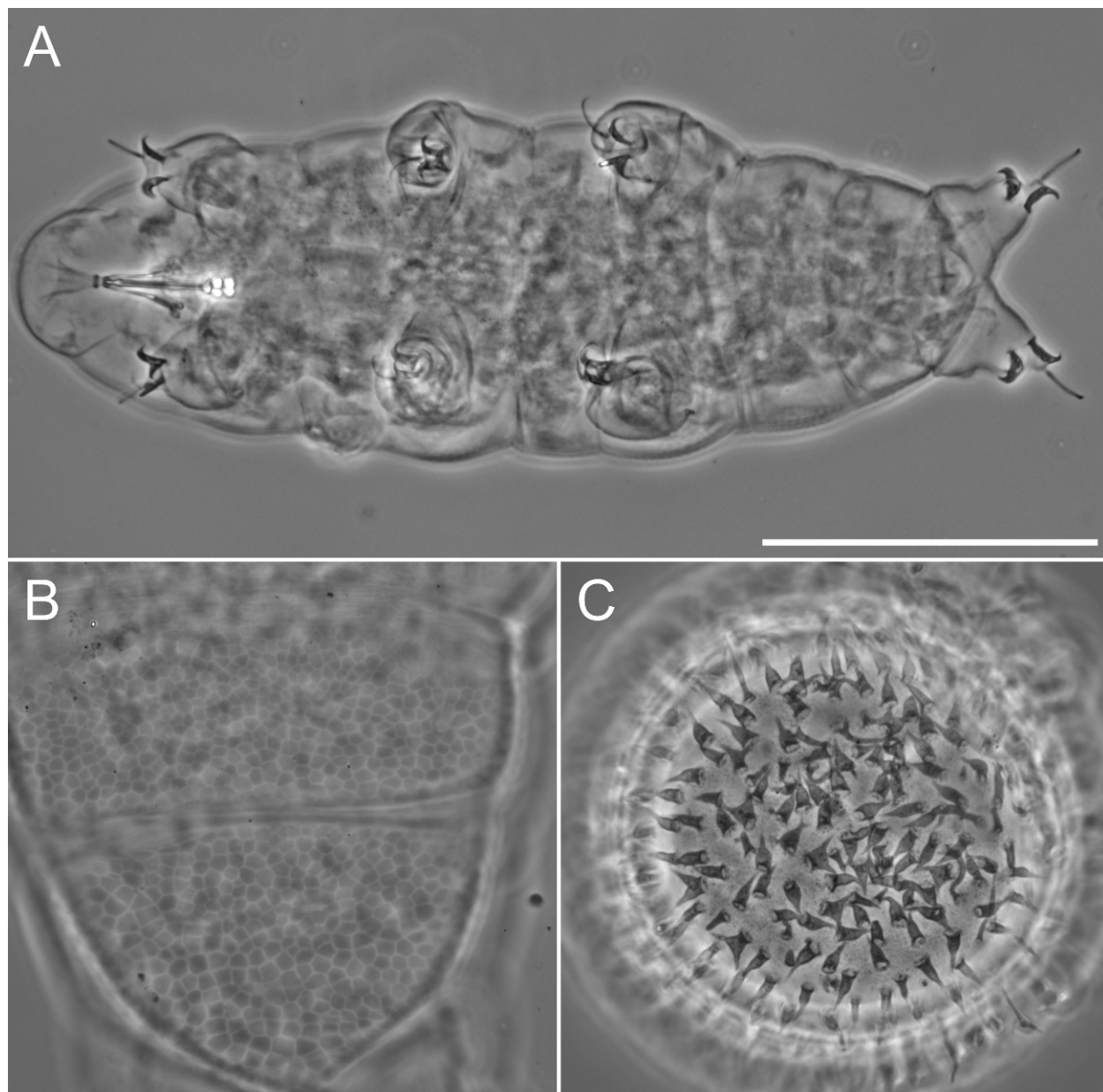


Fig. 3. *Ramazzottius* sp. A) *Ramazzottius* in toto; B) Dorso-caudal cuticle ornamentation; C) Egg in toto. Scale bars: A 100 µm; B-C 20 µm.

Superfamily: Macrobiotoidea Thulin
1928 in Marley *et al.* (2011)

*Macrobiotus hanna*e Nowak
and Stec 2018

Material examined: 15 individuals + 12 eggs
from sample IT.271.

*Macrobiotus sandra*e Bertolani
and Rebecchi 1993

Material examined: 11 individuals + 1 egg
from sample IT.249, 1 individual + 1 egg from sam-
ple IT.259.

Macrobiotus vladimiri Bertolani,
Biserov, Rebecchi and Cesari 2011

Material examined: 7 individuals + 6 eggs
from sample IT.257, 11 individuals and 10 eggs
from sample IT.258.

Macrobiotus sp.

Material examined: 8 individuals from
sample IT.248, 13 individuals from sample IT.264,
3 individuals from sample IT.265, 3 individuals
from sample IT.276.

Notes: As eggs associated with these populations
were not found, it was not possible to confidently
identify them to the species level.

Mesobiotus occultatus Kaczmarek,
Zawierucha, Buda, Stec, Gawlak,
Michalczyk and Roszkowska 2018

Material examined: 12 individuals + 7 eggs from sample IT.259, 18 individuals + 3 eggs from sample IT.262, 6 individuals + 1 egg from sample IT.267.

Mesobiotus sp.

Material examined: 5 individuals from sample IT.252.

Notes: As eggs associated with these populations were not found, it was not possible to confidently identify them to the species level.

Minibiotus cf. *gumersindoi*

Material examined: 8 individuals from sample IT.258, 13 individuals + 6 eggs from sample IT.259, 10 individuals + 3 eggs from sample IT.262, 3 individuals from sample IT.264, 7 individuals + 7 eggs from sample IT.265, 3 eggs from sample IT.267, 6 individuals from sample IT.276.

Notes: Due to the specimen having pores clearly arranged in transverse rows, the most similar taxon is *Minibiotus gumersindoi* Guil and Guidetti 2005; however, a more in-depth analysis including a comparison with *M. gumersindoi* type material is needed to provide a definitive assignment of the examined individuals. The egg processes are screw-like, with each surrounded by a membrane, whereas the eggs of *M. gumersindoi* are unknown.

Paramacrobiotus spatialis Guidetti,
Cesari, Bertolani, Altiero
and Rebecchi 2019

Material examined: 2 individuals + 2 eggs from sample IT.273.

Paramurrayon meieri Guidetti,
Giovannini, Del Papa, Ekrem, Nelson,
Rebecchi and Cesari 2022

Material examined: 3 individuals from sample IT.249.

Notes: No eggs were found; however, the animals matched the species description allowing us to assign them to the species level.

Sisubiotus spectabilis (Thulin 1928)

Material examined: 9 individuals + 7 eggs from sample IT.249.

Discussion

This survey allowed us to provide the first preliminary faunistic checklist of tardigrades from Monviso. While this checklist was derived from a limited sampling effort, the richness found highlights how the Monviso area could be a hotspot for tardigrade alpha diversity.

The tardigrade fauna of Monviso is composed of a mixture of both widespread (*E. blumi*, *M. hanna*, *M. sandrae*, *M. vladimiri*) and Arctic-alpine taxa (*A. victor*, *Claxtonia* sp., *S. spectabilis*), confirming the likeliness of the recent consensus theory on the tardigrades biogeography, indicating the presence of a gradient of taxa ranging from cosmopolitan to endemic, which are often found together (Gąsiorek 2024). It should be noted that in this study the tardigrades were identified only morphologically, which is notoriously a difficult task in some groups (for example, see in the genera *Macrobiotus* and *Hypsibius*; Stec et al. 2021; Warguła et al. 2024). While the identification provided herein provides a first indication on the biodiversity of the Monviso tardigrades, further surveys employing both morphology-based and DNA-based techniques would be advisable.

The finding of the rare *A. victor* gave us the chance to sequence its mitogenome and provide useful data for future phylogenomic studies. While some effort has been recently made to make tardigrade mitochondrial genomes available (Arakawa 2018; Camarda et al. 2025; Vecchi & Stec 2024), the data is still very scarce, and any new piece of information provides a useful contribution. In the assembled mitogenome, the genes nad4l, trnF and trnH were not annotated, most probably due to their high divergence from the reference sequences already present in databases, indicating that an update of the reference database coupled with more sequencing efforts are needed for (but not limited to) this clade of tardigrades (Echiniscidae).

In conclusion, the finding of a diverse community of tardigrade taxa (including rare ones) in a small area on the Monviso massif indicates how, despite years of faunistic studies conducted on Italian and European mountains, a large part of the biodiversity of tardigrades has yet to be uncovered.

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Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Research concept and design: M.V., M.C.L., S.C.; Collection and/or assembly of data: M.V., M.C.L., A.V., S.C.; Data analysis and interpretation: M.V., M.C.L., S.C.; Writing the article: M.V.; Critical revision of the article: M.V., M.C.L., A.V., S.C.; Final approval of article: M.V., M.C.L., A.V., S.C.

Supplementary Materials

Supplementary Materials to this article can be found online at:

<http://www.isez.pan.krakow.pl/en/fovia-biologica.html>
Supplementary files:

SM.01. Mitogenome annotation in a tabular format (feature table). The file can be opened with a text editor.

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