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PROGRAM

November 25th, 2022,
Life Sciences Center, Vilnius University,
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10.00-10.15	**Opening and Welcome**
	Prof. **OSVALDAS RUKŠĖNAS**, *President of the Lithuanian Neuroscience Association*
10.15-11.15	**Keynote lecture**
	Prof. **WALTER SENN**, *University of Bern, Switzerland* **Creative dreams help your brain learn better: generative adversarial networks in the brain**
11.15-11.30	**Coffee/Tea break**
11.30-12.00	**AISTĖ AMBRASĖ**, *University of Tubingen, Germany* **Why are the networks of moral, risky, and ambiguous decision-making distinct in the brain?**
12.00-12.30	**LINA ZABULIENĖ**, *Vilnius University, Lithuania* **Iodine status and the brain: effects and mechanism**
12.30-12.00	**JUSTINAS NARBUTAS**, *Leibniz Research Centre for Working Environment and Human Factors (IfADo), Germany* **Factors involved in the pathophysiology of Alzheimer's disease: new insights about sleep microstructure, chronic stress and cognitive fitness in late midlife**
13.00-14.30	**Lunch. Poster Session**
14.30-14.45	**Meeting of LNA members**
14.45-15.15	**MARIUS BAUZA**, *University College London, UK* **Home cage monitoring system for continuous behavioural and cognitive phenotyping in mice**
15.15-15.45	**JULIJA KRUPIC**, *University of Cambridge, UK* **Unsupervised, frequent and remote: a novel platform for personalised digital phenotyping of spatial working memory and image recognition in humans**
15.45-16.00	**KLAUDIA KUZDROWSKA,** *Adam Mickiewicz University, Poland* **Effects of Nicotine on Neurodegenerative Processes in a Model of Alzheimer's Disease in Drosophila Melanogaster Lineage Appl^{d}**
16.00-16.30	**Coffee/Tea**
16.30-17.00	**JAN RODRIGUEZ PARKITNA**, *Maj Institute of Pharmacology of Polish Academy of Sciences, Poland* **Modeling social reward, empathy and prosocial choice in mice**
17.00-17.30	**JACHIN EDWARD POUSSON**, *Jāzeps Vītols Latvian Academy of Music, Latvia* **Towards Brain-Computer Music Interfacing (BCMI) for music performance**
17.30-18.00	**Closing/Awards**
18.00-20.00	**Closing Party**

Oral presentations

1

Creative Dreams Help your Brain Learn Better: Generative Adversarial Networks in the Brain

Walter Seen

Institute of Physiology, University of Bern, Switzerland
walter.senn@unibe.ch

Dreams help us to digest experiences, clear up our mind, and find new solutions. The beneficial effects of "sleeping over it" is a commonplace, but cognitive sleep research so far mainly focuses on the aspect of memory consolidation. I present a computational model of sleep that extends the classical model of memory consolidation during NREM (non-rapid eye movement) sleep by a creative REM dream phase. The hypothesis is that during REM sleep our brain creates fake sensory experiences out of old memories, and these created experiences are preparing us to correctly behave in new real situations. The dreams improve in realism through an "adversarial" process that shapes the dreams to become more real. The matching of the dreams to reality is made possible by the specific bipolar morphology of cortical layer 5 pyramidal neurons. The surrounding cortical microcircuit further allows for an implementation of error-based learning. Mismatch-errors are expressed as dendrosomatic prediction errors that are minimized, both during wakefulness and sleep.

2

Why are the Networks of Moral, Risky, and Ambiguous Decision-Making Distinct in the Brain?

Aiste Ambrase[1, 2], Veronika Müller[3, 4], Hong Yu Wong[5, 6], Birgit Derntl[1, 7, 8]

[1] Department of Psychiatry and Psychotherapy, Tübingen Center for Mental Health, University of Tübingen, Germany
[2] International Max Planck Research School for Cognitive and Systems Neuroscience, University of Tübingen, Germany
[3] Institute of Neuroscience and Medicine: Brain and Behavior (INM-7), Research Center Jülich, Germany
[4] Institute of Systems Neuroscience, Medical Faculty, Heinrich Heine University Düsseldorf, Germany
[5] Werner Reichardt Centre for Integrative Neuroscience, University of Tübingen, Germany
[6] Department of Philosophy, University of Tübingen, Germany
[7] TübingenNeuroCampus, University of Tübingen, Germany
[8] LEAD Research School and Graduate Network, University of Tübingen, Germany
aiste.ambrase@uni-tuebingen.de

Moral dilemmas have been widely used to identify neural underpinnings of morality. Quite often, choosing between two conflicting options results in decision uncertainty. In this coordinate-based ALE meta-analysis we have compared neural correlates of moral decision-making (n=63 studies) with other types of uncertain value-based decision-making, i.e., risky (n=49) and ambiguous (n=38). Importantly, we have conceptually separated two angles of analysis inquiry as determined by the contrast of interest in the experiments. We investigated within each domain neural networks of 1) Task Performance components, and 2) Response Choice preferences. Additionally, cluster-based functional characterization of the identified regions was performed using the BrainMap database. Finally, resting-state functional connectivity (rsFC) profiles of the meta-analytically identified regions were analysed in an independent female sample (n=114). The meta-analysis showed that in terms of Task Performance, the mentalizing network is activated by moral decision-making, while risk and ambiguity domains require activation of executive control and valuation networks. Convergent activity was found only for risk and ambiguity domains in the right insula, bilateral paracingulate gyrus and the right middle frontal gyrus. In the Response Choice category, networks for morality and ambiguity domains could not be identified, while activity was found in the bilateral caudate and paracingulate gyrus for the risk domain. Investigation of rsFC networks revealed that even at rest the meta-analytically identified regions for moral, risky, and ambiguous decision-making coactivate within each network but have little between-network interaction. We discuss the differences between the networks of moral, risky, and ambiguous decision-making as intrinsic to functional brain architecture as well as the result of different approaches to experimental designs in the different subfields of decision neuroscience.

3

Iodine Status and the Brain: Effects and Mechanisms

Lina Zabuliene, MD, PhD

Faculty of Medicine, Vilnius University, Vilnius, Lithuania
lina.zabuliene@mf.vu.lt

Iodine is essential element for normal growth and for the development of the brain. Iodine is a major component of the thyroid hormones triiodothyronine (T3) and thyroxine (T4). Thyroid hormones regulate many important biochemical reactions, including protein synthesis and enzymatic activity, they are critical determinants of metabolic activity, proper skeletal and central nervous system development in fetuses and infants. Iodine deficiency can be dangerous in women of reproductive age, pregnant and breast-feeding women, and children below three years of age. Its lack can cause irreversible damage, since it is necessary for neuron migration and myelination in the brain. With severe iodine deficiency at this stage a drop of up to 20 points in IQ (Intelligence Quotient) can be observed. Brain development is not concluded during the intrauterine period, and adequate ingestion of iodine during infancy is necessary for the continuous and ideal development of this organ. Iodine deficiency during the first years of a child's life causes changes in brain development that can lead to reduced mental capacity and delayed development. There are studies that also associate the iodine deficiency in children with autism and attention deficit and hyperactivity disorder. Iodine deficiency in infancy has adverse effects on cognitive and motor performance, showing a drop of 7-10 IQ points. The effect of iodine on the adult brain is via thyroid hormones. Most adults with thyroid dysfunction will develop mental symptoms. This can be more prominent in adults with hyperthyroidism or severe hypothyroidism.

4

Factors Involved in the Pathophysiology of Alzheimer's Disease: New Insights About Sleep Microstructure, Chronic Stress and Cognitive Fitness in Late Midlife

Justinas Narbutas[1,2,3,4], Daphne Chylinski[1], Maxime Van Egroo[1], Vincenzo Muto[1], Mohamed Ali Bahri[1], Christian Berthomier[5], Eric Salmon[1,2,6], Christine Bastin[1,2], Christophe Phillips[1,7], Fabienne Collette[1,2], Pierre Maquet[1,6], Julie Carrier[8], Jean-Marc Lina[8], Gilles Vandewalle[1]

[1] GIGA-Cyclotron Research Centre-In Vivo Imaging, University of Liège, Liège, Belgium
[2] Psychology and Cognitive Neuroscience Research Unit, University of Liège, Liège, Belgium
[3] Aging Research Centre (ARC), Karolinska Institutet, Solna, Sweden
[4] Leibniz Research Centre for Working Environment and Human Factors (IfADo), Dortmund, Germany
[5] Physip SA, Paris, France;
[6] Department of Neurology, University Hospital of Liège, Liège, Belgium
[7] GIGA-In Silico Medicine, University of Liège, Liège, Belgium
[8] Centre for Advanced Research in Sleep Medicine, Université de Montréal, Montreal, Canada

narbutas@ifado.de

Introduction. Almost all cognitive functions decline with aging, but some individuals retain excellent memory and other cognitive functions well into their 70s or 80s. The scaffolding theory of aging and cognition posits that cognitive abilities depend on the structurural and functional aspects of the brain. Meanwhile, the structure of the brain is affected by such non-modifiable factors as biological aging, gender and genotype. But brain functions are also affected by cognitive reserve, which refers to lifestyle experiences that can be positive or negative for brain health. Negative factors include depression, chronic stress and sleep problems. Another important group of factors are the pathological deposits of proteins associated with Alzheimer's disease, namely amyloid-beta and tau. One of the factors, sleep quality is important for metabolism, restorative processes in the brain and memory consolidation. But with age, sleep becomes increasingly fragmented. Poor sleep is also associated with a higher concentration of pathological protein complexes in the brain. And finally, episodic memory can be affected both by poor sleep and by the accumulation of these proteins. Two important components of sleep microstructure are sleep spindles and sleep slow waves. Sleep spindles are a positive physiological phenomenon associated with the bursting of neuronal oscillations, which usually occurs in the second stage of sleep. Slow wave sleep can have a slow transition or a fast transition. Fast switching is associated with better memory consolidation. The coupling of both sleep spindles and slow waves of sleep were rarely studied before and espcially in late midlife.

Objective. The aim of our study was to determine whether the pairing of sleep spindles with slow sleep waves may be associated with early amyloid deposits and episodic memory in a group of healthy subjects aged between 50 and 70 years.

Methods. In the initial phase of the study, we examined participants' sleep quality using sleep polysomnography, amyloid deposits with positron emmision tomography, and episodic memory with the Mnemonic Similarity Task. After 2 years, we assessed the subjects' memory again with the same memory test but with different stimuli. We had 2 sleep variables: sleep spindle onset phase on slow-transition slow waves of sleep; and sleep spindle onset phase on fast-transition slow waves of sleep. We chose the medial temporal cortex as the brain region of interest because it is important for the regulation of slow waves in sleep.

Conclusion. Our results revealed that sleep spindle start phase on slow-transition slow waves is associated with amyloid-beta deposits. Also, our results showed that sleep spindle start phase on slow-transition slow waves is associated with worse episodic memory when assessed longitudinally. Taken together, it appears that these specific parameters of sleep microstructure may help predict increased risk for Alzheimer's disease. But these findings require a larger study population and possibly a wider age range.

5

Home Cage Monitoring System for Continuous Behavioural and Cognitive Phenotyping in Mice

Marius Bauza

University College London, UK
m.bauza@ucl.ac.uk

Comprehensive ethologically-relevant behavioural phenotyping in rodent experiments is essential for deciphering the neural basis of animal cognition. Automated home-cage-based testing platforms present a valuable tool to fulfil this need. However, they often involve complex animal training routines, water or food deprivation, and probe a limited range of behaviours. Here, we present a new fully automated AI-driven home-cage system for cognitive and behavioural phenotyping in mice („smart-Kage"). The system incorporates spontaneous alternation T-maze, novel-object recognition and object- in-place recognition tests combined with monitoring of an animal's position, water consumption, quiescence and locomotion patterns, all carried out continuously and simultaneously in an unsupervised fashion over long periods of time (>8 months). Mice learnt the tasks rapidly without any need for water or food restrictions. We applied an ethomics approach to show that combined statistical properties of multiple behaviours can be used to discriminate between mice with hippocampal, medial entorhinal and sham lesions and accurately predict genotype of Alzheimer's disease mouse model (App^{NL-G-F}) on an individual animal level, surpassing the performance of several gold standard cognitive tests. This technology could enable large-scale behavioural screening for genes and neural circuits underlying spatial memory and other cognitive processes.

6

Simultaneous Representation of Multiple Time Horizons by the Entorhinal Grid Cells

Julija Krupic

University of Cambridge, UK
julija@cambridgephenotyping.com

Grid cells and place cells constitute the basic building blocks of the medial entorhinal-hippocampal spatial cognitive map by representing the spatiotemporal continuum of an animal's past, present and future locations. However, the spatiotemporal relationship between these different cell types is unclear. We co-recorded grid and place cells in freely foraging rats and showed that time shifts in grid cells are proportional to their spatial scale, providing a nearly instantaneous read-out of a spectrum of progressively increasing time horizons. Time shifts of place cells also increase with the size of their firing fields and are generally larger compared to grid cells. Long and short time shifts occurred at different parts of the theta cycle which may facilitate their readout. Notably, time shifts were modulated by the animal's trajectories in relation to the local boundaries but not an animal's locomotion cues. Together, these findings suggest that progressively increasing grid cell time-horizons may provide a basis for calculating future animal's trajectories essential for goal directed navigation and planning.

7

Effects of Nicotine on Neurodegenerative Processes in a Model of Alzheimer's Disease in Drosophila Melanogaster Lineage Appl^{d}

Klaudia Kuzdrowska, Michalina Gadomska,
Anetta Lewandowska-Wosik, Ewa Chudzińska

Department of Genetics, Faculty of Biology,
Adam Mickiewicz University, Poznan, Poland
klaudia.kuzdrowska@tprs.stud.vu.lt

Alzheimer's disease (AD) is a progressive, degenerative disease of the central nervous system characterized by worsening of synaptic transmission and the death of neurons. Among other things, amyloid plaques are formed in the brain because of the abnormal accumulation of toxic peptides, including β-amyloid (Aβ).

Drosophila is widely used in AD research because it presents the same markers of the disease like those in humans (Tau, Aβ), which are known for creating phenotypes as neuronal death, cognitive decline, and locomotor disorders.

Nicotine is a commonly used compound in the tobacco industry which is one of the largest in the world and it is linked to addiction. There is a reason why it has been widely studied in terms of its effects on the human body, including the nervous system. Animal models provide a useful tool for examining neurodegenerative processes and Drosophila, is a convenient model has been used in the study of Alzheimer's disease since years. It turned out that nicotine has neuroprotective properties in Parkinson's disease. However, there is little research focusing on the potential neuroprotection of nicotine in Alzheimer's disease.

The aim of our study was to check whether nicotine shows neuroprotective properties in a model of Alzheimer's disease in the Drosophila containing a genetic mutation in the form of a deletion of the Appl gene (Appl^{d}). The research used behavioral tests in response to nicotine administration (adult insect climbing assay). At the cellular level, a comet assay was performed to examine the extent of brain cell damage in Appl^{d} flies treated with nicotine in relation to that seen in untreated flies. Our results show that the effects of nicotine on Appl^{d} fly can impair locomotor activity. This effect was not observed in wild type fly.

Key words: Drosophila melanogaster, Alzheimer's disease, nicotine, climbing assay, comet assay

8

Modeling Social Reward, Empathy and Prosocial Choice in Mice

Jan Rodriguez Parkitna, PhD

Department of Molecular Neuropharmacology, Maj Institute of Pharmacology, Polish Academy of Sciences, Krakow, Poland

janrod@if-pan.krakow.pl

Social interactions can be and often are rewarding. The effect of social contact strongly depends on circumstances, and the reward may be driven by varied motivational processes, ranging from parental or affiliative behaviors to investigation or aggression. The lecture will present mouse models of the rewarding effects of social interaction, from basic social conditioned place preference, to recognition of the affective state of interaction partners, and prosocial choice of actions benefitting others. Behavioral testing reveals social behavior in mice is dependent on sex, age and kinship, with surprising parallels to human behavior. Furthermore, endogenous opioid signaling was observed to be strongly involved in regulating the rewarding effects of social contact, which may open an approach to treatment of disorders affecting social behaviors. Taken together, the results show that rewarding effects of social contact may be robustly modelled in mice, though with clear limitations in more complex behaviors, prosocial in particular.

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I have no conflicts of interest to disclose.

9

Towards Brain-Computer Music Interfacing (BCMI) for Music Performance

Jachin Edward Pousson[1], Inga Griškova-Bulanova[2], Mahrad Ghodousi[2]

[1] Jazeps Vitols Latvian Academy of Music, Riga, Latvia
[2] Department of Neurobiology and Biophysics, Institute of Biosciences, Life Sciences Center, Vilnius University, Vilnius, Lithuania
jachin.edward.pousson@jvlma.lv

Introduction. A Brain-Computer Music Interface (BCMI) harnesses the EEG signal for musical purposes, enabling novel means of musical expression. Music is ubiquitously used to express and transfer emotion or mood. Musicians communicate emotion by means of expressive cues in the act of performance.

Due to several challenges, BCMI system designs reported in the past 20 years mostly involve motionless users which obscures musical intent. These are addressed through BCMI system design for music performance. First, EEG features related to expressive intentions during music performance are investigated for online detection. Second, EEG hardware designed for mobility and software-based filters are used to eliminate external noise. Third, functions for adjusting the detection thresholds of target EEG features are deployed to overcome individual and situational variables.

Method. A total of 2000 samples of 32 channel EEG data were collected from 10 pianists. Subjects were tasked with performing a music score while varying their manner of play to express 1 of 5 contrasting emotions (Neutral, Distressed, Excited, Depressed, Relaxed) upon each repetition. Average power spectra for each subject and emotion were calculated using the FFT into frequency bands (1-4 Hz, 4-8 Hz, 8-12 Hz, 12-30 Hz, 30-45 Hz). Average power spectra during emotional segments was divided by the average power of neutral segments to derive relative power per emotional condition.

Differences in relative power between conditions at 4 electrode clusters (Fp1, AF3, F3; Fp2, AF4, F4; P3, PO3, O1; P4, PO4, O2) were used to determine rules for detecting these features in the online EEG within software and functions to adjust these rules for individuals were deployed. Noisy electrodes were filtered out of the calculation. Target features were grouped into high vs low arousal conditions and detected levels were visually represented on a computer monitor and then mapped to graphical, MIDI and DMX outputs for visualising and musifying them in audio/visual software and hardware in real-time.

Results and Conclusion. The resulting BCMI system was evaluated for accuracy by groups of pianists, expert instrumentalists, and the author. Accuracy was determined by the percentage of time the BCMI feedback matched the performer's intent. Pianists achieved 70.80%, instrumentalists 74.46%, and the author 84.22% accuracy after a setup and training time of less than one hour.

Poster presentations

P1

Associations of VEGFA Gene Polymorphisms with Pituitary Adenoma and its Clinical Manifestations

Linas Ambraziejus, Greta Gedvilaite, Rasa Liutkeviciene

Neurosciences Institute, Lithuanian University of Health Sciences, Medical Academy, Lithuania

linasambraziejus.13@gmail.com

The pituitary gland is surrounded by various nervous, vascular, endocrine, and bony structures, so the most common pathology in this area is a benign pituitary adenoma (PA) tumor [1]. The etiology of this disease is diverse, and in more than half of the cases, no genetic cause is apparent. However, in some cases, germline or somatic genetic defects are associated with the occurrence of PAs. In this study, the association of PA with SNPs and haplotypes of *VEGFA* gene was investigated. This growth factor promotes the proliferation and migration of vascular endothelial cells and is required for both physiological and pathological angiogenesis [2]. Since the *VEGFA* gene and its variants are associated with such biological processes, it can be hypothesized that this gene may be related to the occurrence of PAs.

Aim. To study the associations of *VEGFA* gene polymorphisms (rs1570360, rs699947, rs3025033, rs2146323) with PAs and their clinical manifestations.

Materials and Methods. 112 patients with PA and 245 healthy volunteers participated in the study. DNA samples from peripheral blood leukocytes were purified by DNA salting-out method. RT-PCR performed single nucleotide polymorphisms (rs1570360, rs699947, rs3025033, rs2146323). Results were analyzed using the statistical analysis program "IMB SPSS Statistics 27.0" and SNPstats software.

Results. Statistical analysis of the frequency of PAs showed that individuals with the rare *VEGFA* haplotypes rs1570360, rs699947, rs3025033, and rs2146323 were associated with an increased likelihood of developing a pituitary adenoma (OR=7.54; 95% CI: 1.25-45.29; p=0.028). Statistical analysis also showed that women with these rare *VEGFA* haplotypes were associated with a higher probability of developing a PA (p<0.001). Other results of the studied polymorphisms showed that age, sex, and the size of PA did not affect the association with this benign tumor.

Conclusions. Our study revealed that rare haplotypes of *VEGFA* gene polymorphisms (rs1570360, rs699947, rs3025033, rs2146323) are associated with a 7.5-fold increased probability of developing PA, especially in women.

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P2

Investigation of the Effect of Cannabinol on Sleep in Rats Using Electrocorticography – A Pilot Study

Martynas Arbačiauskas[1], Vytautas Jonkus[2], Osvaldas Rukšėnas[1]

[1] Department of Neurobiology and Biophysics, Institute of Biosciences, Life Sciences Center, Vilnius University, Vilnius, Lithuania
[2] Institute of Applied Electrodynamics and Telecommunications, Vilnius University, Vilnius, Lithuania

martynas.arbaciauskas@gmail.com

Sleep disorders are widespread – around 30% of the human population suffers from at least one symptom of insomnia, including early waking, waking during the night or difficulty falling asleep. The effect of insufficient or disturbed sleep is broad, affecting endocrine, immune, muscular, cardiovascular, and nervous systems. As a consequence, the use of various allegedly sleep-altering substances, such as melatonin or cannabidiol, is increasing. One of such substances is cannabinol, which is researched very little, so further investigation into its effects is necessary if it is to be used as a sleep aid. Sleep is most commonly evaluated using parameters gathered via electroencephalography or electrocorticography, and one popular model organism is the rat (Rattus norvegicus), so for this work it was chosen to evaluate the effect of cannabinol on sleep using 24-hour rat electrocorticography using automated analysis. Novel recording equipment was used, developed in the Faculty of Physics in Vilnius University. The selected method was successfully applied , including development of a program for analysis. Recordings were split into 4 second intervals, denoised, and frequency analysis was performed. The program was run on a high-performance cluster computer in Vilnius University Faculty of Physics. It was revealed that compared to solvent Tween-80, during the light phase of the day, rats affected by cannabinol had lower alpha power. During the dark phase, cannabinol increased the part of high theta/delta intervals. Compared to saline, rats affected by cannabinol had a higher theta/alpha ratio, lower alpha power and lower beta power during the light phase. These parameters are associated with REM sleep and general activity. Importantly, the solvent itself had a significant effect when compared with saline injections. In many parameters, cannabinol and saline groups were more similar to each other than to the solvent group. Therefore, it's possible that Tween-80 alters sleep, while cannabinol restores it to a saline-like state. Additionally, an electromyogram was not recorded, which would allow to get more insights into REM sleep. This study had a small sample size and high variance in the data, so increasing the number of rats per group should be beneficial as well. Thus, it's necessary to conduct further research to clarify the effect of cannabinol on sleep.

P3

An Efficient Raav Vector for Protein Expression in Cortical Parvalbumin Expressing Interneurons

Gytis Baranauskas[1], Tatiana Tkatch[1], Kristina Rysevaite-Kyguoliene[2], Ignas Sabeckis[2], Deimante Sabeckiene[2], Dainius H Pauza[2],

[1] Neurophysiology laboratory, Neuroscience Institute, Lithuanian University of Health Sciences, Kaunas, Lithuania
[2] Anatomy Institute, Lithuanian University of Health Sciences, Kaunas, Lithuania
gytis.baranauskas@lsmuni.lt

Recombinant adeno – associated viruses (rAAV) are extensively used in both research and clinical applications. Despite significant advances, there is a lack of short promoters able to drive the expression of virus delivered genes in specific classes of neurons. We designed an efficient rAAV vector suitable for the rAAV-mediated gene expression in cortical interneurons, mainly in the parvalbumin expressing cells. The vector includes a short parvalbumin promoter and a specialized poly(A) sequence. The degree of conservation of the parvalbumin gene adjoining non-coding regions was used in both the promoter design and the selection of the poly(A) sequence. The specificity was established by co-localizing the fluorescence of the virus delivered eGFP and the antibody for a neuronal marker. rAAV particles were injected in the visual cortex area V1/V2 of adult rats (2 – 4 months old). Neurons expressing the virus delivered eGFP were mainly positive for interneuronal markers: 66.5 ± 2.8 % for parvalbumin, 14.6 ± 2.4 % for somatostatin, 7.1 ± 1.2 % for vasoactive intestinal peptide, 2.8 ± 0.6 % for cholecystokinin. Meanwhile, only 2.1 ± 0.5 % were positive for CaMKII, a marker for principal cells in the cortex. Optogenetic tests confirmed that our vector enables activation of parvalbumin fast spiking interneurons, that leads to elimination of responses to visual stimuli in principal cells. We conclude that our promoter allows highly specific expression of the rAAV delivered cDNAs in cortical interneurons with a strong preference for the parvalbumin positive cells.

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P4

Different Approaches to Purifying TMEM106B and its Possible Interaction with Tau

Rokas Bertašius, Lukas Krasauskas, Vytautas Smirnovas

Amyloid research sector, Institute of Biotechnology, Life Sciences Center, Vilnius University, Lithuania

rokas.bertasius@gmc.stud.vu.lt

The aggregation of amyloid proteins into fibrillar structures is associated with several dozen amyloidoses, including neurodegenerative diseases, which are among the most common disorders in the world, the most common of which – Alzheimer's disease – affects about 50 million people. It is predicted that these numbers will more than triple in the next 30 years. Unfortunately, there is no ultimate cure for it, like for any other tauopathy, so the existing treatment is only symptomatic. [1]. Recently, it was discovered that in some diseases together with Tau tangles, amyloid structures of a lysosomal protein, TMEM106B, can be found. No in vitro studies of TMEM106B interactions with Tau protein have been reported so far, and the main knowledge about the aggregation of this protein comes from postmortem brain research. It is hypothesized that the aggregation of the TMEM106B proteolysis product can directly stimulate Tau protein aggregation and thus activate the progression of various neurodegenerative diseases – tauopathies [2]. Since few protocols of TMEM106B purification exist and are hard to replicate, it is important to find new ways or optimize preexisting protocols to ease the production of TMEM106B for future research, helping to find new possible drug targets involved in tauopathies. TMEM106B genes were fused at N-termini with SENP1 protease cleavable His-Sumo tag. The Tau2N4R gene was inserted into the pET Champion His-Sumo vector using the TA cloning method, while the His-SUMO-TMEM106B gene was inserted into the pET28A expression vector by restriction cloning. Protein was purified using Ni2+ ion affinity and ion exchange chromatography methods. Aggregation of His-SUMO-TMEM106B alone and with Tau was carried out, and kinetics were followed by thioflavin T fluorescence assay. Fibril morphology is observed using atomic force microscopy.

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P5

Illusion of the Size of Incomplete Contours

A. Bielevičius, A. Bertulis, I. Česnavičienė, T. Surkys

Laboratory of Visual Neurophysiology, Institute of Biological Systems and Genetics Research, Lithuanian University of Health Sciences, Kaunas, Lithuania.

arunas.bielevicius@lsmuni.lt

The aim of the study was the illusion of the stimulus size depending on the configuration of the stimulus contour. Incomplete contour stimuli were obtained by removing from the pentagon: either a horizontal, vertical, or diagonal contour line, or a combination of lines forming the angle or rectangle. The expansion effect was always present without any exceptions, as in psychophysical experiments with stimuli of full contours. If the lower horizontal line was not present in the contour of the pentagon, the illusion did not change much, 8 to 9 arc min. When two lower lines, horizontal and diagonal were absent, there was an increase in strength of the illusion from 8 to 13 arc min. Apparently, this happened because the angular component was destroyed and the effect of the Müller-Lyer inner wings, causing a reduction in distance, weakened. If only the angular component, a pair of wings, was exposed, the strength of the illusion did not decrease, although the stimulus became shorter than the entire figure. On the contrary, there was an increase of the illusion from 8 to 13 arc min. Thus, the ratio of the effects of expansion and reduction changed. The expansion was on the decline, and the reduction was also declining, but to a higher degree. If the angular component was absent, and the contour of the open rectangle remained, the stimulus became shorter again. But the illusion significantly increased (8 to 17 arc min) referring to the strengthening of the expansion effect and weakening of reduction. For two horizontal lines, the result slightly increased. For the full rectangle, the illusion has also increased. In general, the ratio of expansion and reduction processes varied greatly in the responses to the stimuli during the length matching procedure. The local components of the stimuli were clearly affected by the configurations to which they belonged. The visual perception of the form cannot be divided into the perception of components and folded back like geometric drawings. When separated, any single segment, such as a line, angle, and the rest of the figure, become new visual wholes, regardless of the fact that the mosaic of excitations caused by them in the retina remains almost unchanged. The main factor of perceived distortions in the size of visual stimuli should be considered the functional relationships of the contour segments forming the shape, and not the integration of neural reactions for each segment.

P6

The Impact of Maternal High-Fat Diet on Offspring Retina

Neda Ieva Biliūtė[1], Gintarė Urbonaitė[1],
Guoda Laurinavičiūtė[2], Urtė Neniškytė[1,3]

[1] Institute of Biosciences, Life Sciences Center, Vilnius University, Lithuania
[2] Institute of Biomedical Sciences, Faculty of Medicine, Vilnius University, Lithuania
[3] VU-EMBL Partnership Institute, Life Sciences Center, Vilnius University, Lithuania

neda.biliute@gmc.stud.vu.lt

Aim. Today the usage of fat-rich Western diet is increasing, and this leads to increasing obesity rates. Many studies show that maternal high-fat diet causes inflammation which can lead to neurodevelopmental disorders of the offspring. It is shown that the retina, as a part of central nervous system, is also affected in the individuals consuming high-fat diet. However, there are no studies investigating the effect of maternal high-fat diet on the retina of the offsprings. In this study we aim to determine whether maternal high-fat diet leads to retinal changes in the offspring.

Methods. We fed female C57Bl/6 mice with a control diet (10% fat) or high-fat diet (60% fat) from weaning to lactation. The offsprings were weaned to CD. The eyes from the offspring were collected, fixed with 4% PFA, frozen and sliced using cryotome. Retinal ganglion cells and Müller cells were labeled immunohistochemically using anti-RBPMS and anti-GFAP antibodies respectively.

Results. We evaluated the number of retinal ganglion cells, GFAP signal area and the thickness of retinal layers. The measurements were compared between the groups of offspring.

Conclusions. Maternal high-fat diet did not have any significant effect on offspring retina.

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P7

KDR Gene rs2071559 and rs1870377 Gene Polymorphisms Association with Pituitary Adenoma

Akvilė Bružaitė[1], Greta Gedvilaite[1], Loresa Kriauciuniene PhD[1], Rasa Liutkeviciene PhD[1,2]

[1] Ophthalmology Laboratory, Neuroscience Institute, Lithuanian University of Health Sciences, Medical Academy, Kaunas, Lithuania, LT-50161.
[2] Neuroscience Institute, Lithuanian University of Health Sciences, Medical Academy, Eiveniu 2, Kaunas, Lithuania, LT-50161.

akvile.bruzaitee@gmail.com

Introduction. Pituitary adenomas (PA) are usually slow-growing benign tumors that do not metastasize to other body tissues. Tumor growth can eventually start to pressure nearby structures and cause endocrine or neurological disorders, such as infertility, headache, or changes in visual function. The exact cause of PA is unknown, and its pathogenesis is multifactorial. Mutations, changes in gene transcription, and epigenetic alterations interact together to promote tumorigenesis. More data on PA genetic factors are needed to predict tumor occurrence, invasiveness and relapse. Kinase insertion domain receptor (*KDR*) gene changes are associated with cancer occurrence. SNP analysis is a valuable predictor of neoplasm/cancer risk in certain populations where this polymorphism is frequently detected. New molecular markers can increase patients' survival and optimize treatment.

The aim. To determine *KDR* gene rs2071559 and rs1870377 polymorphisms association with PA.

Material and methods. The study included 100 individuals with PA and 200 healthy controls. Single nucleotide polymorphisms were determined by RT-PCR. Statistical data analysis was performed using the IBM SPSS program.

Results. Our study showed that *KDR* rs2071559 AA genotype and A allele are statistically significantly more frequent in PA patients than in the control group (p=0.027; p=0.028, respectively). We found that *KDR* rs2071559 AA genotype and A allele are statistically significantly more frequent in patients with invasive PA compared to the control group (p=0.018; p=0.015, respectively). Also, *KDR* rs2071559 AA genotype and A allele are statistically significantly less common and GG genotype is statistically significantly more frequent in relapse-free PA patients compared to the control group (p=0.043; p=0.009 and p=0.029, respectively). There were no statistically significant results of *KDR* rs1870377 polymorphism.

Conclusions:

1. *KDR* rs2071559 AA genotype and A allele are associated with the development of PA.
2. *KDR* rs2071559 AA genotype and A allele are more frequent in patients with invasive PA compared with control group.
3. *KDR* rs2071559 AA genotype and A allele are statistically significantly less common and GG genotype is statistically significantly more frequent in relapse-free PA patients compared to control group.

P8

Retinal Ganglion Cell Topography and Anatomical Spatial Resolution of Common Chaffinch

Ugnė Bytautaitė, Mindaugas Mitkus

Institute of Biosciences, Life Sciences Center, Vilnius University, Vilnius, Lithuania
ugne.bytautaite@gmail.com

Animal vision specializations often represent and help to understand diet, foraging behaviour, activity patterns or adaptations to various habitats of different species. The common chaffinch (*Fringilla coelebs* Linnaeus, 1758) is a small passerine (order Passeriformes) that is one of the most common bird species in many parts of Europe. However, little is known about their visual system.

In this study, using retinal wholemounts and Nissl staining the maximum density and topography of the retinal ganglion cells was investigated to evaluate retinal specializations and to calculate anatomical spatial resolution. These visual parameters were then linked to the species' habitat and diet as well compared to other species. After creating maps of retinal ganglion cell density distribution, it was found that the common chaffinch possesses one central area of sharp vision that also includes a deep central fovea. The maximum density of ganglion cells in the parafoveal region was 114000 ± 6200 cells/mm^2 (mean ± SD) and the average anatomical spatial resolution was 13.0 ± 0.3 cycles/degree (n = 4 eyes).

The common chaffinch is commonly found in various types of forests, parks and gardens. These types of habitats are characterized by denser vegetation, compared to grasslands or savannahs, that places objects of interest in different parts of the visual field. Thus, the topography of the ganglion cells in the retina of the common chaffinch is in line with the "Terrain theory" and reflects adaptation to complex 3D structure of the species habitat. The common chaffinch often forages on the ground and its diet consists mainly of seeds, but small insects can make up to 60-80% of the total food ration during spring and summer. The anatomical spatial resolution found in this study seems to be sufficient for a characteristic mixed diet, prey size and type of foraging.

P9

Computational Modeling of Alzheimer's Disease in Hippocampal CA1 Pyramidal Neurons

Justinas Dainauskas[1], Aušra Saudargienė[2], Helene Marie[3], Michele Migliore[4]

[1] Vytautas Magnus University, Kaunas, Lithuania
[2] Neuroscience Institute, Lithuanian University of Health Sciences, Kaunas, Lithuania
[3] Institut de pharmacologie moléculaire et cellulaire, CNRS, Université Côte d'Azur, Valbonne, France
[4] Institute of Biophysics, National Research Council, Palermo, Italy

justinas.dainauskas@vdu.lt

The most common form of dementia in the world is Alzheimer's disease (AD), a degenerative and irreversible brain illness. Despite the fact that the number of AD patients is rising, no ground-breaking treatments have been suggested recently. In order to understand the intricate molecular, synaptic, cellular, neuronal, and network level causes of impaired learning and memory in the AD, a new multidisciplinary approach is required. We use an integrated experimental and computational modelling approach to explore and better understand the impairment in synaptic plasticity caused by AD-related peptides at hippocampal CA1-CA3 synapses in early AD disease. Amyloid beta (Aβ), Amyloid eta (Aβ), and the Amyloid APP intracellular domain are among the AD-related peptides that are produced as a result of altered amyloid precursor protein (APP) processing and clearance in the early stages of the disease (AICD). While high concentrations of AICD cause LTP disruption and leave LTD intact at glutamatergic synapses, Aβ inhibits long-term potentiation (LTP) and promotes long-term depression (LTD) in hippocampal CA1 pyramidal neurons. The aim of this study is to investigate the joint effect of AICD and Aβ on LTP and LTD at hippocampal CA1-CA3 synapses applying computational modeling approach. We used a newly developed NMDAr-dependent voltage-based model of synaptic plasticity along with a compartmental model of a CA1 pyramidal neuron. The increased AICD levels were modeled, by adjusting the conductances of SK channels, L-type calcium channels, and the contribution of GluN2B-containing NMDA receptor. The heightened levels of Aβ were modeled as increased extracellular glutamate concentration, endocytosis of synaptic AMPA receptors, decreased synaptic density, and altered GluN2B-containing NMDA receptor-mediated activation of calcium/calmodulin-dependent kinase II (CaMKII). Our modeling results show that increased AICD levels disrupt LTP while LTD is unaffected, while increased Aβ levels disrupt LTP and enhance LTD, mirroring the experimental results. Simulation with both AICD and Aβ having pathological concentrations disrupt synapse ability to potentiate weight. Computational modeling study sheds light on the AICD- and Aβ-induced complex processes and their interactions in shaping synaptic plasticity at the hippocampal synapses.

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P10

Estimation of Patient Brain Connectome for Individualized The Virtual Brain Model to Predict Neurosurgical Treatment Outcomes in Parkinson's Disease

Gustavas Davidavičius[1], Paul Jan Triebkorn[2], Andrius Radžiūnas[3], Jan Fousek[2], Justinas Dainauskas[4], Vytautas Kučinskas[4], Viktor Jirsa[2], Aušra Saudargienė[4]

[1] Department of Informatics, Vytautas Magnus University, Kaunas, Lithuania
[2] Institut de neurosciences des systemes, University Aix Marseille Université, Marseille, France
[3] Department of Neurosurgery, Hospital of Lithuanian University of Health Sciences Kauno klinikos, Kaunas, Lithuania
[4] Neuroscience Institute, Lithuanian University of Health Sciences, Kaunas, Lithuania
email: gustavas.davidavicius@stud.vdu.lt

Background and aim: Parkinson's disease (PD) is a neurodegenerative disorder characterized by involuntary, uncontrolled movements. Currently one of the best available treatment options is subthalamic nucleus (STN) deep brain stimulation (DBS). However, this invasive procedure may not lead to the substantial improvement in PD symptoms. The goal of the study is to build an individualized brain connectome to later embed it into The Virtual Brain (TVB) platform for human brain activity simulation. The long-term aim is to predict the outcomes of DBS in PD patients to plan successful treatment.

Materials and methods: Ten PD patients underwent STN DBS implantation surgery. Preoperative T1 and diffusion MRI images and a postoperative CT image were collected. A structural T1 MRI scan was processed with Freesufers recon-all pipeline to obtain tissue segmentation and reconstruction of the cortical surfaces. Diffusion weighted images were processed using MRtrix3, performing artefact corrections, constrained spherical deconvolution and tractography. The structural T1 image was rigidly registered with the diffusion image in order to project the cortical and subcortical parcellation of the brain onto the reconstructed tracts. The Desikan and DISTAL atlas for cortical and subcortical brain areas were used, respectively, to obtain a structural connectome. The DBS electrode was identified on the postoperative CT image and registered with the T1 image.

Results: The structure of the virtual brain model from the patient T1 MRI neuroimaging data was built. The connectome including subcortical areas of globus pallidus internal, globus pallidus external and STN was calculated. The DBS electrode was projected into the virtual brain model to simulate the volume of tissue activated by electric stimulation.

Conclusions: The connectivity extracted will be embedded in the TVB platform to model the activity of the patient brain in deep brain stimulation conditions. A dynamical neural mass model will be equipped to every node of the connectome to simulate neural activity. Perturbations of the dynamics will be modelled by a realistic stimulus through the virtualized DBS electrodes. Patient specific virtual brain modelling will improve our understanding in inter-individual outcomes of DBS treatment.

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P11

Analysis of M6A Modification Level at RRACH Motifs in LINC00461, GAS5, and NEAT1 Genes in Gliomas

Dragunaite R., Skiriute D.

Laboratory of Molecular Neurooncology, Neuroscience Institute,
Medical Academy, Lithuanian University of Health Sciences, Kaunas, Lithuania
rugile.dragunaite@lsmuni.lt

Glioblastoma (GB) is the most common and aggressive brain tumor, characterized by high resistance to therapy and by inter- and intra-tumoral heterogeneity [1]. Epitranscriptomic modifications may modulate key genes involved in glioblastoma cell metabolism and contribute to their pathogenesis by increasing their heterogeneity, plasticity, and malignancy [2]. M6A RNA methylation is a dynamic and reversible modification process which is highly involved in the initiation and development of numerous malignancies [3]. Recent studies propose that the m6A RNA methylation process offers potential targets for cancer therapy in the future. Snap-frozen tumor tissue from 16 GB and 8 LGG patients were used for isolation of total RNA with TRIzol Reagent. Poly-A enriched RNA was used for direct-RNA sequencing by Oxford Nanopore Technologies. The "nf-core/nanoseq" pipeline (ver.:2.0.1) was used for detection of RNA modifications. First, according to the literature in our RNA-seq data we selected three genes (LINC00461, GAS5 and NEAT1) which are involved in glioma progression, regulation of tumor cell growth, invasion, migration and metastasis. Second, our data analysis showed that m6A marks were lower in glioblastoma at gene level in all selected lncRNAs. There were significant differences between survival dependency and m6A modification level in LINC00461. Next, the most frequently modified RRACH motif in tumor samples was found to be AAACT in the LINC00461, GAS, and NEAT1 genes. AAACT motif was found to be mostly modified at the positions 3316 and 3892 of LINC00461 gene transcript 3-exon in GB and LGG samples, with a higher modification detected in GB. While in GAS5 the most modified positions were 513 and 604 in the 11-exon in both GB and LGG, being higher in LGG. NEAT1 gene at the positions 3184 and 3723 of AAACT motif were identified having a higher level of m6A in LGG, whereas were unmodified in GB samples at the 3184 position. Global m6A modification level was higher in LGG samples, as compared to higher malignancy grade glioblastomas. The most frequently modified RRACH motif in analyzed genes was identified AAACT and modification level differed depending on location in the gene. The link between m6A modification and lncRNAs offers a new perspective and suggests that m6A modification and lncRNAs may be important prognostic markers and therapeutic targets for gliomas.

P12

The Associations between STAT4 Gene rs10181656 and rs7574865 Polymorphisms with Optic Neuritis with or without Multiple Sclerosis

Monika Duseikaitė, Greta Gedvilaite,
Loresa Kriauciuniene, Rasa Liutkeviciene

Neurosciences Institute, Lithuanian University of Health Sciences, Medical Academy, Lithuania

monika.duseikaite@lsmu.lt

Abstract. Optic nerve inflammation (ON) is defined as damage to one of the cranial nerves, often associated with multiple sclerosis (MS) and infectious processes (1). In the association of ON and MS, it is often difficult to distinguish the specific signs of these diseases, as ON can be part of the manifestations of MS (2). STAT4 plays an important role in the function of innate and adaptive immune cells and is involved in many autoimmune diseases (3). STAT4 is activated by interleukin (IL)-12 and IL-23. Mentioned interleukins promote the differentiation of CD40+ T cells into Th1 and Th17 cells and the production of interferon-γ (IFN-γ) and IL-17 (4). The Th1 pathway is considered the most important proinflammatory part of pathogenesis in MS, whereas the Th17 pathway has been implicated in the pathogenic mechanisms of MS and ON (5). It is well known that ON is closely related to MS. However, it is often difficult to distinguish the specific symptoms of these diseases; thus, the SNPs studied in our work could directly influence the manifestation of ON.

Aim. To assess the associations of *STAT4* gene rs10181656 and rs7574865 polymorphisms in optic neuritis patients with or without multiple sclerosis.

Materials and Methods. The study included 81 patients with ON, 32 of whom had MS, and 156 healthy subjects. DNA samples from peripheral blood leukocytes were purified by the DNA salting-out method. Single nucleotide polymorphisms (rs10181656, r7574865) were performed using the real-time polymerase chain reaction method (RT-PCR). Results were calculated using the statistical analysis method of ”IBM SPSS Statistics 27.0″.

Results. We found that C allele of *STAT4* gene rs10181656 single nucleotide polymorphism (SNP) was statistically significantly more frequent in the ON patients with MS group than in the control group (79.69% vs. 65.38%, p = 0.024). *STAT4* rs10181656 allele C was statistically significantly more frequent in the ON patients without MS than in the control group (78.57% vs. 65.38%, p = 0.020). *STAT4* rs7574865 allele G was statistically significantly more frequent in the ON patients with MS than in the control group (84.38% vs. 65.93%, p = 0.003).

Conclusions. *STAT4* gene rs10181656 C allele is more frequent in both ON with MS and without MS than in the control group. Also, *STAT4* rs7574865 G allele is more frequent in ON patients with MS than in the control group.

P13

The Association between Relative Leukocyte Telomeres Length and TERT Single Nucleotide Polymorphisms and Pituitary Adenoma

Greta Gedvilaite, Alvita Vilkeviciute, Loresa Kriauciuniene, Rasa Liutkeviciene

Neurosciences Institute, Lithuanian University of Health Sciences, Medical Academy, Kaunas, Lithuania

greta.gedvilaite@lsmuni.lt

Pituitary adenoma (PA) is one of the most common benign tumors of the pituitary gland. Unfortunately, the disease pathogenesis still remains unclear (1). It is known that molecular biomarkers act as an indicators of biological, pathological processes, or pharmacological responses that provide helpful information for diagnosing the disease and predicting its outcome (2). Telomeres are nucleoprotein complexes at the ends of eukaryotic chromosomes (3). Progressive shortening of telomeres leads to senescence, apoptosis, or oncogenic transformation of somatic cells, affecting the health and lifespan of an individual (4). The activity of telomerase is inhibited by regulatory proteins, which limit telomere proliferation, and it is therefore thought that TERT polymorphisms are closely related to telomere length (5). Regarding the telomere length being closely related to tumorigenesis, it is important to determine its impact on pituitary adenoma occurrence.

Aim. To determine the relationship between relative leukocyte telomeres length, TERT gene single nucleotide polymorphisms, and pituitary adenoma.

Methods. The study enrolled 126 patients with pituitary adenoma and 368 healthy subjects. Single nucleotide polymorphisms (rs2736098, rs401681) and relative leukocyte telomere lengths were carried out by RT PCR. The results were assessed using the statistical analysis method of "IBM SPSS Statistics 27.0".

Results. We found that the TERT rs2736098 C allele was statistically significantly less frequent in the group of patients with active pituitary adenoma (66.4 % vs. 79.2 %, p=0.045), and the rs401681 C allele was statistically significantly more common in the group of patients with invasive pituitary adenoma than in the control group (63.9 % vs. 57.8 %, p=0.033). TERT rs2736098 was associated with 2.5-fold increased odds of active pituitary adenoma occurring under codominant and recessive models (OR=2.546; 95 %; CI: 1.042-5.798; p=0.029; (OR=2.464; 95 proc. CI: 1.101-5.485; p=0.024), respectively). Statistically significantly longer relative telomere leukocyte length was found in pituitary adenoma patients with the TERT rs401681 CC genotype compared to controls (median (IQR): 1.176 (1.894) vs. 0.498 (0.567), p=0.037).

Conclusions. TERT gene rs2736098 is associated with 2.5-fold increased odds of pituitary adenoma development. Pituitary adenoma patients with TERT gene rs401681 CC genotype have statistically significant longer telomeres than control group subjects.

P14

EEG Connectivity Analysis for Development of a Brain-Computer Music Interface: a Feasibility Study

Mahrad Ghodousi[1], Jachin Edward Pousson[2], Inga Griškova-Bulanova[1]

[1] Department of Neurobiology and Biophysics, Institute of Biosciences, Life Sciences Center, Vilnius University, Vilnius, Lithuania
[2] Jazeps Vītols Latvian Academy of Music, Riga, Latvia
mahrad.ghodousi@gmc.stud.vu.lt

Introduction. Brain-Computer Interface (BCI) enables the users to control a computer or any other external device using their brain activity. The electroencephalography (EEG) technique has produced the best results in this regard due to its high temporal resolution and affordability. The Brain-Computer Music Interface (BCMI) can be used to convert brain signals into musical features while maintaining the emotional context. However, emotion-related features should first be identified. So far, several methods have been introduced to reveal the information flow and networks. Magnitude Square Coherence (MSC) and Granger Causality (GC) are categorized as connectivity features that have shown promising results in emotion discrimination while their low-processing requirements make them good choices for real-time applications. In this study, we have tried to evaluate the accuracy of these features in recognizing the expressed emotions by the musicians to develop a real-time BCMI system.

Method. 32 channels of EEGs were collected from 10 professional pianists participating in a piano performance task. They were instructed to play a simple learning piece of music several times while trying to change their playing style to express one of five emotions based on a two-dimensional valence-arousal model of affective space (distressed, excited, depressed, relaxed, and neutral). EEG signals were processed in MATLAB using an automated pipeline to remove artefacts and divided into segments containing one of the emotions. Connectivity matrices were calculated for MSC and GC, which were further converted into rows of the final feature matrices. A one-side ANOVA test was performed on the obtained feature matrices, and features with P-value<0.01 that were able to distinguish at least two pairs of emotions were selected. Support Vector Machines (SVMs) were trained for each pair of emotions, and to test the accuracy of the classifier, the data was divided into two parts, known as the training and testing datasets. To remove the effect of outliers, 5-fold cross-validation was used to report the accuracy of the SVM classifier, and the reported accuracies represent the average value and standard deviations.

Results and conclusion. The discrimination accuracy was 86.06±0.62 and 80.51±1.71 for MSC and GC, respectively. The obtained accuracies and simplicity of features indicate that MSC and GC can be good candidates for developing a real-time BCMI system.

P15

The Associations between TAS2R16 Gene Polymorphisms and Early Age – Related Macular Degeneration

Ieva Inokaityte, Greta Gedvilaite, Rasa Liutkeviciene

Ophthalmology laboratory, Neurosciences Institute, Lithuanian University of Health Sciences, Medical Academy, Lithuania

ieva.inokaityte@gmail.com

Abstract. Age-related macular degeneration (AMD), the most common cause of visual impairment in developed countries, is incurable [1]. AMD is the leading cause of registered blindness in people over the age of 50 years in the western world [2]. The disease damages photoreceptors, retinal pigment epithelium, and neurovascular complex. There is an early and late stage of AMD. In the early stage, there is the formation of large drusen and pigmentary abnormalities [3]. AMD is considered a multifactorial disease, with genetic, environmental, lifestyle, and other factors influencing its occurrence. TAS2R16 is a protein-coding gene that binds to the G protein-coupled receptor family located on the taste receptor cells of the tongue and palate epithelium. TAS2R16 gene polymorphisms rs860170, rs978739, and rs1357949 are significantly related to longevity [4]. Although a variety of factors influence AMD, the present study focuses on the association of polymorphisms in the TAS2R16 gene with the occurrence of AMD.

Aim. To determine the associations between TAS2R16 gene polymorphisms and early AMD.

Materials and Methods. The study enrolled 100 patients with early-AMD and 112 healthy subjects. Samples of DNA from peripheral blood leukocytes were purified by DNA salting-out method. Single nucleotide polymorphisms (rs860170, rs978739, rs1357949) were carried out using real-time polymerase chain reaction. The results were assessed using the statistical analysis method of "IBM SPSS Statistics 27.0".

Results. Analysis of TAS2R16 gene rs978739, and rs1357949 polymorphisms did not reveal any differences in genotype distribution between the patients with early-AMD and the reference group (p=>0.05). The TAS2R16 rs860170 C/T genotype was more frequent in females of AMD group compared to control group: 62.5% vs. 61.2%, p=0.019.

Conclusions. TAS2R16 rs860170 gene polymorphism is associated with early AMD.

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P16

How Anxiety Predicts Psychomotor Functions in Stroke Patients?

Jovita Janavičiūtė-Pužauskė, Liuda Šinkariova

Department of Psychology, Vytautas Magnus University, Kaunas, Lithuania
janaviciute.jovita@gmail.com

Background and aim. Stroke is a leading cause of long-term disability around the world. Lower psychomotor speed is associated with a disability and increased risk of brain vulnerability. Affected psychomotor functions manifest in stroke patients along with other impairments. Since psychomotor functions are associated with negative outcomes (e.g. disability, lower quality of life) it is important to reveal factors that predict lower psychomotor functions. It is known that depression is associated with lower psychomotor functions, yet the anxiety role in stroke patients' psychomotor functions is not clear. This work aimed to evaluate whether anxiety could predict psychomotor functions in stroke patients.

Materials and methods. The subjects were 66 stroke patients, 30 females, and 36 males. The age range was between 49 and 84 (M=64.6; SD=9,2). Psychomotor functions were evaluated by the Finger Tapping Test (Reitan, 1959). Anxiety was measured by The Geralized Anxiety Disorder scale – 7 (GAD-7, Spitzer R. et al., 2006). Ethical approval for the study was granted by the Vilnius Regional Biomedical Research Ethics Committee (Nr. 2022/2-1408-880). All participants provided written informed consent before taking part in the study.

Results. Age was included in the regression because it correlated with psychomotor functions. The multiple regression was conducted to explore whether age and anxiety could significantly predict stroke patients' psychomotor functions. The results of the regression indicated that the model explained 19.9% of the variance and that the model was a significant predictor of psychomotor functions, $F(2,41) = 5.1$, $p = .01$. While anxiety contributed significantly to the model ($B = -.609$, $p=0.044$), age did not ($B = -.344$, $p=0.059$). The final predictive model was: Psychomotor functions = 56.12 + (-.609*Anxiety) + (-.344*Age).

Conclusions. The results revealed that stroke patients' psychomotor functions are associated with age and anxiety. While greater anxiety level predicts lower psychomotor functions, age did not.

P17

The Effect of Anaesthesia on Auditory Steady-State Response in Mice

Urte Jasinskyte, Robertas Guzulaitis

Department of Neurobiology and Biophysics, Institute of Biosciences, Life Sciences Centre, Vilnius University

urte.jasinskyte@gmc.stud.vu.lt

The auditory steady-state response (ASSR) is evoked oscillatory activity that is entrained to the frequency and phase of repeated auditory stimulation (Wang et al., 2020). It tests the capacity of auditory pathways to generate a synchronous activity. The ASSR is altered in schizophrenia (O'Donnell et al., 2013), therefore it is used as a biomarker in detecting the pathology (Shahriari et al., 2016). Despite high potential, the mechanisms underlying ASSR are largely unknown. For example, anaesthesia is widely applied in animal studies for immobilization and blocking motor responses to painful stimuli (Moody et al., 2021), however, it is not known how anaesthesia affects ASSR. The aim of this study was to evaluate the impact of anaesthesia on ASSR.

The experiments were performed on C57BL/6 mice. Electrodes were implanted in the primary auditory cortex (A1) and prefrontal cortex (PFC) for ECoG registration at conscious and anaesthetized (sevoflurane and ketamine/xylazine) conditions. ASSR was induced by 2 ms white noise stimuli (clicks) presented at 40 Hz for 1 s at 70 dBa. The Morlet wavelet transformation was used for signal time-frequency analysis. ASSR parameters (power and phase-locking index (PLI)) were calculated at the 35-45 Hz interval.

The results showed that ketamine/xylazine mostly decreases higher frequency oscillations (40-120 Hz) in A1, but also decreases delta (1-4 Hz) and beta (13-30 Hz) oscillations in PFC. In contrast, sevoflurane decreases power across most frequencies in the range of 1-120 Hz both in A1 and PFC. Also, ketamine/xylazine and sevoflurane induce a significant decrease of ASSR parameters in A1. In contrast, both anaesthetics enhance ASSR generation in PFC.

In conclusion, ketamine/xylazine and sevoflurane anaesthesia have a different effect on ASSR parameters in A1 and PFC at the 40 Hz stimulation. Further studies are needed to explain the detailed mechanisms of ASSR generation under anaesthesia.

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P18

Effect of added Sugar on Cognitive Functions and Impulsivity: A Pilot Study

Karolina Jocbalyte, Rytis Stanikunas

Institute of Psychology, Vilnius University, Vilnius, Lithuania
karolina.jocbalyte@fsf.stud.vu.lt

A holistic approach to a person reveals that one's psychological well-being is inseparable from one's physical well-being. Sugar usage has become an important public health issue nowadays. Therefore, the interest in studying the cognitive and emotional effects associated with sugar consumption has increased. The aim of the main study is to investigate how the intake of added sugar affects participants' impulsivity and cognitive functions as monitored during the performance of computerized tasks. Quantitative data for this study was collected via self-report questionnaires, including demographics, the Dietary Fat and free Sugar – Short Questionnaire (DFS), the Yale Food Addiction Scale (YFAS 2.0), and the Barratt impulsiveness scale (BIS-11). Participants also performed computerized tasks: the Reactivity to hint, Stroop and Emotional Stroop (related to food), and the Go-NoGo task. Finally, we used electroencephalography to record the electrical activity of the brain during the task (event-related potentials (ERPs)). Comparing the results of evaluations before and after the added sugar consumption revealed differences in computerized tasks' performance. Intake of added sugar was associated with a shorter reaction time and a larger number of errors immediately after its consumption. The ERPs revealed differences in the P3 and latter components. Overall, the results of the current study suggest that there are performance and electrophysiological differences between the two experimental conditions. However, the pilot study has not revealed how these differences are related to subjects' eating habits.
Keywords: Added sugar, cognitive functions, impulsivity, event-related potentials (ERPs).

P19

The Impact of OPRM1 Single Nucleotide Polymorphisms and Haplotypes on the Alcohol Use Disorder

Migle Kaminskaite[1], Kornelija Bekezaite[1], Auguste Juocyte[1], Darius Jokubonis[1,2], Adomas Bunevicius[1], Ausra Saudargiene[1,3], Ramunas Jokubka[1]

[1] Neuroscience Institute, Lithuanian University of Health Sciences, Kaunas, Lithuania
[2] Republican Centre for Addictive Disorders, Kaunas, Lithuania
[3] Department of Informatics, Vytautas Magnus University, Kaunas, Lithuania
migle.kaminskaite@lsmuni.lt

Background. In modern society, alcohol use disorder (AUD) is a common problem, which is often accompanied by somatic and psychiatric disorders and social problems. Despite widely conducted research, there is no effective treatment for AUD. About 50% of the risk for AUD is inherited. One of the most researched single nucleotide polymorphism (SNP) in AUD pathogenesis is OPRM1 rs1799971. However, the results of this SNP were inconsistent, both A and G alleles were demonstrated to be associated with the AUD. Other SNPs in OPRM1 gene were related with other addiction disorders and may play role in AUD. Therefore, we aimed to study the impact of SNPs rs7758009, rs1074287, rs1799971, rs3778150, rs9479757, rs648893, rs671531, rs1918760, rs2272381 and their haplotypes on the risk for AUD

Methods. The study included 838 participants recruited from local community (N=726) and addictive disorders treatment center (N=112). The risk of AUD was evaluated by Alcohol Use Disorder Identification Test (AUDIT). Impulsivity was measured by Barrat Impulsiviness Scale-11 (BIS-11). Only those samples which were at least half genotyped were included in the prelimany haplotype analysis. Associations of separate SNPs with AUDIT and BIS-11 scores were evaluated by ANOVA. Haplotypes were established by Haplowiev sofware. Haplotype analysis was conducted using haplo.stats package in R software.

Results. Rs1799971 G allele and rs7758009 C allele were associated to AUDIT score ($p < 0.01$). Rs1799971 G allele was associated to BIS. Three haplotype blocks were established (rs7758009-rs1799971, rs1799971-rs3778150, rs648893-rs671531). AUDIT score was associated with haplotypes C-G and T-A in haploblock rs7758009-rs1799971 (p values < 0.05 and <0.01 accordingly and haplotypes G-T and A-T in haploblock rs1799971-rs3778150. BIS-11 scores were associated with haplotypes G-T and A-T in haploblock rs1799971(p values <0.05).

Conclusions. The effect of separate SNP could be influenced by interaction with other SNPs. We plan on genotyping the remaining samples for a better evaluation of haplotypes impact on AUD. Both BIS-11 and AUDIT scores were related to rs1799971 SNP and to the haplotypes in haploblock rs1799971-rs3778150. These results suggest the need of subsequent analysis performing structural equation modeling to evaluate direct or indirect effect of SNPs and haplotypes on the risk of AUD. Better understanding of AUD pathogenesis could benefit the development of more effective treatment methods.

P20

The Electrophysiological Properties of Mouse Hippocampal Pyramidal Neurons During Early Development

Emilija Kavalnyte[1], Kornelija Vitkute[1], Urte Neniskyte[1,2], Aidas Alaburda[1]

[1] Institute of Biosciences, Life Sciences Center, Vilnius University, Vilnius, Lithuania
[2] VU-EMBL Partnership Institute, Life Sciences Center, Vilnius University, Lithuania
emilija.kavalnyte@gmc.stud.vu.lt

Background. During the first weeks of development hippocampal pyramidal neurons undergo morphological and electrophysiological changes. These changes lead to the effective neural network formation and functional maturity of hippocampus. However, it is still not known how electrophysiological properties of mouse hippocampal CA1 pyramidal neurons change during early postnatal development and whether sex has an impact on shaping the electrical activity of the maturing brain.

Aim. To investigate the electrophysiological properties of mouse hippocampal pyramidal neurons during early neural development and to compare them between different sex mice.

Materials and methods. Wild type mice of different sex and age groups (5 to 21 postnatal days) were used in this study. Electrical activity of hippocampal CA1 pyramidal neurons in acute mouse brain slices was evaluated using patch-clamp whole cell configuration method. Python program was developed for optimization of neuron action potential analysis and applied to evaluate action potential parameters.

Results. Electrophysiological properties of mouse hippocampal CA1 pyramidal neurons changed with age: input resistance decreased and rheobase increased, the initial and steady action potential amplitudes, peaks, maximum depolarization and repolarization rates increased, initial and steady widths and thresholds decreased. Differences between sex were also found: rheobase increased with age only in male group, steady action potential peak values increased only in female group and in certain age groups rheobase, initial and steady peak and threshold values were higher in males than females.

Conclusions. Our study confirms that postnatal brain maturation is associated with significant changes of electrophysiological properties of hippocampal pyramidal neurons in mice. Early postnatal development results in ability of hippocampal pyramidal neurons to generate the action potential series of higher frequency, what shapes the connectivity of hippocampal circuitry and leads to more effective information processing in a matured brain. Furthermore, results suggest that sex might have an influence on determining developmental pathways, therefore it requires further investigation.

P21

Metabolic Sialic Acid Labelling and Modulation of Neuronal Sialylation in Organotypic Hippocampal Slice Cultures

Ugne Kisieliute[1], Ugne Kuliesiute [1,2], Urte Neniskyte[1,2]

[1] Institute of Biosciences, Life Sciences Center, Vilnius University, Vilnius, Lithuania
[2] VU-EMBL Partnership Institute, Life Sciences Center, Vilnius University, Vilnius, Lithuania

ugne.kisieliute@gmc.stud.vu.lt

Background and aim. Synaptic pruning is a fundamental process for healthy neuronal circuit maturation and development. Studies have suggested various models of synaptic pruning mechanisms, one of which is mediated by sialic acid – a monosaccharide, which typically terminates the structures of neuronal glycocalyx composing glycoconjugates. The presence of sialic acid inhibits neuron-microglia interaction and microglial phagocytic activity meanwhile after the elimination of sialic acid the residues of de-sialylated glycoconjugates promote microglial elimination of neuronal processes. However, detailed molecular mechanism of such pathway has not been determined yet.

Methods. We use mouse organotypic hippocampal slice cultures as a platform to define how sialylation provides a selective mechanism for the maintenance and strengthening of a subset of synapses. We apply bioorthogonal CLICK chemistry to metabolically label de novo synthesised sialic acid and use chemical inhibitors of sialyltrasferases and sialidases to alter neuronal sialylation.

Results. Mouse organotypic hippocampal slice cultures were optimised and used as a perfect system to study neuronal sialylation ex vivo allowing to visualise the entire tree of dendrite. The visualization and quantitative analysis of newly synthesized sialic acids showed specificity of metabolic sialic acid labelling. The use of chemical inhibitors indicated that the level of neuronal sialylation can be modulated ex vivo enabling to assess the changes in sialic acid abundance on the cell surface.

Conclusions. In conclusion, we show the applicability of mouse organotypic hippocampal slice cultures as a robust model to address de novo synthesis and the turnover of sialic acid in the developing brain tissue. This system enables to target and characterise the under-investigated role of sialic acid in the mechanism of synaptic pruning.

P22

Pro-Inflammatory S100A9 Protein Effects on Tau Protein Aggregation

Lukas Krasauskas, Vytautas Smirnovas

Amyloid research sector, Institute of Biotechnology,
Life Sciences Center, Vilnius University
chemlukras@gmail.com

Neurodegenerative diseases are among the most common disorders in the world. Unfortunately, despite intensive research, the understanding of the mechanism of these diseases is limited, and almost all existing treatments are symptomatic. Alzheimer's disease has attracted the most attention from scientists because it is the most common neurodegenerative disease, affecting about 50 million people worldwide. In addition to amyloid plaques composed of amyloid-β peptides, neurofibrillary tangles formed from the protein Tau are a hallmark of this disease and other tauopathies. Amyloid-β aggregates (and α-synuclein aggregates in Parkinson's disease) have been shown to promote Tau aggregation. It has also been observed that the aggregation of these two peptides involves the pro-inflammatory protein S100A9, whose elevated levels in the brain are recorded after various head injuries [1]. It was found that in post mortem Alzheimer's patient brains Tau tangles colocalizes with S100A9 protein aggregates, raising the question about S100A9 involvement in this disease progression. There has been some speculation from the scientific community that neuroinflammation could induce Tau pathology; thus, it is feasible that S100A9 as a pro-inflammatory protein could be a culprit behind it or at least in part responsible. However, it is strange that there is not much information available, or studies performed to confirm or rule out the potential of the S100A9 protein or its aggregates to participate directly in Tau aggregation. And since amyloid aggregation mechanisms are quite complex and various links between proteins are still unknown, in this work we tried to elucidate the link between Tau and S100A9 proteins. To determine the optimal aggregation conditions for Tau protein prior to experiments with S100A9 protein, polyanion heparin was used as an initiator of amyloid protein aggregation in vitro. Aggregation kinetics were followed using the amyloidophilic dye thioflavin T fluorescence (ThT) assay. Atomic force microscopy was performed to analyze the morphology of the formed aggregates and Fourier-transform infrared spectroscopy was used for the analysis of protein secondary structures.

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P23

Acute Effect of Breathing Exercises on Mental Activity Under Psychological Stress

Wenming Liang[1], Jing Xiao[2], Feifei Ren[3] Zishuai Chen[4], Zhenmin Bai[5], Osvaldas Rukšėnas[1]

[1] Department of Neurobiology and Biophysics, Institute of Biosciences, Life Sciences Center, Vilnius University, Vilnius, Lithuania
[2] Department of Physiotherapy and Rehabilitation, Xiyuan Hospital of Chinese Academy of Chinese Medical Sciences, China
[3] Department of Physical Education, Beijing Language and Culture University, Beijing, China
[4] College of Physical Education, Minzu University of China, Beijing, China
[5] School of Sports Medicine and Rehabilitation, Beijing Sport University, Beijing, China
wenming.liang@gmc.vu.lt

Background and aims: Mindful breathing and slow breathing were found to be able to decrease psychological stress and improve mental health, while fast breathing could increase neuronal excitability. This study aimed to discover the influence of 5min mindful breathing, slow breathing, and fast breathing, compared to music listening, on mental activity during the intensive neuropsychological task.

Methods: 48 participants (men: n=24, age=30±6, BMI=23.2±1.7; women: n=24, age=29±6, BMI=21±1.3) received one-month breathing training online (slow breathing: six reps/min; fast breathing: 30% increase in regular respiration rate). Participants chose the relaxing music they preferred. The mental activity was determined from the accuracy and reaction time of the Stroop Color and Word Test (SCWT). During the experiment, participants performed a one-time baseline test (watched a neutral video for 5min and took 5min of SCWT) and then completed 5min of music listening, slow breathing, and fast breathing (SCWT was taken after each intervention) in a random sequence followed by a 5min rest. Every minute's values were taken for analysis using Generalized Estimating Equation.

Results: For men, during SCWT, there was a significant interactive effect on the accuracy after interventions of slow breathing and music listening, with a higher accuracy after slow breathing at the fifth minute ($z=3.290$, $p=0.001$), and a similar result was found after the slow and fast breathings ($z=3.574$, $p=0.001$), while no significant differences were found for women.

Conclusions: After slow breathing, men's accuracy in doing the neuropsychological task was higher relative to after music listening and fast breathing. 5min breathing exercises or music listening didn't significantly influence women's mental activity.

P24

Psychophysical Study of the Misperception of Length Caused by a Circular Contextual Distractor

Vilius Marma[1], Aleksandr Bulatov[1], Natalia Bulatova[2], Laimutis Kučinskas[2], Edgaras Diržius[2]

[1] Laboratory of Visual Neurophysiology, Institute of Biological Systems and Genetics Research, Lithuanian University of Health Sciences
[2] Institute of Biological Systems and Genetics Research, Lithuanian University of Health Sciences

vilius.marma@lsmuni.lt

Aim. The aim of the study was to further develop a quantitative model of the filled-space illusion and test it to account for the effects caused by stimuli containing an unconventional form of contextual distractor.

Methods. Illusion was measured as a function of the radius of the distracting circle positioned symmetrically with respect to lateral terminator of the three-dot stimulus. Data obtained in two different series were fitted with relevant functions of the model.

Results. It was shown that the model satisfactorily describes all changes in the illusion magnitude for stimulus with the outlined circles and the uniformly filled circles. In addition, it has been demonstrated that the illusion magnitude varies predictably with the size of the circle, and there is no significant difference between the data obtained for stimuli with the outline and filled distractors.

Conclusions. A good correspondence between the experimental and theoretical results supports the suggestion that the context-evoked augmentation of neural excitation can determine the occurrence of the filled-space illusion.

P25

Induction of Experimental Glaucoma in Rats Using Differing Methods of Lasering

Kernius Mickevičius[1], Tomas Paulauskas[1], Justyna Mozyro[1], Inesa Lelyte[1], Odeta Adamoniene[1], Symantas Ragauskas[1], Giedrius Kalesnykas[1,2,3]

[1] UAB Experimentica
[2] Experimentica Ltd.
[3] Tampere University, Tampere, Finland.
kernius@experimentica.com

Purpose. To evaluate RGC loss and IOP elevation in the rat laser-induced ocular hypertension model for glaucoma with differing induction parameters.

Methods. Laser photocoagulation was performed unilaterally (OD) on day 0 at the episcleral veins (treatment group 1, TG1), trabecular meshwork (treatment groups 2 and 3, TG2 and TG3), or a combination of the two (treatment group 4, TG4). The lasering was performed using the following settings of laser power and duration: 0.5 W and 100 ms for TG1, 1 W and 100 ms for TG2, 1 W and 200 ms for TG3, 0.5 W and 100 ms for TG4. The lasering with the same settings for each treatment group was repeated after 7 days. The intraocular pressure was monitored on days 1, 4, 8, 11, 14, 15, 22 and 27. Functional assessment of retinal ganglion cells was performed using pattern electroretinography (pERG) at baseline and on days 14, 21 and 28. Animals were euthanized on day 28, eyes were enucleated, processed as retinal wholemounts, immunostained against RNA-binding protein with multiple spicing (RBPMS) and RBPMS-positive cell numbers were counted. The contralateral eye (OS) was used as control.

Results. Photocoagulation of episcleral veins and trabecular meshwork on Day 0 and Day 7 led to statistically significant increase in the intraocular pressure on Day 1 and Day 8. Ocular hypertension resulted in statistically significant reduction of pERG amplitudes in TG2 on day 21 ($P = 0.02$), TG3 on day 28 ($P = 0.03$) and TG4 at all timepoints ($P = 0.01$ on Day 14; $P < 0.001$ on Day 21; $P < 0.001$ on Day 28). Statistically significant decrease in the total number of RBPMS-positive cells was observed in TG1, TG3 and TG4 (for all $P <= 0.01$) as compared to contralateral control eyes.

Conclusions. A combination of laser photocoagulation of episcleral veins and trabecular meshwork resulted in the highest increase of IOP and the biggest loss of RGC function and cell number as compared to other induction methods of ocular hypertension.

P26

Changes of Functional Brain Connectivity During Depression Treatment with Transcranial Magnetic Stimulation

Gajane Mikalkėnienė[1], Kastytis Dapšys[1,2]

[1] Republican Vilnius Psychiatric Hospital, Vilnius, Lithuania
[2] Department of Neurobiology and Biophysics, Institute of Biosciences, Life Sciences Center, Vilnius University, Vilnius, Lithuania

wel4ou@gmail.com

Background. Functional brain connectivity (FBC) methods allow to research connectivity disorders, such as depression, using a directed transfer function (DTF). It can be depicted by a model of the brain with the presented electroencephalographic (EEG) registration points, their connections and causal interactions (directionality) via the assessment of the areas of bioelectric activity and directions of activity transfer. Transcranial magnetic stimulation (TMS) is used as an alternative treatment for drug-resistant depression and is considered to restore impaired connections. The combination of TMS and EEG allows to study changes in brain connectivity in a non-invasive way. The aim of the study was to research FBC during depression treatment using Matlab add-on Brainstorm.

Methods. Data was collected using Galileo NT software (by EBNeuro, Italy), then processed and analyzed using Matlab add-on Brainstorm. EEG data was calculated as matrices which were processed by Granger causality method to summarize it as a direction image. The averages of the FBC strength were calculated for each direction in each group using the frequency-dependent spectral connectivity assessment. Between-group and within-group differences in FBC were assessed using a permutation t-test variation. Patient groups were evaluated before and after treatment, compared with a control group.

Results. DTF was assessed in each EEG frequency band. The biggest changes were noticed in theta frequency band (4-8 Hz). 28 directions of patients brain electrical activity have changed after treatment with TMS. Comparing DTF between patients before and after treatment in relation to healthy subjects, 11 directions changed after treatment. It was found that TMS changes FBC but patients' after treatment results still bear little resemblance to healthy subjects'.

Conclusions. Directed transfer function assessment is an innovative way of functional brain connectivity assessment. Most of observed connectivity changes after TMS treatment were in EEG theta frequency. Authors hypothesize that artificial neural networks could be created and used as part of DTF assessment research. It could be implemented for prediction of possible treatment efficacy.

P27

Determining Individual Gamma Frequency through Chirp-Based Auditory Stimulation

Aurimas Mockevičius, Inga Griškova-Bulanova

Department of Neurobiology and Biophysics, Institute of Biosciences, Life Sciences Center, Vilnius University, Vilnius, Lithuania

aurimas.mockevicius@gmail.com

Activity in the gamma range is related to many sensory and cognitive processes. Therefore, individualized measures of gamma-band activity are considered to be a potential marker reflecting the state of networks within the brain. However, the methodology for determining the individual gamma frequency (IGF) is not well established. In the present work, we tested an IGF extraction method by applying it to EEG data from either a high (15) or a low (3) number of electrodes in fronto-central regions. During EEG recordings, 80 subjects (42F/38M) received auditory stimulation consisting of clicks with varying inter-click periods, covering 30-60 Hz range. IGFs were determined by estimating the individual-specific frequency that most consistently exhibited high phase locking during the stimulation. The method showed an overall high reliability (98%) of extracted IGFs which were similar to those reported in the previous studies (37±4 Hz, 30-49 Hz). In addition, IGFs extracted from both sets of electrodes (15 and 3) yielded a strong correlation ($r = 0.78$). This work provides a reliable method for IGF estimation and shows that it is possible to determine individual-specific gamma frequency using a limited number of electrodes.

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P28

EEG Study of Mental Fatigue Regarding Long-Term Usage of Volumetric Multiplanar Display

Mehrdad Naderi[1], Albina Abdullayeva[1], Tatjana Pladere[1], Reinis Alksnis[2], Gunta Krumina[1]

[1] Department of Optometry and Vision Science, Faculty of Physics, Mathematics and Optometry, University of Latvia, Riga, Latvia
[2] Laboratory of Statistical Research and Data Analysis, Faculty of Physics, Mathematics and Optometry, University of Latvia, Riga, Latvia

mehrdad.naderi@lu.lv

Stereoscopic technology, which provides highly immersive depth perception, has been investigated massively in many different experiments; however, there is scant research on new technologies that produce actual three-dimensional (3D) images. One of them is the volumetric multiplanar display has been developed recently to show a real 3D image without wearing any stereoscopic goggles, for instance, polarized and anaglyph. Moreover, electroencephalography (EEG) is one of the most reliable methods to study temporal properties of 3D perception and mental fatigue regarding long-term usage of the visual system. Our study aimed to evaluate the degree of mental fatigue after a long-term visual search task on the volumetric display. The study designed based on power spectral analysis of some mental fatigue algorithms and parameters for example, θ, α, β, γ, θ/α, β/α, (α+θ)/β, θ/(θ+α+β), α/(θ+α+β), and β/(θ+α+β). We analyzed the parameters on eleven central electrodes F3, Fz, F4, C3, Cz, C4, P3, Pz, P4, O1, and O2. We recorded brain signals with closed eyes before and after one hour of visual search task on the volumetric multiplanar display. Each trial consisted of a combination of 3D and 2D visual targets.

The results showed a general increase in mental fatigue parameters; however, there were no statistically significant differences between the first rest state (before the task) and the second rest state (after).

In conclusion, a slight difference in brain oscillations due to the long-term visual search task on the volumetric multiplanar display could be a reason to consider a lower load on the accommodation-vergence system concerning stereoscopic displays that induces conflict between accommodation and vergence.

Keywords: Electroencephalography (EEG), visual search task, stereoscopic, volumetric multiplanar, depth perception.

P29

Haplotype Analysis of TAS2R16 (Rs978739, Rs1357949) in the Occurrence of Pituitary Adenoma

Enrika Pileckaite, Alvita Vilkeviciute, Greta Gedvilaite, Loresa Kriauciuniene, Rasa Liutkeviciene

Neurosciences Institute, Lithuanian University of Health Sciences, Medical Academy, Kaunas, Lithuania

enria.pileckaite@lsmu.lt

Pituitary adenomas (PAs) are usually benign tumors that arise in the anterior part of the pituitary gland. It is the third most common intracranial neoplasm after gliomas and meningiomas, accounting for approximately 15% of all intracranial tumors (1). The etiology of PA is diverse, and the actual cause of PA remains undetermined, but it is known that approximately 5% of PA occurs due to hereditary syndromes caused by gene alterations (2). Regarding the impact of genetic changes on the development of PA, new genetic markers can be investigated to determine PA (3). Studies showed that TAS2R16 gene polymorphisms are related to cancer development in rectal and colorectal cancers (4,5). However, Campa et al. determined that the TAS2R16 gene haplotype (rs1357949–rs6466849–rs860170–rs978739: T_A_A_G) shows an association with longevity (6). It is known that some of the functionally active or hereditary syndromes caused by PAs are related to benign tumors and shorter lifespans, which can be affected by gene alterations (7,8). Based on the previously analyzed studies, it is important to determine the connection between haplotypes of TAS2R16 gene single nucleotide polymorphisms (rs978739, rs1357949) and PA development.

Aim. To evaluate the association between pituitary adenoma development and haplotypes of TAS2R16 (rs978739, rs1357949).

Materials and methods. The investigation included 107 patients with PA and 205 healthy individuals. DNA was isolated from peripheral blood leukocytes using the DNA salting-out method. Single nucleotide polymorphisms of TAS2R16 (rs978739, rs1357949) were performed by RT-PCR. The obtained data were statistically evaluated using "IBM SPSS Statistics 27.0" computer program, while haplotype analysis was performed using "SNPStats" web application. Linkage disequilibrium (LD) analysis was estimated by D′ and r2 measures.

Results. The deviation between the expected haplotype frequency and the observed frequency (D') was calculated, which is equal to 0.9018, as well as the square of the correlation coefficient of haplotype frequencies (r2) with a value of 0.1433 was estimated. The TAS2R16 rs978739-T – rs1357949-A haplotype was the most common in the study group and was therefore chosen as the reference (OR – 1, CI = 95%). However, haplotype analysis did not show statistically significant associations with the occurrence of PA.

Conclusion. TAS2R16 gene haplotype (rs978739, rs1357949) is not associated with pituitary adenoma development.

P30

Gender Differences in Serotonergic Control of Rat Social Behaviour

Ieva Poceviciute, Kamile Kasperaviciute, Rokas Buisas, Osvaldas Ruksenas, Valentina Vengeliene

Department of Neurobiology and Biophysics, Institute of Biosciences, Life Sciences Center, Vilnius University, Vilnius, Lithuania

ievapoceviciute04@gmail.com

Rationale. There is increasing evidence that enhancement of the salience of social stimuli can have beneficial effect in managing many psychiatric conditions. There are, however, clear gender-related differences in social behaviour, including neural mechanisms responsible for different aspects of social functions. Objectives. We explored the role of the serotonergic system on rat social behaviour under baseline and under stressful conditions in female and male rats.

Methods. Rats were neonatally treated with the selective serotonin transporter (SERT) inhibitor escitalopram; a procedure known to cause a long-lasting reduction of serotonergic activity. In adulthood, social behaviour was tested in a social interaction test and ultrasonic vocalisations (USVs) were recorded in pair-tested unfamiliar rats before and after yohimbine-induced stress-like state.

Results. Our data demonstrated that both female and, to a lesser extent, male escitalopram treated rats, exposed to a novel social situation, had fewer social exploration events and emitted fewer frequency-modulated calls with trills, trills altogether and step calls, suggesting that impaired function of the serotonergic system reduced the positive valence of social interaction. In a stress-like state, 50 kHz flat calls were increased only in female rats, indicating increased seeking of social contact. However, the number of flat calls in escitalopram treated female rats were significantly lower compared to control rats.

Conclusions. These data suggest that, even though the serotonergic system plays a significant role in controlling social behaviour of both genders, females may benefit more from the serotonergic pharmacotherapy with respect to enhancement of beneficial effects of social support, especially in stress-related situations.

P31

Sialidase Activity Evaluation in Developing Mouse Hippocampus

R. Prokopovicius[1], U. Kuliesiute[1,2], U. Neniskyte[1,2]

[1] Institute of Biosciences, Life Sciences Center, Vilnius University, Vilnius, Lithuania
[2] VU-EMBL Partnership Institute, Life Sciences Center, Vilnius University, Vilnius, Lithuania

rimas.prokopovicius@gmc.stud.vu.lt

Background and aim. Sialidases, enzymes also known as neuraminidases, cleave sialic acid from glycoconjugates and play an important role in the regulation of neuronal sialylation. Sialic acid removal from the neuronal glycocalyx is suggested as one of the mechanisms of synaptic pruning contributing to the removal of unnecessary synapses in the developing brain to ensure healthy neuronal network development. The highest enzymatic activity of sialidases in CNS is reported in the hippocampus, however, the information is limited, and the exact role of sialidases in the process of neuronal network development and maturation remains understudied.

Methods. Enzymatic sialidase activity was measured in freshly collected mouse hippocampus tissue samples of various postnatal age between P0 – P90. Enzymatic activity was normalised to the total amount of protein. Statistical analysis to determine the differences between age groups and sex has been performed.

Results. No enzymatic activity was present in the P0 mice hippocampus, suggesting that sialidases become active in the postnatal development of mice. The highest enzymatic activity of sialidases, around twice as big of an increase compared to other age groups was observed at the age of P14 with significantly higher activity in male hippocampus.

Conclusion. In conclusion, we showed that in mouse hippocampus sialidases demonstrate the highest activity at the age of P14 which corresponds to the time of developmental pruning of synapses in the mammalian CNS. These findings suggest that sialidases have an important role in the mechanism of synaptic pruning in the developing brain.

P32

The Association of TERC Rs12696304, Rs35073794 Gene Polymorphisms with Multiple Sclerosis

Gintare Rumsaite[1], Greta Gedvilaite[1], Renata Balnyte[2], Loresa Kriauciuniene[1], Rasa Liutkeviciene[1]

[1] Neurosciences Institute, Medical Academy, Lithuanian University of Health Sciences, Lithuania
[2] Department of Neurology, Medical Academy, Lithuanian University of Health Sciences, Lithuania

gintare.rumsaite99@gmail.com

Abstract. Multiple sclerosis (MS) is a central nervous system disease (1). It has been determined that the development of MS could be influenced by aging, which is caused by the accelerated shortening of telomeres (2). Telomeres are DNA – protein complexes which protect the ends of chromosomes from genomic instability (3). Telomere length is maintained by a ribonucleoprotein enzyme – telomerase (4). Telomerase activity is inhibited by regulatory proteins that limit telomere elongation, therefore the TERC gene polymorphisms, which affect telomerase activity, are thought to be closely related to changes in telomere length. Taking that into consideration, we selected to discover the association of the telomerase component TERC of single nucleotide polymorphisms with MS.

Aim. To determine the association of TERC rs12696304 and rs35073794 gene polymorphisms with the occurrence of multiple sclerosis.

Material and Methods. The research consists of 200 patients with MS and 240 healthy controls. DNA was extracted from peripheral blood leukocytes by a salting-out method. TERC rs12696304 and rs35073794 genotyping were carried out by using real-time polymerase chain reaction. The statistical analysis of the obtained data was performed by using the "IBM SPSS Statistics 27.0".

Results. Our study determined that TERC rs12696304 G allele is statistically significantly less frequent in the MS group than in the control group (20.5 % vs. 26.52%, p= 0.038). Also, we found that TERC rs35073794 GG genotype is statistically significantly more frequent in MS than in the control group, while AG is statistically significantly less frequent (54.0 vs. 32.6, p<0.001; 45.5 vs. 67.4, p<0.001, respectively). Moreover, A allele is statistically significantly less frequent in the MS group than in the control group (23.25 vs. 33.7, p<0.001). Binary logistic regression revealed that TERC rs12696304 G allele is associated with 1.4-fold decreased odds of MS development under additive model (OR: 0.703, (95% CI: 0.506 – 0.976), p=0.035). TERC rs35073794 is associated with about 2.4-fold decreased odds of MS development under codominant, dominant, over-dominant, and additive model (OR: 0.408, (95% CI: 0.275 – 0.603), p<0.001; OR: 0.412 (95% CI: 0.279 – 0.610), p<0.001; OR: 0.404 (95% CI: 0.273 – 0.598), p<0.001; OR: 0.427 (95% CI: 0.289 – 0.629), p<0,001, respectively).

Conclusion. TERC rs12696304 and rs35073794 are associated with decreased odds of MS development.

P33

The Effect of St. John's Wort Extract on Catalase Activity in Mice Organs

Ilona Sadauskiene[1], Arunas Liekis[1], Asta Kubiliene[2], Mantas Tamkevicius[2], Rima Naginiene[1]

[1] Neuroscience Institute, Lithuanian University of Health Sciences, Kaunas, Lithuania
[2] Department of Analytical and Toxicological Chemistry, Faculty of Pharmacy, Lithuanian University of Health Sciences, Kaunas, Lithuania
Ilona.Sadauskiene@lsmuni.lt

St. John's Wort, botanically known as Hypericum perforatum L., is a widespread medical herb widely used in Lithuania and all over the world. The aerial parts of the plant are rich in antioxidants such as flavonoids, carotene, and vitamin C. Although the plant is well known for its anti-inflammatory, antidepressant, antimicrobial, antiviral and antioxidant effects, the studies for its capability to reduce oxidative stress in the brain are sparse. Though antioxidant properties of some phenolic compounds of St. John's Wort have been proved to be effective in vitro, absorption of these compounds from the gastrointestinal tract, the further metabolism, tissue uptake and possibility to pass blood-brain barrier still remains unclear. There is also insufficient knowledge about the further fate of these compounds, depending on the dose and the mode of entry into the body. The present study aimed to elucidate possible protective effects of Hypericum perforatum L. extract in alleviating the toxicity of aluminum on catalase (CAT) activity in mice brain and liver. The experiments done on BALB/c laboratory mice. The CAT activity in organs homogenates determined spectrophotometrically. Results expressed as the mean ± SEM. Results showed that aluminum decreases CAT activity in the liver and brain of mice by 13.9% and 88.4%, respectively, compared to control group. Meanwhile, the influence of St. John's wort extract on enzyme activity was versatile. In the liver Hypericum perforatum L. extract reduced CAT activity by 19.4% in comparison with control mice. The effect of the extract of St. John's wort for CAT activity in aluminum-treated mice liver was practically minimal. The effect of St. John's wort extract on CAT activity in the liver of aluminum-treated mice was practically minimal, i.e. equal to the control level. However, the effects of St. John's wort extract could be clearly seen in the brains. The extract decreases CAT activity by 74.5%, compared to control. But administration of St. John's wort extract to the aluminum group showed a large increase in CAT activity. Hypericum perforatum L. extract itself may reduce CAT activity in the brain and liver of mice. But can increase CAT activity in the brain and liver of aluminum group, thus reducing the peroxidation induced by aluminum ions.

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Problematic Gaming and Gambling: A Systematic Review of Task-Specific EEG Protocols

Dovile Simkute[1], Artemisa R Dores[2,3], Fernando Barbosa[3], Inga Griskova-Bulanova[1]

[1] Institute of Biosciences, Vilnius University, Vilnius, Lithuania
[2] School of Health, Polytechnic of Porto, Porto, Portugal
[3] Laboratory of Neuropsychophysiology, Faculty of Psychology and Education Sciences, University of Porto, Porto, Portugal

dovile.simkute@gmc.vu.lt

Background. The notion that certain behaviors might be addictive lately has become an interest of research. Particular attention has been paid to the investigation of neurobiological mechanisms underlying problematic behavior disorders with a special focus on gambling and gaming. However, currently existing criteria for discrimination between problematic and non-problematic behavior receives criticism. Electroencephalography (EEG) and Event-Related Potentials (ERPs) are broadly used in addiction-related research and to our knowledge, no attempt was made so far to systematically overview the experimental paradigms and ERP components used in EEG research in the field of gaming and gambling.

Methods and materials. A systematic literature review of PubMed, Scopus, Web of Science (Web of Science Core Collection), EBSCOhost Research Databases (APA PsycINFO; APA PsycArticles; OpenDissertations; ERIC) databases was conducted. Following search terms were used to search the databases: ERP, "event related potential*", EP, "evoked potential*", SS , "steady state", EEG, electroencephal*; gam* NOT gamma. As this is systematic methods review and is focused on a narrative description of methodologies employed by studies, no particular measures of effect within the individual studies were inspected.

Results. A total of 24 studies were revised (problematic gaming – 16, pathological gambling – 8). 3 main target domains (Cue-reactivity, Information processing and Reward Processes & Risk Assessment) implemented to illustrate the experimental protocols.

Conclusions. Gambling-related research is highly focused on the investigation of the reward-related processes, whereas gaming-related research is mostly focused on the altered aspects of more general information processing. A vast heterogeneity regarding the ERP experimental paradigms being used, lack of clear guidelines and standardized procedures leads to having no recognizable measures capable to reliably discriminate or characterize the population susceptible to addictive behavior or being able to diagnose and monitor these disorders. Keywords: behavioral addictions, gaming, gambling, electroencephalography, event related potentials.

P35

Antisense lncRNA CHROMR: Relation to PRKRA and Glioma Patient Survival

Dovydas Širvinskas[1], Daina Skiriutė[2], Giedrius Steponaitis[2], Rytis Stakaitis[2], Paulina Vaitkienė[1]

[1] Laboratory of Molecular Neurobiology, Neuroscience Institute, Lithuanian University of Health Sciences, Kaunas, Lithuania
[2] Laboratory of Molecular Neurooncology, Neuroscience Institute, Lithuanian University of Health Sciences, Kaunas, Lithuania

dovydas.sirvinskas@lsmu.lt

Background. Natural non-coding antisense transcripts (ncNATs) are long non-coding RNA (lncRNA) transcribed from the opposite strand of a separate protein coding or non-coding gene and can affect the overlapped gene through epigenetic, transcriptional, post-transcriptional and/or translational modulations. Through this ncNATs can influence cancerous cell proliferation, migration and therapeutic resistance. lncRNA *CHROMR* is a ncNAT of the *PRKRA* gene (encoding the protein PACT), which, along with its' antagonist *TARBP2* (encoding TRBP), participate in the PKR-dependent part of the integrated stress response (ISR) network. PACT binds to PKR to activate it, while TRBP binding to PKR inhibits it. Activation of the ISR through PKR inhibits protein synthesis and leads cells to apoptosis, which is an important process in the development and survival of cancerous cells.

Methods. We performed RNAseq on post-surgical tumor samples from 26 glioma patients at the Hospital of the Lithuanian University of Health Sciences "Kauno Klinikos", Department of Neurosurgery. This data was then compared to data from the TCGA and GTEx databases.

Results. We found increased levels of CHROMR in glioma cells from both Low-Grade Glioma (LGG) and Glioblastoma Multiforme (GBM) patients compared with healthy brain tissue, without changes to expression of *PRKRA*. We could also observe lower survival rates for patients with a lower *PRKRA* to *CHROMR* ratio compared with high *PRKRA* to *CHROMR* ratio. Lower levels of *TARBP2* were able to rescue survival rates of patients with high *CHROMR*, further linking *CHROMR* with the PKR-dependent ISR.

Conclusions. Here we show that high levels of *CHROMR* (i.e., low ratio of *PRKRA* to *CHROMR*) is a marker of poor prognosis for glioma patients, which could be ameliorated by low levels of *TARBP2*.

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The Effect of Maternal High-Fat Diet on Offspring Behavior and Gut Microbiota

Adomas Smalskys[1], Gintarė Urbonaitė[1], Urtė Neniškytė[1,2]

[1] Institute of Biosciences, Life Sciences Center, Vilnius University, Lithuania
[2] VU-EMBL Partnership Institute, Life Sciences Center, Vilnius University, Lithuania
adomas.smalskys@gmc.stud.vu.lt

Aims. A typical Western diet is excessively fatty, leading to a rapid increase in human obesity worldwide, including the women of reproductive age. There is growing evidence that maternal high-fat diet (mHFD) may cause neurodevelopmental disorders in the offspring, in part due to the changes in the microbiota. Our aim was to determine how mHFD alters the microbiota in the mothers and their offspring and how these changes affect the behavior in offspring using a mouse model.

Methods. Female C57Bl/6 mice were fed a control diet (CD, 10% fat) or high-fat diet (HFD, 60%) from weaning to lactation. Before mating, the metabolic status of the dams was evaluated by the body mass and glucose and insulin tolerance tests. The offspring were weaned to CD. We investigated the behavioral phenotype of the offspring in the three-chamber test, marble burying, Barnes maze test and reciprocal social interaction test. Microbiota composition of the cecum of the dams and their offspring were analyzed using 16S rRNA gene sequencing.

Results. We determined that the consumption of HFD causes metabolic dysfunction in the dams. mHFD decreased relative quantity of gut bacteria in both dams and offspring. Microbiota alterations at the genus level were more prominent in mHFD female versus male offspring. mHFD females demonstrated grater relative decrease in bacteria in genus level similar to HFD mothers. Decreased sociability was noticed in both mHFD males and females although only males had shown increased activity and only females had showed decreased repetitive behavior.

Conclusions. Our findings show, that mHFD altered the composition of the offspring gut microbiota which may contribute to abnormal behavior in a sex-specific manner.

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Optic Neuritis: a Case Report

Almina Stramkauskaitė[1], Paulina Mikulėnaitė[2], Brigita Glebauskienė[2], Rasa Liutkevičienė[2,3], Arvydas Gelžinis[2], Reda Žemaitienė[2]

[1] Lithuanian University of Health Sciences, Medical Academy, A. Mickeviciaus 9 str., Kaunas LT-44307, Lithuania
[2] Department of Ophthalmology, Lithuanian University of Health Sciences, Medical Academy, Eiveniu 2 str., Kaunas LT-50161, Lithuania
[3] Neuroscience Institute, Ophthalmology laborratory, Lithuanian University of Health Sciences, Medical Academy, Eiveniu 2 str., Kaunas LT-50161, Lithuania
stramkauskaitealmina@gmail.com

Optic neuritis (ON) is an inflammatory demyelinating disorder of the optic nerve. The disease occurs in young healthy 20-45-year-old adults and predominantly affects females. ON is a clinical diagnosis that is made on the basis of history and clinical features. Corticosteroids and immunomodulatory drugs are assigned to patients with ON [1,2,3]. Case report. We present the case of a 29-year-old woman from Lithuania. In January 2021 she complained of decreased VA, photophobia, and discomfort on the left side of the head. She was consulted by an ophthalmologist and after 5 months by a neurologist, but no pathological changes were found, and MRI was planned. In July 2021 the patient was consulted by a neuro-ophthalmologist. On examination, the VA of both eyes was 1.0, however, the patient claimed she was "seeing through the fog" with her left eye. A slit-lamp examination, tonometry, color perimetry, and OCT tests were normal. VEP was performed by an otoneurologist and increased latency of the P100 wave was observed, and MRI showed signs of left eye ON. The patient was hospitalized in the Hospital of LUHS in KC in the Department of Ophthalmology. On examination, the VA of both eyes was 1.0, but 'seeing through the fog' in the left eye remained. Intraocular pressure was normal in both eyes. Colors were paler with the left eye, eye movements were not painful. Full-field perimetry was normal. No changes in chest radiography and blood tests were observed. Treatment with intravenous pulse steroids therapy with methylprednisolone 1g was started. In October 2021 OCT was repeated, showing RNFL within the normal range. An optical examination was performed before discharging the patient, and no pathological changes were seen. Oral prednisolone was assigned, and the dose was reduced gradually. An ophthalmologist consultation after 3-4 weeks was recommended.

Conclusions. ON can present without typical symptoms (decreased VA, difficulties perceiving colors, central scotoma, painful eye movements). Sometimes ON can only be diagnosed by performing brain and orbital MRI, and VEP.

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P38

Blood Protein Profile for Astrocytoma Diagnosis and Prognosis

Rūta Urbanavičiūtė, Daina Skiriutė

Laboratory of Molecular Neurooncology, Neuroscience Institute,
Lithuanian University of Health Sciences, Kaunas, Lithuania
urbanaviciute.ruta@gmail.com

Relative five-year survival for brain cancers has hardly changed in 30 years, increasing by 1%, when in all cancers combined, it increased nearly 20%. The most frequent group of primary brain tumours, astrocytomas, and especially glioblastoma (GBM), is very aggressive. In adult GBM group 1-year and 5-years relative survival is 41% and 5%. The treatment of astrocytoma is complicated due to the absence of reliable tools, which would allow monitoring of essential aspects of tumorigenesis. Present study aimed to find profiles of circulating blood serum proteins, specific for astrocytomas, in order to track cancerous processes in brain tissue. Study consisted of two parts – selection and validation studies. In the first part, 79 different grade astrocytoma patients' tumour tissue and serum samples were analysed. For the validation study – 162 independent serum samples were used. In the part one, ten blood circulating markers were evaluated using multiplexing antibody array technology in blood samples of astrocytoma patients and healthy participants. Profile, consisting of four proteins – ANGPT1, IP-10, TIMP-1 and TGF-β1, was identified as the most promising for astrocytomas diagnostic. With the same sample set, patients' survival prediction tool (Patients Survival Score) was created, and 2-years survival was predicted with the accuracy of 83.8%. It consisted of two molecular variables – values of CHI3L1 and OPN expression in serum, together with patient's IDH1 mutational status. With different sample set, second part of the investigation was performed and improved diagnostic serum profile for astrocytomas was revealed, consisting of TGF-β1, TIMP-1 and CHI3L1 protein values. The accuracy of calculated PSS was also confirmed.

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Visual Attention to Erotic Stimuli: An Eye-Tracking Study in Men, Naturally Cycling Women and Oral Contraceptives Users

Miglė Usonytė[1, 2], Ingrida Zelionkaitė[1], Jolvita Briazkalaitė[1], Erik Ilkevič[1], Rimantė Gaižauskaitė[1], Ramunė Grikšienė[1]

[1] Department of Neurobiology and Biophysics, Life Sciences Center, Vilnius University, Lithuania
[2] Institute of Philosophy, Faculty of Philosophy, Vilnius University, Lithuania
m.usonyte@gmail.com

Everybody "knows" that men and women differ in their attitude towards erotic stimuli, and that women's attitudes might be modulated by sex steroids. However, there is a lack of objective evidence as to whether men and women with distinct hormonal statuses look at these stimuli differently. Therefore, the aim of our study was to evaluate the effect of sex and sex steroids on visual attention to erotic images in men, naturally cycling women (NC) and oral contraceptives (OC) users.

The study included 38 men (23.4±4.0 yrs), 35 NC women (26.1±4.5 yrs) in the follicular phase, and 27 OC users (24.2±4.1 yrs). Eye movements were recorded with Eye Link 1000 while participants freely viewed the images. Subjects rated evoked arousal and valence (pleasantness) after each stimulus. To analyze visual attention, pictures were divided into interest areas (female/male body, female/male face, erogenous zones, and neutral surroundings). The gazing time and the number of entries to the specific area were measured. Saliva samples were collected to evaluate sex steroid concentration.

There were no significant differences in subjective evaluations of stimuli between groups. However, correlation analysis revealed that longer use of OC was negatively related to arousal evoked by erotic stimuli ($r = -0.55$, $p=0.01$). As expected, men looked longer than NC women at erogenous zones ($p=0.009$) and they paid more attention to female bodies than NC ($p=0.007$) and OC ($p=0.06$) women. Interestingly, faces attracted significantly more attention from NC women, as compared to men and OC women (both $p=0.001$). Attention to different zones was related to subjective evaluations: OC women were less likely to enter men's faces when images evoked higher valence to them ($r=-0.62$, $p=0.002$); men spent more time looking at female faces ($r=0.37$, $p=0.03$) when images were more arousing but entered more at erogenous zones ($r=0.35$, $p=0.04$) when images evoked higher valence; NC women gazed longer ($r=0.42$, $p=0.03$) to erogenous zones when images were more arousing. Sex steroids modulated women's attention: in NC women higher progesterone was related to shorter looking at erogenous zones ($r = -0.40$, $p=0.04$); while OC women with higher testosterone looked at female bodies longer ($r = 0.46$, $p=0.03$).

To summarize, results suggest that visual attention to erotic images is modulated not only by sex but also depends on the concentration of sex steroids as well as on subjective feelings evoked by erotic stimuli.

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Mix of Solutions for Effective Food Package Development: Neuromarketing & AI Perspective

Egle Vaiciukynaite

School of Economics and Business, Kaunas University of Technology, Kaunas, Lithuania

egle.vaiciukynaite@ktu.lt

Food packaging creates the first impression for customers and plays a key role in the selection process, especially when customers have no idea about a new product. Indeed, many different packaging components, like branding, shape, design, and nutritional information, might influence customers' willingness to buy a product (Viejo et al., 2022). Although companies and brands seek to create products that customers might love, they are still developing their food packages using traditional, neuromarketing or combining both methods. Nevertheless, emerging solutions have also been explored for packaging assessment, such as Artificial Intelligence (AI) tools or webcam-based eye-tracking solutions. Such tools can be quite beneficial in saving time and effort in the food package development processes. Despite mentioned opportunities, companies and brands face a challenge on how to create effective food packages for physical and online stores and have a social media presence. The main question remains: What methods and tools should companies and brands use to develop successful food packages? Therefore, this pilot research seeks to examine how diverse neuromarketing (e.g., mobile eye-tracking, webcam-based eye-tracking), consumer tests, and ML/AI solutions can serve as leverage for effective food packages? Stimuli included six food packages of protein-related bars, while four packages were in the development phase, and two were competitors (exceptions). This research used AI prediction tools for food packages, a consumer test, and two neuromarketing techniques (e.g., mobile eye-tracking and ML-based eye-tracking). Based on the test using ML/AI solution results, the most visual attention was on the textual information of packages (e.g., nutrition, logo). Meanwhile, the red and pink colours received more user attention in comparison with other colours of the packages. These results suggest that testing is critical for effective food packages, but current eye-tracking related AI prediction tools might be used for the first stages of the packaging design evaluations. For the final stages, the mobile or ML-based eye-tracking solution, combined with a consumer test, is recommended.

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MiRNA Expression Profile in the Serum of Patients with Parkinson's Disease

Giedrė Miniotaitė[1], Violeta Belickienė[1], Goda Debesiūnaitė[1], Aistė Pranckevičienė[2], Andrius Radžiūnas[3], Paulina Vaitkienė[1]

[1] Laboratory of Molecular Neurobiology, Lithuanian University of Health Sciences, Kaunas, Lithuania
[2] Health Psychology Department, Faculty of Public Health, Lithuania University of Health Sciences, Kaunas, Lithuania
[3] Department of Neurosurgery, Lithuanian University of Health Sciences, Kaunas, Lithuania

paulina.vaitkiene@lsmuni.lt

Parkinson's disease (PD) is a neurodegenerative disorder that is characterized by both motor and non-motor manifestations. Motor symptoms include resting tremor, bradykinesia, rigidity, shuffling gait, or postural instability. Non-motor symptoms of PD are cognitive changes, behavioral/neuropsychiatric changes, autonomic nervous system failure, sensory and sleep disturbances. PD progresses for several years until clinical diagnosis is made and it's treatment varies considerably from patient to patient. Recently, miRNA interference has been extensively studied due to it's affects in many biological processes, including manifestation of neurodegenerative diseases such as PD. MiRNA molecules formed in various body cells can travel through biological fluids providing long lasting expression of disease – related genes. Circulating miRNAs could possibly be used as one of the non-invasive biomarkers to help differentiate diseases, their stages, monitor their progression and could also be used in the development of a new treatment. The aim of this study was to determine 9 different miRNA expression levels in the serum of patients with PD and check for relations with clinical symptoms or other patient related data. First of all, extracelular vesicle miRNAs were isolated from collected samples of blood serum, transcribed into cDNA and its expression was measured by RT-PCR. Statistical analysis was performed using Student's t test, ANOVA criteria and Pearsons correlation coefficient in GraphPad Software. MiRNA expression was evaluated by age, sex, the onset of the disease, its duration, severity of symptoms and selected method of treatment for 88 individuals with PD. 36 control group patients received medicational treatment, 39 deep brain stimulation and 13 gamma knife surgery. The results revealed that patients showed different miRNA expression levels when comparing control group to surgical treatment groups. Statistical data confirmed, that miRNA expression level variation was dependent on severity of presented clinical appearance of the disease. Also patients age, the onset of the disease and it's duration had an influence in altered miRNA levels. In conclusion, primary data suggest that different miRNA expression levels showed patient heterogeneity and indicate a potential role of miRNA's in PD pathogenesis. However, more research is needed to further evaluate the potential of miRNAs as candidate biomarkers before application in clinical practice.

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Modulation of Microglia Functions through Diet in Ageing Mice

Akshay Kumar Vijaya, Simonas Kuras, Egidijus Šimoliūnas, Jonas Mingaila, Daiva Baltriukienė, Aurelijus Burokas

Department of Biological Models, Institute of Biochemistry, Life Sciences Center, Vilnius University

akshay.vijaya@gmc.vu.lt

Aging is epitomized by a progressive increase in neuroinflammation, which contributes to cognitive impairment and eventually leads to neurodegenerative diseases. Microglia are the resident immune cells of the brain that play a crucial role in maintaining homeostasis. The activation and deactivation of microglia dictates the type of immune response. Microglia dysfunction has major implications on neuroinflammation. The importance of the gut microbiota in the CNS has long been recognized. Metabolites in the gut can trigger immune response in the brain leading to neuroinflammation. The gut microbiota has shown to significantly influence microglia from birth until adulthood and the metabolites released by the microbiota can regulate the inflammation mediated by microglial activation in the CNS. Diet is a key modulating factor influencing the composition of the gut microbiota. To understand the diet effects on microglia cells we used C57BL/6JRj mice for our research. The animals were divided into two groups (old and young) and subjected to a different diets (control, control & prebiotics, high-fat and high-fat & prebiotics). After 10-month diet (old group) or 1-month diet (young group), the animals were culled, and microglial cells were isolated to perform phagocytosis, chemotaxis, ROS and senescence experiments which directly correlate to microglial activation and functioning in the CNS of aged and young animals. We observed that microglia showed a decline in functionality in aged animals when compared to young animals. Moreover, microglia from animals fed with high-fat diet showed a bigger decline even when compared with other diets.

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Evaluation of the Antioxidant Effects of Aronia, Pomegranate and Elderberry on the Brains of Laboratory Mice

A. Žentelytė, R. Bernotienė

Neurosciences Institute and Department of Biochemistry, Medical Academy, Lithuanian University of Health Sciences, Kaunas, Lithuania

agne.zentelyte@stud.lsmu.lt

Antioxidants are compounds that help protect the cells of your body from damage caused by free radicals. Free radicals are always present in your body, but having too many of them can be harmful and contribute to a number of chronic diseases. Aronia, pomegranate and elederberry are rich in antioxidants and polyphenolic compounds that offer protection from this damage. The antioxidant properties of various berries are measured by the polyphenol content each has. Polyphenol content is the marker for bioactivity of antioxidants. So, getting antioxidants from berries and fruits such as aronia, pomegranate and elderberry is a great way to support overall health and help prevent against the activity of radical oxygen species which would otherwise cause long-term damage. This study was performed to evaluate the antioxidant effects of aronia, pomegranate and elderberry extracts on the brains of laboratory mice. Our experiments were performed on outbred white laboratory mice by changing drinking water with plant extract solutions of aronia, pomegranate and elderberry. Exposure time was 21 days. Lipid peroxidation level was estimated spectrophotometrically by measuring the concentration of MDA produced by reaction with TBA at 535 nm and 520 nm light wavelengths. The concentration of antioxidant GSH was measured spectrophotometrically by reaction with DTNB to give compound TNB, which absorbs light wavelength at 412 nm . GSH is important in protecting cells against damage from radiation, free oxygen radicals, heat, and sulfhydryl reactive agents, and provides the bulk of sulfhydryl groups for the detoxication of electrophilic xenobiotics. So, in our experiments we showed that after 21 days of exposure to aronia, pomegranate and elderberry, the content of GSH was increased by 281 % ($p<0.001$), 302 % ($p<0.0001$) and 297 % ($p<0.0001$), respectively, as compared to control mice group. In further experiments we determined the content of MDA in mice brain. It is very important, becouse determining the level of MDA is usually the most practical and reliable method for detecting and screening oxidative stress. Our results showed that after treatment with aronia, pomegranate and elderberry, the content of MDA was significantly increased by 50 % ($p<0.001$) in all treated groups, as compared to control mice group. Our experiments showed that extracts of aronia, pomegranate and elderberry increased antioxidant GSH level, but unfortunately did not protect lipids from peroxidation.

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9 Saulėtekio Av., III Building, LT-10222 Vilnius
info@leidykla.vu.lt, www.leidykla.vu.lt/en/
www.knygynas.vu.lt, www.zurnalai.vu.lt