

Bison from Alazeya river basin



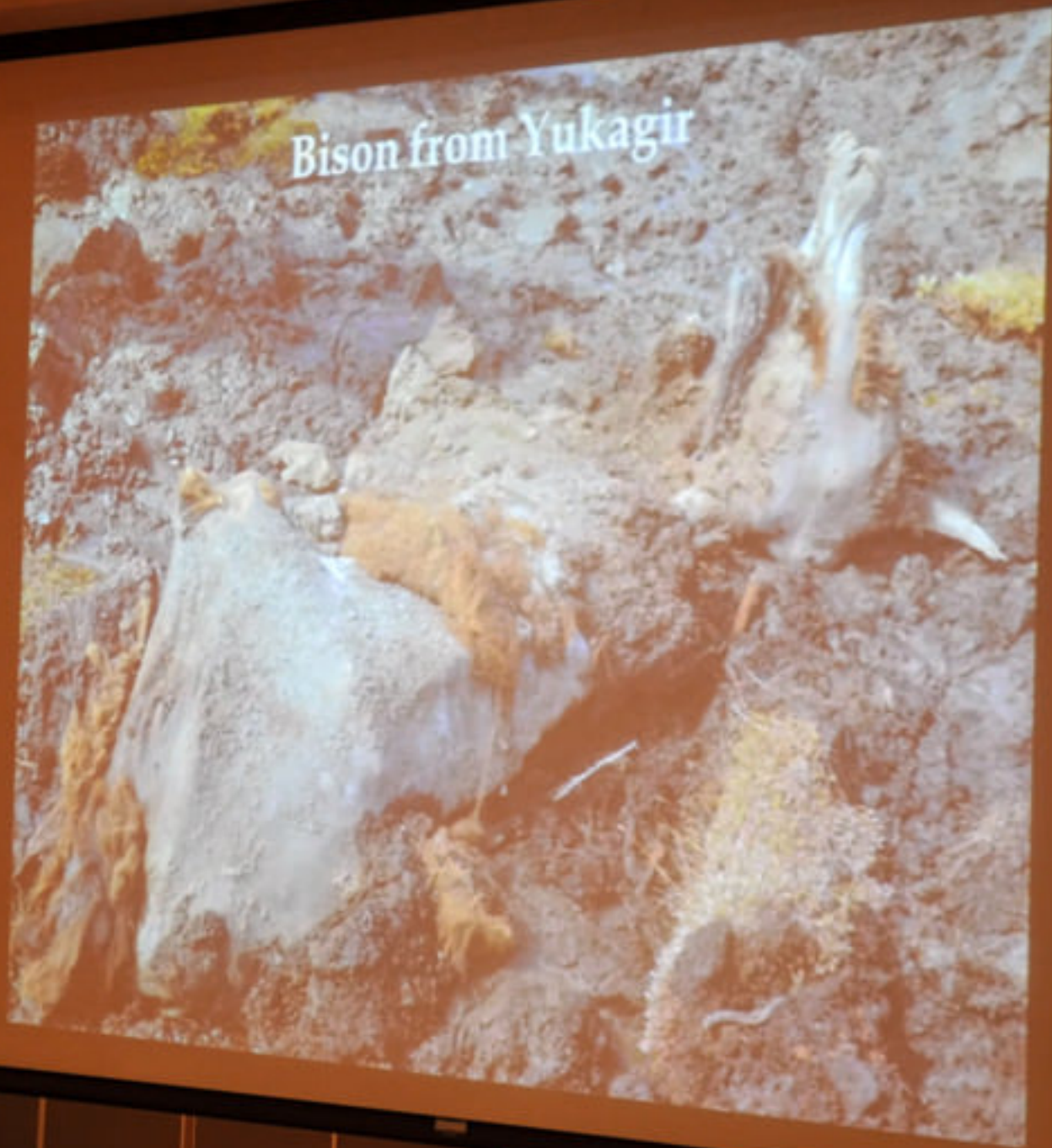
# Omoloyskiy elk



Mummy of ancient wolf pup, 2011



Bison from Yukagir







## Mammoth Yuka, 2010





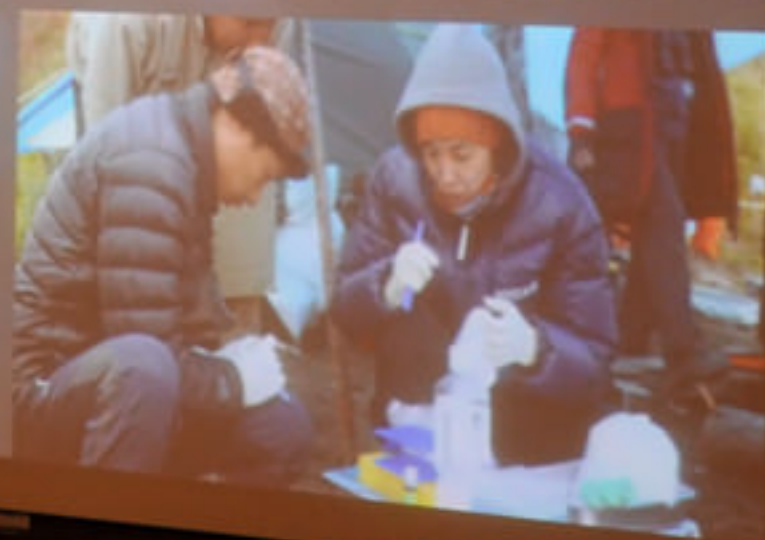


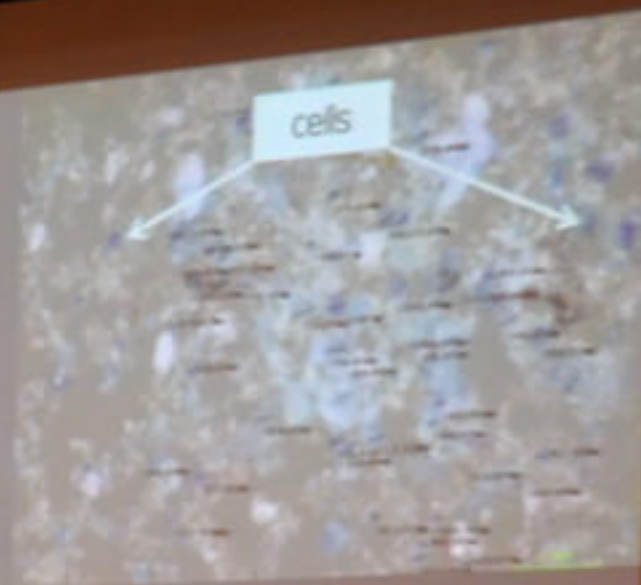
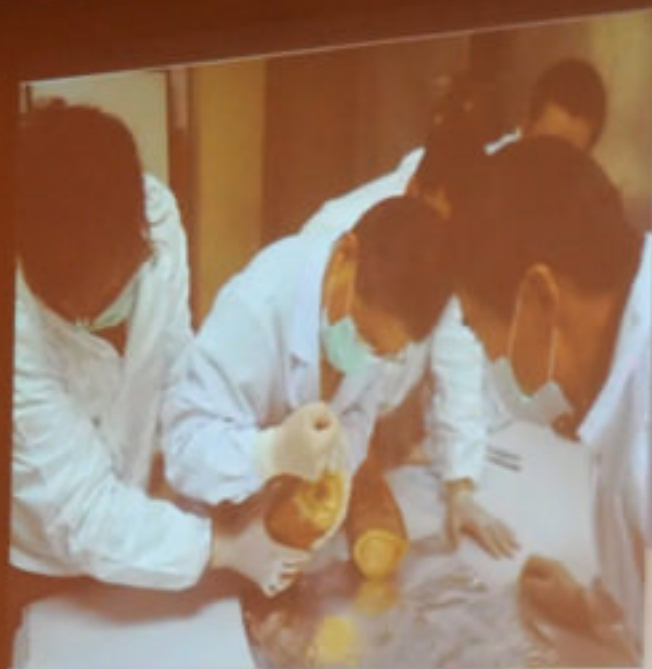
Yuka fu underground natural freezer





The first Russian-Korean expedition to the North Yakutia  
to search for the remains of mammoths





The study of mammoth samples in the laboratory of Mammoth museum



Malolyakhovskiy mammoth









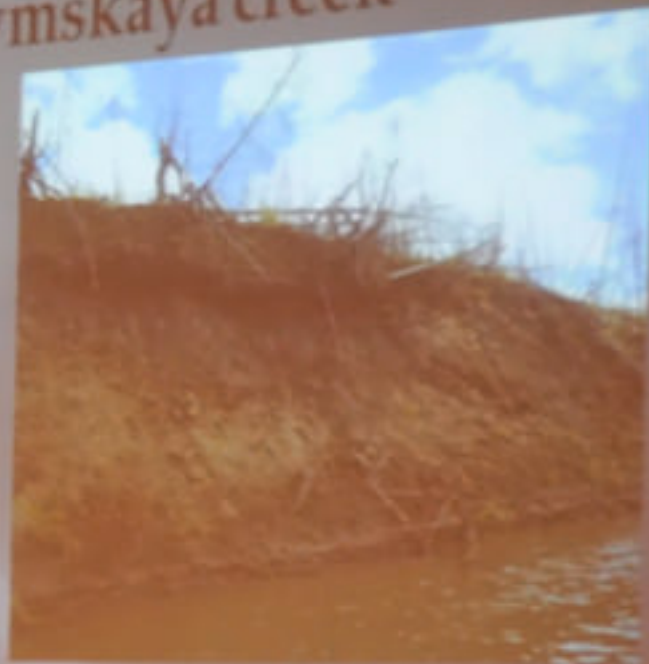
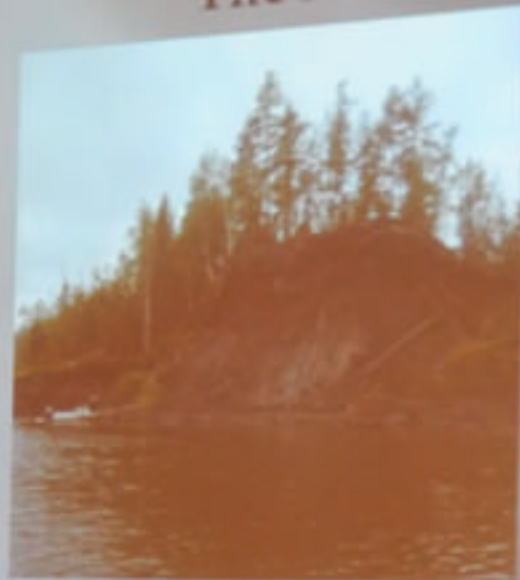


1. The Omulevka River
2. The Pravokolymskaya creek
3. The Irileah Siene River
4. The Berezovka River
5. The Korkodon River





## The Pravokolymskaya creek





## The Irileah Siene River





*Mammuthus primigenius primigenius* (=a later form of mammoth)



The tusk with abnormal painful growths





The tusks with abnormal painful growths from other places

Toybohoy village

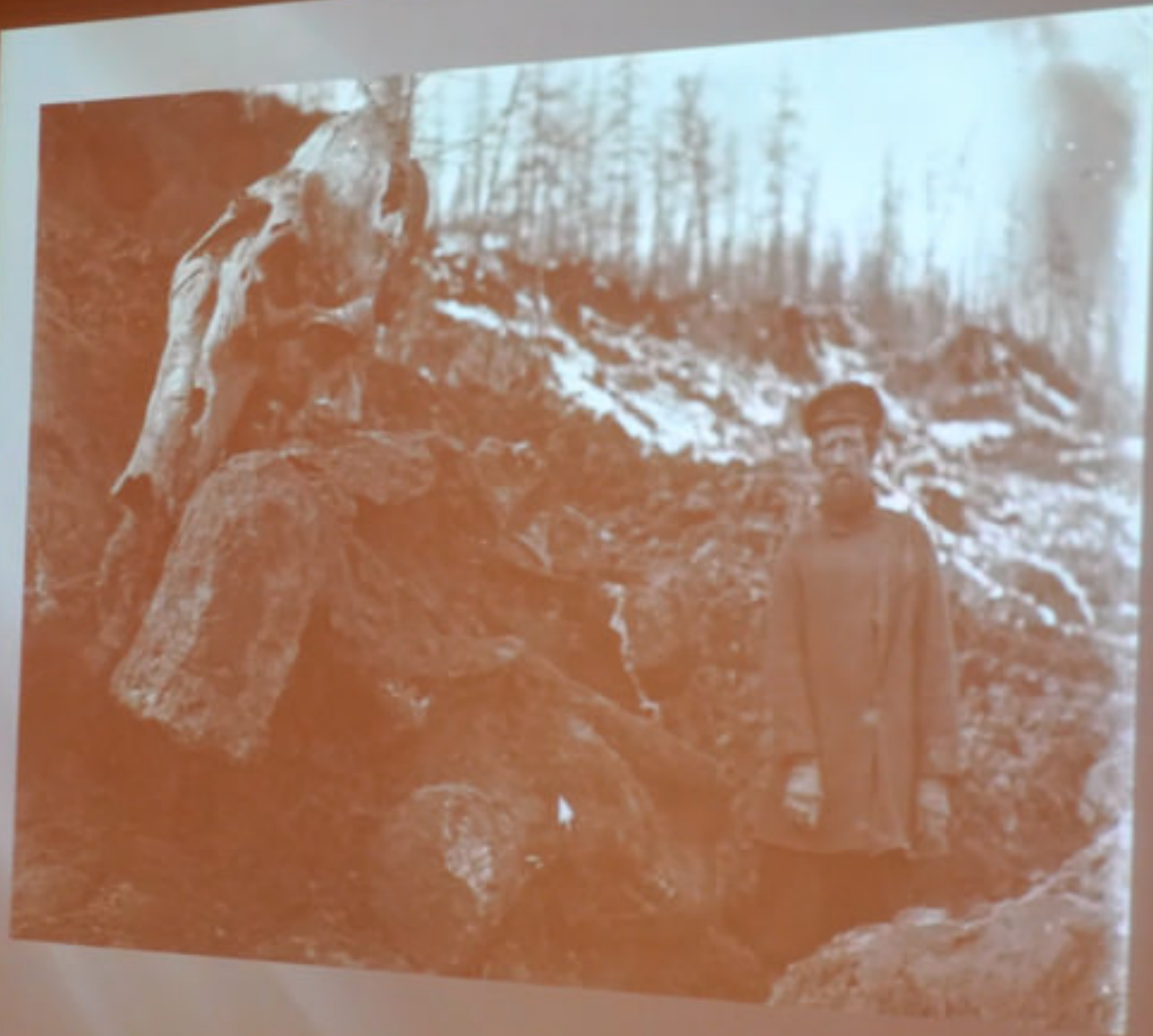


Bolshoi Lyakhovskiy Islands



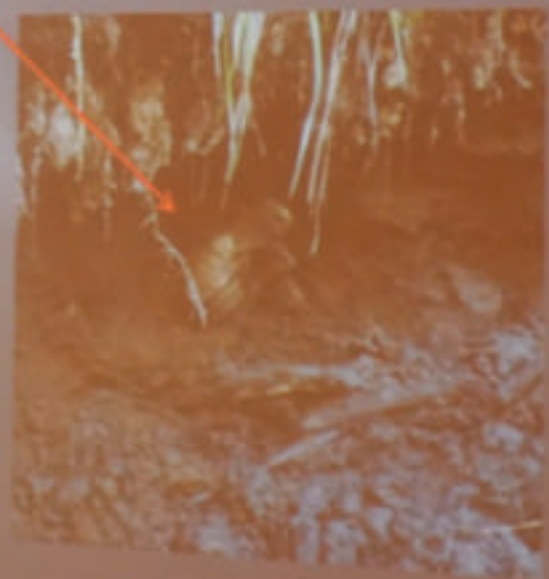
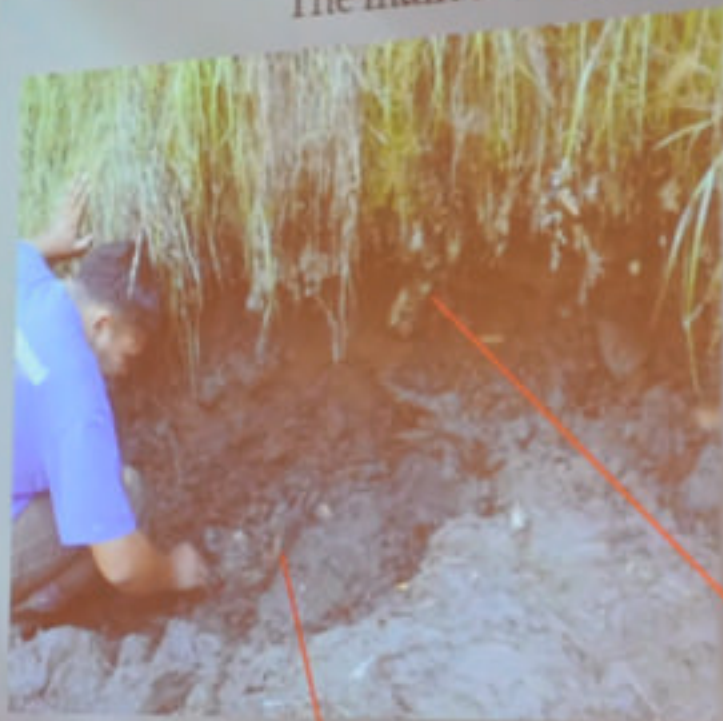
The Berezovka River





Berezovskiy mammoth, 1900

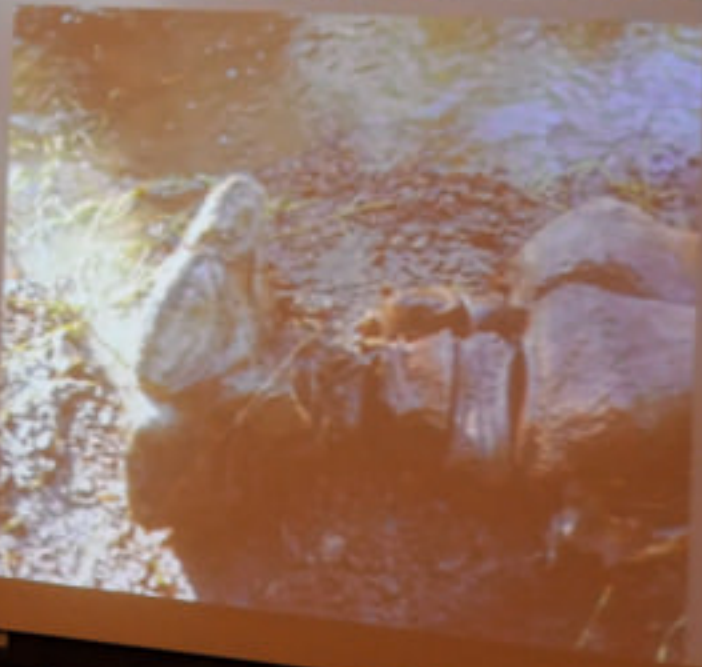
# The main carcass in the permafrost



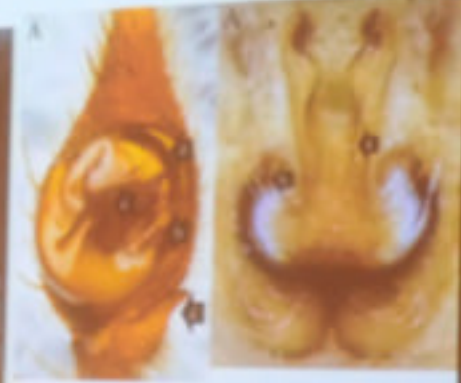
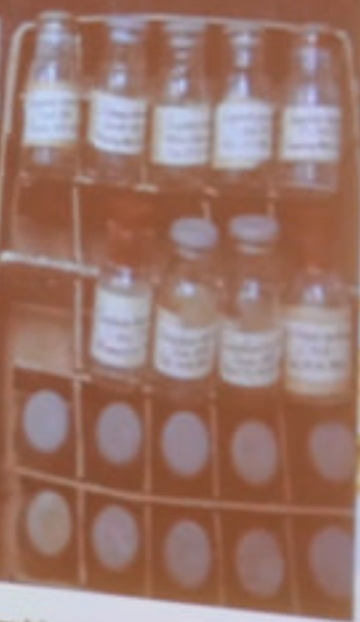
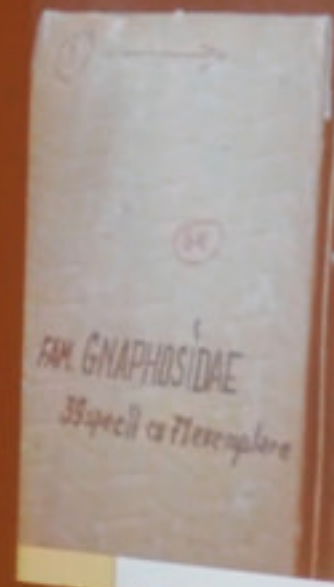
vertebra



# Front leg from the permafrost



"ALEXANDRU ROȘCA" spider collection in  
"GRIGORE ANTIPA" NATIONAL MUSEUM OF  
NATURAL HISTORY (BUCHAREST)



*Pisaura novicia* (L. Koch, 1878)



*Pholcus ponticus* Thorell, 1875



# THE INTEGUMENT OF *TRACHELIPUS TROGLOBIUS* - EVOLUTIONARY ADAPTATIONS LINKED TO THE CAVE ENVIRONMENT

Andrei GIURGINCA<sup>1</sup>, Vladimir ŠUSTR<sup>2</sup>, Karel TAJOVSKÝ<sup>3</sup>

<sup>1</sup>"Emin Racoviță" Institute of Speleology, 13 September Road, no. 13, Sector 5, 050711 Bucharest, Romania, e-mail: andrei.giurginca@icr.ro  
<sup>2</sup>Faculty of Science, Masaryk University of Brno, 602 00 Brno, Czech Republic, e-mail: vustr@sci.muni.cz  
<sup>3</sup>Institute of Zoology, Faculty of Science, Masaryk University of Brno, 602 00 Brno, Czech Republic, e-mail: karel.tajovsky@sci.muni.cz

## INTRODUCTION

Different specific evolutionary adaptations are known in terrestrial invertebrates inhabiting permanently the cave environment. Morphological structures of the integument of troglodytic isopods represent one example of such adaptations. The micro-structure and other corresponding structures of the troglodytic integument have a significant role in minimizing the mortality and the normal functioning of their bodies by preventing small particles of sediment from sticking to the body surface (Schubert 1976). *Trachelipus troglodytes* (Tajovský & Bugeja 1988) is one of the three terrestrial troglodytic isopods (Troglodytes, Oribotroglodytes) described from the Moravia Caves, one of the most important and unique troglodytic cave systems (Tajovský & Bugeja 1988, Giurginca & Cizik 2003, Giurginca, Nis & Vláčilová 2009). Detailed investigations of the integument structure has been undertaken using scanning electron microscopy (SEM, 20kV-5000X) in order to elucidate to which extent the cave environment continuously influenced the morphological structure of the body surface of this species.

## NEW DESCRIPTION OF THE *Trachelipus troglodytes* INTEGUMENT STRUCTURES



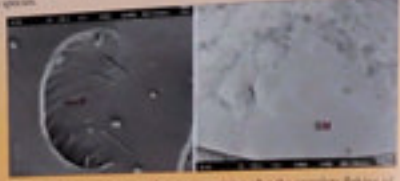
The anterior is covered by dense simple flaking scales (a) the coxite fields bear a smoother surface than the rest of the integument with oval-shaped protuberances (b) between scales.



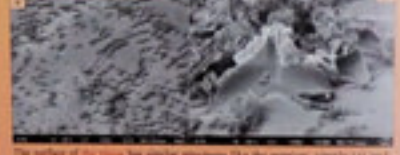
Simple flaking scales (a) and half-moon pits (P). Two types of protuberances: (a) simple formed by a single flaking scale and (b) formed by several flaking scales.



There is a tubercle surrounded small tubercle (T) because the tubercle is covered by scales (a), (b) simple or (c) complex, while the tubercle (b) formation is covered by several flaking scales.



The pila (P) seem to represent the scales remaining after the complete flaking of the scales. Alternatively, the integument is completely smooth (SM).



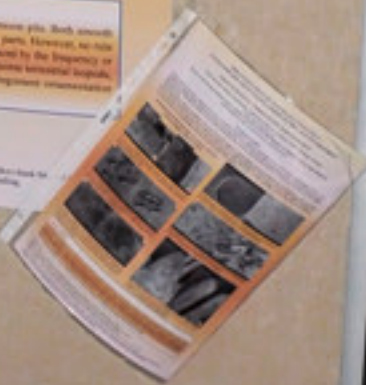
The surface of the pila has similar structures like the previous simple (a) and complex (b) flaking scales and pits cover the integument.



The surface of the pila (a) is densely covered by scales with the presence of a few scales bearing only pits. The tubercles (b) of the integument are covered by dense large scales.

The integument of *Trachelipus troglodytes* has an unique appearance involving the presence of flaking scales and half-moon pits. Both smooth and pits on the body surface are completely covered by scales and generally characteristic for individual body parts. However, the smooth and pits on the body surface are observed. Presence of tubercles and pits seem to be influenced by the frequency of the other integument structures with cave sediment or walls. Tubercles, characteristic for body surface of some troglodytic isopods, are the evolutionary derived of a species permanently inhabiting the highly humid cave environment.

Andrei Giurginca, Institute of Speleology, 13 September Road, no. 13, Sector 5, Bucharest, Romania, 050711  
 Vladimir Šustr, Faculty of Science, Masaryk University of Brno, 602 00 Brno, Czech Republic, e-mail: vustr@sci.muni.cz  
 Karel Tajovský, Institute of Zoology, Faculty of Science, Masaryk University of Brno, 602 00 Brno, Czech Republic, e-mail: karel.tajovsky@sci.muni.cz



# Molecular confirmation of *Anadara kagoshimensis* (Tokunaga, 1906) (Mollusca: Bivalvia) in Adriatic and Black Seas

Ana-Maria Krapan<sup>1</sup>, Alexandra-Florina Levandi<sup>2</sup>, Dana Pasia Popa<sup>3</sup>, Elena Julia Iorgu<sup>4</sup> and Luk Drdica Popa<sup>5</sup>

<sup>1</sup>Department of Biology, Faculty of Natural Sciences, Babeş-Bolyai University, Cluj-Napoca, Romania (e-mail: ana.krapan@ubbcluj.ro)  
<sup>2</sup>Department of Biology, Faculty of Natural Sciences, Babeş-Bolyai University, Cluj-Napoca, Romania (e-mail: alexandra.florina.levandi@ubbcluj.ro)  
<sup>3</sup>Department of Biology, Faculty of Natural Sciences, Babeş-Bolyai University, Cluj-Napoca, Romania (e-mail: dana.pasia@ubbcluj.ro)  
<sup>4</sup>Department of Biology, Faculty of Natural Sciences, Babeş-Bolyai University, Cluj-Napoca, Romania (e-mail: elena.julia.iorgu@ubbcluj.ro)  
<sup>5</sup>Department of Biology, Faculty of Natural Sciences, Babeş-Bolyai University, Cluj-Napoca, Romania (e-mail: luk.drdica@ubbcluj.ro)

## INTRODUCTION

*Anadara kagoshimensis* (Tokunaga, 1906) (Fig. 1A) and *A. inaequalis* (Bougais, 1796) (Fig. 1B) are two very similar shell species originating from the Indo-Pacific region. *A. kagoshimensis* has been introduced to the Mediterranean and the Black Seas under the name of *Anadara inaequalis* (Thiers, 1844) and *A. inaequalis*, respectively, as an alien invasive species. An alien species was observed in the Adriatic Sea since the 1960s and was later recorded as *A. kagoshimensis* (Gardner, 1971) in the Black Sea. The species was first recorded in 1964 by Gardner in the Philippines and specimens of *A. kagoshimensis* from Europe were collected by Levandi in 2008. Mader (2010) determined that *Anadara kagoshimensis* (Tokunaga, 1906) is the most recent of the invasive alien species observed in Europe. The authors concluded that there are no marked differences in shell features, respectively, number of ribs, rib sculpture and selenite color between studied specimens from Japan, the native area of *A. kagoshimensis* and European specimens. It is presumed that the European *A. kagoshimensis* has been introduced from cultured water from Japan.



Figure 1. A: *Anadara kagoshimensis* from Japan (Tokunaga, 1906); B: *A. kagoshimensis* from the Adriatic (Levandi, 2010); C: *A. kagoshimensis* from the Black Sea (Mader, 2010); D: *A. inaequalis* from the Adriatic Sea (Gardner, 1971). (C) and (D) were assessed according to Levandi (2008).

## METHODS

Our study was performed on specimens collected from both the Black Sea (Yevlev, 2008) and Adriatic Sea (Mader, 2010) (Fig. 2). The morphology of shells collected from Adriatic Sea (Fig. 1C) and Black Sea (Fig. 1D) was assessed according to Levandi (2008). Total genomic DNA was extracted from muscle or mantle tissue of each individual using 'NucleoSpin' Tissue kit (Machery-Nagel GmbH & Co. KG, Sion, Germany) according to the producer's protocol. We analyzed the nuclear DNA marker ITS1 (Internal Transcribed Spacer 1) of our specimens and we compared them with sequences of *A. kagoshimensis* from the native area of the species available from GenBank (accession no.: AB277036.1). A total number of 56 sequences were analyzed: two from the Black Sea (one for each population), two from the Adriatic Sea and one from the Pacific Ocean. The sequences were obtained using the GCG 4.0.5. software following the producer's specifications.



Figure 2. The native area of *A. kagoshimensis* (Japan) and the European Adriatic and the western Black Sea populations.

## RESULTS AND CONCLUSIONS

The homogeneity of the study from the analyzed European specimens is similar to that of *A. kagoshimensis* from Japan. We also obtained an identity of 99.99% between the sequences from the European specimens and those from the native area. The above data, respectively, also the high percentage identity between the ITS1 DNA sequences confirm the presence of *A. kagoshimensis* in the two European seas.

Keywords: *Anadara kagoshimensis*; *Anadara inaequalis*; Adriatic Sea; Black Sea; DNA; ITS1; Mollusca; Bivalvia; Invasive species; Molecular biology; Phylogenetics; Genetic diversity; Genetic structure; Genetic differentiation; Genetic drift; Genetic bottleneck; Genetic expansion; Genetic migration; Genetic introgression; Genetic admixture; Genetic hybridization; Genetic recombination; Genetic selection; Genetic drift; Genetic bottleneck; Genetic expansion; Genetic migration; Genetic introgression; Genetic admixture; Genetic hybridization; Genetic recombination; Genetic selection.





Author: ANDREI GIURGINCA, GEORGE-JOEL NAZAREANU  
Institution: "Grigore Antipa" Museum, Bucharest, Romania  
E-mail: andrei.giurginca@antipa.ro, nazareanu@antipa.ro

Annual Zoological Congress of "Grigore Antipa" Museum

## First record of *Sterna hirundo* nesting inside Bucharest

Andrei GIURGINCA\*, George-Joel NAZAREANU\*

\* "Grigore Antipa" National Museum of Natural History, 12 September Blvd., 060711, Sector 4, Bucharest, Romania. e-mail: andrei.giurginca@antipa.ro, nazareanu@antipa.ro

**INTRODUCTION**

The common tern (*Sterna hirundo* Linnaeus, 1758), is a frequent summer guest, arriving from their nesting grounds in the second half of April. The species is breeding on coastal wetlands and islands, but also on the shores of inland lakes, on pebbly beaches (where it makes extraordinary waves) or on floating vegetation, in which case the nest is more substantial including vegetal debris.

The bird nests in groups or near colonies and, more rarely, in isolated pairs.

The breed consists of between one and three eggs incubated for 28-33 days by both parents. The chicks are able to swim at a few days and are fed by both parents for up to 28 days when they are able to fly (Călinescu, 1981, 2002; Săvescu, 2009).





An isolated pair of common terns has nested on an artificial "island" formed between two logs on the Trandafirilor Lake for four years: 2014, 2015, 2017 and 2018.




**CONCLUSIONS**

This is the first recorded case of a pair of common terns nesting inside Bucharest on an artificial "island" formed between two logs on the Trandafirilor Lake for four years: 2014, 2015, 2017 and 2018.

More, we record the presence of *Sterna* at several places in Bucharest: near the Park, near the Trandafirilor Lake, near the Park, near the Trandafirilor Lake.

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**Population genetics of *Anadara kagoshimensis* (Tokunaga, 1906) (Bivalvia, Arcidae) from two European Seas**

Alexandra Florina Levintsi<sup>1</sup>, Ana-Maria Răduță<sup>2</sup>, Dana Paula Popa<sup>3</sup>, Fabio Crocetta<sup>4</sup>, Elena Iulia Iorga<sup>5</sup>, Marieta Costache<sup>6</sup>, Luis David Popa<sup>7</sup>

<sup>1</sup>Department of Marine Biology, Babeş-Bolyai University, Cluj-Napoca, Romania; <sup>2</sup>Department of Marine Biology, Babeş-Bolyai University, Cluj-Napoca, Romania; <sup>3</sup>Department of Marine Biology, Babeş-Bolyai University, Cluj-Napoca, Romania; <sup>4</sup>Department of Marine Biology, Babeş-Bolyai University, Cluj-Napoca, Romania; <sup>5</sup>Department of Marine Biology, Babeş-Bolyai University, Cluj-Napoca, Romania; <sup>6</sup>Department of Marine Biology, Babeş-Bolyai University, Cluj-Napoca, Romania; <sup>7</sup>Department of Marine Biology, Babeş-Bolyai University, Cluj-Napoca, Romania

**INTRODUCTION**

Several species of ark shells were accidentally introduced through shipping of ballast water in certain areas where they have found good conditions to survive and develop. *Anadara kagoshimensis* (Tokunaga, 1906) (Figure 1) is considered an invasive species in European Seas. The species originating in the Indo-Pacific region, after being introduced as a bivalve for aquaculture (Togaki, 1986; Popa, 2012), has been found around 1900 in the Atlantic Sea (Petersen, 1972) and in 1982 in the Black Sea (Dimitrova, 1988).

Ark shells have been intensively studied from a morphological point of view because they possess long-lived and effective in their larval phase (Dimitrova et al., 2012). Clonal reproduction of *Anadara kagoshimensis* has been recorded along the coast of Ukraine (D. Iorga et al., 2017).

In this study, we used microsatellites (SNP markers) to analyze the population genetics of *A. kagoshimensis* from 2 studied European Seas (Black Sea and Adriatic Sea).



Figure 1. *Anadara kagoshimensis* (Tokunaga, 1906).

**METHODS**

We identified 10 microsatellite markers for *A. kagoshimensis* by cross-amplifying 26 markers isolated for other species of ark shells, 2 single- and 2 tri-allelic.

We analyzed 32 individuals each from 2 different invasive populations: Black Sea (Izvoare, Tulcea coast), Mureș and Orșida Cluj-Napoca (Romania coast) (Figure 2).

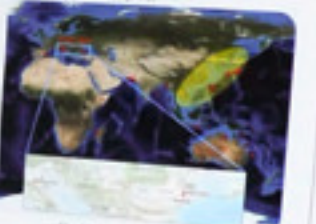


Figure 2. Study locations of *A. kagoshimensis*.

The microsatellite data generated using a LI-COR 4300XL microsatellite reader and the data were analyzed using GenAlEx 6.5 (Peakall & Smouse, 2006).

Marker	Number of alleles	Gene diversity	Polymorphism information content
AK1	2	0.143	0.143
AK2	2	0.143	0.143
AK3	2	0.143	0.143
AK4	2	0.143	0.143
AK5	2	0.143	0.143
AK6	2	0.143	0.143
AK7	2	0.143	0.143
AK8	2	0.143	0.143
AK9	2	0.143	0.143
AK10	2	0.143	0.143

**RESULTS AND DISCUSSION**

The characteristics of the ten microsatellite markers described for *A. kagoshimensis* are presented in Table 1. The genetic diversity was moderate (low diversity) as measured by the number of alleles (2-10) and polymorphism information content (0.143-0.217). No gene flow was observed between the populations of the Black and Adriatic Seas despite the high genetic diversity.

The level of variability within an individual (het) in all populations is presented in the following table (Table 2) and a significant number of heterozygotes are present in other marine bivalve species (Dimitrova et al., 2018).

We tested the presence of a 1:1 Mendelian gene flow between the two studied Black Sea populations, meaning that the proportion of the parental genotypes would be equal with respect to the population. However, in our study, the microsatellite data indicated using a Mendelian approach identified a significantly higher gene flow from Izvoare to Tulcea along the western Black Sea coast as compared to the main studied Sea.

Similar results of the Black Sea genetic data applied to certain regions of the European coast. Possible causes of this phenomenon have been studied at the level of gene gene flow and the variation in the structure of the European coast. Possible causes of this phenomenon have been studied at the level of gene gene flow and the variation in the structure of the European coast.





**Population genetics of *Anadara kagoshimensis* (Tokunaga, 1906) (Bivalvia, Arcidae) from two European Seas**

Alexandra Florina Lovinski<sup>1</sup>, Ana-Maria Krupar<sup>1</sup>, Dana Paula Popa<sup>1</sup>, Fabio Crescetti<sup>2</sup>, Elena Iulia Iorga<sup>1</sup>, Marieta Costache<sup>1</sup>, Lutz Oudiziu Popa<sup>1</sup>

<sup>1</sup>Department of Biology, "Babeş-Bolyai" University of Cluj-Napoca, Cluj-Napoca, Romania; <sup>2</sup>Department of Biology, University of Turin, Turin, Italy

**INTRODUCTION**

Several species of *Anadara* were independently introduced through shipping or ballast water to certain sea-shells that have found good conditions to survive and develop. *Anadara kagoshimensis* (Tokunaga, 1906) (Bivalvia) is considered an invasive species in European Seas. The species originating in the Indo-Pacific region, also known as *Anadara kagoshimensis* (Tokunaga, 1906) (Bivalvia), was first found around 1980 in the Atlantic Sea (Pascarella, 1979) and in 1981 in the Black Sea (Crescetti, 1984).

Its shells have been intensively studied from a phylogenetic point of view (Muller, 1998; Krupar, 2010) and morphological and ecological in Black Sea (Crescetti et al., 2010). The genetic data regarding its invasive spread was published along the coast of China (Li, Tang et al., 2011).

In this study we used microsatellite DNA markers to analyse the population genetics of *Anadara kagoshimensis* from 2 European Seas (Black Sea and Baltic Sea).



Figure 1. *Anadara kagoshimensis* shells from the Black Sea.

**METHODS**

We applied 10 microsatellite markers for *Anadara kagoshimensis* by cross-amplifying 20 individuals collected in other species of similar sizes of *Anadara* and *Chorax*.

We analysed 20 individuals from 2 different invasive populations from the Black Sea (Black Sea, Eastern coast) (Figure 2).

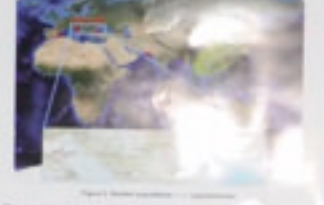


Figure 2. Sampling locations in the Black Sea.

Population	Sample Size	Number of Alleles	Heterozygosity
Black Sea (Eastern coast)	20	10	0.45
Black Sea (Western coast)	20	10	0.45

Table 1. Genetic diversity of *Anadara kagoshimensis* in the Black Sea.

**RESULTS AND DISCUSSION**

The microsatellite analysis of the *Anadara kagoshimensis* population in the Black Sea revealed a high genetic diversity, as indicated by the number of alleles and the heterozygosity. The genetic diversity was similar to that reported for the Black Sea (Crescetti et al., 2010) and the Baltic Sea (Crescetti et al., 2010).

The level of genetic diversity was similar to that reported for the Black Sea (Crescetti et al., 2010) and the Baltic Sea (Crescetti et al., 2010).

The genetic diversity of *Anadara kagoshimensis* in the Black Sea was similar to that reported for the Black Sea (Crescetti et al., 2010) and the Baltic Sea (Crescetti et al., 2010).

Genetic diversity of the Black Sea coastal area was similar to that reported for the Black Sea (Crescetti et al., 2010) and the Baltic Sea (Crescetti et al., 2010).

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**Author(s):** Ana-Maria Krasniqi, Alexandra-Florina Levischi, Dana Paula Popa, Elena Iulia Torcu, and Luis Ordoñez Pizarro

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### Molecular confirmation of *Anadara kagoshimensis* (Tokunaga, 1906) (Mollusca: Bivalvia) in Adriatic and Black Seas

Ana-Maria Krasniqi<sup>1</sup>, Alexandra-Florina Levischi<sup>2</sup>, Dana Paula Popa<sup>3</sup>, Elena Iulia Torcu<sup>4</sup> and Luis Ordoñez Pizarro<sup>5</sup>

**INTRODUCTION**  
*Anadara kagoshimensis* (Tokunaga, 1906) (Fig. 1A) and *A. inaequalis* (Gmelin, 1791) (Fig. 1B) are two very similar and invasive species originating from the Indo-Pacific region.

Since 2010, *A. kagoshimensis* has been recorded in the Mediterranean and the Black Seas, under the name of *Scapharca vesica* (Risso, 1846) and *S. inaequalis*, respectively, as an alien invasive species. An *in situ* specimen was obtained in the Adriatic Sea since the 1980s and was later reported as *S. vesica* by Ghidoui (2017). In the Black Sea, the species was first recorded in 1988 by Gornik as *S. inaequalis*. The morphological differences between *A. kagoshimensis* specimens from the native area (Japan and Philippines) and specimens of *A. inaequalis* from Europe were noticed by Levischi et al. (2020). Further (2020) determined that *Anadara kagoshimensis* (Tokunaga, 1906) is the valid name for the invasive *in situ* specimen present in Europe. The authors concluded that there are no marked differences in shape, ligament, ornamentation of the shell sculpture and even color between studied specimens from Japan (the native area of *A. kagoshimensis*) and European specimens. It is presumed that the European *A. inaequalis* has been introduced from Japan.



Figure 1. A) *Anadara kagoshimensis* (Tokunaga, 1906) (Fig. 1A) and B) *Anadara inaequalis* (Gmelin, 1791) (Fig. 1B) are two very similar and invasive species originating from the Indo-Pacific region. C) *A. kagoshimensis* from the Black Sea (the native area of *A. kagoshimensis*) and D) *A. inaequalis* from the Adriatic Sea (the native area of *A. inaequalis*).

**METHODS**

The study was performed on specimens collected from both the Black Sea (Ljubanica Island and Belenevo) and the Adriatic Sea (Istria) in 2017. The morphology of shells collected from Belenevo (Fig. 1C) and Istria (Fig. 1D) was assessed according to Levischi (2020).

Total genomic DNA was extracted from muscle or mantle tissue of each individual using 'BioSprint' (Qiagen) kit (BioSprint High Pure DNA & RNA Spin Kit - Germany), according to the producer's protocol.

We produced the nuclear DNA using D36 (Universal Transcribed Sequence 1), in our specimens and we compared them with sequences of *A. kagoshimensis* from the native area of the species, available in GenBank (accession no. AB277595-7), a set of numbers of the sequences were deposited from the Black Sea and the Adriatic Sea, from the Adriatic Sea and from the Pacific Ocean. The sequences were obtained using the online tool: BioEdit following the producer's specifications.



Figure 2. The native area of *A. kagoshimensis* (Japan) and the introduced area (Adriatic and Black Seas).

**RESULTS AND CONCLUSIONS**

The phylogenetic analysis of the studied European specimens is similar to that of *A. kagoshimensis* from Japan. We also observed an identity of 100% between the sequences from the European specimens and those from the native area. The unique shell morphology and the high percentage identity between the *in situ* Black specimens confirm the presence of *A. kagoshimensis* in the sea European area.





## Molecular confirmation of *Anadara kagoshimensis* (Tokunaga, 1906) (Mollusca: Bivalvia) in Adriatic and Black Seas

Ana-Maria Krupar<sup>1</sup>, Alexandra-Florina Levănda<sup>2</sup>, Oana Paula Popa<sup>3</sup>, Elena Iulia Iorgu<sup>4</sup> and Lutz Oettler Popa<sup>5</sup>

<sup>1</sup>Department of Biology, Faculty of Biology, Babeş-Bolyai University, Cluj-Napoca, Romania; <sup>2</sup>Department of Biology, Faculty of Biology, Babeş-Bolyai University, Cluj-Napoca, Romania; <sup>3</sup>Department of Biology, Faculty of Biology, Babeş-Bolyai University, Cluj-Napoca, Romania; <sup>4</sup>Department of Biology, Faculty of Biology, Babeş-Bolyai University, Cluj-Napoca, Romania; <sup>5</sup>Department of Biology, Faculty of Biology, Babeş-Bolyai University, Cluj-Napoca, Romania

**INTRODUCTION**  
*Anadara kagoshimensis* (Tokunaga, 1906) (Fig. 1A) and *A. inaequalis* (Shufeldt, 1796) (Fig. 1B) are two very similar bivalve species originating from the Indo-Pacific region.  
 Until 2010, *A. kagoshimensis* has been misidentified in the Mediterranean and the Black Seas under the name of *Anadara inaequalis* (Peters, 1844) and *A. inaequalis* (Shufeldt, 1796), as an alien invasive species.  
 The first *A. kagoshimensis* specimens were reported in the Adriatic Sea since the 1980s and were later identified as *A. kagoshimensis* (Tokunaga, 1906) in the Black Sea. The species was first recorded in 1994 by Gurev et al. (1994) and specimens of *A. kagoshimensis* (Tokunaga, 1906) were later found by Lăzărescu et al. (2016). Most (2016) determined that *Anadara kagoshimensis* (Tokunaga, 1906) is the valid name for the invasive alien species present in Europe. The authors concluded that there are no relevant differences in shell, siphon, muscularis, number of ribs, etc. between the native and introduced specimens from Japan. The native area of *A. kagoshimensis* and European specimens, it is presumed that the European *A. kagoshimensis* has been introduced from Japan.



Fig. 1. A: *Anadara kagoshimensis* (Tokunaga, 1906) (Fig. 1A) and *A. inaequalis* (Shufeldt, 1796) (Fig. 1B) are two very similar bivalve species originating from the Indo-Pacific region. B: *A. kagoshimensis* (Tokunaga, 1906) (Fig. 1C) and *A. inaequalis* (Shufeldt, 1796) (Fig. 1D) are two very similar bivalve species originating from the Indo-Pacific region.

**METHODS**  
 Our study was performed on specimens collected from both the Black Sea (Greece (Samsun and Trabzon) and the Adriatic Sea (Croatia (Zadar) (Fig. 2). The morphology of shells collected from Samsun (Fig. 2C) and Zadar (Fig. 2D) was assessed according to Lăzărescu et al. (2016).  
 Total genomic DNA was extracted from muscle or mantle tissue of each individual using 'DNeasy Blood & Tissue' (Qiagen, Germany) according to the producer's protocol.  
 We sequenced the nuclear DNA region (1751 bp) Internal Transcribed Spacer 1 in our specimens and we compared them with sequences of *A. kagoshimensis* from the native area of the species available from GenBank (accession no. AB073997). A set number of ten sequences were analyzed: two from the Black Sea (one for each population), two from the Adriatic Sea and one from the Pacific Ocean. The sequences were obtained using the 1000 bp region following the producer's specifications.



Fig. 2. The native area of *A. kagoshimensis* (Japan) and a representative area of the Adriatic European population.

**RESULTS AND CONCLUSIONS**  
 Consistently, the study from the western European specimens is similar to that of *A. kagoshimensis* from Japan. We observed an identity of 99.99% between the sequences from the European specimens, and those from the native area. Similar shell morphology and the high percentage identity between the 1751 bp DNA sequences, confirm the presence of *A. kagoshimensis* in the European area.

Correspondence: Ana-Maria Krupar, Department of Biology, Faculty of Biology, Babeş-Bolyai University, Cluj-Napoca, Romania. E-mail: amkrupar@biologie.ubbcluj.ro



Molecular confirmation of *Anadara kagoshimensis* (Tokunaga, 1906) (Mollusca: Bivalvia) in Adriatic and Black Seas

Ana Maria Krupar<sup>1,2</sup>, Aleksandra Platica Lubrdic<sup>1</sup>, Doris Pavic Popic<sup>1</sup>, Elvira Jula Jorgic<sup>1</sup> and Ljilja Dujic Popic<sup>1</sup>

*Anadara kagoshimensis* (Tokunaga, 1906) (Mollusca: Bivalvia) is a species of bivalve that is native to the Japanese archipelago. It was first described by Tokunaga in 1906 and later reclassified as *A. kagoshimensis* by Tokunaga in 1910. The species is characterized by its large size and distinctive shell shape. It is found in the Adriatic and Black Seas, where it is considered an invasive species. The authors of this study used molecular techniques to confirm the identity of *A. kagoshimensis* in these regions. The study involved the collection of samples from various locations in the Adriatic and Black Seas, followed by DNA extraction and sequencing. The resulting sequences were compared to those of the type material of *A. kagoshimensis* from Japan. The results of the study show that the samples collected in the Adriatic and Black Seas are indeed *A. kagoshimensis*, confirming its presence in these regions. This finding is important for understanding the spread of this species and its potential impact on local bivalve populations.





# Feeding activity and stress response evaluation of transgenic *Caenorhabditis elegans* induced by some cationic and amphoteric surfactants

Marina CICCHOLA, Stefano IVAN, Alice DINISCIOLOTTI, David de PIZZIERA  
The University of Nottingham, School of Life Sciences, University Park, Nottingham, Nottingham, UK, NG7 2RD

## Introduction

*Caenorhabditis elegans* is a free living nematode is exposed naturally to different contaminants, and has been used as toxicity testing for several decades. Various surfactants widely used in consumer products, detergents or cleaners are discharged in sewage which may contaminate the local fresh water and soil. Organisms exposed to surfactants may activate several well-conserved defence pathways such as food shock or oxidative stress responses.

## Material and Methods

**Surfactants:** Amphoterics: Cocamidopropyl betaine (CAPB), SLES, SLS, SLES/CO. Cationic: Nonylphenol ethoxylate (NPE), DBPHE. Nonionic: SLES, Dioctylsulfosuccinate (DOS), SLS, SLES/CO, SLS/CO and SLES/CO + SLES/CO. Quaternary ammonium: Nonylphenol ethoxylate (NPE), SLES, SLES/CO, SLS, SLES/CO, SLS/CO, SLES/CO + SLES/CO.



## Stress response in developmental larval stages



**Figure 1.** Relative expression of GFP under developmental larval stages in a representative population, induced by 0.1 mg/L CAPB, SLES and SLS. The graphs indicate relative expression of GFP in response to different surfactants (CAPB, SLES, SLS) and to different concentrations (0.1, 1, 10, 100, 1000 mg/L) of surfactants. The relative expression of GFP was significantly higher (p < 0.05) in response to CAPB and SLES at all concentrations, and to SLS at 0.1, 1, 10, 100 and 1000 mg/L. The relative expression of GFP was significantly higher (p < 0.05) in response to CAPB, SLES and SLS at all concentrations. Error bars represent standard deviation. CAPB, Cocamidopropyl betaine; SLES, SLES/CO; SLS, SLS/CO. \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001.

## It is

It is shown that food uptake is inhibited in response to surfactants.



oxidative is produced by 0.01 mg/l Myosmine acid.



## Discussion

*C. elegans* nervous system responds to the tested cationic and amphoteric surfactants, reducing its pharyngeal pumping and thus feeding is inhibited in this population (Panel 1). Dose-dependent development was not observed after synchronization. Patterns of gene expression (Fig. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11) indicate that most of the end can respond to other surfactants. However, some of these genes as well as all different larval stages during development, in order to respond to be harmful in various organisms, producing reactive oxygen species that generate oxidative stress.

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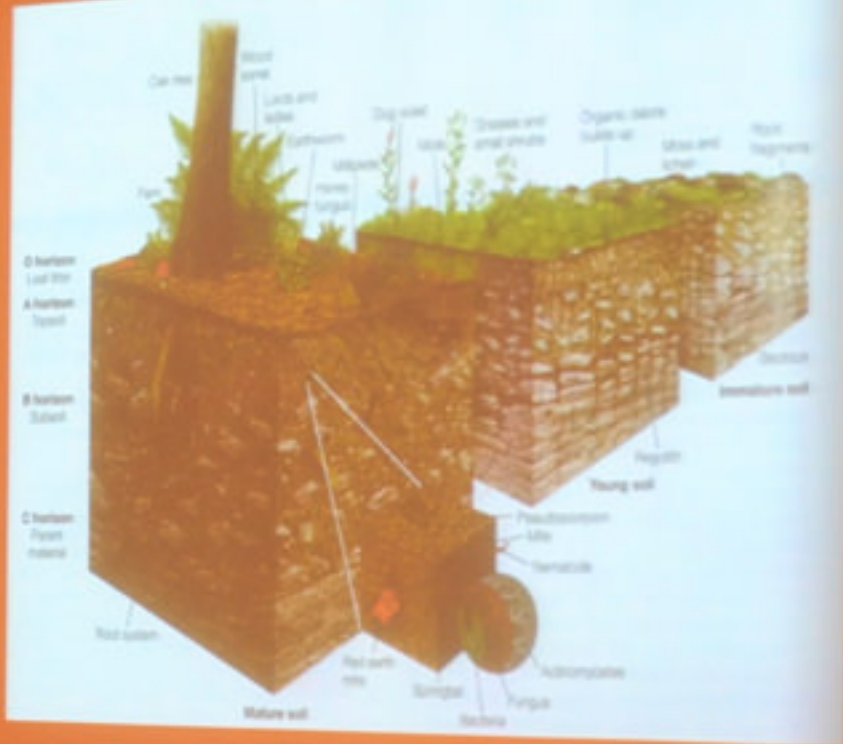
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## THE SOIL FAUNA



• "full-time inhabitants" (many micro- and mesoarthropods, earthworms and macroinvertebrates) (Walters, 2001)

• "part-time inhabitants" of soil (like many vertebrates, soil dwelling insect, larvae or mound-building insects) (Walters, 2001).







Coprophilous beetles (Coleoptera) associated with  
feces of brown bear (*Ursus arctos* Linnaeus, 1758)  
in the Carpathians

Eugen NITZU<sup>1</sup>, Radu MOȚ<sup>2</sup>

<sup>1</sup> "Emile Racovitza" Institute of Speleology

<sup>2</sup> Zarand Association