DSB CONFERENCE 2023

Program & Abstracts

Budapest, 6th December 2023

ANNUAL MEETING OF EÖTVÖS LORÁND UNIVERSITY DOCTORAL SCHOOL OF BIOLOGY

ELTE
EÖTVÖS LORÁND
TUDOMÁNYEGYETEM

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DSB CONFERENCE 2023

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USE OF SOCIAL MEDIA

The official hash tag of the event is **#DSB2023**. The organizers encourage attendees to tweet/post about the amazing science they experience during the meeting. However, please be polite and respectful of others in all of your online activities.

Welcome

Greetings to all participants!

It is our great pleasure to welcome you to DSB Conference 2023. The aim of this event is to bring together PhD students in Biology Doctoral School to discuss their work, but also to find out about lectures of broader interest and to get to know each other. This event is open for all students enrolled in a PhD program at Eötvös Loránd University. Thanks to your enthusiastic participation, DSB Conference 2023 will be a memorable event full of exciting moments and surprising experiences. Get ready for stunning science coming your way.

We wish you all a successful and enjoyable meeting!

Loretta László
Head of the Organizing Committee

Prof. László Nyitray, Head
Head of the Biology Doctoral School

Introduction

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Dr. Péter Lőw	Professor of Department of Anatomy, Cell and Developmental Biology, ELTE
Dr. Péter Pongrácz	Professor of Department of Ethology, ELTE
Dr. Balázs Rosivall	Professor of Department of Systematic Zoology and Ecology, ELTE

ORGANIZING COMMITTEE

Head

Loretta László	PhD student at Signal Transduction and Functional Genomics Research Group, Institute of Enzymology, Research Center for Natural Sciences

Members

Éva Moussong	PhD student at ELTE NAP Neuroimmunology Research Group, Department of Biochemistry, ELTE
János Pálinkás	PhD student at ELTE-MTA "Lendület" Motorenzymology Research Group, Department of Biochemistry, ELTE
Regina Martinek	PhD student at Genome Stability Research Group, Institute of Enzymology, Research Center for Natural Sciences
Vivien Szendi	PhD student at Laboratory of Molecular and Systems Neurobiology, Department of Physiology and Neurobiology, ELTE
Luca Eszter Balog	PhD student at Department of Systematic Zoology and Ecology, ELTE

THE VENUE

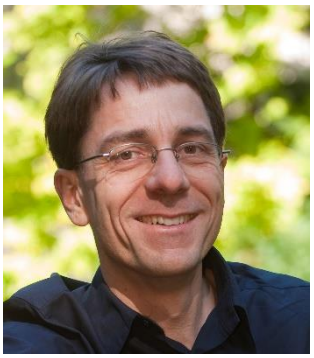
Research Centre for Natural Sciences (Main lecture room) Budapest, Magyar Tudósok Körútja 2, 1117

HUN-REN Magyar Kutatási Hálózat

Scientific Program

8:00-8:45 Registration

8:45-9:00 Opening ceremony



Keynote Lecture I

9:00-9:30

László Acsády: Neurowonders - wander around the brain

member of the HAS Thalamus Research Group, Institute of Experimental Medicine, Hungarian Reserach Network

Session I

9:30-9:45 Tamás Lakatos: Importance of forested village edges for bird communities

9:45-10:00 Dániel Kovács: Age-dependent hormesis to HSF-1 deficiency suggests a compensatory mechanism mediated by unfolded protein response of the ER in Caenorhabditis elegans

10:00-10:15 Thi Phuong Hoang Nguyen: Iodine Biofortification of cabbage plants cultivating in a hydroponic system

10:15-10:30 Tímea Kovács: Training style-dependent associations of dogs' inattention and learning performance

10:30-11:00 Coffee break

Flash posters I: Each participant gives a 3-minute presentation

11:00-11:05 Introduction of the Hungarian Biotechnology Students Association (MaBE)

11:05-11:30 7 flash poster talks. (1. Liza Tóth, 2. Karola Anna Barta, 3. Márton Péter Nyiri, 4. Laura Gillet, 5. Hana Kaci, 6. Zhanerke Kenzhebayeva, 7. Shany Dror)

Session II

11:30-11:45 Máté Winternitz: The effect of a smooth muscle myosin inhibitor in a no-reflow animal model

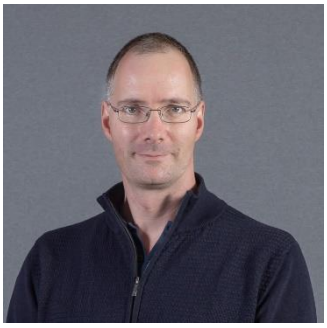
11:45-12:00 Ágota Réka Szabó: Milkweed (Asclepias syriaca) invasion, fragment size and connectivity determine arthropod communities and their functional traits

12:00-12:15 Maissa Ben Mahmoud: Multifactorial approach is needed to unravel the maturation phases of human neurons derived from induced pluripotent stem cells

12:15-12:30 Bálint Halpern: Individual behavioral variation of juvenile Hungarian meadow vipers (Vipera ursinii rakosiensis)

12:30-13:20 Lunch break with group photo

Keynote Lecture II



13:20-13:50

Péter Batáry: Landscape ecological perspectives of biodiversity conservation

Landscape and Conservation Ecology Group, Institute of Ecology and Botany Centre for Ecological Research

Session III

13:50-14:05 Gantuya Batdelger: Traditional herders' knowledge on plants, ongoing ecological changes and herding, case study in the mountain forest-steppe region in Mongolia

14:05-14:20 Levente Lakatos: Intracellular activity of new potent antitubercular compounds inhibiting a mycobacterial essential enzyme for the biosynthesis of arabinose

14:20-14:35 Amira Fatime Vörös: Biomass allocation of a semi-arid grassland under altered precipitation regime

14:50-15:05 István Oszoli: Group-selection via aggregative propagule-formation enables cooperative multicellularity in an individual based, spatial model

15:05-15:35 Coffee break

Flash posters II: Each participant gives a 3-minute presentation

15:35-16:00 7 flash poster talks. (1. Dániel Vörös, 2. Orsolya Oravecz, 3. Fanni Keresztes, 4. Ankita Murmu, 5. Ferenc Fekete, 6. Rebeka Szőke, 7. Nandakishor Krishnan)

Closing ceremony

16:20-16:40 Award ceremony

16:40-16:50 Concluding remarks

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Tamás Lakatos	I	Ecology and Evolution	lakatos.tamas@ecolres.hu
Dániel Kovács	I	Genetics	d.kowacs@gmail.com
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Amira Fatime Vörös	III	Ecology, Conservation Biology and Systematics	amira.voros@ttk.elte.hu
István Oszoli	III	Ecology and Evolution	oszolipisti@student.elte.hu

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Abstracts of oral presentations

Importance of forested village edges for bird communities

Tamás Lakatos[1,2], András Báldi[3], Zoltán Benkő, István Kovács, Zoltán László[4], Szabolcs Mizser[7,8], Jenő Purger[5], Krisztina Sándor[6], Gábor Seress[6], Béla Tóthmérész[7,8], István Urák[9], Péter Batáry[1]

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Urbanization combined with agricultural intensification is responsible for global biodiversity decline, which happens through habitat loss and fragmentation. Therefore, biodiversity conservation cannot rely solely on protected areas; human-dominated landscapes (e.g. agricultural areas and neighbouring villages) should also be involved in the creation of conservation strategies. Villages represent an interface between urbanized and agricultural landscapes, but studies focusing on their biodiversity-retaining capacity are still scarce. In order to fill this gap, we designed our study for Hungarian and Romanian villages (N = 72) in semi-natural (deciduous forests) vs. agricultural landscapes with varying distances from mid-sized cities. Our study design included two villages in the agglomeration zone of cities, with rather modern, ornamental gardens and two villages far from the cities, characterized mainly by traditional gardening practices. We studied birds of these villages with the point count method in two periods during the peak breeding season. Village centres and edges were sampled between April and June 2022. According to our results, species richness was highest in forested landscapes and at the edge of villages, but distant village centres were more species-rich. The abundance of birds was higher in centres than village edges, but mainly synanthropic species were observed. Villages in the agglomeration had lower abundances even in forested landscapes. We also assigned functional traits (diet, foraging technique, nesting location, body mass) to birds to understand their role in ecosystem functioning. We found that insectivores were more abundant on forested village edges, as well as species that nest close to the ground. Overall, our study showed that villages are also prone to urbanization effect, especially the centres of villages and those that are situated in the agglomeration zone. Village centres prevent the spread of insectivores and ground nesting species, thus ecosystem services provided by these species cannot function properly. At the same time, villages situated in simplified, agricultural landscapes were able to maintain high bird abundance, which indicates that these settlements can function as wildlife refuges up to a certain level.

Age-dependent hormesis to HSF-1 deficiency suggests a compensatory mechanism mediated by unfolded protein response of the ER in *Caenorhabditis elegans*

Dániel Kovács[1*], János Barnabás Biró[1*], Saqib Ahmed[1], Márton Kovács[1], Tímea Sigmond[1], Bernadette Hotzi[1], Umar Mohammad[1], Tibor Vellai[1,2], János Barna[1,2]

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[*] *These authors contributed equally to this work*

The master regulator of the heat shock response is the heat shock factor HSF1, which acts as a conserved transcription factor in eukaryotes and plays a pivotal role in the maintenance of cellular proteostasis. HSF1 also has a protective role in the progression of aging and neurodegenerative diseases, and has been implicated in carcinogenesis and tumour development. Thus, manipulation of HSF1 activity has a promising therapeutic potential for these disorders. Lack of HSF-1 function is usually associated with impaired stress tolerance. Contrary to this knowledge, here we show that inactivation of HSF-1 in the nematode *Caenorhabditis elegans* results in increased thermotolerance in young adult worms, whereas the thermotolerance of older animals depleted for HSF-1 is actually decreased compared to wild type. Furthermore, a gene expression analysis supports that in young worms, distinct cellular stress signaling are induced upon HSF-1 deficiency. We also demonstrate that increased proteotoxic stress tolerance in HSF-1 depleted worms requires the activity of the unfolded protein response of the endoplasmic reticulum and the SKN-1/Nrf2-mediated oxidative stress response pathway, suggesting a mutual compensatory interaction between HSF-1 and these conserved stress response systems. Based on these results, it is plausible that a such compensatory network also operates in higher organisms, raising the possibility of an unexpected outcome when activity of HSF1 is manipulated.

Keywords: autophagy, C. elegans, cellular stress response, heat shock factor 1, heat shock proteins, heat shock response, hormesis, insulin-like signalling pathway, proteostasis, thermotolerance, unfolded protein response, skn-1.

Iodine Biofortification of cabbage plants cultivating in a hydroponic system

Nguyen Thi Phuong Hoang [1,4], Ferenc Fodor[4], Gyula Záray[1], Anett Endrédi[1], Christina Streli[2], Dieter Ingerle[2], Philipp Ziegler[2], Martin Radtke[3], Ana Guilherme Buzanich[3], Péter Dobosy[1*]

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Iodine is a trace element needed in the human diet because it creates thyroid hormones. Iodine intake recommendations range from 90 to 270 µg per day: 90 µg for early children (1–8 years), 120 µg for older children (9–13 years), 150 µg for adults, and 220-270 µg for pregnant and lactating women. Iodine insufficiency affects over 2.2 billion people globally, making it challenging to locate a plant-based source of iodine that meets the necessary dietary intake.

The iodine biofortification of cabbage was examined in this study by cultivating plants in a hydroponic system containing iodine at concentrations ranging from 0.01 to 1.0 mg/L as potassium iodide or potassium iodate. Plant physiological parameters (chlorophyll content, photosynthetic efficiency), biomass production, concentration variations of iodine, and as well as selected essential elements were all studied during the experiment.

Based on the experimental results, iodine addition did not influence photosynthetic efficiency or chlorophyll concentration. The iodide treatment boosted biomass production at all dosages; however, this effect was only detected at low concentrations; at 0.5 mg/L, the yield was reduced. Increasing the iodine concentration in the nutrient solutions resulted in higher iodine content in all plant parts; the presence of iodide caused 2–7 times higher accumulation compared to the iodate treatment, and the highest accumulation was observed in the roots and the lowest in the edible plant tissues. The accumulated iodine form in the roots was I- in both treatment types, and IO¬3- was converted to I-, indicating that reductive chemical reactions are dominant in the roots. The type of iodine treatment had a varied effect on essential element transport; when iodide was added to the nutrient solution, the content of all elements decreased, whereas adding 1.0 mg/L iodate increased the transport compared to control plants.

Training style-dependent associations of dogs' inattention and learning performance

Tímea Kovács [1, 2], Vivien Reicher[3], Barbara Csibra[1, 2], Márta Gácsi[2, 4]

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The interconnections between learning, emotion, and sleep are well-established; deficits in learning efficiency can stem from factors such as social stress, insufficient sleep, or neurodevelopmental disorders. Attention Deficit Hyperactivity Disorder (ADHD) is one of the most prevalent neurodevelopmental disorders in humans, and its symptoms of inattention result in academic impairments. Considering that dogs are ideal models of ADHD, our aim was to investigate the associations between dogs' inattention and learning performance under two Conditions, using permissive vs controlling training styles. We expected more inattentive dogs to perform worse and have poorer sleep-dependent memory consolidation (less improvement from pre- to post-sleep), and explored potential differences between training styles.
We measured the behaviour of N=25 companion dogs in a within-subject design, employing a command-learning task. Dogs were trained by dog trainers to perform already known actions to newly learned commands on two Occasions, in permissive and controlling training styles. The order of Conditions was balanced between subjects. After both training sessions, an experimenter assessed the dogs' learning performance in a neutral style. The test was followed by a 2-hour-long sleep and a post-sleep retest. Dogs' general Inattention was assessed using an ADHD-questionnaire adapted for dogs.
Condition and Inattention had no main effect on pre-sleep test performance, but dogs performed better on the first occasion ($p<0.001$), and an Occasion × Inattention interaction indicated that on the second occasion, more inattentive dogs performed better ($p=0.015$). Regarding the post-sleep retest performance, again, dogs performed better on the first occasion ($p=0.008$). Furthermore, a Condition × Inattention interaction revealed that in the controlling condition, more inattentive dogs performed better after sleep ($p=0.022$). Performance change (from test to retest) was affected by Condition × Inattention; in the permissive condition, more inattentive dogs showed poorer improvement ($p=0.007$).
The occasion effect on both test and retest performance implies proactive interference, wherein previously acquired knowledge hampers subsequent learning. However, suggested by the test performance results on the second occasion, more inattentive dogs might have been less affected by interference, and gained more from the repetitive nature of our training procedure - as it has been described in the human ADHD literature. The retest and performance change results suggest that more inattentive dogs might not benefit from a permissive training style and

the complete lack of control/inhibition, and that these processes are interlinked with sleep. Ultimately, our study lays a foundational framework toward identifying the optimal training approach tailored for inattentive dogs.

The effect of a myosin-2 inhibitor in a no-reflow animal model

Máté Winternitz

Doctoral School of Biology and Institute of Biology, ELTE Eötvös Loránd University, Budapest

Acute ischemic stroke is a major clinical challenge, with many patients experiencing poor functional outcome despite the revolutionary evolution of mechanical thrombectomy (MT). Cerebral capillary constriction, mediated by the actomyosin system in precapillary smooth muscle cells and capillary pericytes, contributes to the no-reflow phenomenon observed after thrombectomy. Therefore, direct targeting of the actomyosin system of these cells can be a promising therapeutic approach. For that purpose, we developed an in vivo 2-photon microscope animal model for investigating the blood flow parameters related to the stroke and the following no-reflow phenomenon. As the model proved to be relevant, we successfully administrated a blebbistatin derivative molecule, developed by our laboratory, named MPH-222. This molecule is strongly able to inhibit myosin-2 isoforms. The targeted delivery ensures that the molecule is administrated directly to the stroke-affected regions, potentially maximizing its therapeutic efficacy while minimizing off-target consequences. The developed catheter-based delivery method for MPH-222 administration is a potential add-on therapy to MT. According to the results, MPH-222 demonstrated local and transient accumulation in the stroke-affected brain region. It has also shown promising results as demonstrated by 2-photon measurements, indicating that MPH-222 may play a substantial role in rapidly restoring blood flow in the stroke-affected region. These results support the importance of direct myosin inhibition in the brain as the optimal therapeutic pathway following emergency intervention.

Milkweed (*Asclepias syriaca*) invasion, fragment size and connectivity determine arthropod communities and their functional traits

Ágota Réka Szabó[1,2], Edina Török[1], Tamás Lakatos[1,2], Dávid Korányi[1], Attila Torma[1,3], Nikolett Gallé-Szpisjak[1], Péter Batáry[1], Róbert Gallé[1,4]

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Land-use change, including habitat fragmentation, has far-reaching negative impacts on the environment, resulting in biodiversity loss, soil quality degradation and alteration of water availability changes. The combination of consequences may cause invasive plants to establish and spread affecting plant negatively affecting native arthropod communities as well. We investigated the impact of fragmentation and milkweed invasion on invertebrate communities in sandy grasslands of forest-steppe habitats in Hungary. We sampled ground-dwelling arthropods, mainly herbivore true bugs and predator spiders, with pitfall traps and pollinators by direct observations along transects in invaded vs. control patches of each fragment. We considered arthropod species' body size and feeding (all groups), dispersal ability (herbivores and predators) and nesting location (pollinators) traits in our analyses. In non-invaded patches, the number of monophagous herbivores showed an increasing trend, while in invaded fragments, there were more polyphagous individuals with increasing connectivity and fragment size. The dispersal ability of predators was lower as connectivity increased in non-invaded patches but higher in patches invaded by milkweed. The primary focus of restoration projects should be the restoration of habitat and eradication of invasive species while concurrently supporting the revival of native species and their ecological relationships.

Multifactorial approach is needed to unravel the maturation phases of human neurons derived from induced pluripotent stem cells

Maissa Ben Mahmoud[1], Anikó Rátkai[1], Krisztina Bauer[1], Norbert Bencsik[1], Attila Szücs[1,2], Katalin Schlett[1], Krisztián Tárnok[1]

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Neurons derived from induced pluripotent stem cells (h-iPSC-Ns) provide an invaluable model for studying the physiological aspects of neuronal development and diseases. However, multiple studies have also demonstrated that h-iPSC-Ns exhibit a high degree of functional and epigenetic diversity. Due to the imprecise characterization and significant variation among the currently available maturation protocols, it is essential to establish a set of criteria to standardize models and accurately characterize and define the developmental properties of neurons derived from iPSCs.
In this study, we conducted a comprehensive analysis of the h-iPSC-Ns via electrophysiological and microscopic techniques to follow their functional development at the cellular and network levels. This enabled us to provide a thorough description of the maturation process of h-iPSC-Ns over a 10-week period *in vitro*. Specifically, we have used conventional whole-cell patch-clamp and dynamic clamp techniques, alongside morphometry, to assess the characteristics of maturing h-iPSC-Ns. Additionally, we utilized calcium imaging to monitor the progression of synaptic activity and network communication. At the single cell level, human neurons exhibited gradually decreasing membrane resistance in parallel with improved excitability by 5 weeks of maturation. Their firing profiles were consistent with those of mature regular firing type of neurons. At the network level we observed the development of abundant fast glutamatergic and depolarizing GABAergic synaptic connections together with synchronized network activity. The identified sequence of differentiation events are consistent and offers a robust framework for developing targeted experiments at varying stages of neuronal maturation. This framework allows for the use of different, age-related methodologies or a singular set of experiments for a culture's maturation.

Keywords: induced pluripotent stem cell, human neuron, differentiation, maturation, electrophysiology, morphometry

Individual behavioral variation of juvenile Hungarian meadow vipers (*Vipera ursinii rakosiensis*)

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The Hungarian meadow viper (*Vipera ursinii rakosiensis*) conservation program started captive breeding of the species in 2004. Over the past years altogether nearly 4900 vipers were born in the Hungarian Meadow Viper Conservation Centre and over 900 vipers were released to eleven habitats in Kiskunság and Fertő-Hanság National Parks in Hungary. As captive environment affect development of individual behavior and though future survival of reintroduced vipers, we decided to test different variables with the intention to fine-tune future captive breeding techniques. In a controlled study, post-release behavior in seminatural enclosure, origin and sex of the vipers and structural diversity of captive environment was tested on 48 juvenile vipers, representing 12 families. Vipers were kept in small or large indoor terraria, or small outdoor terraria individually after birth in August 2021. Those in indoor terraria were continuously fed over the winter. In the end of May 2022 they were translocated to large outdoor terraria individually. The vipers behavior was observed in a standardized way: recording their position, posture, external body tempterature every hour over the whole day at least once a week over a four week period. Consistency of individual behavior was tested by using R-statistic. We detected difference between sexes and various origins, showing slower adaptation to new environment by those who spent their early life stages in indoor conditions, and females tending to be slower in reacting to changing environmental conditions.

Traditional herders' knowledge on plants, ongoing ecological changes and herding, case study in the mountain forest-steppe region in Mongolia

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An understanding of traditional knowledge and practices of plants, habitats and livestock herding is increasingly acknowledged as vital for the sustainability and efficient nature conservation. However, some scientists argue that traditional knowledge may become inadequate, while reciprocal relationships loosen, because locals are unable to adapt to the rapid socio-ecological changes, and thus knowledge, practices and values become outdated and irrelevant over time. We hope that a deeper understanding of how herders perceive ecological changes in their landscape and their traditional herding knowledge and practices would be useful for improving pasture management and promoting regeneration processes. Our main objectives were 1) to reconstruct the folk habitats locals use to partition landscapes, 2) to reveal how herders perceive ongoing ecological changes, and 3) to test whether the knowledge about the 'proper' ways of grazing, the adequacy of the applied traditional practices, or the ways herders actually manage herds and pastures changed most. Our study areas were located in the mountain forest-steppe region in Mongolia. In 2017-2023, we interviewed over 70 herders using photos of plant species and habitats and semi-structured interviews focusing on landscape change and folk plant classification. We also studied the present-day understanding, reported validity and relevance of best herding practices documented during a dialogue workshop with best herders 80 years ago by Sambuu Jamsran, together with the socio-ecological drivers of experienced changes. Mongolian herders distinguished altogether 88 folk habitat types, habitat classification was multidimensional; key dimensions were geomorphological and edaphic. There were some well-known species (e.g., *botyuul, hyag, shireg*) and species groups (hot plants and leafy plants) that were often used to describe habitat types. We found 32 indicators on how herders perceived landscape and vegetation changes for the 14 main habitat types studied. Our findings on traditional herding practices shows that most advices (53 from 69) were agreed with by Mongolian herders as still valid today, however, only 34 advices were followed.

Intracellular activity of new potent antitubercular compounds inhibiting a mycobacterial essential enzyme for the biosynthesis of arabinose

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The “classical” examples of intracellular bacteria are species from the *Mycobacterium* genus with over one hundred environmental and pathogenic species. Tuberculosis remains a major public health threat [1]; the causative pathogen, *Mycobacterium tuberculosis* (MTB), kills approximately two million people each year and is thought to be present as a latent infection in one-third of the world’s population. Non-tuberculous (atypical) mycobacteria (NTM) are increasingly recognized as causative agents of various opportunistic human infections, most often originating from contaminated water supplies, and their incidence (skin, postoperative, etc.) is not limited to immunocompromised patients. MTB and NTM central nervous system infections also take a variety of forms (meningitis, meningoencephalitis, etc.). In addition, the increasing incidence of circulating multidrug-resistant (MDR) and extensively drug-resistant (XDR) TB strains threatens to return to such an era when half of TB patients died. To make TB

treatment more effective, safer, and shorter, new anti-TB agents are being developed. Based on our new collaborative work a new class of small molecular weight antitubercular compounds were defined [2]. These compounds are decaprenylphosphoryl-β-d-ribose oxidase (DprE1; EC:1.1.98.3]. inhibitors. DprE1 is crucial for the biosynthesis of mycobacterial cell wall polysaccharides lipoarabinomannan and arabinogalactan [3]. First antimycobacterial activity – structure relationship was determined. Next, we have investigated the *in vitro* selectivity of the hit compounds on various human cell cultures. The intracellular activity was tested on infected MonoMac-6 cells. The extensive structure-activity relationships study underlined the importance of the naphthalen-2-yl methyl moiety to retain antitubercular activity with acceptable *in vitro* cytotoxicity profile. Compound 56 showed intracellular killing activity on infected model host cell MonoMac6 culture.

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Biomass allocation of a semi-arid grassland under altered precipitation regime

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During climate change altered precipitation pattern can significantly affect ecosystems functioning and stability. The sensitivity of grasslands productivity to increased or decreased water availability has already been documented, which can have a strong impact on carbon-cycling. The majority of studies focused on aboveground plant biomass, but a large proportion of grasslands plant biomass exist below ground. Thus, tracking changes in allocation is of paramount importance.
We studied the response of aboveground biomass, belowground biomass, and root : shoot ratio to altered precipitation in a semi-arid temperate grassland. We applied a single extreme drought event and recurrent precipitation change with two level of drought and increased precipitation. In additional analyses we estimated to what extent intraspecific response influenced the vegetation's biomass allocation under the experimental conditions, by using dominant species' root : shoot ratio in ambient climate.
We found that aboveground biomass was reduced in response to recurrent drought, and the effects of extreme drought effect was also detectable after five years.
For total belowground biomass, we observed the effect of chronic drought, with significant negative effect of severe drought. Even though the total belowground biomass was not affected by extreme drought, we detected its effect on the vertical distribution, as in the shallower (0-10 cm) soil layer, the phytomass was reduced significantly.
The root : shoot ratio was not affected by the single extreme drought, but was significantly increased in chronic drought. This increment in the biomass ratio was due to a stronger reduction of aboveground biomass compared to belowground biomass. We also found that most likely there is a strong intraspecific response to altered water availability, since there was a much stronger allocation to belowground biomass than it is expected from shifts in species composition.
These results indicate that chronic drought has an important role in shaping grasslands biomass allocation. Our results highlight the importance of belowground biomass studies, as focussing only on aboveground response would give inaccurate predictions, as belowground biomass is less sensitive to altered water access.

Group-selection via aggregative propagule-formation enables cooperative multicellularity in an individual based, spatial model

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The emergence of multicellularity is one of the major transitions in evolution that happened multiple times independently. During aggregative multicellularity, genetically unrelated lineages cooperate to form transient multicellular groups. Unlike clonal multicellularity, aggregative multicellular organisms do not rely on kin selection instead other group selection mechanisms maintain cooperation against cheater phenotypes that benefit from cooperators but do not contribute to groups. Spatiality with limited diffusion can cause group selection, as interactions among individuals are restricted to local neighbourhoods only. Predation may help the emergence of aggregation through the size increase of stuck-together-cells.

We have investigated the effect of spatiality on the stability of aggregative multicellularity via individual-based modelling. We have examined whether aggregation facilitates the survival of cooperators in a temporally heterogeneous environment against cheaters, where only a subset of the population is allowed to periodically colonize a new, resource-rich habitat. Cooperators constitutively produce adhesive molecules to promote aggregation and propagule-formation while cheaters spare this expense to grow faster but cannot aggregate on their own, hence depending on cooperators for long-term survival. We have compared different population-level reproduction modes with and without predation to evaluate the different hypotheses.

In a temporally homogeneous environment without the bottleneck of propagule-based colonization, cheaters always win. Predation can benefit cooperators better, but it is not enough to maintain the necessary cooperator amount in successive dispersals, either randomly or by fragmentation. Aggregation-based population reproduction however can ensure the adequate ratio of cooperators-to-cheaters in the propagule when a new habitat is colonized and is sufficient to do so even without predation. Spatiality combined with temporal heterogeneity helps cooperators via group selection, facilitating thus aggregative multicellularity. External stress (predation) may facilitate aggregation, however, according to our results, it is neither necessary nor sufficient for aggregative multicellularity to be maintained when there is effective group-selection.

Abstracts of flash posters

Preliminary study on visual classification of stress and aggression between horses and riders in show jumping

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Show jumping has been the most popular equestrian sport for decades. It involves the horse-rider dyad riding through a course in an arena, jumping the obstacles in their way. The sport requires immense training and perfect cooperation and communication between the pair. Sometimes conflicts happen between the two, that can lead to the non-completion of the course. The rider has to react to and correct these undesired behaviours, but unfortunately, it is traditional and still widespread to react to any misbehaviour of the horse aggressively on the rider's part.

Our goal is to investigate these interspecies conflicts in the cases of non-completion events to identify patters of success and search for cases where the horse is not abused, but still performs well. Our method is video analysis and we coded N=500 videos of non-completion events. We also analyse the corresponding data gathered from the Hungarian National Horse Sport Federation database as well as the FEI (International Horse Sport Federation) database's Hungarian section, which contains the extensive competition history data of more than 4000 active competition riders.

During the coding, we recorded various data of the horse-rider dyads (e.g. sex, course height) and coded the conflict in detail (e.g. at which obstacle did the conflict happen, the type of conflict and the rider's reaction to it). Our preliminary results show, that out of the three possible non-completion events, Elimination is the most dominant (~60%), with the Retirement being second (~40%) and Withdrawal only happened in three cases. Out of all of the subcategories non-completion events ~90% of the cases was directly caused by a conflict between horse and rider. We found, that out of all of the (both female and male) rider's reactions to a conflict ~70% reacted negatively, punishing the horse in some way, and that female riders overall reacted more negatively to a conflict, than male riders (females in 55% and the males only in 42%).

Our findings show, that abusive behaviour towards show jumping horses in conflict situations during competitions is still frequent and highlight the need for stricter rules in penalizing abuse of the animals. We highlight the importance of avoiding such aggressive behaviours towards the animals and emphasize the focus on avoiding these conflicts in order to reduce stress and better the welfare of show jumping horses. Our research is a joint project of the ELTE Dept. of Ethology, the National Horse Sports Federation and Oxford One Innovation Center Zrt.

Effects of positive frequency-dependent learning, learning mistakes, and immigration on complex cultures – Validation on the song of collared flycatcher (*Ficedula albicollis*) by individual-based modeling

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Cultural diversity and stability of a population affect the adaptive capacity and survival of individuals. In addition to field studies, cultural diversity and stability have been studied using different modelling approaches in relatively simple cultures. These theoretical studies have helped to identify mechanisms that generate cultural diversity by increasing the proportion of new elements in the population, for example through immigration or erroneous learning. Copy-the-majority learning strategies, forms of positive frequency-dependent learning, have the opposite effect: while they help maintain cultural stability by promoting the spread of common elements, they also reduce cultural diversity. We investigated whether these fundamental, opposing mechanisms are sufficient together to create a complex, polymorphic cultural system and to maintain its diversity and stability. To do this, we developed an individual-based model that simulates song learning in birds, incorporating the extent of immigration, the frequency of learning errors and the strength of positive frequency-dependent learning as modifiable parameters. The model provided information on the composition and temporal changes of individual and population repertoires. A comparison was also made with long-term field data on a European passerine species with moderate song complexity, the collared flycatcher (Ficedula albicollis). Our results confirmed that certain combinations of the three mechanisms studied were indeed able to generate patterns that showed certain aspects of polymorphic cultures. However, when comparing the simulation results with the field data, several discrepancies were found, which emphasise the implementation of other mechanisms, especially those with a stabilising effect. Long-term metastable states found in cultural diversity at the population level raise awareness of the possible sensitivity of animal cultures to external factors.

Investigation of the effect of nanomaterials on the structure of amyloidogenic proteins

Flash poster I

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Interest in the study of nanoparticles has increased significantly in recent years because of their enormous potential and threat. Micro- and nanomaterials are present in our everyday environment and have been detected in several living organisms and products for human consumption, such as honey, beer, sugar, and tap water. They have also been detected in several human organs and tissues, including the human placenta. Inhibition of growth and development and immune responses have been described as effects of nanoparticles. They can also affect mitochondria and thus lead to metabolic disorders. They have the potential to affect proteins in the body and in the environment (Hildebrand et al., 2018). Interactions with nanoparticles can lead to conformational changes and the denaturation of proteins (Roach et al., 2005). Therefore, understanding the consequences of the formation of interactions between proteins and nanoparticles is essential to map their biological effects. We investigated the effects of nanoparticles on protein structure using ThT fluorescence, CD and SRCD spectroscopy, electron microscopy, and cytotoxicity measurements. Our results indicate that polystyrene nanoparticles, even in small amounts, affect the aggregation process of the amyloid-β protein involved in Alzheimer's disease. We also revealed that the particles can rapidly and in relatively large amounts bind the monomeric form of the protein on their surface, which affects the aggregation capabilities of the protein. Our results also suggest that the presence of nanoparticles may reduce the toxicity of amyloid-β in cellular medium. In our recent measurements, we observed that ready-made amyloid fibrils can depolymerize when in contact with polystyrene particles.

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When dogs are more than just pets: Exploring the links between anthropomorphism, behavior, and keeping practices

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Anthropomorphism is a cognitive process by which humans attribute human characteristics, emotions, mental states, and behaviours to non-human agents, including non-human animals. In Western countries, dogs are often regarded as family members or even as “children”, i.e., owners attribute them a social function that relies on anthropomorphism. This phenomenon might benefit the owner (also known as the “pet effect”) and is extensively investigated, but findings about the consequences for the dog are more scarce and contradictory. Some studies suggest that anthropomorphism can lead owners to misinterpret their dog’s behaviour, display inadequate emotional reactions that could result in more distress and problem behaviour in the dog. Our questionnaire study aimed to investigate the relationship between the perception of the dog-human relationship, the educational practices of the owner, and the behaviour of the dog. We hypothesized that an anthropomorphic perception of the dog-human relationship would result in specific issues in dog keeping and in the dog’s behaviour. We collected data from 799 Hungarian dog owners between February and March 2022. A principal component analysis identified three main perceived roles of the dog: a human-like (anthropomorphic) role, an animal-like role and a practical role. Preliminary results indicate that a higher score on the practical role dimension is negatively associated with dog and owner-related issues in raising the dog (e.g. associated with fewer socialization problems, less impatience), with higher perceived obedience and with fewer problematic behaviours in dogs (e.g, less fear). On the other hand, both the human-like and the animal-like roles of the dog are positively associated with problematic behaviours in dogs (i.e. more fear, more excitability). We conclude that the perception of the dog-human relationship is linked to the dog’s socialization and keeping practices via influencing general obedience and problematic behaviours in dogs.

The study of the interaction between ampelopsin, myricetin, and their sulfate conjugates and multispecific organic anion transporting polypeptides (OATP1B1, OATP2B1)

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Organic anion-transporting polypeptides (OATPs) are transmembrane transporters that can facilitate the cellular uptake of various substances. Among them, OATP1B1 is a key hepatic uptake transporter whose inhibition could lead to adverse food- and drug-drug interactions. Additionally, the ubiquitously expressed OATP2B1 is essential for the intestinal absorption of many orally administered drugs. Flavonoids such as ampelopsin and myricetin are commonly present in various foods and beverages, known for their biological effects. Yet, except for myricetin, no data have been reported about the potential inhibitory effect of these flavonoids on OATPs. Therefore, the investigation of the interactions between OATP1B1 and OATP2B1 and ampelopsin, myricetin, and their sulfate metabolites could be of great significance. The inhibitory impacts of ampelopsin, myricetin, and their sulfate metabolites were examined on A431 cells, a line of human epidermoid carcinoma cells overexpressing human OATP1B1 or OATP2B transporters. Our research revealed that the majority of the compounds tested proved to be strong inhibitors of OATP1B1 and OATP2B1 transport activity with low micromolar or even nanomolar IC50 values. In addition, the uptake of myricetin-3'-sulfate was detected in A431 cells overexpressing OATP1B1 or OATP1B1, using our recently developed fluorescence-based method, which incorporates 2-aminoethoxydiphenyl borate (2-APB), a cell-permeable molecule that, upon forming a complex with flavonoids, leads to enhanced fluorescence. Our findings show that not only the original flavonoids but also some of their conjugates can interact with drug transporters. Myricetin-3'-sulfate is enriched in cells expressing OATP1B1 and OATP2B1 transporters. Consequently, a high intake of ampelopsin, myricetin, and their sulfate metabolites may disrupt the pharmacokinetic profiles of pharmaceutical substances.

Keywords:
Organic Anion transporting polypeptides, fluorescence enhancer, Ampelopsin, Myricetin, Sulfate metabolites

The role of Ca2+ ATPases in autophagy

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Autophagy is a conserved process involved in the degradation of unnecessary or damaged organelles and proteins in eukaryotic cells. As a first step of autophagy, cytosolic material are sequestered into double-membrane vesicles called autophagosomes that then fuse with lysosomes to create autolysosomes where the isolated material is degraded. Autophagy is strictly regulated by multiple signaling and metabolic pathways, and growing body of evidence suggest that Ca^{2+}, one of the most important second messenger in cells, is acting as a critical regulator of the autophagic process. The basis of Ca^{2+} signalling is the high Ca^{2+} gradient between the cytoplasm and the extracellular space that is maintained by Ca2+ pumps both in the plasma membrane (PMCAs) and intracellular organelles (SERCAs and SPCAs). Lysosomes are important intracellular Ca^{2+} stores with high luminal Ca^{2+} concentration. While in the lysosomal membrane several Ca^{2+} channels with a variety of function have been reported no high affinity Ca^{2+} pumps filling the lysosomal lumen with Ca^{2+} have been identified. It is well known that the TRPML1 Ca^{2+} channel and a subunit of the Drosophila voltage gated Ca^{2+} channel, the Straightjacket protein, regulate autolysosome formation and autophagic degradation. Among the Ca^{2+} pumps only SERCA is known to affect autophagy but the exact mechanism of its function has not been determined. Our group has shown that upon starvation the plasma membrane Ca^{2+} pump PMCA4b and its only Drosophila homologe dPMCA internalized and localized to the membrane of autolysosomes both in human HEK293 and Drosophila fat cells suggesting a role of PMCAs in autophagy. Moreover, we observed that silencing SERCA in Drosophila changed the morphology of fat cell autophagic structures after starvation. Based on these data we aim to characterize the role of Ca^{2+} pumps PMCA and SERCA, and their interactors CD147 (Robo2) and the autophagy associated protein VMP1 in the regulation of autophagy using both human and Drosophila cell model systems. We hypothesise that the SERCA pump and VMP1 regulate the early steps of the autophagic process while the PMCAs and CD147 (ROBO2) are involved in maintaining the high free Ca^{2+} concentration of the lysosomal lumen.

Eavesdropping in dogs: Dogs with a vocabulary of object labels can learn new labels by observing social interactions

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18-month-old infants can learn words by observing 3rd-party interactions. Label learning by observation has also been demonstrated in a few individual grey parrots and bonobos. Word-knowledgeable (WK) dogs learn object labels (e.g., dog toy names) by engaging in playful social interactions with their owners. To examine whether WK dogs also learn object labels by observing 3rd-party interactions, and how this compares to their typical learning context, we exposed WK dogs (N=9) to two conditions. In the Observational Learning Condition (OLC), dogs observed two of their owners as they engaged in a triadic interaction with a toy. One of the owners repeatedly named the toy, gave it to the other owner, and asked them to hand it back. While doing so the owners looked at each other and at the toy in an ostensive manner, but not at the dog. These one-minute-long interactions were repeated for 4 days, after which the process was repeated with a second toy. In the Active Learning Condition (ALC), dogs were exposed to the same process but instead of observing the owners, one of the owners played with the dog with a new toy. To test the learning outcome, after the completion of each condition, both of the toys were placed together and the owner asked the dog to retrieve each toy six times, in a semi-random order. The dogs' performance did not differ between conditions (Wilcoxon matched pairs test, $p= 0.248$). In each condition 6 out of 9 dogs performed significantly above chance (binomial test; chance level = 0.5, $p \leq 0.02$). These results show that WK dogs can learn labels after only eight minutes of exposure and by observing 3rd-party interactions.

Flash poster II

Transition from surface metabolism to vesicles at the origin of life

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The genetic apparatus of contemporary cells represents a highly intricate and complex structure that has evolved over millions of years 1. Consequently, early lifeforms lacked the regulatory capacity of modern genetic machinery. Rather, simple dynamic rules must have existed to regulate early replicators and ensure their survival, thereby preventing competitive exclusion 2,3. The most probable candidate for the spatial context of first living systems is the surface of minerals 4,5, where early replicators and metabolites were attached to the mineral surface. This may have provided them (among other factors) with spatial segregation and rudimentary regulatory mechanisms, which enabled different replicators to coexist and evolve 6,7. However, concurrent life is cellular and not surface-bound, which hypothesises a transition of living systems from a 2D to a 3D spatial context with potentially different dynamical properties. In our project, we analysed the differences between these two spatial environments and developed a possible scenario for this transition by bridging well-established models of prebiotic surface 6 and vesicle metabolism 8. To achieve this, we have employed the same cooperative regime of RNA replicators in both environments with realistic genotypephenotype mapping based on RNA sequences. Our findings suggest, that whilst it is unlikely for complex living systems to intialize in vesicles, surface metabolism may have acted as a preadaptation for the cellular stage despite significant differences in the trends of evolution in the two contexts.

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Regulation Of Placental Protein Expression In Healthy And Diseased Pregnancies

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Proteins expressed in the placenta are pivotal in orchestrating the intricate processes of pregnancy. They wield a profound influence over the differentiation of trophoblast cells, the preservation of immunological tolerance towards the developing fetus, and influencing the overall outcome of pregnancy. Among these, the placental galectins – the galectin-13 and galectin-14 - are primarily expressed in the syncytiotrophoblast layer of the placenta and play an important role in maternal-fetal immune tolerance. Furthermore, their altered expression is linked to obstetrical syndromes like preeclampsia and recurrent pregnancy loss.
To extend our knowledge, this study was aimed at uncovering the transcriptional and post-transcriptional regulation of *LGALS13* and *LGALS14* by bioinformatics analysis.
For the identification of relevant transcription factors and miRNAs targeting *LGALS13* and *LGALS14*, prediction tools and high dimensional single cell data were used. Additionally, microarray and qRT-PCR data from our previous and ongoing studies were used to intersect potential transcription factors with those which are differentially expressed in obstetrical syndromes.
The analysis identified several putative transcription factors that can regulate galectin genes at the transcriptional level. From these transcription factors, 14 were found to be downregulated in preeclampsia and recurrent pregnancy loss. miRNAs for *LGALS13* and for *LGALS14* were predicted by all the applied platforms, from which two were identical. According to our search, four miRNAs were already found in obstetrical syndromes to be upregulated, which could contribute to the downregulation of placental galectins in these pathological pregnancies.
Overall, this research enhances our understanding of the transcriptional and post-transcriptional regulation of placental galectins and their potential role in pregnancy complications. However, further in vitro experiments are needed to validate these findings and to reveal their impact on maternal-fetal immunotolerance.

Small GTPase proteins' effect on lifespan and autophagy

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Autophagy is an essential cytoprotective degradation pathway which is responsible for the elimination of damaged proteins and organelles, therefore it maintains cellular homeostasis. Its function is of great significance, especially in postmitotic cells like neurons, which require high basal autophagy to ensure their survival and prevent neuronal loss. The process starts with the phagophore formation, which closes into an autophagosome. Fusion with a lysosome will create the autolysosome. During lysosomal degradation, the enclosed cargo is degraded by acidic lysosomal hydrolases.

Studying the degradation process is crucial, because the autophagic activity has been found to decrease with age, which can lead to the appearance and accumulation of toxic components that cause the neurons to die. Many neurodegenerative disorders are known to correlate with the damage of the degradation pathway, but the amount of toxins can be lowered by the activation of autophagy. A potential approach of treatment is to enhance lysosomal degradation. In our research we investigated small GTPase proteins effect on autophagy and lifespan.

Our results revealed that the activation of small GTPase proteins have different effects. Rab2 and Arl8 are both beneficial in a constitutively active form, they can elongate lifespan, improve climbing ability, and induce autophagy. But the activation of Rab7 is damaging and has an overall negative effect on autophagy and lifespan.

Based on these findings we continued our experiments with the investigation of GAP enzymes which influence the activity of small GTPase proteins. These enzymes can inactivate the small G proteins by catalyzing the hydrolysis of GTP. The RNAi silencing of specific GAPs can lead to elongated activation of small GTPases and potentially activate autophagy.

Our aims are to find GAPs that affect Rab2 and to examine lysosome biogenesis. Results revealed that the silencing of CG42795 can increase the amount of Rab2 positive structures, elongate lifespan and activate lysosomal degradation. The lysosome biogenesis can be analyzed by measuring the number of Arl8 positive structures. We found that CG11727 RNAi can increase the amount of lysosomes and acidic compartments.

As a conclusion we can state that between GAPs there is probably a redundancy, so many GAP can affect a small GTPase protein. The silencing of GAPs was sufficient to activate small G proteins and also autophagy. These enzymes can be a potential drug molecule targets in the future.

Identification of Cell Types from Ovarian Cancer Single-Cell Transcriptomics Data

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Single-cell RNA sequencing (scRNA-Seq) has emerged as a powerful tool in various fields, including oncology. This has led to an increase in publicly available scRNA-Seq cancer-related datasets, including those of ovarian cancer. In this study, we analyzed four ovarian cancer scRNA-Seq datasets, GSE217517, GSE173682, GSE154600, and GSE184880, from the publicly available National Center for Biotechnology Information (NCBI) Gene Expression Omnibus (GEO) database to identify normal and ovarian cancer cell types. Our entire analysis workflow was performed using Seurat, an R package for scRNA-Seq data analysis. We first pre-processed the four datasets through quality control and filtering of all samples to remove low-quality cells, followed by normalization and scaling. We then performed dimensional reduction using principal component analysis and the uniform approximation and projection method for the visualization of our data. Furthermore, we integrated the four datasets using an anchor-based approach which resulted in a total of 153,226 cells. For cell-level downstream analysis, we performed clustering to group the cells based on the similarity of their gene expression profiles. We identified T cells, B cells, epithelial cells, myocytes, endothelial cells, fibroblasts, dendritic cells, plasma cells, natural killer cells and cell cycling cells based on the expression of positive marker genes in each cluster and using automatic cell type annotation tool, SingleR. We found enriched expression of ovarian cancer marker genes expressed in cluster 1, which was identified as epithelial cell cluster. As 90% of ovarian tumors occur through epithelial-to-mesenchymal transition, the expression of marker genes of epithelial cells and ovarian cancer cells in the same cluster supports our findings. Based on this evidence, we labeled the cell type of cluster 1 as ovarian cancer cell. Finally, we incorporated the cell type information to the expression matrix consisting of genes and cells. We further plan to perform statistical analyses to understand cell-cell communication between normal and ovarian cancer cells at single-cell resolution and find an association between the expression of genes in different cell types. We believe that these analyses may reveal the in-depth mechanisms and how communication is regulated and maintained underlying crucial biological processes in ovarian cancer.

Genetic and non-genetic factors influencing drug metabolizing CYP1A2 and CYP2C9 enzymes

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The drug-metabolizing CYP1A2 and CYP2C9 enzymes, abundantly expressed in the liver, are highly polymorphic resulting in substantial variability in pharmacokinetics of drugs. We observed significant inter-individual differences in CYP1A2 and CYP2C9 activities and mRNA levels in human liver tissue samples as well as in psychiatric patients belonging to the Caucasian population. This variability is often attributed to genetic factors; however, the contribution of *CYP1A2* polymorphisms to CYP1A2 phenotype (CYP1A2 enzyme activity) is controversial. Therefore, we aimed to investigate the effect of *CYP1A2* single nucleotide polymorphisms (-3860G>A, -2467delT, - 739T>G, -163C>A, 2159G>A) on the CYP1A2 selective phenacetin *O*-dealkylation and mRNA expression as well as on CYP1A2-substrate olanzapine blood concentrations. The *CYP1A2*1F* allele considered to be associated with increased CYP1A2 inducibility is generally identified by the presence of -163C>A polymorphism; however, -163C>A existed in several haplotypes (*CYP1A2*1F*, *CYP1A2*1L*, *CYP1A2*1M*, *CYP1A2*1V*, *CYP1A2*1W*); consequently, *CYP1A2*1F* was a less prevalent variant than reported in Caucasian populations (0-0.4% *vs* 32-57%). None of the tested *CYP1A2* polymorphisms had a significant effect either on CYP1A2 activity or on olanzapine plasma concentrations in patients with psychiatric disorders. In contrast, significant contribution of *CYP2C9*2* and *CYP2C9*3* polymorphisms to the CYP2C9-selective tolbutamide 4'-hydroxylase activity was confirmed. Furthermore, significant correlation was observed between CYP1A2 and CYP2C9 activities and mRNA levels in the liver and those in the leukocytes, as well as between the CYP activities/expression and some non-genetic factors. Co-medication with CYP2C9-specific inducer/inhibitor agents, CYP1A2-inducing smoking, chronic alcohol consumption and amoxicillin+clavulanic acid are known to have a significant effect on CYP activity, and consequently on pharmacokinetics of CYP-substrate drugs. We have clearly demonstrated that the severe ibuprofen toxicity developed in a patient was due to the loss-of-function polymorphisms in CYP2C9 (*CYP2C9*2/*3* genotype), while CYP1A2 expression and related smoking showed a strong correlation with olanzapine plasma concentrations in patients with psychiatric disorders. These results demonstrated that revealing the relevant factors in CYP activities and considering both genetic and non-genetic factors can contribute to personalized pharmacotherapy adjusted to the patients' drug-metabolizing ability, and can facilitate to avoid adverse drug reaction or the lack of therapeutic effect due to inappropriate dosing.

The impact of story visualization and social context on children's creativity

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Storytelling is important in both learning and secure parent-child attachment providing a basis for creative abilities. New technology allows various forms of storytelling which can affects creativity and imagination differently. Digital stories and audiobooks can deprive storytelling from the social context by listening to a stranger's audio and not the caretaker's voice. Since cartoons contain several nonverbal multimodal features and readymade images (e.g., animations, sound effects) children's fantasy might be used less compared to traditional books. We investigated whether the social context of storytelling (parent reading or stranger's voice) and the intensity of visualization (animations and pictures) of a story affect children's creativity and imagination in short-term, and whether engaging in different forms of storytelling associates with trait creativity in the long-term. We expected stories told by the audio and with more intense visualization to be linked to lower creativity and mental imaginary scores. We also expected an association between trait creativity and the frequency of digital/traditional storytelling.

Participants were 5-8-year-old children (N=70) and their parents. Parents reported their child's digital media use, storytelling habits, and trait creativity. In an experiment, children's creativity was assessed (Alternative Uses Test, Figure Association Test, Test for Creative Thinking – Drawing Production, and the Mental Comparison Task) before and after watching/hearing a story on a tablet either red by the parent or heard from the original audio of the cartoon. Stories also varied on the level of visualization (full animation, pictures, no image).

Results suggest that children reading for themselves increases creativity in 7.4-8.2-year-old children, while it does not increase creativity in 5-7.3-year-old children. Furthermore, the creativity of 5-7-year-old children increases significantly if parents tell them a lot of stories by heart. For 7-7.3-year-olds, a smaller effect can be observed, and for 7.4-8.2-year-olds, it has almost no effect on creativity. Finally, the creativity of children decreases as a result of digital games if the parent has lower education, while the creativity of children improves if the parent has higher education.

Ectosymbiosis in eukaryotic evolution

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The symbiogenetic origin of eukaryotes with mitochondria is considered a major evolutionary transition. The initial interactions and conditions of symbiosis, along with the phylogenetic affinity of the host, are widely debated. Here, we focus on a possible evolutionary path toward an association of individuals of two species based on unidirectional syntrophy. With the backing of a theoretical model, we hypothesize that the first step in the evolution of such symbiosis could be the appearance of a linking structure on the symbiont's membrane, using which it forms an ectocommensalism with its obligate host. We consider a commensalistic model based on the syntrophy hypothesis in the framework of coevolutionary dynamics and mutant invasion into a monomorphic resident system (evolutionary substitution). We investigate the ecological and evolutionary stability of the consortium (or symbiotic merger), with vertical transmissions playing a crucial role. The dynamics of the population densities of the involved species are represented using a set of ordinary differential equations, and the growth rates of each species are represented using novel Malthusian functions. We utilize the concept of evolutionary substitution, and the ecological fixation of the ecto-commensalistic association is mathematically modelled in terms of the local asymptotic stability (using linearization) of certain fixed points corresponding to the coevolutionary dynamical system. The impact of the 'effectiveness of vertical transmission' on the dynamics is also analysed. We find that the transmission of symbionts and the additional costs incurred by the mutant determine the conditions of fixation of the consortia. Additionally, we observe that small and highly metabolically active symbionts are likely to form the consortia.

Acknowledgments

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