18th INTERNATIONAL SYMPOSIUM OF BIOLOGY AND ANIMAL NUTRITION









BOOK OF ABSTRACTS

September 26th 2025, INCDBNA
Balotesti, Romania

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INCDBNA IBNA Balotesti, Romania

NATIONAL RESEARCH-DEVELOPMENT INSTITUTE FOR BIOLOGY AND ANIMAL NUTRITION

26 September 2025

IBNA Headquarters, Balotesti

18th International Symposium of Biology and Animal Nutrition

Symposium Program

08.00 - 8.45 REGISTRATION

08.45 - 9.00 WELCOME (*Dr. Catalin Dragomir; Dr. Ionelia Țăranu*)

09.00- 10.15 FIRST SESSION OF SCIENTIFIC COMMUNICATIONS

(*Moderators: Catalin Dragomir, Vasiliki Makri)*

09.00 -09.15

Water-Soluble Oregano Supplementation Improves Growth Performance and Intestinal Integrity in Broilers Under Coccidial Challenge
I. Giannenas, V.Makri, D. Galamatis, G. Symeon, I. Panitsidis, S. Quarki, I. Stylianaki, P. Sakkas

09.15-09.30

Plant-Mediated Synthesis of Silver Nanoparticles for Biomedical Applications
Adriana-Maria Andreica, Mihaela Cecilia Vlassa, Rahela Carpa, Ioan Petean

09.30-09.45

The Effects of Apple Pomace Extract on the Intestinal Barrier Integrity in an *in Vitro* Cellular Model
Gina Cecilia Pistol, Ana Maria Ciupitu, Valeria Cristina Bulgaru, Ionelia Taranu

09.45-10.00

Effects of Encapsulated and Urease-Active Urea Addition on Aerobic Stability and Microbial Activity in Corn Silage
Maryama Khalif Mohamud, Selma Buyukkilic Beyzi, Berrin Okuyucu, Levent Özdüven, Yusuf Konca

12.00-12.15

The genetic parameters for average daily gain and Kleiber ratio in Limousine breed
Pelmuș Rodica Ștefania, Rotar Mircea Cătălin, Gras Mihail Alexandru, Van Cristina.

12.15-12.30

Effects of dietary cowpea seeds and rye grain supplementation on performance and metabolic blood profile in Aberdeen Angus fattening bulls
Smaranda Mariana Toma, Nicoleta Aurelia Lefter, Georgeta Ciurescu, Dan Traian Râmbu, Mihaela Dumitru, Madalin Manole

12.30 - 13.30 LUNCH BREAK

13.30-14.30 THIRD SESSION OF SCIENTIFIC COMMUNICATIONS

(Moderators: *Daniela Marin, Arabela Untea*)

13.30-13.45

Effects of Chronic Thermal Stress (Heat/Cold) and Supplementation with Apple and White Grape Pomace on Organ Morphology, Intestinal Traits, and Nutrient Digestibility in Laying Hens
Gabriela Maria Cornescu, Tatiana Dumitra Panaite, Ana Cismileanu

13.45-14.00

Use of INS-1 cell line in Type 2 Diabetes mellitus research
Costin Dragomir

14.00-14.15
Play behaviour as a part of social interaction in weaned pigs
Sonya Ivanova, Maryana Petrova.

14.15 – 14.30

Reduction of GHG without decreasing profitability – a case study of small ruminants' Romanian farms
Catalin Dragomir, Mihai Gras, Lin Bautze, Josselin Andurand, Katja Klump, Durba Kashyap, Catalin Mircea Rotar, Madalin Manole

14.30 – 14.45

Phylogenetic Relationships Among Eurasian Otter (Lutra lutra) Based on the Complete Mitogenomes from Türkiye and Iran
Husham Abdulrahman Mahdi Alabbasi

ORAL PRESENTATIONS

Phylogenetic relationships among Eurasian Otter (Lutra lutra) based on the complete mitogenomes from Türkiye and Iran

Saffet Teber[1] ; Ahmet Yesari Selçuk[2] ; *Husham Abdulrahman Mahdi Al-Abbasi[3,4]; Mohammad Moradi[5] ; Mehmet Baran[6] ; Akif Keten[7] ; Tarkan Yorulmaz[8] ; Alaettin Kaya[9] ; Servet Ulutürk[10]; Haluk Kefelioğlu[11]; Coşkun Tez[12,13]; Osman İbiş[1,13]

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The Eurasian otter (*Lutra lutra*), a Near Threatened species and a key indicator of aquatic ecosystem health, has experienced significant population declines due to anthropogenic pressures and historical climatic fluctuations. While extensive genetic studies have been conducted across Europe and parts of Asia, data from Anatolia and Iran—regions considered potential Pleistocene refugia—remain scarce. In this study, we sequenced and analyzed complete mitochondrial genomes (mitogenomes) of 13 *L. lutra* collected from Türkiye (n=9) and Iran (n=4). The assembled mitogenomes were approximately 16,535 bp in length and exhibited the typical gene composition of mammals, including 13 proteincoding genes, 22 tRNAs, and two rRNAs. Phylogenetic analyses based on Bayesian Inference (BI) and Maximum Likelihood (ML) approaches revealed two major haplogroups within *L. lutra*: an East Asian clade and a Western Palearctic clade comprising samples from Europe, Türkiye, and Iran. Within the dataset, six haplotypes were identified among Turkish samples and one among Iranian samples, indicating low nucleotide diversity ($\pi = 0.00081$) across the region. Comparative analysis with sequences from GenBank showed strong haplotype sharing between Türkiye, Iran, and European populations, suggesting historical colonization routes and limited genetic differentiation. CYTB and control region analyses supported these findings, revealing low variation consistent with previous reports for Eurasian populations. The observed genetic homogeneity likely reflects historical bottlenecks associated with Pleistocene climatic oscillations and recent anthropogenic impacts. This study fills an important gap in the phylogeographic knowledge of *L. lutra* and highlights the role of Anatolia and Iran in shaping the evolutionary history of this species. The results provide a genomic resource for future conservation genetics studies and reinforce the necessity of regional monitoring strategies for sustaining genetic diversity in fragmented otter populations.

Keywords: *Lutra lutra*, Mitogenome, Genetic diversity, Phylogeny, Türkiye, Iran.

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IBNA BALOTESTI

Certificate of attendance

This certificate guarantees that

Husham Abdulrahman Mahdi Alabbasi

has attended

18th International Symposium of Animal Biology and Nutrition

which has been held on 26 September 2025, and presented the paper entitled:

"Phylogenetic Relationships Among Eurasian Otter (Lutra lutra) Based on the Complete Mitogenomes from Türkiye and Iran"

Scientific Director
Dr. Ionelia TARANU

Scientific Secretary
Dr. Daniela MARIN