

ABSTRACT BOOK

ICMB 2026

3rd Edition

Molecular
regulation across
the domains of life
— from DNA to
proteins

September 21-24,
2026

INTERNATIONAL CONFERENCE

MOLECULAR BIOLOGY

CURRENT ASPECTS AND PROSPECTS



organizer: **Science and
Research Association**

ABSTRACT BOOK

WELCOME TO ICMB 2026



organizer: **Science and
Research Association**

SPONSORS & PARTNERS

We would like to express our sincere appreciation to all the sponsors and partners of ICMB 2026. Your support and contributions have been very important in making this conference possible and creating a great space for scientific exchange. Thank you for being an essential part of ICMB 2026!

SPONSORS

SILVER SPONSORS:



BRONZE SPONSOR:

vetimex capital

AWARD SPONSORS:



targets

an Open Access Journal by MDPI



cells

an Open Access Journal by MDPI



genes

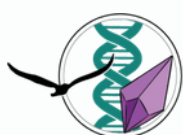
an Open Access Journal by MDPI

SPONSORS

CONFERENCE BAG SPONSORS:



PARTNERS



**Facultatea de
Biologie și Geologie**
UNIVERSITATEA BABEȘ-BOLYAI



FULBRIGHT
Romania



HEART
Healthcare, Education And Research Talks



MEDIA PARTNERS:



ALL CONFERENCE ALERT
ACADEMIC CONFERENCES AT A GLANCE

E fain la Cluj!

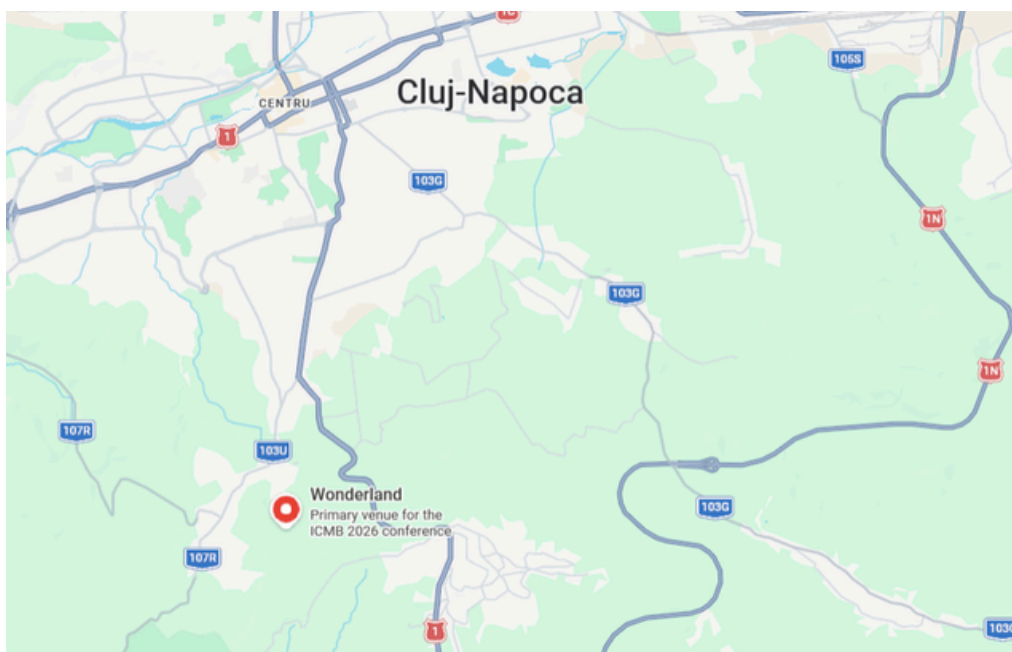
ROMEDIC
EFORTURI PENTRU SĂNĂTATE

TABLE OF CONTENTS

Locations	6
Participants-only information	9
About us	10
Prices	15
Schedule Details	17
Session 1: Molecular regulation from genes to cellular function	39
Session 2: Decoding the genome: DNA, chromatin & transcription	42
Session 3: From transcription to regulatory RNA	48
Session 4: RNA processing and post-transcriptional regulation	50
Session 5: From molecular information to protein function	55
Session 6: Regulatory networks across biological systems	58
Session 7: Gene regulation across molecular and cellular scales	63
Session 8: Molecular regulation, proteins & disease	67
Session 9: From molecular networks to systems biology	70
Poster Exhibition	73
Prizes and Awards	87

LOCATIONS

Wonderland Resort in Cluj-Napoca, Romania



**Plenary & Keynote
Lectures:**

TBA

Poster Sessions:

TBA

**Workshops and Round
Table discussions:**

TBA

How to get there

Cluj-Napoca benefits from an extensive air network with direct flights from many major cities in Europe and Romania. Land connections (road and rail) are also well developed for longer trips.

1. LOCAL TRANSPORTATION IN CLUJ-NAPOCA

Cluj-Napoca features an extensive public transport network, alongside rideshare services and taxis.

- From Avram Iancu International Airport (CLJ) → City Center:
 - Public Transit (Bus): Lines A1E, 5, 8
 - Alternatives: Rideshare (Uber / Bolt), Taxi, Rent-a-car
- From Cluj-Napoca Main Railway Station (Gara CFR) → City Center:
 - Bus: Lines 3, 32B, 35, 9, 4, 5
 - Tram: Line 101

2. DOMESTIC TRAVEL (WITHIN ROMANIA)

Departure City	Flight	Train (InterRegio)	Car
Bucharest (~450 km)	Direct (~1h)	9–10 hours	6–8 hours via E60 / A3
Iași (~400 km)	Direct (~1h)	8–10 hours (direct)	6–7 hours via DN15 / DN17 / DN1C
Timișoara (~300 km)	Direct (~50 min)	6–7 hours	4–5 hours via DN6 / E81
Brașov (~270 km)	—	7–8 hours (direct)	5–6 hours via DN1 / DN13
Constanța (~600 km)	Layover via OTP (~2–3h)	12–14 hours (via Bucharest)	9–10 hours via A2 / A3 / E60
Oradea (~150 km)	—	2–3 hours (direct)	2–2.5 hours via DN1 / E60

3. INTERNATIONAL TRAVEL (FROM EUROPE)

Direct Flights to Cluj-Napoca International Airport (CLJ):

- Germany: Direct flights (~1.5–2h) from Frankfurt, Munich, Berlin, Stuttgart, Dortmund.
- Italy: Direct flights (~1.5–2h) from Milan, Rome, Bologna, Venice, Naples.
- United Kingdom: Direct flights (~2.5–3h) from London (Heathrow, Luton, Stansted).
- France: Direct flights (~2.5h) from Paris and Lyon.
- Spain: Direct flights (~3–4h) from Madrid, Barcelona, Valencia.
- Austria: Direct flights (~1.5h) from Vienna.
- Hungary: Direct flights (~1h) from Budapest.
- Poland: Direct flights from Warsaw.
- Nordic Countries (DK, SE, NO): Direct flights (~2–3h) from Copenhagen, Stockholm, Oslo (seasonal).

4. OVERLAND TRAVEL (CAR / TRAIN / COACH):

- Hungary: Car: 4–5 hours (M3 / DN1 / E60) | Train: 7–8 hours (direct from Budapest).
- Austria: Car: 8–10 hours (A1 / E60 via Hungary) | Train: 12–14 hours.
- Germany: Car: ~12–14 hours (from Munich) | Coach / Train: 15–20 hours.
- Poland: Car: 10–12 hours (via Slovakia) | Train: 12–15 hours.
- Italy: Car: 12–14 hours (via Austria & Hungary) | Coach: 20–25 hours.
- France: Coach / Train: 20–30 hours.
- Spain: Car / Coach: 25–35 hours.

PARTICIPANTS-ONLY

Special Offer

ICMB 2026 participants receive a **15% discount** on all in-stock Romanian and English titles at carturesti.ro.

- Promo Code: **ICMB15**
 - Redemption: Enter the code in the shopping cart prior to payment
 - Validity Period: September 5 – 30, 2026
 - Eligible Items: In-stock Romanian and English books
-

Participants-only information

Scan this QR code to access further conference information, real-time photos, materials, and event updates.



ABOUT US

The Organiser

Science and Research Association (in Romanian: Asociația pentru Știință și Cercetare) is a non-governmental organization from Romania dedicated to promoting science, research, and scientific education within society. Formally founded in 2021, with its main activity in Cluj-Napoca, the association aims to bring science closer to the public and support the development of the scientific community.



About the Conference

The International Conference – Molecular Biology: Current Aspects and Prospects (ICMB) is organized by the Science and Research Association and supported by our partners. The association is a non-profit, non-governmental organization registered in the Romanian National Registry under number 45691402.

The main aim of ICMB 2026 is to bring together researchers, students, and experts from around the world to share knowledge, present new scientific results, and foster future collaborations.

For more details and collaborations, find us at:
contact@stiinta-cercetare.ro
 social media: @science.ongoing
www.stiinta-cercetare.ro



ABOUT US

About the Conference

Through lectures, poster sessions, workshops, and scientific discussions, participants will have the opportunity to explore the latest discoveries and innovations in molecular biology and related fields. ICMB 2026 is designed not only as a scientific conference but also as a platform for networking and professional development. Those who attend the conference can present their research through oral presentations or posters, interact with leading scientists, and establish connections that may end with future research projects and collaborations. The conference will cover a broad range of topics in the area of molecular biology and life sciences.



Conference History

ICMB was first organized in 2015 and brought together researchers, academics, and students interested in advances in molecular biology and related scientific fields. The inaugural edition created an international platform for scientific exchange, allowing participants to present their research, discuss emerging trends, and establish collaborations across institutions and disciplines. Following the success of the first conference, ICMB quickly gained recognition as a valuable meeting point for scientists working in molecular biology, biotechnology, genetics, and other life science disciplines. The event fostered meaningful discussions, encouraged interdisciplinary collaboration, and supported the visibility of young researchers within the scientific community.



Organizing Team

Our team is proudly formed by:

Coordinators

Octavia Roman, Postdoctoral Researcher, Institute of Microbiology, ETH Zurich, Switzerland; President of the Science and Research Association

Partners, Scientific and Financial Aspects: octavia@stiinta-cercetare.ro

Paula Groza, Postdoctoral Researcher, Department of Medical Biochemistry and Cell Biology, Institute of Biomedicine, Sahlgrenska Academy, University of Gothenburg, Sweden

General Management Speakers Related Information: paula@stiinta-cercetare.ro

Diana Pandichi, M.Sc. in Food Quality Management, University of Agricultural Sciences and Veterinary Medicine (USAMV), Cluj-Napoca; Biotechnology graduate, Babeş-Bolyai University

Partners, Sponsors and PR: diana_p@stiinta-cercetare.ro

Mădălina Marinescu, M.Sc. in Medical Biology and Bioinformatics; B.Sc. in Biochemistry, Babeş-Bolyai University, Cluj-Napoca, Romania

Participants Management and Design: madalina@stiinta-cercetare.ro

Volunteers

Diana Panait, Research Assistant, PhD, Institute for Research, Development and Innovation in Applied Natural Sciences & Electron Microscopy Center, Babeş-Bolyai University, Cluj-Napoca, Romania

Sponsors and Communication: diana@stiinta-cercetare.ro

Iris Ionescu, upcoming freshman at University of Pennsylvania, USA

Social Media: iris@stiinta-cercetare.ro

Gabriela Popescu, Faculty of Automatic Control and Computer Science, National University of Science and Technology POLITEHNICA Bucharest, Romania

Social Media and Design: gabriela@stiinta-cercetare.ro

Mirela Buda, M.Sc. in Molecular Biotechnology at Babeş-Bolyai University, Cluj-Napoca, Romania

Social Media and Design: mirela@stiinta-cercetare.ro

Volunteers

Cristina Bledea, First-year Master's student, Faculty of Medical and Health Sciences, Babeş-Bolyai University, Cluj-Napoca, Romania
Social Media: cristina@stiinta-cercetare.ro

Oana Tofan, M.Sc. in Molecular Biotechnology, Babeş-Bolyai University; Molecular Biologist and Curation Scientist
Social Media and PR: oana@stiinta-cercetare.ro

Abrudan Maria Anastasia, Second-year Master's student in Molecular Biotechnology, Faculty of Biology and Geology, Babeş-Bolyai University, Cluj-Napoca, Romania
anastasia@stiinta-cercetare.ro

Larisa-Gabriela Rus, M.Sc. in Medical Biology, Faculty of Biology and Geology, Babeş-Bolyai University, Cluj-Napoca, Romania
Newsletter Editor: larisa@stiinta-cercetare.ro

Alex Cipleu, Second-year Bachelor's student in Biology, Faculty of Biology and Geology, Babeş-Bolyai University, Cluj-Napoca, Romania
alexandru_c@stiinta-cercetare.ro

Dana-Maria Crişan, Graduate of University of Medicine and Pharmacy "Iuliu Haţieganu" Cluj-Napoca, Medical Doctor
Social Events: dana@stiinta-cercetare.ro

Acknowledgements

ICMB2026 also benefits from the support of additional volunteers who contribute to the preparation and successful organization of the conference:

Andreea Stănciulescu (andreea_s@stiinta-cercetare.ro)

Mara Ciora (mara@stiinta-cercetare.ro)

Iulia Gaiţă (iulia@stiinta-cercetare.ro)

Miruna Trantea (miruna@stiinta-cercetare.ro)

Bianca-Andreea Floarea (bianca@stiinta-cercetare.ro)

Alexandru Tudor Petrişor (alexandru@stiinta-cercetare.ro)

Scientific Committee

Gabriel Ichim	Group Leader Cancer Research Center of Lyon (CRCL); Lyon, France
Martin Ott	Professor University of Gothenburg, Sahlgrenska Academy; Gothenburg, Sweden
Ion Cîrstea	Group Leader Ulm University; Ulm, Germany
Ioana Berindan Neagoe	Professor "Iuliu Hațieganu" University of Medicine and Pharmacy; Cluj-Napoca, Romania
Dorina Podar	Associate Professor Babeş-Bolyai University (UBB); Cluj- Napoca, Romania

Advisory board

Fulvio Reggiori	Professor Aarhus University, Denmark
Tim Hunt	Emeritus Professor The Francis Crick Institute, United Kingdom

PRICES

Early Bird	Basic Package	Academia - 350€
		Industry - 450€
		Postdoctoral Researcher - 235€
		PhD Students - 185€ (PhD fee waiver possibility)*
		HighSchool, Bachelor and Master students - 100€
	Festive Package	includes Basic Package (special offers apply) + 90 € (dinner + open bar drinks)
	Complete Package	Standard: Basic Package (special offers apply) + Accommodation for 3 nights (or more)
		Deluxe: Festive Package + Accommodation for 3 nights (or more)

PRICES

Late Bird	Basic Package	450€
Very Late Bird	Basic Package	550€

PhD Fee Waiver

* The **Cancer Cell Death Team from CRCL (Lyon, France)** offers two conference fee waivers for PhD students to attend **ICMB2026 – International Conference: Molecular Biology – Current Aspects and Prospects**, which will take place in Cluj-Napoca, Romania, from 21–24 September 2026. This opportunity is intended to support doctoral students who will benefit from participating in the conference and who can demonstrate how attendance will contribute to their scientific development.

SCHEDULE DETAILS

**SHORT
PROGRAMME**

DAY 1 - MONDAY, 21 SEPTEMBER 2026

THE GENOME DAY

09:30 - 10:30	Registration
10:30 - 11:00	Opening Ceremony
11:00 - 12:30	Plenary Talks <i>Session 1 - Molecular regulation from genes to cellular function</i>
12:30 - 13:30	Lunch
13:30 - 16:00	Plenary Talks <i>Session 2 - Decoding the genome: DNA, chromatin & transcription</i>
15:30 - 16:00	Coffee Break
16:00 - 16:35	Plenary Talks <i>Session 3 - From transcription to regulatory RNA</i>
16:35 - 17:00	Flash Talks
17:00 - 18:00	Poster session and mingle
18:00 - 19:00	Dinner
22:00	Astronomical Observatory

DAY 2 - TUESDAY, 22 SEPTEMBER 2026

THE RNA WORLD (RNA- PROCESSING- REGULATION- TRANSLATION)

09:25 - 11:00	Plenary Talks <i>Session 4 - RNA processing and post-transcriptional regulation</i>
11:00 - 11:30	Coffee Break
11:30 - 12:30	Plenary Talks <i>Session 5 - From molecular information to protein function</i>
12:30 - 13:30	Lunch
13:30 - 15:20	Plenary Talks <i>Session 6 - Regulatory networks across biological systems</i>
15:20 - 15:30	Preventive Medicine Activities
15:30 - 16:00	Coffee Break
16:00 - 18:00	Workshop / Round Tables
18:00 - 19:20	Dinner
20:00 - 22:00	Pub Quiz

DAY 3 - WEDNESDAY, 23 SEPTEMBER 2026

THE SYSTEM

09:25 - 11:00	Plenary Talks <i>Session 7 - Gene regulation across molecular and cellular scales</i>
11:00 - 11:30	Coffee Break
11:30 - 12:30	Plenary Talks <i>Session 8 - Molecular regulation, proteins & disease</i>
12:30 - 13:30	Lunch
13:30 - 14:00	Preventive Medicine Activities
14:00 - 15:00	Round Table
15:00 - 16:00	Plenary Talks <i>Session 9 - From molecular networks to systems biology</i>
16:00 - 17:00	Workshops
17:00 - 17:55	Keynote Talk
17:55 - 18:10	Prizes announcement
18:10 - 19:00	Break / Free Time
19:00 - 20:30	Festive Dinner

DAY 4 - THURSDAY, 24 SEPTEMBER 2026

09:00 - 10:00 Zoology/ Vivarium Museum

09:15 - 10:00 Museum

10:00 - 10:15 Departure to Workshops

10:15 - 12:15 Workshops

10:15 - 12:15 Workshops/ Institute Visit

12:30 - 13:30 Brunch

13:30 - 15:30 City Tour

14:45 - 15:30 Pharmacy Museum

14:45 - 15:30 Mineralogy Museum

SCHEDULE DETAILS

PROGRAMME

DAY 1 - MONDAY, 21 SEPTEMBER 2026

09:30 – 10:30 **Registration**

10:30 – 11:00 **Opening Ceremony**

Session 1: **Molecular regulation from genes to cellular function**

11:05 – 11:45

Keynote Speaker
Éva Kondorosi
 Biological Research Centre, Hungarian Academy of Sciences, Szeged, Hungary

Molecular Dialogue Across the Domains of Life: Chemical and Peptide Signaling, Coordinated Gene Regulation in Legume–Rhizobium Symbiosis

11:45 – 12:00

Diana Petre
Characterisation of Retinal Ganglion Cells of the Area Centralis in Brn3cCre; Brn3bCKOAP mice

12:00 – 12:30

Paul Chiroi
Blood Transcriptomic Signatures in Ischemic Stroke: From Discovery to Diagnostic Value

12:30 – 13:30 **Lunch**

Session 2: **Decoding the genome: DNA, chromatin & transcription**

13:35 – 14:05

Invited Speaker
Tudor Badea
 Research and Development Institute, Transylvania University of Braşov, Romania

Transcriptional Programmes for Retinal Ganglion Cell Type Specification

DAY 1 - MONDAY, 21 SEPTEMBER 2026

14:05 – 14:20	Adina Teodora Gontea <i>The Role of Pou4f Transcription Factors Brn3a and Brn3b in Retinal Ganglion Cell Midline Crossing</i>
14:20 – 14:50	Invited Speaker Finn Werner University College London, United Kingdom <i>Integration of Transcription and Translation in Archaea</i>
14:50 – 15:05	Edwin Humberto Hodelin Maynard <i>Mapping Brn3b+ cell populations of the Superior Colliculus and the Periaqueductal Grey involved in visual evoked defensive behaviours using Brn3bCre mice</i>
15:05 – 15:25	Cornelia Braicu <i>TNBC Drug Resistance: A Systems Biology Approach</i>
15:30 – 16:00	Coffee break

Session 3: From transcription to regulatory RNA

16:05 – 16:35	Invited Speaker Ioana Neagoe Iuliu Hațieganu University of Medicine and Pharmacy, Cluj-Napoca, Romania: <i>From the RNA World to RNA Medicine</i> <i>From the RNA World to RNA Medicine: Non-Coding RNAs in Cancer, Biomarkers, and Therapeutic Innovation</i>
----------------------	--

DAY 1 - MONDAY, 21 SEPTEMBER 2026

16:35 – 17:00 **FLASH TALKS**

17:00 – 18:00 **Poster session and mingle**

18:00 – 19:00 **Dinner**

22:00

Astronomical Observatory

self-paid - 20 lei (aprox. 5€)

students with proof - 50% discount

DAY 2 - TUESDAY, 22 SEPTEMBER 2026

Session 4:

RNA processing and post-transcriptional regulation

09:30 – 10:00

Invited Speaker

David Stanek

Charles University and Institute of Molecular Genetics,
Czech Academy of Sciences, Prague, Czech Republic

*Characterization and targeted rescue of a novel
PRPF31 mutation in retinitis pigmentosa*

10:00 – 10:15

Weronika Wiktorja Pawlik

*Discovery of a mutation-containing circRNA in
polyglutamine disease through systematic analysis of
RNAs with CAG repeats*

10:15 – 10:30

Anna Zsófia Poscher

*Integrative Multiomics Approaches Reveal Hypoxia-
Dependent Reprogramming of IL-4 Macrophage
Polarization*

DAY 2 - TUESDAY, 22 SEPTEMBER 2026

Session 4: RNA processing and post-transcriptional regulation

10:30 – 11:00

Invited Speaker

Joanna Rorbach

Department of Medical Biochemistry and Biophysics,
Karolinska Institutet, Stockholm, Sweden

Distinctive features of protein synthesis in mammalian mitochondria

11:00 – 11:30

Coffee Break

Session 5: From molecular information to protein function

11:35 – 12:15

Keynote Speaker

Andrei Lupas

Department of Protein Evolution, Max Planck Institute
for Biology Tübingen, Germany

Proteins as nanomachines: from sequence to structure to mechanism

12:15 – 12:30

Robert Pasieka

Waking the sleepers: lincRNA overexpression compromises DHX36 activity and global protein synthesis

12:30 – 13:30

Lunch

DAY 2 - TUESDAY, 22 SEPTEMBER 2026

Session 6: Regulatory networks across biological systems

13:35 – 14:05

Invited Speaker

Paweł Bednarek

Institute of Bioorganic Chemistry, Polish Academy of Sciences, Poznań, Poland

Evolution of glucosinolate-hydrolysing enzymes for cellular immune defence

14:05 – 14:30

Rivka Dikstein

Structural and molecular basis of specialized translation mediated by the ribosome mRNA-binding channel

14:30 – 15:00

Invited Speaker

Alessio Mengoni

Biology Department, University of Florence, Italy

Interkingdom Interactions and Epigenomic Plasticity in the Evolution of Symbiotic Bacterial Genomes

15:00 – 15:20

Christa Kanstrup

Intron-dependent regulation of the Glucosinolate Transporter GTR2

15:20 – 15:30

Alecsandra Andreea Budihoi

Preventive Medicine Activities

15:30 – 16:00

Coffee Break

16:00 – 18:00

Parallel Sessions

Workshop 16:00 - 18:00

Diana Mitrea

Achieving your goals: one intentional step after another

DAY 2 - TUESDAY, 22 SEPTEMBER 2026

Round Table 16:00 - 17:00

Éva Kondorosi

Navigating ERC Grants: From Research Idea to Competitive Proposal

Round Table 17:00 - 18:00

Alessio Mengoni

Science, Risk and Entrepreneurship: Building a Biotech Company

18:00 – 19:20

Dinner

19:20 – 20:00

Departure Pub Quiz

20:00 – 22:00

Pub Quiz

DAY 3 - WEDNESDAY, 23 SEPTEMBER 2026

Session 7:

Gene regulation across molecular and cellular scales

09:30 – 10:00

Invited Speaker

Anca Gafencu

Institute of Cellular Biology and Pathology “Nicolae Simionescu” of the Romanian Academy, Bucharest, Romania

Gene Regulation, Expression, and Metabolic Functions of Major HDL-Apolipoproteins

DAY 3 - WEDNESDAY, 23 SEPTEMBER 2026

Session 7:

Gene regulation across molecular and cellular scales

10:00 – 10:20

Christopher Dulson

Targeting the Transcription System of African Swine Fever Virus for Antiviral Drug Discovery

10:20 – 10:30

Sponsor Talk (ZEISS)

From 2D to 3D — ZEISS Microscopy Solutions for Spatial Biology

Cicerone Tudor, Business Developer / PASS EMEA, ZEISS Research Microscopy Solution

10:30 – 11:00

Invited Speaker

Radu Zabet

Blizard Institute, Queen Mary University of London, London, United Kingdom

Explainable AI identifies H3K18ac as a new marker of active enhancers

11:00 – 11:30

Coffee Break

Session 8:

Molecular regulation, proteins & disease

11:35 – 12:05

Invited Speaker

Alina Seserman

Faculty of Medical and Health Sciences, Babeş-Bolyai University, Romania

The Road to Chemoresistance: Decoding Early Adaptation in 3D Melanoma Models

DAY 3 - WEDNESDAY, 23 SEPTEMBER 2026

Session 8: Molecular regulation, proteins & disease

12:05 – 12:30

Claudia Gabriela Tugui

Proteins in the Pipes: Wastewater Metaproteomics for Public Health Monitoring

12:30 – 13:30

Lunch

13:30 - 14:00

Alecsandra Andreea Budihoi

Preventive Medicine Activities

14:00 - 15:00

Round Table

Radu Zabet & Marek Mutwil

AI in Science: Tool, Collaborator or Disruptor?

Session 9: From molecular networks to systems biology

15:05 - 15:30

Dorina Podar

TBA

15:30 – 16:00

Invited Speaker

Marek Mutwil

Section for Plant Biochemistry, Department of Plant and Environmental Sciences, University of Copenhagen, Denmark

Gene function prediction with knowledge graphs

16:00 – 17:00

Workshop

Andra Ciucă

What does it take to become a genetic counsellor?

DAY 3 - WEDNESDAY, 23 SEPTEMBER 2026

Session 9: From molecular networks to systems biology

17:00 – 17:40	Keynote Speaker Nikolaus Rajewsky Max-Delbrück-Center for Molecular Medicine (MDC) and Charité University Berlin, Germany <i>Molecular Mechanisms from Spatial Omics</i>
17:40 – 17:55	Keynote Chat
17:55 – 18:10	Prizes Announcement
18:10 – 19:00	Break / Free Time
19:00 - 20:30	Festive Dinner and networking

DAY 4 - THURSDAY, 24 SEPTEMBER 2026

09:00 - 09:15	Activity: Museum Meeting Point
09:15 - 10:00	Activity: Museum Zoology/Vivarium Museum Visit

DAY 4 - THURSDAY, 24 SEPTEMBER 2026

10:00 - 10:15	Departure to Workshops
10:15 - 12:15 Parallel Sessions	Workshop Adorjan Cristea <i>Basics of PCR and Electrophoresis</i>
	Workshop - Institute Visit Cornelia Braicu <i>Research Center for Functional Genomics, Biomedicine and Translational Medicine, Iuliu Hatieganu University of Medicine and Pharmacy</i>
12:30 - 13:30	Brunch Organising Team <i>optional/self-paid</i>
13:30 - 15:30	Activity: City Center Tour <i>City Tour includes one of the museums below to visit, subject to attendance</i>
14:45 - 15:30 Parallel Sessions	Pharmacy Museum <i>self-paid entrance</i>
	Mineralogy Museum

SCHEDULE DETAILS

WORKSHOPS

1 - ACHIEVING YOUR GOALS: ONE INTENTIONAL STEP AFTER ANOTHER

TUE., 22 SEP.
16:00 - 18:00

Trainer: Diana Mitrea, PhD (Founder & CEO at DeMix Solutions, LLC, USA)

Description: A practical framework for turning ambitious long-term goals into manageable steps using SMART goal setting. This session blends proven project, time, and resource management principles with the speaker's real-world experience navigating academia, biotech, and entrepreneurship, offering perspectives on building a meaningful path while maintaining a healthy work-life balance.

Target audience: trainees

[high school students | undergraduate & graduate students | postdocs]

2 - WHAT DOES IT TAKE TO BECOME A GENETIC COUNSELLOR?

WED., 23 SEP.
16:00 -17:00

Trainer: Andra Ciucă, Postdoctoral Researcher, Babeş-Bolyai University; Lead, Genetic Counsellors Branch, European Board of Medical Genetics

Description: This workshop introduces genetic counselling as a career for students who are interested in genetics, biology, psychology, and helping people make sense of their complex health and genetics information. Through my own experience, I'll talk about how my career evolved from psychology to genetic counselling to research. We will explore together what genetic counsellors do, what skills matter, and how you can start building a career into this field.

Target audience: trainees

[high school students | undergraduate & graduate students]

3 - BASICS OF PCR AND ELECTROPHORESIS

THU., 24 SEP.
10:15 -12:15

Trainer: Adorjan Cristea

Description: Hands-on workshop

Target audience: trainees

[high school students | undergraduate & graduate students]

SCHEDULE DETAILS

ROUND TABLES

1 - NAVIGATING ERC GRANTS: FROM RESEARCH IDEA TO COMPETITIVE PROPOSAL

TUE., 22 SEP.
16:00 - 17:00

Discussion Leader: Professor Dr. Éva Kondorosi,
Biological Research Centre, Hungarian Academy of
Sciences, Szeged, Hungary

Description: A practical discussion on preparing competitive ERC grant applications. Prof. Dr. Éva Kondorosi will share insights on developing a strong research vision, structuring a proposal, and avoiding common pitfalls throughout the application process.

Target audience: graduate students | postdoctoral researchers
principal investigators | early-career group leaders

2 - AI IN SCIENCE: TOOL, COLLABORATOR OR DISRUPTOR?

WED., 23 SEP.
14:00 - 15:00

Discussion Leaders:
Group Leader Dr. Radu Zabet, Blizard Institute,
Queen Mary University of London, United Kingdom
Associate Professor Dr. Marek Mutwil, Section for
Plant Biochemistry, Department of Plant and
Environmental Sciences, University of Copenhagen,
Denmark

Description: Artificial intelligence is rapidly reshaping scientific research. This roundtable will discuss the opportunities, limitations, and ethical considerations of AI in research, from experimental design and data analysis to scientific writing and reproducibility.

Target audience: undergraduate students | graduate students
postdoctoral researchers | principal investigators

3 - SCIENCE, RISK AND ENTREPRENEURSHIP: BUILDING A BIOTECH COMPANY

TUE., 22 SEP.
17:00 - 18:00

Discussion Leader: Professor Dr. Alessio Mengoni,
Biology Department, University of Florence, Italy

Description: An interactive discussion exploring the journey from academic research to biotech entrepreneurship. Topics will include translating scientific discoveries into real-world applications, managing risk, securing funding, and building successful research-driven companies.

Target audience: graduate students | postdoctoral researchers
principal investigators | researchers interested in entrepreneurship

SESSION 1:
**MOLECULAR REGULATION
FROM GENES TO CELLULAR
FUNCTION**

KEYNOTE SPEAKER

MOLECULAR DIALOGUE ACROSS THE DOMAINS OF LIFE: CHEMICAL AND PEPTIDE SIGNALING, COORDINATED GENE REGULATION IN LEGUME-RHIZOBIUM SYMBIOSIS

Éva Kondorosi^{1,2}

¹ Institute of Plant Biology, HUN-REN Biological Research Centre, Szeged, Hungary

² Centre for Translational Medicine, Semmelweis University, Budapest, Hungary

Life on Earth has evolved in close association with microorganisms. Among these interactions, symbiosis represents one of the most intimate and mutually beneficial relationships between organisms from different domains of life. A remarkable example is the partnership between legume plants and Rhizobium soil bacteria, which enables plant growth under nitrogen-limiting conditions through biological nitrogen fixation.

The establishment of this symbiosis relies on an intricate molecular dialogue between the two partners. Mutual recognition by reciprocal chemical signaling in the rhizosphere initiates the formation of a new, symbiotic plant organ, the root nodule, where the bacteria become intracellular endosymbionts. Development of functional nodules requires the coordinated differentiation of both the host plant cells and their bacterial partners.

In the model legume *Medicago truncatula*, successful symbiosis involves the activation of nearly 1,000 symbiosis-specific plant genes, accompanied by extensive physiological and transcriptional reprogramming of the bacteria, including induction of the nitrogen fixation machinery that converts atmospheric N₂ into ammonia, thereby supporting plant growth without an external nitrogen source.

During nodule development, both the infected plant cells and the endosymbiotic bacteria undergo repeated rounds of endoreduplication. This process gives rise to giant polyploid plant cells containing highly polyploid and elongated, terminally differentiated bacteroids that irreversibly lose their capacity for cell division. Bacterial terminal differentiation is orchestrated by more than 700 sequentially expressed host-derived peptides, predominantly by the nodule-specific cysteine-rich (NCR) peptides.

This lecture will present recent advances in our understanding of the chemical and peptide signaling networks that coordinate bacterial and plant gene expression throughout symbiosis. I will also discuss how changes in nuclear ploidy and epigenetic modifications shape symbiosis-specific gene expression in the host, and how key transcription factors regulate the activation of NCR genes that govern bacterial differentiation and the establishment of an efficient nitrogen-fixing symbiosis.

Keywords: *signaling molecules; developmental effectors; gene evolution; gene activation; transcription factors; Medicago truncatula; Sinorhizobium meliloti.*

CHARACTERISATION OF RETINAL GANGLION CELLS OF THE AREA CENTRALIS IN BRN3CCRE; BRN3BCKOAP MICE

Diana Petre¹, Ileana Daria Dobre (Madan)¹, Ana-Maria Sisman (Taranciuc)¹, Elangovan Boobalan², Brian Brooks², Tudor C. Badea^{1,3}

¹Transilvania University of Brasov, Research And Development Institute, Brasov, Romania

²National Eye Institute, Ophthalmic Genetics and Visual Function Branch, National Eye Institute, NIH, Bethesda, MD

³National Brain Research Center, Romanian Academy of Sciences, Bucharest, Romania

Among mammals, mice present a unique structure for the analysis of retinal development and function by using large-scale chemical mutagenesis and targeted genetic manipulation (Badea and Nathans, 2004), however a region of high visual acuity was not previously described.

Using POU4F transcription factors that orchestrate the development and cell-type specification of neurons like Brn3b and Brn3c, a cell marking strategy involving Cre-mediated recombinase to effect the recombination of a pair of LoxP target sites in the Brn3b conditional allele and human placental Alkaline Phosphatase, we discovered a central region of higher density of retinal ganglion cells in the mouse flatmount retina, called Area Centralis, placed in a naso-temporal fashion. We verified experimentally Brn3cBrn3b expression in the mouse retinal ganglion cells timeline: embryonic day 12, E15, postnatal day 0, P7, P15, P19, adults. In order to track the neurons and visualize the dendritic morphologies of RGCs, we used sparse anterograde AAVFLEXeGFP virus infections in the Brn3c^{Cre}; Brn3b^{CKOAP} mice retinas, combined with anti-Brn3b and anti AP imunostainings; we also did retrograde labelling injections with Choleratoxin in both Superior Colliculus and Lateral Geniculate Nucleus for the visualization of ventro-temporal retinal crescent (VTC) containing ipsi projecting RGCs.

We found that the majority of Brn3b⁺Brn3c⁺ RGCs belong to the OFF-DS (JamB) and OFF-delta (OFF-sustained) types, with a few instances of midget-like and small bistratified cells, ArCe placement position relative to mouse ipsi-contra territories and consequences on visual function of Brn3c⁺Brn3b⁺ RGC ablation. Using Tyr^{Cj/Cj}; Brn3c^{Cre}; Brn3b^{CKOAP} mice and appropriate controls we also found that albinism does not significantly affect position and density gradient of ArCe RGCs. The Brn3b⁺Brn3c⁺ RGCs transcriptomic studies will provide the molecular candidates for the early stages of RGC specification, axon guidance and navigation, which are essential clues for all attempts at RGC regeneration and optic nerve navigation.

Keywords: *Molecular Cell Type Specification; Retinal Ganglion Cells; Brn3c; Brn3b; Visual Acuity; AAVFLEXeGFP virus infections; Alkaline Phosphatase staining.*

Reference:

Badea, T. C., & Nathans, J. (2004). Quantitative analysis of neuronal morphologies in the mouse retina visualized by using a genetically directed reporter. *Journal of Comparative Neurology*, 480(4), 331-351.

SESSION 2:
**DECODING THE GENOME:
DNA, CHROMATIN &
TRANSCRIPTION**

PLENARY SPEAKER

TRANSCRIPTIONAL PROGRAMS FOR RETINAL GANGLION CELL TYPE SPECIFICATION

Tudor C. Badea^{1,2}

¹ Transilvania University of Brasov, Research And Development Institute, Brasov, Romania

² National Brain Research Center, ICIA, Romanian Academy, Bucharest, Romania

Visual information collected by photoreceptors is processed by retinal neurons, separated into distinct features and passed on to the brain by 20-40 distinct Retinal Ganglion Cell (RGC) types. RGCs are amongst the best understood classes of neuronal cell types, and can be distinguished by morphological, physiological and molecular criteria. However, the mechanisms by which individual RGC types are specified and acquire their unique features are not understood. We use a combinatorial genetic approach based on Cre and Cre-dependent conditional knock-in alleles through which we can identify individual RGCs expressing specific combinations of transcription factors and/or neurotrophic receptors, and generate genetic mosaics in mice. Using these tools we have uncovered a combinatorial transcriptional code for RGC type specification, involving the three POU domain transcription factors Brn3a, Brn3b and Brn3c. We discovered the cell-autonomous effects of transcription factor ablation in Brn3-expressing RGCs, including cell survival, morphological changes and transcriptomic programs. Using intersectional genetics based on the tools we have generated, we and others are cataloguing RGC types with increasing specificity, and study dendritic arbor morphologies, projections to specific retinorecipient areas of the brain, and involvement in visual circuitry linked to specific brain nuclei. By labelling specific neuronal cell types, we can follow their developmental history and uncover the molecular mechanisms leading to cell type specification.

Keywords: *Retinal Ganglion Cells; Transcription Factors; Development; Cre recombination; Molecular Genetic Manipulations.*

References

1. Badea, T.C. (2003) Journal of Neuroscience 2003 Mar 15;23(6):2314-22.
2. Badea, T.C. (2004) Journal of Comparative Neurology 2004 Dec 20;480(4): 331-51.
3. Badea T.C. (2009) Neuron 2009 Mar 26;61(6):852-64.
4. Badea T.C. (2011) Vision Res. 2011 Jan 28;51(2):269-79.
5. Chen S.K., (2011) Nature 2011 Jul 17;476(7358):92-5.
6. Shi M, PLoS One. 2013 Oct 8;8(10):e76347.
7. Sajgo S, Proc Natl Acad Sci U S A. 2017 May 16;114(20):E3974-E3983.
8. Parmhans N J Comp Neurol. 2018 Mar 1;526(4):742-766.
9. Muzyka VV, Neural Dev. 2018 Jun 29;33(1):15.
10. Kiyama T, Cell Rep. 2019 Apr 16;27(3):900-915.e5.
11. Parmhans N, J Comp Neurol. 2021 Jun;529(8):1926-1953.
12. Chen CK, J Comp Neurol 2021 doi: 10.1002/cne.25208
13. Muzyka, VV (2021) Neural Development vol 36: 5 September 21
14. Tien NW, (2022), J. of Neuroscience,
15. Kiyama T (2023) Front. Ophthalmol., 2023 May 18
16. Rodgers J. (2025) Molecular Therapy 2025 Jan

THE ROLE OF POU4F TRANSCRIPTION FACTORS BRN3A AND BRN3B IN RETINAL GANGLION CELL MIDLINE CROSSING

Adina Teodora Gontea^{1,2}, Tudor Constantin Badea^{1,3}, Ugo Ala⁴,
Ghania Zubair⁴

¹ Research and Development Institute, Transilvania University, Brasov, Romania

² SCDEP of Brasov, "Marin Dracea" National Institute for Research and Development in Forestry,

³ National Center for Brain Research, Romanian Academy, Bucharest, Romania

⁴ University of Turin, Italy

The Pou4f transcription factors Brn3a and Brn3b are required for the development of Retinal Ganglion Cells (RGCs), which convey visual information from the eye to the brain. RGC axons reach the midline at the optic chiasm and either cross contralaterally or turn away from the midline and project ipsilaterally (only 3-5% of all mouse RGCs). It was previously reported that Brn3a is enriched in contralaterally projecting RGCs, but its role remains unclear, since germline Brn3a^{KO} mice die at birth. We therefore specifically deleted Brn3a from RGCs using our Cre-dependent Brn3a conditional allele (Brn3a^{CKOAP}) and a retina - specific Cre driver (Rax:Cre). We labelled RGC projections by injecting the fluorescent tracers ChTB-A555 in the right eye and ChTB-A488 in the left eye of retinal Brn3a KO (Rax:Cre; Brn3a^{CKOAP/KO}), heterozygote (Rax:Cre, Brn3a^{CKOAP/WT}), or wild type control (Brn3a^{CKOAP/WT}) adult mice. We quantitated ipsi and contra A488 and A555 fluorescence intensities in LGN, OPN, SCN and SC). No significant differences between ipsi/contra projections to retinorecipient areas were observed across the three genotypes. To identify candidate genes that could be involved in the ipsi-contra specification we developed a statistical method based public single-cell data from mouse RGCs. The pattern of distribution of well-established ipsi and contra markers have enabled us to create profiles that led to the identification of several new candidate genes for both ipsilateral and contralateral identities. We then compared the expression patterns of the new markers in the Brn3b^{KO/KO} and WT animals and we found a consistent upregulation for the genes potentially involved in the ipsilateral identity. Therefore, we performed the ChTB experiment also in these genotypes and we identified an increase in ipsilateral projections in Brn3b^{KO/KO} compared to WT. In conclusion, Brn3a does not play a role in ipsi vs. contra specification and Brn3b is inhibiting the ipsilateral pathway.

Keywords: Retinal Ganglion Cells; Superior Colliculus; gene expression; visual information.

PLENARY SPEAKER

INTEGRATION OF TRANSCRIPTION AND TRANSLATION IN ARCHAEA

Finn Werner¹

¹ RNAP laboratory, Institute for Structural and Molecular Biology, University College London, Gower Street, WC1E 6BT London, United Kingdom.

Promoter-proximal pausing and gene control is often thought to be a eukaryotic trait, but key components including RNA polymerase subunits Rpo4/7, the elongation factor Spt4/5 and termination factor aCPSF1 arose much earlier in evolution – in the Archaea. We have shown that promoter-proximal transcription termination anticorrelates with mRNA levels at genome-scale; this is a bona fide regulatory mechanism as it responds to changes in the environment including stress and nutrient availability. This regulation is brought about by balancing aCPSF1-facilitated premature termination and antitermination, proximal to the promoter. I will present plausible mechanisms that enable this type of global gene control including the role of elongation factors and chromatin, but in particular make the case for transcription-translation coupling, TTC. Globally, during amino acid starvation, the cell down-adjusts the yield of transcription to meet the reduced needs for translation, thereby achieving a tight resource economy fit for a microbe. Simultaneously, a small subset of genes that mitigate the starvation, like *cimA*, is upregulated – and our results suggest that this induction involves alternative translation initiation and ribosome frame shifting.

Thus, in response of amino acid starvation, the dual regulatory response of repression and induction of gene expression involve both transcription and translation machineries.

MAPPING BRN3B+ CELL POPULATIONS OF THE SUPERIOR COLLICULUS AND THE PERIAQUEDUCTAL GREY INVOLVED IN VISUAL EVOKED DEFENSIVE BEHAVIOURS USING BRN3B^{CRE} MICE

Edwin Humberto Hodelin Maynard^{1,2}, Ionut-Dimitrie Atasiei³ and Tudor Constantin Badea^{1,4}

¹ Transilvania University of Brasov, Faculty of Medicine, Research and Development Institute.

² University of Medical Sciences of Havana.

³ Neurosurgery Department, Emergency Clinical Hospital "Sf. Pantelimon", Bucharest.

⁴ National Brain Research Centre, ICIA, Romanian Academy.

Aims: To understand the neuroanatomy of Superior Colliculus (SC) and Periaqueductal Grey (PAG) Neurons expressing Brn3b and involved in visual evoked defensive behaviours (VEDB) by using Brn3b^{Cre} mice.

Methods: We targeted different dorsoventral and mediolateral positions of the superior colliculus using stereotactic injections of Cre-dependent AAV-FLEX-tdTomato virus in Brn3b^{Cre} mice. Intracardiac paraformaldehyde fixation was performed on day 30 after injection, followed by retina and brain dissection/sectioning, and imaging at low (X5) and high-resolution (X20).

Results: Brn3b+ neurons located from the superficial to the deep layers of the medial SC specifically project to the ipsilateral dorsal terminal nucleus of the accessory optic tract and the bilateral epimicrocellular, microcellular tegmental, cuneiform and lateral posterior thalamic nuclei. Additionally, we observed that neurons located in the intermediate and deep layers of the lateral SC specifically project to the ipsilateral dorsal half of the PAG, substantia nigra, zona incerta, internal capsule, and paraventricular thalamic nucleus. Moreover, they also project to the bilateral peripeduncular nucleus, hypothalamic area, preoptic area, central thalamic nuclei and lateral posterior thalamic nucleus. Brn3b+ neurons located in the dorsal part of the PAG do not project outside of this region. A common pathway of ipsi-contralateral dissemination of the information for all Brn3b+ neurons located in the SC includes the optic tracts with crossing fibres in the optic chiasm. In addition, Brn3b+ neurons of the lateral SC also send projections to the contralateral side towards the centrolateral and paracentral thalamic nuclei with crossing fibres in the central medial thalamic nucleus.

Conclusions: AAVFLEX-tdTomato injections in Brn3b^{Cre} mice reveal Brn3b+ cell bodies in several layers of the ipsilateral SC and PAG. The target selection of Brn3b neurons, as well as their ipsi-contralateral dissemination of the information, follows a specific pattern related to the location of these neurons in the mediolateral axis of the SC.

Keywords: brain circuit; visual evoked defensive behaviour; transcription factors; visual system.

SESSION 3:
**FROM TRANSCRIPTION TO
REGULATORY RNA**

PLENARY SPEAKER

FROM THE RNA WORLD TO RNA MEDICINE: NON-CODING RNAS IN CANCER, BIOMARKERS, AND THERAPEUTIC INNOVATION

Ioana Berindan-Neagoe^{1,2}

¹ Department of Genomics, MEDFUTURE Institute for Biomedical Research, Iuliu Hațieganu University of Medicine and Pharmacy, Cluj-Napoca, Romania

² Doctoral School, "Iuliu Hațieganu" University of Medicine and Pharmacy, 23 Marinescu, 400337 Cluj-Napoca, Romania

The discovery that much of the human genome is transcribed without encoding proteins has fundamentally changed our understanding of cancer biology. Once considered transcriptional noise, non-coding RNAs are now recognized as key components of regulatory networks controlling cell identity, proliferation, differentiation, immune responses, and adaptation to cellular stress. Their dysregulation is increasingly linked to tumor initiation, progression, metastatic dissemination, and resistance to therapy, positioning the "RNA world" at the centre of contemporary precision oncology.

This presentation follows the evolution of non-coding RNA research from mechanistic cancer biology toward translational applications in RNA medicine. Drawing on studies across different tumor models, it will focus on microRNAs and other regulatory RNAs as molecular signatures of malignant transformation and tumor progression, and on their integration with genomic, transcriptomic, and clinical information. The potential of circulating RNAs and extracellular-vesicle-associated RNA as minimally invasive biomarkers will be discussed in the context of liquid biopsy, where molecular signatures obtained from blood may complement tissue-based diagnostics, contribute to patient stratification, and provide dynamic information on disease evolution.

However, RNA's clinical relevance extends beyond biomarker discovery. Non-coding RNAs participate in complex regulatory networks involving oncogenic signaling, apoptosis, inflammation, immune escape, and drug response, creating opportunities to identify therapeutically actionable vulnerabilities. Integrating RNA signatures with functional genomics, multi-omics datasets, computational biology, and drug-repurposing strategies can therefore transform descriptive molecular profiles into hypotheses for therapeutic intervention.

The shift from studying RNA as a regulatory layer of cancer biology to exploiting RNA-derived information for diagnosis, patient stratification, and therapeutic discovery reflects a broader transformation in biomedical research. RNA medicine is emerging not as a single technology, but as an integrated framework connecting molecular mechanisms, biomarkers, computational discovery, and precision therapeutics. Non-coding RNAs sit at this intersection and may become a key bridge between understanding cancer complexity and developing more individualized approaches to clinical management.

Keywords: Non-coding RNAs, Liquid biopsy, Precision oncology.

SESSION 4:
**RNA PROCESSING AND
POST-TRANSCRIPTIONAL
REGULATION**

PLENARY SPEAKER

CHARACTERIZATION AND TARGETED RESCUE OF A NOVEL PRPF31 MUTATION IN RETINITIS PIGMENTOSA

David Stanek¹

¹ *Charles University and Institute of Molecular Genetics, Czech Academy of Sciences, Prague, Czech Republic*

Retinitis pigmentosa (RP) is a hereditary retinal disease characterized by photoreceptor loss and currently lacks an effective therapy. RP is caused by mutations in numerous genes, with mutations in PRPF31 accounting for approximately 10% of autosomal dominant RP cases. Here, we characterized patients carrying a pathogenic variant in the PRPF31 gene containing a point mutation in intron 10. This mutation reduces normal PRPF31 splicing and activates a cryptic splice site, resulting in the production of an aberrant transcript. The pathogenic mRNA and protein are unstable, leading to reduced expression of functional PRPF31 protein in patient-derived samples. To rescue the splicing defect, we designed modified antisense oligonucleotides (ASOs) targeting several regions surrounding the mutation in intron 10. We identified an ASO that improved PRPF31 splicing in patient-derived iPSCs and retinal pigment epithelium (RPE) cells and increased PRPF31 protein levels. These findings provide a foundation for ASO-based splice correction therapies targeting splicing defects in RP.

DISCOVERY OF A MUTATION-CONTAINING CIRC RNA IN POLYGLUTAMINE DISEASE THROUGH SYSTEMATIC ANALYSIS OF RNAs WITH CAG REPEATS

Weronika Pawlik¹, Magdalena Woźna-Wysocka¹, Magdalena Jazurek-Ciesiołka¹, Jarosław Dulski², Tomasz M. Witkoś¹, Agata Ciołak¹, Emilia Kozłowska¹, Edyta Kościańska¹, Luke C. Bartelt³, Julien Philippe⁴, Jarosław Sławek², Paweł M. Świtoński⁵, Albert R. La Spada⁴, Agnieszka Fiszer¹

¹ Department of Medical Biotechnology, Institute of Bioorganic Chemistry Polish Academy of Sciences, Poznan, Poland

² Department of Neurology, Neurodegenerative Diseases and Neuroimmunology, Medical University of Gdansk, Gdansk, Poland

³ Department of Molecular Genetics and Microbiology, Duke University Medical Center, Durham, NC 27710, USA

⁴ Departments of Pathology & Laboratory Medicine, Neurology, Biological Chemistry, and Neurobiology & Behavior, and the Center for Neurotherapeutics, University of California, Irvine; Irvine, CA, USA

⁵ Department of Neuronal Cell Biology, Institute of Bioorganic Chemistry Polish Academy of Sciences, Poznan, Poland

CAG repeat tracts occur in both non-coding and translated RNAs, have tended to lengthen throughout evolution, and are thought to enhance neuronal function. We identified over 600 human RNAs (including mRNAs, lncRNAs, and circRNAs) with at least 10 CAG repeats, originating from 58 genomic loci, which vary, e.g., in the rate of CAG length polymorphism. Several circRNAs originate from the ATXN7 locus, where CAG expansion causes spinocerebellar ataxia type 7 (SCA7). For selected circATXN7(3,4).1 (circ1), we demonstrated its cytoplasmic localization, as well as its presence in 40S, monosome and polysome fractions. We showed that circ1 is expressed in human fibroblasts, blood and cerebellum, and, importantly, we identified a mutation-containing circRNA with potential implications in SCA7.

Keywords: CAG repeats; non-coding RNA; circRNA; lncRNA; polyglutamine diseases; SCA7.

INTEGRATIVE MULTIOMICS APPROACHES REVEAL HYPOXIA-DEPENDENT REPROGRAMMING OF IL-4 MACROPHAGE POLARIZATION

Anna Poscher^{1;2,*}, Gyöngyi Ilona Cinege^{1,*}, Zsófia Varga^{1,*}, Apolka Domokos^{3;4}, Szilárd Pólisha³, Petros Tzerpos³, Csilla Sajben⁵, Viktória Jeney⁶, Krisztián Pál Bene^{3;7}, Roland Tengölics⁵, László Nagy^{3;7}, Zsolt Czimmerer^{1;#}

¹HUN-REN Biological Research Centre, Institute of Genetics, Szeged, Hungary

²University of Szeged, Faculty of Science and Informatics, Doctoral School in Biology, Szeged, Hungary

³University of Debrecen, Faculty of Medicine, Department of Biochemistry and Molecular Biology, Debrecen, Hungary

⁴University of Debrecen, Faculty of Medicine, Molecular Cell and Immunobiology Doctoral School, Debrecen, Hungary

⁵Laboratory of Metabolomics, Complex Molecular and Cell Biology Service Centre, HUN-REN Biological Research Centre, Szeged, Hungary

⁶University of Debrecen, Faculty of Medicine, Research Centre of Molecular Medicine, MTA-DE Lendület Vascular Pathophysiology Research Group, Debrecen, Hungary

⁷Johns Hopkins University School of Medicine, Institute for Fundamental Biomedical Research Johns Hopkins All Children's Hospital, Department of Medicine and Biological Chemistry, St. Petersburg, Florida, USA

* These authors contributed equally

Corresponding author (czimmerer.zsolt@brc.hu)

Macrophages are highly plastic myeloid cells that adopt diverse functional states in response to environmental cues, ranging from IFN γ -induced classical (M1) to IL-4-induced alternative (M2) polarization. M2 polarization frequently occurs under hypoxic conditions, including wound healing, fibrosis, and tumor development, but the effects of hypoxia on the M2 polarization program remain poorly understood. In this study, we aimed to identify the microenvironmental signals shaping IL-4-driven M2 polarization during murine wound healing in vivo and to investigate the molecular mechanisms underlying signal integration using an in vitro BMDM model and integrative multiomics analyses.

Reanalysis of a time-course wound-healing scRNA-seq dataset revealed two macrophage subpopulations with high IL-4 response signatures at later stages of healing. Although both populations displayed features of alternative activation, one exhibited a markedly stronger hypoxia gene signature suggesting that hypoxia contributes to shaping alternative macrophage polarization in vivo. In vitro bulk RNA-seq of IL-4-stimulated BMDMs demonstrated that hypoxia substantially reshapes the IL-4-induced transcriptional program, repressing 500 IL-4-inducible genes while enhancing 271.

Hypoxia-enhanced IL-4-inducible genes were preferentially expressed in the hypoxic M2 macrophage population identified in vivo and were enriched for wound healing-associated processes. To characterize the epigenetic regulation of this gene set, ATAC-seq and RNAPII ChIP-seq was used and revealed that hypoxia increased IL-4-induced activation of regulatory elements associated with hypoxia-enhanced IL-4-inducible genes. Additional metabolomic profiling showed the accumulation of polyamine biosynthetic intermediates in hypoxic IL-4-stimulated BMDMs, consistent with the enhanced transcriptional induction of enzymes involved in polyamine biosynthesis.

Our results indicate that hypoxia reshapes IL-4-driven macrophage polarization through coordinated transcriptional, epigenetic and metabolomic reprogramming, connecting environmental signal integration to macrophage functional states in vivo and in vitro.

Keywords: *macrophage polarization; single-cell RNA-sequencing; interleukin-4; hypoxia; epigenetic regulation; polyamine biosynthesis*

PLENARY SPEAKER

STRUCTURAL AND FUNCTIONAL INSIGHTS INTO HUMAN MITOCHONDRIAL GENE EXPRESSION

Joanna Rorbach¹

¹ *Department of Medical Biochemistry and Biophysics, Karolinska Institute, Stockholm, Sweden*

Mitochondria retain their own genome and a dedicated protein synthesis machinery, distinct from the cytosolic system, to produce essential components of the oxidative phosphorylation system. This machinery depends on a large network of auxiliary factors that regulate RNA maturation, mitoribosome assembly, translation and quality control, many of which remain incompletely understood. Mutations in several of these factors cause human disease, yet the molecular mechanisms linking defective mitochondrial gene expression to pathogenesis are often unclear. In this talk, I will present our recent structural and functional studies revealing unique features of the human mitochondrial translation machinery, from mitoribosome biogenesis and translation to the surveillance pathways that ensure the fidelity and integrity of these processes.

Keywords: *Mitochondrial RNA; mitoribosome; translation; quality control; mitochondrial diseases.*

SESSION 5:
**FROM MOLECULAR
INFORMATION TO PROTEIN
FUNCTION**

KEYNOTE SPEAKER

PROTEINS AS NANOMACHINES: FROM SEQUENCE TO STRUCTURE TO MECHANISM

Andrei Lupas¹

¹ Max Planck Institute for Biology, Department of Protein Evolution, Max-Planck-Ring 5, 72076 Tübingen, Germany

Proteins are essential components of all living systems. In fact, it is fair to say that life results substantially from the chemical activity of proteins. For this activity, proteins must adopt defined three-dimensional structures which are fully encoded in their amino-acid sequences. However, the sequences encode far more than just static structures. They also specify the path by which the structures will be reached, the dynamic adjustments they will undergo in response to changing conditions and binding partners, the components of the cellular machinery they will need to engage to reach their native location. From the information in their sequence, proteins can recognize their binding partners and know whether they will alter them by catalysis or through conformational changes, and whether they will fold or unfold conditionally upon encountering them. All these aspects we subsume under the term mechanism and the chemical mechanisms of proteins are fully specified in their sequences. In the department of Protein Evolution at the MPI for Biology we have focussed for 25 years on the relationship between sequence, structure, and mechanism from an evolutionary perspective. In this talk, I will discuss insights we have gained, using Two Component Signal Transduction and exopolysaccharide export as examples. Our work has been greatly boosted by progress in structure modeling and computational biophysics.

Keywords: *Proteins, structure, structure prediction, chemical mechanism, computational biophysics, transmembrane signal transduction, exopolysaccharide export*

WAKING THE SLEEPERS: LINCRNA OVEREXPRESSION COMPROMISES DHX36 ACTIVITY AND GLOBAL PROTEIN SYNTHESIS

Robert Pasięka¹, Patrycja Plewka¹, Emanuele Vitale², Iga Kapuścińska¹, Mateusz Bajczyk³, Dawid Bielewicz⁴, Tomasz Skrzypczak⁴, Kishor Gawade¹, Bartosz Koch¹, Alessia Ciarrocchi², Katarzyna Dorota Raczyńska^{1,4}

¹ Department of Gene Expression, Laboratory of RNA Processing, Institute of Molecular Biology and Biotechnology, Faculty of Biology, Adam Mickiewicz University, Poznan, Poland;

² Laboratory of Translational Research, Azienda Unita Sanitaria Locale-IRCCS di Reggio Emilia, Reggio Emilia, Italy;

³ Department of Gene Expression, Institute of Molecular Biology and Biotechnology, Adam Mickiewicz University, Poznan, Poland;

⁴ Centre for Advanced Technologies, Adam Mickiewicz University, Poznan 61-614, Poland

Transposable element-derived long intergenic noncoding RNAs are increasingly recognized as context-dependent regulators of gene expression, but the functional consequences of their ectopic activation in somatic cells remain poorly understood. We previously showed that U7 snRNA represses a subset of LTR12-associated lincRNAs, including Inc-ARRDC4-1 and Inc-ADCYAP1-2, two testis-enriched lincRNAs with minimal expression in somatic cells. Here, we examined the consequences of their increased expression in somatic cells. We showed that overexpression of either lincRNA led to overlapping transcriptomic and proteomic changes, impaired migration, altered adhesion and proliferation, and a ~50% reduction in protein synthesis. Furthermore, we identified Inc-ARRDC4-1 as an upstream regulator of Inc-ADCYAP1-2 transcription. Downstream of this event, Inc-ADCYAP1-2 interacts with the RNA helicase DHX36, a regulator of G-quadruplex-containing mRNAs. Inc-ADCYAP1-2 activation reduces DHX36 protein levels which is accompanied by decreased protein output from a subset of DHX36 mRNA targets. At the cellular level, these effects correlate with altered cell proliferation, migration, adhesion, and global translation. Our results suggest a Inc-ARRDC4-1 : Inc-ADCYAP1-2 : DHX36 regulatory cascade linking de-repression of LTR12-containing lincRNAs to reduced protein synthesis and altered cellular processes in somatic cells.

Keywords: long intergenic non-coding RNAs, U7 snRNA; transposable elements; LTR12 elements; transcription; gene expression regulation; DHX36 helicase; G-quadruplexes; translation.

SESSION 6:
**REGULATORY NETWORKS
ACROSS BIOLOGICAL
SYSTEMS**

PLENARY SPEAKER

LOSS OF A CONSERVED DISULFIDE BOND LINKS SPECIALIZED METABOLISM WITH PLANT IMMUNITY

Gopal Singh^{1*}, Himani Agrawal^{1*}, Mariola Piślewska-Bednarek¹,
Suthitar Ogawa², Chujia Jin², Anna Piasecka¹, Monidipa Bose¹,
Aleksander Strugała¹, Łukasz Marczak¹, Miłosz Ruszkowski¹,
Yoshitaka Takano² and Paweł Bednarek¹

¹ Institute of Bioorganic Chemistry, Polish Academy of Sciences, Noskowskiego 12/14, 61-704 Poznań, Poland;

² Laboratory of Plant Pathology, Graduate School of Agriculture, Kyoto University, Kyoto 606-8502, Japan.

Plants deploy specialized metabolism as a spatially controlled component of immunity. In *Arabidopsis thaliana*, the mitochondrial outer-membrane thio-glucosidase PENETRATION2 (PEN2/BGLU26) hydrolyses indole glucosinolates at attempted fungal entry sites, but the molecular features that distinguish PEN2 from related β -glucosidases remain unclear. We tested whether other EE-type thio-glucosidases can replace PEN2 when expressed in the *pen2-2* mutant and redirected to the same subcellular context. AtBGLU27 and the Brassica rapa brassinin-associated β -glucosidase BrBABG.a partially restored indole glucosinolate hydrolysis and resistance to *Colletotrichum tropicale*, whereas AtBGLU18, AtBGLU23 and AtBGLU28 did not accumulate as detectable proteins. Unlike PEN2, AtBGLU27 and BrBABG.a acted predominantly constitutively and displayed distinct substrate preferences, indicating that PEN2 carries additional regulatory features that couple metabolism to pathogen perception. Sequence, structural and phylogenetic analyses revealed that PEN2, BGLU27 and BABG proteins have lost conserved residues associated with secretory-pathway-dependent post-translational modifications, including a disulfide bond broadly retained in plant family-1 β -glucosidases. Reintroduction of this disulfide bond into PEN2 produced the intended covalent linkage but abolished glucosinolate-hydrolysing activity. The loss of this structural constraint is conserved across PEN2-related Brassicaceae proteins. These findings define an immune-associated thio-glucosidase lineage in which loss of a conserved disulfide bond enabled function outside the secretory pathway, while PEN2-specific regulation restricts defensive metabolite activation to pathogen contact sites.

Keywords: *β -glucosidases; glucosinolates; thio-glucosidases; plant immunity; specialized metabolism.*

STRUCTURAL AND MOLECULAR BASIS OF SPECIALIZED TRANSLATION MEDIATED BY THE RIBOSOME MRNA-BINDING CHANNEL

Davide Fraticelli¹, Disha-Gajanan Hiregange², Benjamin Weiss¹, Ariel Ogran¹, Anat Bashan², Ada Yanath², Rivka Dikstein¹

¹ Weizmann Institute, Department of Biomolecular Sciences, Rehovot, Israel

² Weizmann Institute, Department of Structural Biology, Rehovot, Israel

Translation is a major step of gene expression, yet the molecular mechanisms underlying transcript-specific regulation remain incompletely understood. Emerging evidence suggests that heterologous ribosome composition and modification are involved in the translation of specific mRNAs. Here, we investigate a previously underexplored regulatory mechanism inherent to the ribosome, in which certain ribosomal proteins within the small ribosomal subunit (40S) interact directly with mRNA and decode 5'UTR regulatory information to control translation. Using cryo-EM, translome profiling, and ribosome mutants impaired in RPS26/eS26 mRNA binding, we demonstrated that distinct mRNAs induce specific conformations within the mRNA channel, resulting in differential translation outcomes. We uncovered a previously unrecognized role for RPS26/eS26 in regulating initiation, scanning dynamics, and selective translation of transcripts, including replication-dependent histone mRNAs. These transcripts have very short 5'UTRs and suboptimal Kozak sequences yet exhibit robust translation activity that is RPS26/eS26-dependent. We identified a translational enhancer in histones 5'UTR, overlapping the predicted RPS26/eS26-binding sites. Exploiting these features, we designed a high-efficiency translational cassette with minimal leaky scanning, improving efficacy and safety for mRNA-based therapy. These findings suggest that transcript-specific regulatory information can be decoded through specific interactions within the ribosomal mRNA channel, revealing new principles of translational control with therapeutic potential.

Keywords: Ribosomal proteins, Ribosome specialization, mRNA translation, mRNA binding, RPS26, eS26, 5'UTR

PLENARY SPEAKER

INTERKINGDOM INTERACTIONS AND EPIGENOMIC PLASTICITY IN THE EVOLUTION OF SYMBIOTIC BACTERIAL GENOMES

Francesca Coscione¹, Camilla Fagorzi¹, Iacopo Passeri¹ and
Francesca Vaccaro¹, Alessio Mengoni¹

¹ Department of Biology, University of Florence, Italy

Understanding how bacterial genomes generate functional diversity in complex environments remains a central challenge in microbiology. Symbiotic systems provide a powerful framework to investigate how ecological interactions shape gene regulation, genome organization, and evolutionary trajectories. The nitrogen-fixing symbiosis between rhizobia and leguminous plants offers a compelling model to explore how bacterial adaptation emerges from the interplay between genomic architecture and environmental context.

Here, I discuss how epigenomic plasticity and interkingdom interactions contribute to the functional and evolutionary dynamics of the symbiotic bacterium *Sinorhizobium meliloti*. Genome-wide analyses of DNA methylation patterns reveal a highly dynamic and heterogeneous epigenomic landscape across its multipartite genome, supporting the existence of a “pan-epigenome” that may modulate gene expression and generate phenotypic variability [1]. Moreover, by examining genotype-by-genotype interactions between *S. meliloti*, host plants and soil fungi, extensive transcriptomic reprogramming in both partners are present which involve a large fraction of genes with unknown function, suggesting that interaction-dependent traits are embedded within the “unknome” and are largely invisible under standard laboratory conditions [2–4].

From an evolutionary perspective, these findings highlight how ecological interactions may expose and select for context-dependent gene functions, contributing to genome diversification. The multipartite genome of *S. meliloti*, shaped by horizontal gene transfer, provides a flexible substrate for novel function integration, while epistatic interactions among regulatory layers — including epigenetic modifications — may further constrain or enable adaptive responses. Gene function thus emerges not as an intrinsic property, but as a context-dependent feature shaped by networks of interactions across genomes and environments.

By integrating epigenomics and cross-omics approaches within ecologically relevant systems, this work frames symbiosis as a model to investigate how bacterial genomes evolve and function in interaction-rich environments, shedding light on hidden layers of regulation and evolution in microbial life.

Keywords: *Symbiotic bacteria; multipartite genome; unknown function genes; DNA methylation; biotic interactions.*

References

1. Passeri, I. et al. (2025). *Genome Biol. Evol.* 17
2. Vaccaro, F. et al. (2025). *Microbiol. Res.* 297, 128180
3. Vaccaro, F. et al. (2024). *Microbiol. Res.* 285, 127768
4. Fagorzi, C. et al. (2021). *mSystems* 6, 10–1128

INTRON-DEPENDENT REGULATION OF THE GLUCOSINOLATE TRANSPORTER GTR2

Adam T. Henriksen¹, Meike Burow¹ and Christa Kanstrup¹

¹ *Copenhagen Plant Science Centre, Department of Plant and Environmental Sciences, University of Copenhagen, Denmark*

Introns are an essential feature of eukaryotic genes, yet their functional contribution beyond RNA splicing remains poorly understood. Although introns are removed during mRNA maturation, they have been suggested to influence gene regulation and enhance gene expression at multiple levels, including transcription, mRNA processing, nuclear export and translation¹⁻³.

In this study, we investigate the role of introns in the context of the *Arabidopsis thaliana* glucosinolate transporter 2 (GTR2). GTR2 belongs to the Nitrate and Peptide transporter Family (NPF), part of the Major Facilitator Superfamily (MFS), a large and diverse group of membrane transporters. While many NPF members transport primary metabolites such as nitrate and peptides, GTR2 is specialized for the transport of the defense metabolites, glucosinolates, and plays a key role in their root-shoot translocation and seed loading. Despite detailed knowledge of GTR2s function and substrate specificity, little is known about how GTR2 is regulated. Previous work has shown that introns are required for full functional complementation of *gtr2* knockout plants, whereas the coding sequence achieved reduced complementation. As these constructs encode identical protein sequences, this suggests that introns influence GTR2 expression, protein abundance or function through regulatory mechanisms rather than changes in protein structure.

Building on these findings, our ongoing work aims to study how introns influence the function of GTR2. We are comparing intron-containing and intron-less GTR2 variants in planta to assess their impact on transcript accumulation, protein abundance, and transporter activity. These efforts continuously deepen our understanding of how transporter abundance and activity is regulated.

Keywords: *Introns; Regulation; Glucosinolate transporter 2.*

References

1. Hir H. L., Nott A., Moore M. J (2003). How introns influence and enhance eukaryotic gene expression. *Trends in Biochemical Sciences*.
2. Jo B-S., Choi S. S (2015). Introns: The Functional Benefits of Introns in Genomes. *Genomics & Informatics*.
3. Shaul O. (2017). How introns enhance gene expression. *Biochemistry and Cell Biology*.

SESSION 7:

**GENE REGULATION ACROSS
MOLECULAR AND
CELLULAR SCALES**

PLENARY SPEAKER

GENE REGULATION, EXPRESSION, AND METABOLIC FUNCTIONS OF MAJOR HDL-APOLIPOPROTEINS

Anca Violeta Gafencu¹

¹*Institute of Cellular Biology and Pathology "Nicolae Simionescu", Romanian Academy*

Lipoproteins are the plasma carriers of lipids in the blood, and their protein component, the apolipoproteins, was long thought to play a structural role in stabilizing the particles and mediating their interactions with the enzymes and receptors involved in lipid metabolism. However, many functions of these proteins have recently been uncovered. High-density lipoproteins (HDL) mediate cholesterol efflux, removing excess cholesterol from peripheral tissues and transporting it back to the liver. The main apolipoproteins of HDL, ApoA1, ApoA2, and ApoE, are synthesized primarily by the liver, with minor contributions from other tissues. Our data show that the stress factors Bisphenol A and LPS downregulate ApoA1 and ApoE, respectively, through engagement of NF- κ B signaling. AP-1 transcription factors are also involved in ApoE gene regulation, driving upregulation in the liver but downregulation in macrophages due to different distal regulatory mechanisms. Anti-inflammatory ligands such as glucocorticoids and transcription factors such as KLF4 and STAT1, increase ApoE expression by acting on proximal or distal regulatory elements. ApoA2 expression is controlled by HNF4 acting on the proximal promoter region, together with additional transcription factors such as RXR/TR β and SREBP, acting on distal promoter elements. Modulation of ApoA2 expression influences processes ranging from lipid metabolism to energy homeostasis. Taken together, the gene regulation of these apolipoproteins plays a central role in lipid metabolism, contributing to the maintenance of normal HDL levels and the preservation its atheroprotective properties, and may also extend to other metabolic processes, including glucose homeostasis and energy balance.

This work was supported by a project funded by UEFISCDI (PN-II ID_PCE-2011-3-0591 and project # 10CoEx/02/03.2026 within PNCDI IV), the European Union (NextGenerationEU, PNRR/2022/C9/MCID/I8, contract #760060, STROMA), and the Romanian Academy.

Keywords: *apolipoproteins; promoter; enhancer; gene regulation.*

TARGETING THE TRANSCRIPTION SYSTEM OF AFRICAN SWINE FEVER VIRUS FOR ANTIVIRAL DRUG DISCOVERY

Christopher Dulson¹, Simona Pilotto¹, Gwenny Cackett¹, Michal Sýkora¹, Sophia Hazlett¹, Christopher Waudby¹, Chris Netherton¹, Linda Dixon¹, Finn Werner¹

¹ University College London

Introduction: African Swine Fever Virus (ASFV) infects domestic pigs in most cases causing a lethal haemorrhagic fever in greater than 90% of cases. Outbreaks occur frequently in Europe, Africa and Asia, consequentially the swine farming industry has suffered devastating losses which in turn threatens global food security. Currently, there are no antiviral drugs approved for use against ASFV. Therefore, we are investigating promising therapeutic targets in the viral transcription system, which includes the viral DNA dependent RNA polymerase (RNAP). **Objective:** To recombinantly produce active viral RNAP and develop assays for the discovery of inhibitors. **Methodology:** Recombinant production of the eight subunit RNAP core and transcription factors and structural determination by cryo-electron microscopy. The viral RNAP was also active at in vitro transcription and compounds were screened for inhibitory effects. The hit inhibitory compounds identified were further characterised for the ability to bind the viral RNAP using ligand observed nuclear magnetic resonance (NMR). **Results:** The structure of the recombinant eight subunit viral RNAP resembles that of eukaryotic RNAP II, however greater than two thirds of the sequence is not conserved offering the potential for selective inhibition. A high-throughput in vitro transcription assay was developed and a series of inhibitors of viral transcription were discovered with IC₅₀ 25-50 µM with selectivity for inhibition of ASFV RNAP activity over eukaryotic RNAP II. Additionally, the inhibitors were observed to bind the ASFV RNAP with two of which exhibiting competitive binding. **Conclusions:** Active recombinant ASFV RNAP was produced, the structure was determined and selective inhibitors of transcription discovered. Further derivatisation of these inhibitors guided by structural studies has the potential to develop an efficient antiviral drug which can limit the spread of outbreaks and bolster global food security.

Keywords: African Swine Fever Virus; RNA Polymerase; Transcription; Drug Discovery; Ligand Observed Nuclear Magnetic Resonance; Single Particle Cryo-Electron Microscopy.

Reference

1. Pilotto, S., Sýkora, M., Cackett, G., Dulson, C. and Werner, F., 2024. Structure of the recombinant RNA polymerase from African Swine Fever Virus. *Nature Communications*, 15(1), p.1606.
2. Cackett, G., Sýkora, M., Portugal, R., Dulson, C., Dixon, L. and Werner, F., 2024. Transcription termination and readthrough in African swine fever virus. *Frontiers in Immunology*, 15, p.1350267.
3. Cackett, G., Portugal, R., Matelska, D., Dixon, L. and Werner, F., 2022. African swine fever virus and host response: transcriptome profiling of the Georgia 2007/1 strain and porcine macrophages. *Journal of virology*, 96(5), pp.e01939-21.
4. Cackett, G., Sýkora, M. and Werner, F., 2020. Transcriptome view of a killer: African swine fever virus. *Biochemical Society Transactions*, 48(4), pp.1569-1581.

PLENARY SPEAKER

EXPLAINABLE AI IDENTIFIES H3K18AC AS A NEW MARKER OF ACTIVE ENHANCERS

Khizra Maqsood^{1,2,3,†}, Duarte Polvora Brandao^{1,3,†}, Jareth Wolfe^{1,2,4}, Bhavana Kayyar¹, Catalin-George Clinciu¹, Roxana Andreea Bosnea¹, Olivia A. Grant^{1,4}, Fanny Boulet^{1,3}, Christopher G. Bell^{3,5}, Gabriella Ficuz^{3,6}, Madapura M. Pradeepa^{1,3}, Hani Hagraas^{2*}, Nicolae Radu Zabet^{1,3,4,*}

¹ Blizard Institute, Barts and The London School of Medicine and Dentistry, Queen Mary University of London, London, E1 2AT, UK

² School of Computer Science and Electronic Engineering, University of Essex, Colchester, CO4 3SQ, UK

³ Centre for Epigenetics, Queen Mary University of London, London, E1 2AT, UK

⁴ School of Life Sciences, University of Essex, Colchester, CO4 3SQ, UK

⁵ William Harvey Research Institute, Queen Mary University of London, London, UK, EC1M 6BQ

⁶ Centre for Haemato-Oncology, Barts Cancer Institute, Queen Mary University of London, London, UK, EC1M 6BQ

Enhancers are non-coding regions of DNA that regulate transcription, yet the mechanisms underlying enhancer activity remain incompletely understood. Histone modifications and chromatin accessibility are widely used to predict candidate enhancers, but most studies focus on H3K27ac, H3K4me1 and/or ATAC-seq only. Here, we trained several AI models (Convolutional Neural Networks (CNN), eXtreme Gradient Boosting (XGBoost), Logistic Regression (LR) and type2 Fuzzy Logic System (type2-FLS)) to predict enhancers across different human and mouse cell lines using multiple epigenetic datasets. All models display mixed performances, with type2-FLS generalising better in cell lines unseen during training (despite a drop in performance), while the others performing better on the withheld data in cells they were trained on. Crucially, type2-FLS identified H3K18ac as an important enhancer mark. All models predict hundreds of thousands of candidate enhancers, with approximately 100 thousand detected by multiple models. We validated some of these novel enhancers by both global epigenetic perturbations (targeting H3K18ac) and directed epigenetic rewriting (CRISPRi). Interestingly, seven epigenetic marks in humans and five in mouse (including H3K18ac) are sufficient to annotate enhancers without losing accuracy. Overall, we identified H3K18ac as a novel epigenetic modification of mammalian enhancers and predicted candidate enhancers in multiple human and mouse cell lines.

Keywords: Gene regulation; cis-regulatory elements; epigenetics; Artificial Intelligence; H3K18ac; Transposable Elements.

SESSION 8:
**MOLECULAR REGULATION,
PROTEINS & DISEASE**

PLENARY SPEAKER

THE ROAD TO CHEMORESISTANCE: DECODING EARLY ADAPTATION IN 3D MELANOMA MODELS

Alina Seserman¹

¹ Group of Nanomedicine, Faculty of Medical and Health Sciences, Babeş-Bolyai University, Cluj-Napoca, ROMANIA

Despite therapeutic advances, resistance remains a major challenge in melanoma. We investigated early adaptive responses to doxorubicin (DOX) in B16.F10 melanoma spheroids exposed to two sub-inhibitory treatments ($\sim$ IC₃₀) separated by a drug-free recovery period. Multi-level molecular analyses revealed a biphasic response: initial cell-cycle arrest followed by survival-associated reprogramming involving Notch1 signaling, angiogenesis, and ECM remodeling. DOX re-exposure reinforced a pro-invasive phenotype, with increased Aqp1, VEGF, Ackr3, MMP-2, and MMP-9 activity. These findings highlight early adaptive pathways underlying chemoresistance and support melanoma spheroids for identifying potential targets for therapeutic intervention.

PROTEINS IN THE PIPES: WASTEWATER METAPROTEOMICS FOR PUBLIC HEALTH MONITORING

Claudia Tugui¹, Willem van Holthe¹, Filine Cordesius¹, Mark van Loosdrecht¹, Martin Pabst¹

¹*Department of Biotechnology, Delft University of Technology, 2629 HZ Delft, The Netherlands*

Wastewater-based surveillance is an increasingly important approach for monitoring infectious diseases, antimicrobial resistance, and population-level exposure to pharmaceuticals and environmental contaminants. While current surveillance efforts primarily focus on small molecules and nucleic acids, wastewater also contains a rich and largely unexplored proteomic landscape. Despite recent advances in environmental proteomics, routine large-scale monitoring of protein biomarkers in wastewater remains limited, largely due to the complexity of the matrix. Raw wastewater comprises a heterogeneous mixture of organic and inorganic matter, microorganisms, cellular debris, and chemical pollutants, posing significant analytical challenges.

Here, we introduce a high-throughput wastewater metaproteomics workflow that combines efficient protein extraction using a hybrid FASP and in-solution digestion strategy with HPLC-MS/MS-based proteomic analysis and an optimized data-processing pipeline. This integrated approach enables robust and accurate profiling of complex wastewater proteomes of both microbial and human origin. The bioinformatic workflow leverages de novo peptide sequencing to tailor large public protein sequence databases, thereby maximizing metaproteomic coverage across diverse taxa. Applying this workflow, we analyzed wastewater samples collected over a three-month period from two wastewater treatment plants, demonstrating its suitability for longitudinal, population-level surveillance and overcoming key matrix-related challenges.

Applying this workflow to wastewater samples collected, we identified a stable core microbiome encompassing diverse microbial taxa, including gut-associated bacteria and potential opportunistic pathogens. In addition, nearly 200 human proteins were detected, including candidate population-level health biomarkers such as immunoglobulins, uromodulin, and cancer-associated proteins. These findings demonstrate the potential of wastewater metaproteomics as a complementary tool for public health surveillance.

Keywords: *human proteins; mass-spectrometry; metaproteomics; pathogens; wastewater.*

References

1. C.G. Tugui, F. Cordesius, W. van Holthe, M.C. van Loosdrecht, M. Pabst – Wastewater metaproteomics: tracking microbial and human protein biomarkers, ISME Communications, 2025 Dec 18, 6(1):ycaf243, DOI: 10.1093/ismeco/ycaf243

SESSION 9:
**FROM MOLECULAR
NETWORKS TO SYSTEMS
BIOLOGY**

PLENARY SPEAKER

GENE FUNCTION PREDICTION WITH KNOWLEDGE GRAPHS

Mads Harder Møller¹, Peng Ken Lim, Ruoxi Wang, Shan Chun Lim, Jenet Princy Antony Velankanni, Manoj Itharajula², Marek Mutwil¹

¹ Department of Plant and Environmental Sciences, University of Copenhagen, Thorvaldsensvej 40, 1871 Frederiksberg, Denmark

² School of Biological Sciences, Nanyang Technological University, 60 Nanyang Drive, 637551, Singapore

Despite decades of research, only about 12% of Arabidopsis genes are fully experimentally characterized, and the rate of new functional discoveries has plateaued, leaving most genes across the plant kingdom without known functions. Two bottlenecks stand out: most functional knowledge is locked in millions of publications in a machine-unreadable form, and standard co-expression networks blur condition-specific signals by averaging across all samples. I will present two complementary resources addressing these bottlenecks. First, PlantConnectome, a knowledge graph constructed by processing over 200,000 plant science articles with large language models, captures millions of relationships between genes, metabolites, stresses, tissues, and other biological entities at approximately 90% accuracy. It recovers thousands of protein-protein interactions and transcription factor-target relationships absent from existing databases, substantially expanding the gold standards available for gene function prediction. Second, TEA-GCN, a two-tier ensemble approach, partitions public transcriptomes into condition-specific clusters before aggregating multiple correlation metrics, yielding gene co-functional and co-regulatory networks that outperform conventional co-expression methods and annotate gene pairs with the experimental contexts that drive their association. I will discuss how cross-species conservation strengthens functional inferences, and how these resources feed into graph neural networks for gene function prediction. Finally, I will present our vision for AI-driven biological discovery, in which knowledge graphs, comparative omics across the plant kingdom, and experimental validation form a closed loop for accelerating gene function discovery and engineering stress-resilient crops. All resources are freely available at plant.connectome.tools.

Keywords: *knowledge graphs; gene function prediction; co-expression networks; large language models; plant stress resilience.*

KEYNOTE SPEAKER

MOLECULAR MECHANISMS FROM SPATIAL OMICSNikolaus Rajewsky^{1,2}

¹ Laboratory for Systems Biology of Regulatory Elements, Berlin Institute for Medical Systems Biology (MDC-BIMSB), Max-Delbrück-Centrum for Molecular Medicine in the Helmholtz Association (MDC), Berlin, Germany

² Charité-Universitätsmedizin, Berlin, Germany

Gene expression in cells within tissues is of key importance to understand and control the space-time trajectory of diseases. I will summarize the current state-of-the-art to quantify gene expression, at sub-cellular resolution, across tissues, including our own approach (Schott et al Cell 2024) and unpublished improvements towards long-read sequencing and analyses of clinical samples. The quality of these data is becoming so good that computational analyses can reveal the molecular mechanisms that are driving phenotypes – a profound improvement of computational biology. I will also talk about our “Google for RNA” – a new way to search, instantly, for RNA sequences in the universe of published “Cell Atlases” – comprising ~70 million single cells, thousands of experiments, and hundreds of diseases. With this approach we are working towards a “universal coordinate system” for human biology, enabling to instantly map a new experiment into the space of existing data and thus enabling to learn (including AI) new biology and to discover clinically actionable properties of samples².

Keywords: Gene Expression, RNA, Spatial Transcriptomics.

References

1. Schott M., León-Periñán D., Splendiani E., Strenger L., Licha J. R., Pentimalli T. M., Schallenberg S., Alles J., Samut Tagliaferro S., Boltengagen A., Ehrig S., Abbiati S., Dommerich S., Pagani M., Ferretti E., Macino G., Karaiskos N., and Rajewsky N. Open-ST: High-resolution spatial transcriptomics in 3D. Cell (2024). DOI: 10.1016/j.cell.2024.05.055
2. León-Periñán D., Karaiskos N. and Rajewsky N. Ultrafast and reference-free sequence discovery in single-cell data. Nature (2026). <https://doi.org/10.1038/s41586-026-10975-w>

POSTER EXHIBITION:
**POSTER SESSION AND
NETWORKING**

P01_BIOACTIVE DIETARY COMPONENTS IN THE REGULATION OF HOMOCYSTEINE METABOLISM AND BMI: A CASE STUDY

Camelia Râtea, Mitogenix Innovations Targu-Mures.

P02_DETECTION OF BIOMOLECULES ON CITRATE-CAPPED SILVER NANOPARTICLES: COMPARISON BETWEEN COLLOIDAL AND DRIED SUBSTRATE CONFIGURATIONS

Andreea Türke, Faculty of Physics, Babeş-Bolyai University, Cluj-Napoca.

P03_THE EFFECT OF LIPOSOME LIPID MEMBRANE DEFORMATION ON ITS SWELLING TIME

Valentin Niculescu, National Institute - INFLPR, Atomistilor 409, Magurele, Ilfov, Romania.

P04_A TRANSCRIPTOMIC FRAMEWORK FOR IDENTIFYING MOLECULAR SIGNATURES OF MERCURY AND LINDANE STRESS IN NATURALLY ADAPTED LEGUME GENOTYPES

Mihaela Gălean, Doctoral School of Integrative Biology, Faculty of Biology and Geology, Babeş-Bolyai University, Cluj-Napoca, Romania; Centre for Systems Biology, Biodiversity and Bioresources (3B), Babeş-Bolyai University, Cluj-Napoca, Romania.

P05_DIETARY REGULATION OF INFLAMMATORY CYTOKINE OUTPUT ALONG THE GUT-LIVER AXIS: FEWER PRODUCER CELLS, UNCHANGED PER-CELL SIGNAL

Alena Bohdanecká, Institute for Clinical and Experimental Medicine (IKEM), Prague, Czech Republic; First Faculty of Medicine, Charles University, Prague, Czech Republic.

P06_SELENIUM NANOPARTICLE IDENTITY AND CELLULAR RESPONSE: TOWARD REDOX-SENSITIVE MICRORNA INVESTIGATION

Vlad Andrei Moldovan, Doctoral School of Biomedical Sciences, University of Oradea, 410087 Oradea, Romania

P07_EVALUATION OF THE GENE ENCODING MERCURIC REDUCTASE IN THE RHIZOSPHERE OF TWO PLANTS SPECIES NATIVE ON A HISTORICALLY MERCURY-CONTAMINATED SITE

Mihai C. Grimm, Doctoral School of Integrative Biology, Babeş-Bolyai University, Cluj-Napoca, Romania; Centre for Systems Biology, Biodiversity and Bioresources (3B), Babeş-Bolyai University, Cluj-Napoca, Romania.

P08_THE INTERACTION BETWEEN VDR POLYMORPHISMS, VITAMIN D STATUS AND MYOCARDIAL INFARCTION

Erica Baidauz, Facultatea de Biologie, Universitatea din Bucureşti, România.

P09_BACTERIAL AND FUNGAL COMMUNITY RESPONSE AFTER 20 YEARS OF NATURE-BASED REMEDIATION AT MOLDOVA NOUĂ, A FORMER COPPER MINING SITE

Emanuela D. Tiodar, Centre for Systems Biology, Biodiversity and Bioresources (3B), Babeş-Bolyai University, Cluj-Napoca, Romania.

P10_TESTING THE RELATIONSHIP BETWEEN THE OXYTOCIN RECEPTOR (OXTR) AND COLORECTAL CANCER IN A COHORT OF SUBJECTS FROM ROMANIA

Bratu Cristina-Mihaela, Faculty of Biology, University of Bucharest, Romania.

P11_MUTATIONAL PROFILE OF RAS GENES IN COLORECTAL CANCER: A MOLECULAR ANALYSIS OF A ROMANIAN PATIENT COHORT

Alexandra Chelaru, Faculty of Biology, University of Bucharest, Bucharest, Romania.

P12_PHYLOGENETIC ANALYSIS OF MERCURIC REDUCTASES REVEALS DISTINCT CLUSTERS OF PUTATIVE FUNGAL HOMOLOGUES

Cristina Lorena Văcar, Centre for Systems Biology, Biodiversity and Bioresources (3B), Babeş-Bolyai University, Cluj-Napoca, Romania.

BIOACTIVE DIETARY COMPONENTS IN THE REGULATION OF HOMOCYSTEINE METABOLISM AND BMI: A CASE STUDY

Camelia Râtea¹

¹Mitogenix Innovations Targu-Mures

Objectives: This study evaluated the impact of personalized functional foods and targeted nutritional interventions on serum homocysteine levels and Body Mass Index (BMI) response in an overweight patient with hyperhomocysteinemia.

Materials and Methods: A case study was conducted over a two-year period (April 23, 2021 – May 11, 2023) focusing on a 39-year-old overweight male with confirmed elevated serum homocysteine ($>15 \mu\text{mol/L}$). The evaluation consisted of two dietary phases separated by an 8-month period of dietary relapse. The first 9-month intervention included supplementation with Quatrefolic (1 mg/day), Choline (250 mg/day), Omega-3 fatty acids, and an 80% plant-based diet. The second 8-month intervention reintroduced the protocol with additions of beetroot/kale juice, a nitric oxide precursor complex, and standardized daily antioxidant intake. Biomarkers and clinical symptoms were regularly monitored.

Results: At baseline, the person had a homocysteine level of $50 \mu\text{mol/L}$ and a BMI of 28.73 kg/m^2 . After the first intervention, homocysteine decreased to $21.3 \mu\text{mol/L}$ and BMI reached 25.0 kg/m^2 , resolving chronic fatigue, migraines, and insomnia. Discontinuation of the protocol led to a relapse (homocysteine: $50 \mu\text{mol/L}$, BMI: 28.6 kg/m^2). Following the second functional food-based intervention, homocysteine normalized to $11.2 \mu\text{mol/L}$ and BMI to 24.0 kg/m^2 , resulting in complete symptom remission.

Conclusions: Personalized, functional food-based interventions targeting methylation and oxidative stress are effective in lowering homocysteine and optimizing BMI. Long-term dietary adherence and lifestyle maintenance are crucial for managing chronic metabolic conditions.

Keywords: *Hyperhomocysteinemia, Functional Foods, Overweight, Nutritional Intervention, Methylation.*

References

1. Homocysteine Lowering Trialists Collaboration. (1998). Lowering blood homocysteine with folic acid based supplements: Meta-analysis of randomized trials. *BMJ*, 316(7135), 894–898.
2. O'Leary, F., & Samman, S. (2010). Vitamin B12 in health and disease. *Nutrients*, 2(3), 299–316.
3. Robinson, K., Arheart, K., Refsum, H., Brattström, L., Boers, G., et al. (1998). Low circulating folate and vitamin B6 concentrations: Risk factors for stroke, peripheral vascular disease, and coronary artery disease. *Circulation*, 97(5), 437–443.
4. Konstantinova, S. V., Tell, G. S., Vollset, S. E., Ulvik, A., & Ueland, P. M. (2008). Divergent associations of plasma choline and betaine with components of metabolic syndrome in middle age and elderly men and women. *Journal of Nutrition*, 138(5), 914–920.
5. Huang, T., Tucker, K. L., & Lee, Y. (2010). Dietary patterns, n-3 fatty acids intake, and plasma homocysteine concentrations in the US population: NHANES 1999–2002. *American Journal of Clinical Nutrition*, 92(2), 399–406.
6. Kumar, A., Palfrey, H. A., Pathak, R., et al. (2017). The metabolism and significance of homocysteine in nutrition and health. *Nutrition & Metabolism*, 14, 78.

POSTER ABSTRACT_P02

DETECTION OF BIOMOLECULES ON CITRATE-CAPPED SILVER NANOPARTICLES: COMPARISON BETWEEN COLLOIDAL AND DRIED SUBSTRATE CONFIGURATIONS

Andreea Türke¹, Nicolae Leopold¹, Ștefania D. Iancu¹

¹Faculty of Physics, Babeș-Bolyai University, Kogălniceanu 1, 400084, Cluj-Napoca

Analytes were added to the colloid as 10 μ L aqueous solutions at concentrations of 10^{-4} M for uric acid, hypoxanthine, and creatine, and 10^{-3} M for urea and salicylic acid. Spectra were recorded with Ca^{2+} , Cl^- , or $\text{Ca}^{2+} + \text{Cl}^-$, which modify citrate coverage and analyte adsorption. Salicylic acid and creatine produced detectable signals mainly with Ca^{2+} , whereas chloride generated Ag-Cl spectral features and reduced analyte band intensities. Hypoxanthine and uric acid yielded intense spectra, particularly in the combined ionic system, although several bands shifted or disappeared. Urea was not reliably detected.

Two solid substrates were evaluated: a centrifuged cit-AgNP layer and a dried colloidal droplet deposited on glass. On both substrates, Ca^{2+} was unnecessary for adsorption of anionic analytes. Nevertheless, SERS intensities were lower than in colloidal systems, and citrate partially masked analyte bands. The centrifuged layer showed strong citrate contributions, probably because citrate accumulated between nanoparticles during centrifugation. By contrast, the simply dried layer exhibited reduced citrate interference and enabled clearer detection of salicylic acid, creatine, hypoxanthine, and uric acid. Although its spatial signal distribution was less uniform, analyte features were more pronounced.

Overall, ionic composition and substrate preparation strongly affected molecular adsorption and SERS spectral quality. The simply dried cit-AgNP substrate provided favorable conditions for detecting biologically relevant molecules. Controlling these adsorption processes may reduce metabolic interference in biofluids and improve nucleic-acid accessibility to plasmonic surfaces. These findings provide a basis for future SERS studies targeting circulating cell-free DNA and DNA-associated epigenetic biomarkers relevant to early cancer diagnosis.

Keywords: SERS; silver nanoparticles; adsorption; dried substrates; biomolecules.

POSTER ABSTRACT_P03

THE EFFECT OF LIPOSOME LIPID MEMBRANE DEFORMATION ON ITS SWELLING TIME

Dumitru Popescu¹, Diana R. Radnef-Constantin², Valentin I. R. Niculescu³ and Agneta A. Mocanu⁴

¹"Gheorghe Mihoc-Caius Iacob" Institute of Mathematical Statistics and Applied Mathematics of Romanian Academy, Calea 13 Septembrie, 13, Bucharest, Romania.

²Astronomical Institute of the Romanian Academy, Cutitul de Argint 5, sector 4, Bucharest, Romania, ghe12constantin@yahoo.com

³National Institute - INFLPR, Atomistilor 409, Magurele, Ilfov, Romania.

⁴Hyperion University of Bucharest, Romania.

In this paper we consider an unilamellar liposome (lipid vesicle) filled with aqueous solution of osmotic solute which is introduced in a large box filled with an aqueous medium. Due to the process of osmosis, the liposome swells until, suddenly, a transbilayer pore appears. This is the critical state of the liposome. Some of the internal solution leaks through this pore and the liposome relaxes until its initial size. The swelling starts again and the liposome begins a new cycle and so on. The evolution of the liposome is a dynamic and cyclical process. The swelling of the liposome is described by a differential equation and algebraic one. The appearance of the pore changes the evolution of the liposome. All the processes which contribute to the liposome relaxing are described by three differential equations. This system of differential equations describes the evolution of the pulsatory liposome during a cycle and can be integrated using numerical and analytical [1] methods. After performing a number of cycles, the pulsatory liposome stops. During each cycle, the pulsatory liposome releases a certain amount of osmotic solute. The osmotic solute can be a pharmacological substance, genetic material or a special substance. So the pulsatory liposome can be used in biomedical applications. It can be assimilated to a two strokes biophysical engine. We investigated the effect of liposome membrane deformation during swelling on its swelling time [2].

Keywords: *Pulsatory liposome; biophysical engine; swelling time.*

References

1. Radnef-Constantin D R et al., 2026, U.P.B. Sci. Bull., Series A, 88, 3 (in press)
2. Constantin D R, Popescu D, 2024, Romanian Journal of Physics 69, 701

POSTER ABSTRACT_P04

A TRANSCRIPTOMIC FRAMEWORK FOR IDENTIFYING MOLECULAR SIGNATURES OF MERCURY AND LINDANE STRESS IN NATURALLY ADAPTED LEGUME GENOTYPES

Mihaela Gălean^{1,3}, Csaba Timár², Emanuela D. Tiodar³, Cristina L. Văcar³, Zoltan R. Balázs^{1,2}, Chiel Jonker⁴, Simona Radutoiu⁵, Horia L. Banciu^{1,2,3}, Dorina Podar^{2,3}

¹Doctoral School of Integrative Biology, Faculty of Biology and Geology, Babeş-Bolyai University, Cluj-Napoca, Romania;

²Department of Molecular Biology and Biotechnology, Faculty of Biology and Geology, Babeş-Bolyai University, Cluj-Napoca, Romania;

³Centre for Systems Biology, Biodiversity and Bioresources (3B), Babeş-Bolyai University, Cluj-Napoca, Romania;

⁴Department of Population Health Sciences, Institute for Risk Assessment Sciences, Utrecht University, Utrecht, The Netherlands;

⁵Department of Molecular Biology and Genetics, Aarhus University, Aarhus, Denmark.

Soil contamination with mercury (Hg) and γ -hexachlorocyclohexane (γ -HCH, lindane) poses a major threat to living organisms, disrupting plant metabolism and growth while impairing the nervous, immune, and reproductive systems of animals. Despite high contaminant concentrations, certain plants can thrive in such environments in association with specialised resident bacteria and fungi, thereby acting as pioneer species of land revegetation. However, the molecular mechanisms underlying Hg or γ -HCH stress have not yet been elucidated, with only generic plant stress responses being well characterised. Moreover, transcriptomic studies have predominantly relied on non-adapted model or crop species subjected to experimental contaminant exposure, and little is known about the transcriptional responses of naturally adapted species under long-term contaminant pressure. The present study aims to characterise the molecular basis of Hg and γ -HCH resistance in a perennial legume naturally occurring at historically contaminated sites. Three contrasting genotypes, originating from Hg-contaminated, γ -HCH-contaminated, and uncontaminated (control) environments, were propagated through vegetative cuttings to preserve their genetic identity. An optimized soil-based exposure system was used for 5 weeks of cutting establishment. Plants were then exposed to environmentally relevant concentrations of Hg (25 ppm) or γ -HCH (0.183 ppm) for seven days, before roots were harvested for RNA extraction. RNA sequencing and downstream bioinformatic analyses are currently underway. We hypothesize that long-term adapted genotypes will exhibit distinct or attenuated transcriptional responses than the non-adapted genotype, reflecting mechanisms associated with contaminant resistance. Rhizosphere microbiome analyses of the plant genotypes growing at these sites showed distinct microbial clustering (beta-diversity, ANCOM-BC2), suggesting site-specific microbial adaptation that may complement the plant's own transcriptional strategies. Redundancy analysis (RDA) identified site-specific physico-chemical properties associated with microbial community assemblage. Differentially expressed plant genes (DEGs) will be identified to characterise genotype and contaminant specific responses, providing insights into potentially long-term adaptation. The transcriptomic dataset may support the future development of phytomanagement strategies.

Keywords: soil contamination, plant resistance, phytoremediation, rhizosphere, microbiomes.

Funding: This work is supported by a grant of the Ministry of Research, Innovation and Digitization, CNCS - UEFISCDI, project number PN-IV-P1-PCE-2023-2016, contract no: 76PCE, within PNCDI IV.

POSTER ABSTRACT_P05

DIETARY REGULATION OF INFLAMMATORY CYTOKINE OUTPUT ALONG THE GUT-LIVER AXIS: FEWER PRODUCER CELLS, UNCHANGED PER-CELL SIGNAL

Alena Bohdanecká^{1,3}, Motúzová V.², Kverka M.², Kraus M.², Heczková M.¹, Brátová M.¹, Bartelik O.², Cahová M.¹

¹ Institute for Clinical and Experimental Medicine (IKEM), Prague, Czech Republic

² The Institute of Microbiology of the Czech Academy of Sciences (IMIC CAS), Prague, Czech Republic

³ First Faculty of Medicine, Charles University, Prague, Czech Republic

Background. Cytokine output can be set either by the number of signalling-competent cells or by the amount each cell produces, and which level a nutritional input acts on is rarely resolved. We addressed this in *Mdr2*^{-/-} (*Abcb4*^{-/-}) mice, a sclerosing cholangitis model in which a gluten-free diet (GFD) attenuates liver injury by an unknown mechanism.

Methods. Mice of both sexes received GFD or standard diet from four weeks of age and were analysed at 20 weeks (n = 44). Flow cytometry quantified in parallel the proportion of cells producing IFN- γ , IL-17A or TNF- α and the per-cell production intensity, in CD4⁺, CD8⁺, $\gamma\delta$ T, NK and NKT populations from liver, mesenteric lymph nodes (MLN) and spleen, at baseline and after PMA/ionomycin stimulation. Linear models included diet, sex and acquisition day.

Results. GFD reduced the proportion of cytokine-producing cells (39 of 49 parameters in liver, $p < 0.001$), whereas per-cell intensity was unchanged (median ratio 1.00) and varied without directional consistency. Effect size followed an ordered gradient from the site of exposure, MLN > liver > spleen, in both basal and stimulated states. Females showed broader basal engagement of hepatic lymphocytes without higher per-cell output. In $\gamma\delta$ T cells, GFD affected IL-17A in opposite directions in males and females.

Conclusions. A dietary input tunes inflammatory signalling by contracting the pool of cytokine-competent cells rather than by changing per-cell signal amplitude, along a gradient from gut to liver. Liver RNA sequencing from the same animals is under way.

Keywords: Sclerosing cholangitis; *Mdr2*^{-/-} (*Abcb4*^{-/-}) mice; Gluten-free diet; Cytokine-producing cells; IFN- γ ; IL-17A; TNF- α ; Mesenteric lymph nodes; Sex differences.

POSTER ABSTRACT_P06

SELENIUM NANOPARTICLE IDENTITY AND CELLULAR RESPONSE: TOWARD REDOX-SENSITIVE MICRORNA INVESTIGATION

Vlad Andrei Moldovan¹, Simona Ioana Vicaș^{1,2}, Monica Baia³ and Agnieszka Śmieszek⁴

¹ Doctoral School of Biomedical Sciences, University of Oradea, 410087 Oradea, Romania

² Faculty of Environmental Protection, University of Oradea, 26 Gen. Magheru Street, 410048 Oradea, Romania

³ Faculty of Physics, Babeș-Bolyai University, 1 M. Kogălniceanu Street, 400084 Cluj-Napoca, Romania

⁴ Department of Pharmacology and Toxicology, Wrocław University of Environmental and Life Sciences, 50-375 Wrocław, Poland

Selenium nanoparticles (SeNPs) are redox-active nanomaterials whose biological effects depend strongly on synthesis route and physicochemical properties. Published evidence linking SeNPs to microRNA regulation converges on the same redox-sensitive hubs, yet employs particles of unrelated origin, size and surface chemistry, leaving the relationship between physicochemical descriptors and gene-regulatory outcomes undefined [1]. Reproducible formulations are therefore required before such effects can be evaluated.

This study compared SeNPs synthesized by ascorbic acid reduction of sodium selenite with particles obtained using aqueous extracts of *Lentinula edodes*. Nanoparticle formation and colloidal stability were evaluated by ultraviolet-visible spectroscopy, dynamic light scattering, polydispersity index and zeta potential measurements, and selected formulations were subsequently assessed for metabolic viability in tumor and non-tumor adherent cell lines.

Preliminary results showed that the synthesis route influenced SeNP size distribution, dispersity, surface charge and colloidal stability. Chemically synthesized and extract-mediated nanoparticles exhibited distinct physicochemical profiles, supporting the selection of representative formulations for subsequent cellular assessment. Initial screening indicated a formulation- and concentration-dependent cellular response. In addition, intrinsic absorbance of some SeNP dispersions overlapped with the detection range of the viability assay, demonstrating the importance of particle-only controls for reliable data interpretation.

Based on the redox-active nature of selenium and on the observed formulation-dependent cellular responses, we hypothesize that physicochemically distinct SeNP populations may differentially affect redox-sensitive signaling pathways and, consequently, the expression of microRNAs involved in oxidative stress adaptation. Candidate targets include the Nrf2-related miR-200a axis, NF-κB-associated miR-21, miR-155 and miR-146a, and p53-regulated miR-34a and miR-15a/16. This hypothesis will be tested by correlating intracellular oxidative status with microRNA expression determined by RT-qPCR.

The identification of stable and reproducible formulations therefore represents an essential step toward investigating SeNP-mediated modulation of redox-sensitive microRNA networks.

Keywords: *colloidal stability; green synthesis; microRNA; redox signaling; selenium nanoparticles.*

References

[1] Moldovan VA, Cavalu SD, Baia M, Leopold LF, Laslo V, Śmieszek A, Vicaș SI, 2026, Journal of Trace Elements in Medicine and Biology, 97, 127925. doi:10.1016/j.jtemb.2026.127925

POSTER ABSTRACT_P07

EVALUATION OF THE GENE ENCODING MERCURIC REDUCTASE IN THE RHIZOSPHERE OF TWO PLANTS SPECIES NATIVE ON A HISTORICALLY MERCURY-CONTAMINATED SITE

Mihai C. Grimm^{1,3}, Emanuela D. Tiodar^{2,3}, Horia L. Banciu^{2,3}, Dorina Podar^{2,3}

¹Doctoral School of Integrative Biology, Babeş-Bolyai University, Cluj-Napoca, Romania;

²Department of Molecular Biology and Biotechnology, Faculty of Biology and Geology, Babeş-Bolyai University, Cluj-Napoca, Romania;

³Centre for Systems Biology, Biodiversity and Bioresources (3B), Babeş-Bolyai University, Cluj-Napoca, Romania

Mercury (Hg) pollution represents a serious risk to both ecosystem and human health. Almost 10% of European soils exceed the threshold of 100 µg kg⁻¹ of Hg¹, and with estimated global release of 2200 Mg of Hg from anthropogenic activities per year², there is an urgent need for its decontamination. Sustainable and non-destructive techniques to remediate large areas that are cost-effective are emerging as suitable technologies. Microorganisms-assisted phytoremediation uses the ability of plants native to contaminated sites and their associated microorganisms to remediate soils. Central to this approach is the microbial resistance largely mediated by the mercuric reductase encoded by merA gene, by converting ionic mercury, Hg²⁺, to a less toxic form, Hg⁰. This study aimed to quantify by qPCR the merA gene in the rhizosphere of the two most dominant herbaceous plant species native to a highly Hg-polluted site (*Lotus tenuis* and *Diplotaxis muralis*). Gene copy numbers were normalized per unit soil mass.

merA was present in 83% of the *D. muralis* rhizosphere samples, while in *L. tenuis* it was present in all samples. For *L. tenuis*, samples from a control site were collected and merA was absent in all samples with one exception.

These findings offer preliminary evidence that microbial resistance to mercury from the rhizosphere of different plant species varies within the same polluted site. Expected outcome: identification of plant species suitable for phytoremediation techniques by assessing the Hg-resistance of their associated rhizosphere.

Keywords: *Diplotaxis muralis*; *Lotus tenuis*; merA; bioremediation; phytoremediation.

Acknowledgements: This work was supported by a grant from the Ministry of Research, Innovation and Digitization, CNCS - UEFISCDI, project number PN-IV-P1-PCE-2023-2016, contract no. 76PCE/2025 within PNCDI IV.

References

1. Panagos, P., Jiskra, M., Borrelli, P., Liakos, L. & Ballabio, C. Mercury in European topsoils: Anthropogenic sources, stocks and fluxes. *Environ. Res.* 201, 111556 (2021).
2. Sonke, J. E. et al. Global change effects on biogeochemical mercury cycling. *Ambio* 52, 853–876 (2023).

POSTER ABSTRACT_P08

THE INTERACTION BETWEEN VDR POLYMORPHISMS, VITAMIN D STATUS AND MYOCARDIAL INFARCTION

Erica Baidauz¹, Alexandra-Valentina Ene (Danciu)^{1,2}, Cristina Mihaela Bratu¹, Alexandra Chelaru¹, Mihai Toma², Dănuț Cimponeriu¹

¹Facultatea de Biologie, Universitatea din București, România

²Spitalul Universitar de Urgență Militar Central București, România

Introduction: Acute myocardial infarction is a major contributor to cardiovascular morbidity and mortality worldwide. In addition to established cardiometabolic risk factors, vitamin D deficiency and genetic variation in the vitamin D receptor gene (VDR) have been investigated as potential contributors to cardiovascular susceptibility. However, the relationships among VDR variants, serum vitamin D status, and acute myocardial infarction remain insufficiently characterized.

Objective: This study aimed to evaluate the associations of the VDR Apal, TaqI, and FokI variants, serum 25-hydroxyvitamin D concentrations, and selected cardiometabolic risk factors with acute myocardial infarction.

Methodology: This case-control study included 66 patients with acute myocardial infarction and 34 healthy control subjects. The VDR Apal, TaqI, and FokI variants were genotyped using PCR-RFLP. Serum 25(OH)D concentrations were measured using an enzyme-linked immunosorbent assay. Additionally, clinical and cardiometabolic characteristics were also evaluated.

Results: The VDR FokI FF genotype was associated with higher odds of acute myocardial infarction (OR = 2.55, 95% CI: 1.06-6.16, p = 0.03). Haplotype analysis identified two haplotypes associated with myocardial infarction, with the risk-associated haplotypes containing the FokI F allele. Serum 25(OH)D concentrations were significantly lower in patients than in control subjects (15.97±22.71 vs. 35.99±24.54 ng/mL, p < 0.001). Active smoking was more frequent among patients (26 vs 5, p = 0.01). The association of the FF genotype with myocardial infarction remained significant after adjustment for other relevant variables (e.g. age).

Conclusions: The findings indicate that the VDR FokI FF genotype and reduced serum 25(OH)D concentrations are associated with acute myocardial infarction in the investigated groups. The presence of the F allele in risk-associated haplotypes further supports the potential relevance of the FokI polymorphism. Nevertheless, given the relatively small sample size and the case-control design, these findings should be interpreted cautiously and require validation in larger, independent populations.

Keywords: 25-hydroxyvitamin D; acute myocardial infarction; cardiometabolic risk; FokI; genetic polymorphism; haplotype; rs2228570; vitamin D receptor; VDR.

POSTER ABSTRACT_P09

BACTERIAL AND FUNGAL COMMUNITY RESPONSE AFTER 20 YEARS OF NATURE-BASED REMEDIATION AT MOLDOVA NOUĂ, A FORMER COPPER MINING SITE

Emanuela D. Tiodar¹, Karsten Raulund-Rasmussen², Adrienn Micsinai³, Rita Sipos³, Peter Bondgaard Mortensen⁴, Cristina L. Văcar¹, Zoltan R. Balázs¹, and Dorina Podar^{1,5}

¹Centre for Systems Biology, Biodiversity and Bioresources (3B), Babeş-Bolyai University, Cluj-Napoca, Romania

²Department of Geosciences and Natural Resource Management, Forest and Bioresources, University of Copenhagen, Denmark

³Eurofins BIOMI Kft., Gödöllő, Hungary

⁴Eurofins Miljø A/S, Galten, Denmark

⁵Department of Molecular Biology and Biotechnology, Faculty of biology and Geology, Babeş-Bolyai University, Cluj-Napoca, Romania

Soil metal contamination creates persistent risks for ecosystems and human health, making effective remediation essential. We investigated soil microbial communities two decades after revegetation at Moldova Nouă, Romania, where mining led to elevated Cu, Zn, Pb, and As levels. Without removing contaminants, applied nature-based solutions limited metal mobility and erosion via (i) perennial grass revegetation and (ii) afforestation, mainly with *Robinia pseudoacacia* and *Elaeagnus angustifolia*.

The study assessed whether these interventions promoted ecosystem recovery by evaluating soil microbial diversity and community structure across revegetated (treated), untreated (control), and reference trajectory sites via eDNA metabarcoding. Recovery success was inferred based on similarities/differences to reference communities.

Diversity levels were largely similar across trajectories for both bacteria and fungi, indicating that elevated metal concentrations did not primarily drive diversity loss. However, community identity shifted with trajectory. Bacterial communities overlapped partially, with treated forest communities positioning between control and reference sites. Fungal communities reorganized along the remediation gradient, each trajectory hosting a distinct composition. Both domains retained fingerprints of unresolved contamination: bacterial phyla typical of pristine soils (e.g., Verrucomicrobiota) were absent from treated and control sites, while a phylum restricted to the control trajectory (Chloroflexota) was absent from treated trajectories. The profile of fungal relative abundance in treated soils resembled an intermediate position between the control and the Basidiomycota-dominated references. Unlike control soils, dominated by Ascomycota, treated soils showed comparable Ascomycota and Basidiomycota abundances, with Basidiomycota reaching similar or higher levels than Ascomycota. This indicates a partial transition from the control's phylum-level profile. Mortierellomycota's shared presence in treated and reference soils, but not control, reinforces this early recovery signal. Treated soils across both domains, however, remained linked to residual metals concentrations, unlike references, which tracked organic matter.

Together, these results suggest that 20 years of nature-based remediation shifted soil microbial communities away from the contaminated state, but neither domain fully converging toward reference communities.

Keywords: eDNA; copper; metals; nature-based solutions (NbS); phytoremediation; pollution; remediation; soil microbiota.

Acknowledgements: The research is funded by the Horizon Europe project ARAGORN under grant agreement 101112723

POSTER ABSTRACT_P10

TESTING THE RELATIONSHIP BETWEEN THE OXYTOCIN RECEPTOR (OXTR) AND COLORECTAL CANCER IN A COHORT OF SUBJECTS FROM ROMANIA

Bratu Cristina-Mihaela¹, Chelaru Alexandra¹, Baidauz Erica¹ and Cimponeriu Dănuț^{1,2}

¹Faculty of Biology, University of Bucharest, Romania

²Molecular Biology Laboratory, National Institute of Research and Development for Food Bioresources, Bucharest, Romania

Background: Approximately 60% of colon cancer cases in Romania are diagnosed in advanced stages (3 and 4), raising the need to analyze local factors influencing outcome in Eastern Europe, such as smoking, drinking, education and body mass index.

Aim: This study evaluates the relationship between OXTR rs53576 variants and colon cancer risk, through analysis of genotypic and allelic distribution in case and control groups.

Methods: A total of 280 subjects from Romania were included in a case-control design: 130 patients with histopathologically confirmed colon adenocarcinoma and 150 controls with no history of colon neoplasia.

Results: Genotype distribution matched Hardy-Weinberg distribution across all subgroups and risk was estimated for each genotype using Odds Ratios with 95% confidence intervals. Genotype distribution differed significantly between cases and controls (chi square = 6.14; $p < 0.05$), consistent with Hardy-Weinberg equilibrium in each subgroup. The GG genotype was associated with an increased colon cancer risk (OR = 1.78; 95% CI: 1.105–2.854; $p = 0.017$), whereas the GA genotype conferred a protective effect (OR = 0.56; 95% CI: 0.34–0.91; $p < 0.05$); this protective association was more pronounced among men (OR = 0.45; $p < 0.05$), suggesting a possible sex-specific modulation of OXTR-related risk.

Conclusions: These results point to OXTR rs53576 as a genetic factor worth considering in colon cancer risk assessment and offer the first data on its allele frequencies for a Romanian cohort.

Keywords: colon cancer; OXTR; rs53576; genetic polymorphism; lifestyle factors.

POSTER ABSTRACT_P11

MUTATIONAL PROFILE OF RAS GENES IN COLORECTAL CANCER: A MOLECULAR ANALYSIS OF A ROMANIAN PATIENT COHORT

Alexandra Chelaru¹, Mihai-Viorel Dionisie², Cristina-Mihaela Bratu¹, Erica Baidauz¹, Gheorghe Dănuț Cimponeriu¹, Maria-Daniela Pojoga¹, Ecaterina Tataru²

¹Faculty of Biology, University of Bucharest, Bucharest, Romania

² Molecular Biology Laboratory, GRAL Medical, OncoFort Hospital, Bucharest, Romania

Background: Colorectal cancer (CRC) is a molecularly heterogeneous disease in which alterations of the RAS signalling pathway have major implications for tumor biology and therapeutic decision-making. This study aimed to characterize the KRAS and NRAS mutational profile in patients with locally advanced or metastatic CRC investigated within the Romanian National Genetic Testing Program.

Methods: Tumour tissue from 194 patients with CRC was analysed at the Molecular Biology Laboratory of GRAL Medical, Bucharest, between November 2025 and February 2026. Genomic DNA was extracted from formalin-fixed paraffin-embedded tissue and analysed for KRAS and NRAS mutations in exons 2, 3, and 4 using allele-specific real-time PCR and a CE-IVD RAS mutation analysis kit.

Results: The cohort was predominantly male (64%), with patients aged 50–80 years. RAS mutations were identified in 89 patients (45.9%), while 104 (53.6%) were negative and one sample was inconclusive. KRAS alterations predominated, being detected in 80 patients, mainly in exon 2, codon 12 (74 cases), followed by exon 3 (4 cases) and exon 4 (1 case). NRAS mutations were identified in 4 patients. One patient harboured concomitant KRAS G12S and an NRAS mutation, while 4 patients presented multiple KRAS mutations. Additional testing confirmed KRAS G12C in 7 of 9 samples initially assigned to the G12C/G12S group.

Conclusions: The heterogeneous RAS mutational landscape observed emphasizes the importance of comprehensive molecular testing in CRC. Accurate RAS genotyping provides clinically relevant information for therapeutic stratification and supports personalized management of patients with advanced disease.

Keywords: colorectal cancer; molecular diagnostic; KRAS; NRAS; RAS mutations.

POSTER ABSTRACT_P12

PHYLOGENETIC ANALYSIS OF MERCURIC REDUCTASES REVEALS DISTINCT CLUSTERS OF PUTATIVE FUNGAL HOMOLOGUES**Cristina Lorena Văcar¹, Dorina Podar²**¹Centre for Systems Biology, Biodiversity and Bioresources (3B), Babeş -Bolyai University, Cluj-Napoca, Romania²Department of Molecular Biology and Biotechnology, Faculty of Biology and Geology, Babeş-Bolyai University, Cluj-Napoca, Romania

The bacterial mercuric reductase MerA is the best-characterised enzyme involved in Hg²⁺ detoxification. Conserved pairs of cysteine residues bind Hg²⁺ at the active site and facilitate its reduction to elemental mercury (Hg⁰), a volatile form that readily diffuses out of the cell. Although this mechanism is well established in prokaryotes, whether fungi possess functionally equivalent enzymes remains unclear, despite reports that some fungal species can volatilise mercury. The recent functional characterisation of a mercuric reductase gene in *Metarhizium robertsii* (Wu et al., 2022), together with Hg²⁺ volatilisation observed in a resistant *Fusarium oxysporum* isolate (MT913528) from our laboratory, suggests that fungi may harbour previously unrecognised MerA homologues. In this isolate, a 1,437-bp fragment of a putative merA gene was expressed both in the presence and absence of Hg²⁺, suggesting constitutive rather than Hg-induced expression.

To investigate the evolutionary origin of putative fungal MerA homologues and their relationship to established prokaryotic enzymes, we analysed 336 homologous sequences from Bacteria, Archaea and Fungi retrieved from NCBI. Sequences were aligned using MUSCLE in MEGA X and examined for conserved catalytic motifs and cysteine pairs. A Neighbour-Joining phylogenetic tree was then constructed and annotated in iTOL with sequence annotation scores and structural features.

Most fungal sequences clustered with cyanobacterial homologues, whereas several sequences from more recently diverged Ascomycota showed relationships with Bacteroidetes, consistent with distinct horizontal gene transfer events. The association with Cyanobacteriota is also compatible with the constitutive merA expression reported in *Synechocystis* sp. (Singh et al., 2019). Overall, the results suggest at least two evolutionary histories for fungal MerA homologues: inheritance from an ancestor shared with Cyanobacteriota and independent acquisition from Bacteroidetes. These findings indicate that MerA-like proteins may be more widely distributed among fungi than previously recognised and provide a basis for their future functional and biochemical characterisation.

Keywords: *Fusarium oxysporum*; Mercury volatilization; Mercury detoxification; Cyanobacteriota; Mercury contamination.

Funding: This work is supported by a grant from the Ministry of Research, Innovation and Digitization, CNCS - UEFISCDI, project number PN-IV-P1-PCE-2023-2016, contract no: 76PCE, within PNCDI IV.

References

1. Wu, C., Tang, D., Dai, J., Tang, X., Bao, Y., Ning, J., Zhen, Q., Song, H., St. Leger, R. J., Fang, W., 2022. Proceedings of the National Academy of Sciences 119, e2214513119.
2. Singh, D. K., Lingaswamy, B., Koduru, T. N., Nagu, P. P., Jogadhenu, P. S. S., 2019. Microbiology Open 8, e00838.

PRIZES

Best Poster Award

Cells 235€

Genes 185€

Best Talk Award

Targets 250€

ABSTRACT BOOK

ICMB 2026

3rd Edition

Molecular
regulation across
the domains of life
– from DNA to
proteins

September 21-24,
2026

INTERNATIONAL CONFERENCE
**MOLECULAR
BIOLOGY**

CURRENT ASPECTS AND PROSPECTS



organizer: **Science and
Research Association**

Designed by: Mirela Buda, mirela@stiinta-cercetare.ro
Text Editor: Larisa-Gabriela Rus, larisa@stiinta-cercetare.ro
©Science and Research Association