Università degli Studi dell'Insubria

Centro di Ricerca in

Neuroscienze

GIORNATA SCIENTIFICA 2021

8 luglio 2021

Aula 10MTG, Via Monte Generoso 71, VARESE

Accesso online disponibile a questo link

Centro NeuroScienze

Università degli Studi dell'Insubria

Segreteria del Centro: Dipartimento di Biotecnologie e Scienze della Vita, Via J.H. Dunant n. 2, 21100 Varese VA - Tel. 0332 421392, E-mail: Centro.Neuroscienze@uninsubria.it

Indice

Giornata Scientifica 2021

PRESENTAZIONE DEL CENTRO DI RICERCA IN NEUROSCIENZE

Il Centro di Ricerca in Neuroscienze dell'Università dell'Insubria è stato fondato nel 2003. L'obiettivo del Centro è stato, sin dalla sua nascita, quello di costituire un punto di incontro tra i gruppi di ricerca dell'area biomedica e clinica presenti nell'Ateneo, favorendo lo scambio di conoscenze e la nascita di collaborazioni su tematiche attinenti alle Neuroscienze.

Il Centro opera organizzando riunioni annuali dei laboratori di ricerca dei suoi membri, afferenti a diversi Dipartimenti dell'Ateneo, in cui i giovani collaboratori sono invitati a presentare comunicazioni sulle loro attività. Inoltre, il Centro collabora all'organizzazione di Seminari specialistici e divulgativi su tematiche neuroscientifiche, promuovendo la conoscenza dei meccanismi fisiologici e patologici alla base del funzionamento del sistema nervoso.

Gli organi direttivi del Centro si compongono del Direttore e del Consiglio Scientifico. Il Centro di Ricerca in Neuroscienze ha avuto come Direttori, in passato, la prof.ssa Daniela Parolaro, il prof. Riccardo Fesce, il prof. Mauro Fasano ed il dr. Sergio Balbi. Il Direttore attuale, per il triennio 2020-2022, è la dr.ssa Lia Forti, ed il Consiglio Scientifico è composto dai professori Marco Cosentino, Charlotte Kilstrup-Nielsen, Cristina Roseti e Silvia Sacchi.

REGOLAMENTO
DEL CENTRO DI RICERCA
IN NEUROSCIENZE

INDICE

Art. 1 - Denominazione del Centro

1. Presso l'Università degli Studi dell'Insubria è istituito il Centro di Ricerca in Neuroscienze.

Art. 2 - Sede del Centro

1. Il Centro afferisce al Dipartimento di Biotecnologie e Scienze della Vita, è ivi funzionalmente e logisticamente allocato e usufruisce degli spazi, dei finanziamenti, delle attrezzature tecnico-scientifiche e del personale messi a disposizione dal Dipartimento o da altri enti pubblici o privati.

Art. 3 - Finalità del Centro

1. Il Centro ha lo scopo di:
   a. promuovere la ricerca nell'ambito delle Neuroscienze, ovvero sulla biologia cellulare, genetica, biochimica e fisiologia delle cellule nervose, sulla neurofarmacologia e neuroimmunologia, sulle patologie funzionali e degenerative del sistema nervoso;
   b. favorire lo sviluppo di un approccio interdisciplinare e multidisciplinare per approfondire le conoscenze nel campo delle Neuroscienze raccordando le competenze dei gruppi operanti presso l'Università degli Studi dell' Insubria;
   c. trasmettere e scambiare informazioni sulle tematiche sopraindicate tra le unità di ricerca del settore operanti presso altri dipartimenti o istituzioni di ricerca o laboratori di aziende industriali;
   d. contribuire alla formazione di ricercatori, esperti e docenti delle discipline ricomprese nelle sue finalità;
   e. promuovere rapporti con altre istituzioni di ricerca in Italia e all'estero, per proporre progetti a livello locale, nazionale ed internazionale, al fine di configurarsi come nodo di network di eccellenza nell'ambito delle Neuroscienze;
   f. favorire il confronto, la diffusione e la divulgazione delle conoscenze mediante comunicazioni, convegni, corsi, iniziative editoriali e pubblicistiche e ogni altro programma formativo ed informativo utile al perseguimento delle sue finalità;
   g. provvedere all'acquisizione e gestione di apparecchiature, strumenti scientifici e servizi tecnici in dotazione al Centro.

Art. 4 - Attività del Centro

1. Nell'ambito dell'attività del Centro verranno organizzati seminari, attività di aggiornamento e convegni, nazionali ed internazionali, relativi ad argomenti di cui all'art. 3 e nel rispetto delle disposizioni in vigore per l'amministrazione universitaria.
2. Tali attività potranno essere svolte anche in collaborazione con Enti pubblici e privati ed associazioni con interessi convergenti.
3. Nel rispetto della normativa vigente e con finanziamenti specificamente destinati a tale scopo dai finanziatori potranno essere istituiti premi di ricerca o borse di studio.

4. Rientra tra le attività del Centro la possibilità di curare la pubblicazione di articoli, testi e rapporti sugli argomenti elencati nell'articolo 3.

Ogni anno il Centro predisporrà una relazione sull'attività svolta. L'attività del Centro è verificata ogni due anni dal Senato Accademico, sentito il Nucleo di Valutazione, nelle forme, nei tempi e nei modi previsti dallo Statuto di Ateneo e dal Regolamento generale di Ateneo.

Art. 5 - Aderenti al Centro

1. Oltre ai professori e ricercatori proponenti, possono aderire al Centro:
   a. professori e ricercatori dell'Università dell'Insubria, di altri Atenei italiani e stranieri;
   b. studiosi afferenti a centri e enti di ricerca pubblici e/o privati;
   c. professionisti esperti nei settori di attività del Centro;
2. L'adesione al Centro può essere richiesta mediante domanda di adesione corredata da curriculum scientifico e/o professionale e dalla descrizione dettagliata dei temi di interesse, che devono essere in linea con le finalità del Centro. Sulla domanda di adesione si esprime entro 30 giorni il Consiglio Scientifico del Centro. Contro il diniego decidono definitivamente gli organi accademici competenti.
3. I componenti del Centro che sono esterni all'Università dell'Insubria possono esprimere solo parere consultivo sulle materie oggetto di deliberazione da parte del Centro e non concorrono alla formazione del numero legale.
4. Possono svolgere attività nell'ambito del Centro, oltre agli aderenti, a seguito di deliberazione favorevole del Consiglio Scientifico, laureandi, specializzandi, dottorandi di ricerca, borsisti, assegnisti di ricerca ed altro personale di enti di ricerca e/o strutture pubbliche o private.
5. Per il personale esterno alle Università ammesso a frequentare le strutture del Centro, sulla base di specifici accordi, il Direttore Scientifico del Centro dovrà accertare l'esistenza di idonea copertura assicurativa, relativa a infortuni e responsabilità civile.
6. Il Centro si avvale per il proprio funzionamento di personale messo a disposizione da Dipartimenti dell'Università o da terzi mediante convenzioni con l'Università.
7. Il Centro può utilizzare, previa approvazione del Dipartimento ospitante, i locali e le apparecchiature in dotazione alle strutture ove afferiscono gli aderenti al Centro.

Art. 6 - Organi del Centro

1. Sono organi del Centro:
   a. il Direttore Scientifico;
   b. il Consiglio Scientifico.

Art. 7 - Direttore Scientifico

1. Il Direttore Scientifico del Centro è eletto dal Consiglio Scientifico del Centro fra i professori di prima e di seconda fascia e i ricercatori

dell'Università degli Studi dell'Insubria aderenti al Centro ed esterni al Consiglio stesso. Il Direttore è nominato con decreto del Direttore del Dipartimento a cui afferisce il Centro.

2. Il Direttore dura in carica tre anni e può essere confermato. Almeno tre mesi prima dalla scadenza del triennio il Consiglio Scientifico procede alla designazione del Direttore Scientifico.
3. La durata del mandato del Direttore Scientifico coincide con quella del Consiglio Scientifico.
4. Il Direttore scientifico:
   a. rappresenta il Centro, ne sovrintende e coordina l'attività, mantiene i rapporti con le autorità accademiche;
   b. convoca e presiede il Consiglio Scientifico, ne coordina l'attività e provvede all'esecuzione delle deliberazioni assunte;
   c. presenta al Consiglio Scientifico, all'inizio di ogni anno di attività, il programma dettagliato delle ricerche unitamente al preventivo dell'utilizzazione dei fondi disponibili nell'anno;
   d. predispone e sottopone al Consiglio Scientifico e al Consiglio del Dipartimento a cui afferisce il Centro, la relazione sull'attività svolta nell'anno, sui fondi ottenuti e sulla loro utilizzazione;
   e. designa un Vice Direttore tra gli aderenti al Centro che lo supplisce in caso di impedimento o di assenza.

Art. 8 - Consiglio Scientifico

1. Il Consiglio Scientifico del Centro è composto dal Direttore Scientifico, e da 4 membri eletti dall'assemblea degli aderenti, tra i membri del Centro.
2. Il Consiglio Scientifico è nominato con decreto del Direttore del Dipartimento a cui afferisce il Centro e dura in carica tre anni.
3. Il Consiglio Scientifico:
   a. individua e programma le linee dell'attività scientifica del Centro;
   b. approva il programma delle ricerche e il piano finanziario annuale proposto dal Direttore Scientifico;
   c. approva il rendiconto finale predisposto dal Direttore Scientifico;
   d. delibera sulle questioni riguardanti l'amministrazione dei fondi del Centro;
   e. delibera sulle forme di collaborazione e convenzione con altri Organismi pubblici e privati;
   f. delibera in merito alle richieste di nuove adesioni al Centro.
4. Il Direttore Scientifico convoca il Consiglio Scientifico almeno due volte all'anno o quando non meno di un terzo dei membri ne facciano richiesta. La convocazione è inviata, anche solo mediante posta elettronica, almeno 5 giorni prima della data fissata per la riunione.
5. Le riunioni del Consiglio Scientifico sono valide se è presente un terzo dei componenti. Le deliberazioni sono valide se approvate da più della metà dei presenti; in caso di parità prevale il voto del Direttore Scientifico.
6. Di ogni riunione viene redatto verbale, che viene approvato dal Consiglio Scientifico.

Art. 9 - Finanziamenti

1. Il Centro opera con i finanziamenti derivanti da:
   a. Ministero dell'Università e della Ricerca Scientifica ed altri ministeri interessati nell'area di ricerca;
   b. Consiglio Nazionale delle Ricerche;
   c. eventuali contributi del Dipartimento di Biotecnologie e Scienze della Vita;
   d. Regioni, enti locali ed altri Enti pubblici o privati, imprese o Fondazioni;
   e. Unione Europea o altri organismi internazionali;
   f. eventuali contributi di altri organismi italiani o stranieri;
   g. donazioni e lasciti;
   h. entrate diverse.

Art. 10 - Amministrazione

1. Il Centro è qualificato come centro di costo del Dipartimento e ad esso si applicano le norme previste dallo Statuto di Ateneo e dal Regolamento per l'amministrazione, la finanza e la contabilità.
2. La gestione amministrativa e contabile fa capo al Dipartimento di Biotecnologie e Scienze della Vita.

Art. 11 - Modifiche al regolamento

1. Le modifiche al presente regolamento sono proposte dal Consiglio Scientifico con la maggioranza qualificata dei 2/3 degli aventi diritto al voto e approvate dagli organi accademici competenti.

Art. 12 - Cessazione del Centro

1. Il centro cessa su proposta degli aderenti, con delibera approvata a maggioranza qualificata dei 2/3 e comunicata agli organi accademici competenti e nei casi stabiliti dall'art 62 dello Statuto dell'Università degli studi dell'Insubria.

Art. 13 - Norma di rinvio

1. Per quanto non previsto nel presente regolamento si applicano lo Statuto, il Regolamento per l'Amministrazione, la Finanza e la Contabilità ed il Regolamento Generale di Ateneo dell'Università degli Studi dell'Insubria.

Membri del Centro

Tiziana Alberio
Dipartimento di Scienza e Alta Tecnologia
Università dell'Insubria

Sergio Balbi
Dipartimento di Biotecnologie e Scienze della Vita
Università dell'Insubria

Elena Bossi
Dipartimento di Biotecnologie e Scienze della Vita
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Camilla Callegari
Dipartimento di Medicina e Chirurgia
Università dell'Insubria

Marco Cosentino
Dipartimento di Medicina e Chirurgia
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Mauro Fasano
Dipartimento di Scienza e Alta Tecnologia
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Lia Forti
Dipartimento di Biotecnologie e Scienze della Vita
Università dell'Insubria

Cristina Giaroni
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Stefano Giovannardi
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Università dell'Insubria

Charlotte Kilstrup-Nielsen
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Franca Marino
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Marco Mauri
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Università degli Studi dell'Insubria

Erica Zamberletti
Dipartimento di Biotecnologie e Scienze della Vita
Università degli Studi dell'Insubria

Linee di ricerca dei membri del Centro

Tiziana Alberio, Mauro Fasano
Biochemistry and Functional Proteomics Laboratory

The Biochemistry and Functional Proteomics lab research is mainly focused on protein biochemistry. Our projects focus on Parkinson's Disease with two main goals: the elucidation of pathogenetic mechanisms and the discovery of peripheral biomarkers. We both use standard biochemistry methods and proteomics to find proteins and pathways involved in neurodegenerative processes. We employ in-house routines to statistically analyze omics data and the systems biology approach to interpret complex results. We have established several collaborations to describe Parkinson's Disease specific mechanisms from general pathways of neurodegeneration and we are often involved in other neuroscience projects in order to analyze and interpret complex data.

Elena Bossi, Cristina Roseti
Laboratory of Cellular and Molecular Physiology

Our research topics are focused on the structure, function and regulation of ion channels and membrane transporters involved in numerous diseases, such as Parkinson and chronic pain. By using electrophysiological techniques, molecular biology, immunochemical, biochemical and fluorimetric techniques, several proteins involved in the membrane translocation of ions and solutes have been studied and characterized by the laboratory of cellular and molecular physiology. Electrogenic membrane transporters are the main subject of research: the protein belonging to neurotransmitter sodium symporter or SLC6 family, like GAT1, GlyT1, DAT and B0AT1 are studied. Moreover, other transporters involved in neurotransmission are also investigated, like SLC1 glutamate transporters and in gut-brain relationships also SLC15a family (PEPT1 oligo-peptides transporters) is also deeply studied. Recently we have also investigated some TRP channels and their role in chronic pain onset and persistence. The proteins are studied in heterologous systems: Xenopus oocytes or cell lines. In these cells cDNAs coding for wild type or recombinant proteins are transfected or membrane collected from healthy or pathological human tissue transplanted. The functional and/or pharmacological characterization is usually conducted by two-electrode voltage clamp, but also by uptake

using fluorescent probes and HPLC methods. Quantification or alteration in protein expression is studied by immunochemistry or qPCR approaches.

Marco Cosentino, Franca Marino
Center of Research in Medical Pharmacology

Our main research interests concern neuro- and immunopharmacology with particular regard to the neuroendocrine modulation of immune response. Recent research: pharmacological modulation of endogenous catecholamines in human lymphocytes and its functional relevance in health and disease such as multiple sclerosis and Parkinson's disease. Other interests: clinical pharmacology and pharmacogenetics, pharmacoepidemiology and pharmacovigilance, pharmacology of herbal medicines.

Lia Forti
Laboratory of Cellular Neurophysiology

The recent research topic in the lab is the study of functional effects of acute stress (AS) on synaptic transmission and membrane excitability of neurons in the rodent prefrontal cortex (PFC). We are exploring AS effects on miniature and spontaneous synaptic currents, on synaptic plasticity (LTP, LTD) and membrane firing regulation in various regions and layers of the PFC. Our expertise includes electrophysiological patch-clamp recordings, field potential recordings, planar multielectrode arrays recordings and Ca^{2+} imaging, in brain slices and cultured cells. Our past interests were focused mainly on cerebellar physiology, including patch-clamp and Ca^{2+} imaging studies of synaptic inputs to cerebellar granular layer interneurons, regulation of their pacemaker firing, and axonal action potential propagation in molecular layer interneurons.

Cristina Giaroni
Laboratory of enteric nervous system physiopharmacology

Our main research topics are centered on the cellular and molecular mechanisms involved in the adaptive changes occurring in the enteric nervous system which underlay the pathophysiology of main gut diseases, such as intestinal ischemia/reperfusion injury, intestinal inflammation and irritable bowel syndrome. In this regard, we are currently focusing our research on the relevance of the enteric microenvironment and the microbiota in the development of enteric neuropathies underlying intestinal ischemia and inflammation

Charlotte Kilstrup-Nielsen
Laboratory of Molecular Biology

The research focus of the laboratory of Molecular Neurobiology is to characterize the functions of X-linked kinase CDKL5 in the nervous system and the consequences of its deficiency, leading in humans to a severe neurologic disorder. The goal of our studies is to provide data that can pave the way for therapeutic approaches. For these studies we make large use of *Cdkl5*-KO neurons and mice. We have through our studies contributed significantly to the current knowledge of CDKL5 functions and the consequences of some pathologic mutations. We also showed that in neurons, CDKL5 levels are tightly controlled by phosphorylation-dependent degradation. Our present focus is to characterize synaptic defects in CDKL5 deficient neurons and the role of CDKL5 in regulating microtubule dynamics. We have demonstrated that surface expression of the AMPA-receptor subunit GluA2 is reduced in *Cdkl5*-KO neurons but can be restored upon treatment with the antidepressant drug Tianeptine. Regarding microtubules, we have identified the +TIP CLIP170 as an import downstream effector of CDKL5 possibly representing a novel druggable target for CDKL5 deficiency disorder.

Tiziana Rubino, Erica Zamberletti
Neuropsychopharmacology Group

Ongoing research lines in the lab are aimed at evaluating: 1) The therapeutic potential of some phytocannabinoids in models of autism; 2) The role of the endocannabinoid system in the pathogenesis of psychiatric disorders; 3) The ability of cannabidiol to modulate the long-term negative consequences of adolescent delta-9-tetrahydrocannabinol exposure on the brain; 4) the role of the endocannabinoid system in adolescent brain maturation/remodeling

Silvia Sacchi
Laboratory "The Protein Factory 2.0"

We work in molecular mechanisms involved in the regulation of the catabolism of the atypical neuromodulators D-serine (D-Ser) and D-aspartate (D-Asp) in the brain. D-Ser is an essential activator of the NMDA receptors since it acts as the principal co-agonist, while D-Asp is an alternative agonist. Alterations in their metabolism have been shown to affect the receptor functionality, thus being implicated in several neurological disorders, among which schizophrenia, AD and ALS. In particular, we are interested in deciphering how the functional properties of the two human FAD-dependent flavooxidases responsible for the degradation of D-Ser and D-Asp - D-amino acid oxidase (hDAAO) and D-aspartate oxidase (hDDO), respectively - are modulated (cofactor/ligand binding, interaction with regulatory proteins, subcellular localization, degradation pathway). Indeed, despite their relevant physiological role,

little is known about the processes entailed in establishing hDAAO and hDDO cellular levels and activity. Investigating them will provide crucial information concerning the regulation of D-Ser and D-Asp levels in the brain, with remarkable implications for the understanding of the modulation of NMDAR-mediated neurotransmission in physiological and pathological conditions. Furthermore, since the precursor L-Ser, synthesized via the so called "phosphorylated pathway", is the key rate-limiting factor for maintaining steady-state levels of D-Ser in the adult brain (it is converted to the D-enantiomer by serine racemase), we recently started to study the enzymes catalyzing the different biosynthetc steps: phosphoglycerate dehydrogenase (PHGDH), phosphoserine aminotransferase (PSAT) and phosphoserine phosphatase (PSP). Again, the factors affecting the amount and the activity of these enzymes are still largely elusive. Thus we are investingating the L-Ser pathway using various biochemical approaches, cell model systems and brain samples, with the ambitious aim to identify potential molecular targets and propose alternative strategies to modulate D-Ser levels.

GIORNATA SCIENTIFICA 2021

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Programme

10:50 **Welcome – Session Opening**

Lia Forti
Director of the Center for Research in Neuroscience

11:00 **First session**

Chair: Lia Forti

Manan Bhatt
Is Betaine a substrate also for GABA transporter 1 (GAT1)?

Tiziana Romanazzi
The pharmacological interaction of the obeticholic acid on dopamine transporter expressed in *Xenopus laevis* oocytes

Roberta De Rosa
A novel role of CDKL5 at inhibitory synapses and a possible therapeutic strategy for CDKL5-related defects

12:00 **Coffee break**

12:15 **Second session**

Chair: Elena Bossi

Angela Di Iacovo
LRRK2 G2019S plays a role in the excitatory/inhibitory imbalance of Parkinson's disease

Edoardo Pedrini
Showcase of two analytical workflows for omic data analysis

13:00 **Lunch break**

14:30 **Third session**

Chair: Franca Marino

Alessandra Gasparini
Inflammatory biomarkers and antidepressant response in Major Depressive Disorder: the role of C-Reactive Protein

Luca Magistrelli
A longitudinal evaluation of the peripheral immune phenotype in a cohort of Parkinson's disease patients

Alessia Furgiuele
Effect of dopaminergic agents on human peripheral CD4+T lymphocytes: relevance for Parkinson's disease

Lucia Princiotta Cariddi
Pilot study aimed to identify the role of peripheral adaptive immunity in the mechanism of Alzheimer's disease Neuroinflammation

16:00 -17:00 **Plenary lecture**

Francesco Rusconi
Forgetting matters: a link between memory and stress resilience?

Plenary lecture

Francesco Rusconi

Dr. Rusconi graduated in Molecular Biology of the Cell at the University of Milan, (Dept. Life Science) in 2007 (Project: Hippocampus proteomics of a model of THC tolerance). He undertook the PhD program in Molecular and Cellular Biology in the same institution, and after the third year abroad at the Baylor College of Medicine, he graduated in 2010 (Project: Proteomics of Myotonic Dystrophy 2 (DM2) patients-derived myotubes). He joined the Lab of Prof. Battaglioli (Dept. Medical Biotechnology and Translational Medicine) in 2011, since that moment, he studies epigenetic mechanisms of environmental adaptation in excitatory neurons. This topic led him to approach neuropsychiatric disorders. He is now working to understand whether an aberrant fine tuning of excitatory synapses is a potential unifying pathogenic mechanisms of psychiatric disorders.

Forgetting matters: a link between memory and stress resilience?

Since more than a hundred years, the brain has been studied to understand the mechanisms of memory formation and consolidation, considering forgetting as a passive process. However nowadays, researchers suggest that also forgetting could represent an active process, highlighting the importance of the biology of forgetting, which will be fundamental to understand psychiatric disorders such as post-traumatic syndromes.

Trauma-induced neuroplastic modifications in the hippocampus, enhance contextual fear learning, anxiety and avoidant behaviors. This process requires experience-evoked transcription of neuroplasticity genes and is facilitated by epigenetic processes including histone acetylation. However, stress also induces different epigenetic processes displaying an opposite transcriptional outcome (histone deacetylation) on the same genes, instrumentally to restrain excitatory neuroplasticity and limiting fear memory consolidation. The role of the CoREST/HDAC2/LSD1 corepressor complex will be discussed in this context.

The existence of pro-and anti-neuroplasticity epigenetic mechanisms suggests that a balanced hippocampal function could limit traumatic memory consolidation. In support of this hypothesis, it is widely known that trauma induces *per se* a window of restrained hippocampal neuroplasticity temporarily limiting memory consolidation. However, it is

unknown if the nature of this process is simply a toxic consequence of stress perception, or whether it represents an adaptive mnemonic reduction with protective purposes. Through the characterization of trauma-engaged epigenetic mechanisms aimed at restraining hippocampal neuroplasticity, I will discuss a framework to interpret posttraumatic susceptibility as excessive contextual memory consolidation, of stressful experiences. In line, posttraumatic syndrome (PTSD) has been described as a fear-memory disease, showing extensive signs of excessive fear consolidation and generalization along with decreased extinction of traumatic memory.

Abstracts

Is Betaine a substrate also for GABA transporter 1 (GAT1)?

Manan Bhatt[1,2], Angela Di Iacovo[1], Tiziana Romanazzi[1], Raffaella Cinquetti[1], Cristina Roseti[1,3], Elena Bossi[1,2,3].

[1]Department of Biotechnology and Life Sciences, University of Insubria, Italy. [2]NeuroTrans: European Training Network (ETN) from MSCA ITN of the European Commission's Horizon 2020 framework. [3]Center for Research in Neuroscience, University of Insubria, Italy.

The plasma membrane γ-aminobutyric acid (GABA) transporters are responsible for the re-uptake of GABA in central nervous system (CNS). Among these four sodium- and chloride dependent GABA transporters (GAT1-3 and BGT1), GAT1 is investigated the most, as it is considered the primary regulator of GABA, whereas the physiological role of BGT1 (betaine/GABA transporter) in the brain is little understood and still very much under debate. Betaine (N-trimethylglycine) is usually associated with osmoregulation in kidney and liver, but the presence of BGT1 in blood brain barrier, and betaine accumulation in nervous tissues raise questions around its possible influence on neuronal functions. A number of clinical reports also suggest that betaine supplements provide neuroprotection and improve cognition. The recent studies on the nematode *C. elegans* showing betaine regulated ion channels in the nervous system, and possible therapeutic roles of betaine for schizophrenia, make it even more important to understand the functions of betaine in the brain.

Our recent electrophysiological experiments on *X. laevis* oocytes heterogeneously expressing rGAT1, have shown transport currents elicited under the influx of betaine. The pre-steady state currents were significantly reduced in the presence of betaine, and almost (but not completely) disappeared at higher concentrations. The experiments on competitive assay between GABA and betaine provide some interesting results and indicate that the affinity of GAT1 for betaine is very low compared to GABA. The I-V, Q-V, and τ-V relationships for betaine reflected similar observations to those of other GAT1 substrates like GABA and Nipecotic acid. These preliminary results exhibit how important it could be to explore the effects of betaine not only on GAT1, but also on all other GABA transporters.

THE PHARMACOLOGICAL INTERACTION OF THE OBETICHOLIC ACID ON DOPAMINE TRANSPORTER EXPRESSED IN XENOPUS LAEVIS OOCYTES

[1] Tiziana Romanazzi, [1] A. Di Iacovo, [1] M. Bhatt, [1,2] C. Roseti, [1] R. Cinquetti, [3] D. Zanella, [1,2] E. Bossi, [3] A.Galli.

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Dopamine (DA) is a catecholamine neurotransmitter involved in several physiological functions, such as movement control, learning and reward behaviour. Addictive drugs such as cocaine and amphetamine act on the mesolimbic circuit evoking an increase in DA activity. Interestingly, the gut-brain axis also displays significant control over motivated behaviour. Even though several studies report that the bile acids can be detected in the brain, their physiological role in the central nervous system (CNS) is still little understood. Recently, it was discovered that bile diversion, a bariatric surgery used to treat obesity and to reduce food addiction, causes an increase of bile acid level into the blood and reduces reward-related behaviour induced by cocaine. Using a knockout model for the bile acid receptor, it has been shown that the main actor of the post-operative effects is the Takeda G protein coupled bile acid receptor (TGR5), expressed in intestine, ileum, colon, as well as in some population of astrocytes and neurons inside the CNS. Obeticholic acid (OCA) is a bile acid analogue, FDA approved drug for primary biliary cholangitis, a selective agonist of nuclear farnesol-X-receptor (FXR) and of TGR5. Inside a dopaminergic synapse, the dopamine transporter (DAT) mediates the re-uptake of the DA from the synaptic cleft, thereby terminating the postsynaptic dopamine action. Due to the electrogenicity of DAT, it was expressed in the presence and in the absence of the TGR5 receptor in *Xenopus laevis* oocytes, and the possible interaction between the DAT and the OCA was studied by two electrode voltage clamp technique (TEVC). The collected data show that the OCA acts directly on the mDAT causing a fast inward current independently from the presence of the receptor, suggesting the binding of OCA with the transporter mediating a small fast conductance of sodium ions. This hypothesis was confirmed by substituting the sodium with lithium buffer during TEVC recording. It is known that the lithium ions generate a leaking current in the DA transporter and the perfusion of DA partially blocks it. Because the same electrophysiological behaviour is highlighted also perfusing the OCA, the partial block of the leak current supports the idea of direct binding of OCA to mDAT. Furthermore, chelating intracellular calcium with the injection of EGTA did not affect the OCA-associated current, supporting the hypothesis of direct effect on transporter. The I_{max} and $K_{0.5}$ in the presence and in the absence of OCA are not altered. These preliminary results shed a light on the possible direct mechanism of OCA on DAT activity. The next step will be to test other bile acid and the action of OCA on other SLC6 transporters. Moreover, it could be fascinating to investigate the role of OCA on dopamine transporter in the presence of addictive drugs. Understanding the mechanism of action of OCA on DAT would certainly open interesting therapeutic perspectives given the fundamental role of this transporter in several addictions.

A novel role of CDKL5 at inhibitory synapses and a possible therapeutic strategy for CDKL5-related defects

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Mutations in the cyclin-dependent kinase like 5 gene (*CDKL5*) have been found in individuals with a rare X-linked neurodevelopmental disorder characterised by early-onset epileptic encephalopathy, severe intellectual disability, developmental delay, and autistic-like features. The disorder affects mostly females who are heterozygous for CDKL5 deficiency and mosaic for the mutated allele. At present, no cure exists for patients with CDKL5 deficiency disorder.
Although the role of CDKL5 at excitatory synapses is widely accepted, its possible role in regulating inhibitory neurotransmission is still unknown. The investigation of its possible function at the inhibitory synapses would allow characterising, in more details, the molecular aspects underlying the epileptic, cognitive and autistic phenotypes. Our data suggest that CDKL5 resides in the postsynaptic inhibitory compartment where it interacts with both collybistin (CB) and gephyrin. While gephyrin represents the main inhibitory scaffolding protein, CB is a brain-specific GDP/GTP-exchange factor, which regulates gephyrin recruitment from intracellular deposits to postsynaptic membranes.
We here describe functional data suggesting that CDKL5 through its interaction with CB regulates the conformation of the protein and thus its activity in recruiting gephyrin to submembraneous clusters. Such model could explain the reduction in the number of gephyrin-positive puncta along with the reduced surface exposure of γ_2 subunit-containing $GABA_ARs$ ($GABA_AR\ \gamma_2$) that we found in *Cdkl5*-KO primary hippocampal neurons.
The above defects were accompanied by a decrease in the frequency of miniature inhibitory postsynaptic currents. A similar result was observed when CDKL5 expression was acutely silenced, indicating that the impact of CDKL5 on the inhibitory neurotransmission could be ascribed to its effect at the postsynaptic site. Furthermore, *ex vivo* findings corroborated the *in vitro* ones; indeed, a deranged surface expression of synaptic $GABA_ARs$ was also found both in hippocampal slices and in synaptosomal fractions of fully symptomatic *Cdkl5*-KO mice.
Interestingly, we found a restoration of surface expressed $GABA_AR\ \gamma_2$ and gephyrin clusters in *Cdkl5*-KO neurons treated with a synthetic pregnenolone derivative, pregnenolone-methyl-ether (PME). The latter showed a beneficial effect also *in vivo* as it was able to normalise the reduced surface expression of synaptic $GABA_ARs$. We therefore hypothesise that CDKL5 may regulate $GABA_AR$ expression also through its control of microtubule dynamics.

LRRK2 G2019S plays a role in the excitatory/inhibitory imbalance of Parkinson's disease

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Parkinson's disease (PD) is characterized by the loss of dopaminergic neurons in the substantia nigra pars compacta, with consequent reduction of striatum projections and widespread involvement of other central nervous system structures.
Recently, *Leucine-rich repeat kinase 2* (LRRK2) has been discovered to play a role in both monogenic and sporadic forms of PD. The most common mutation in PD is the substitution Gly2019Ser in the LRRK2 gene, associated with the increased kinase activity.
Our previous data suggested a role of LRRK2 G2019S in excitotoxicity since the mutated kinase caused a reduced activity of glutamate transporters EAAT2. To investigate the possible effect of the LRRK2 kinase also on GABAergic transmission, membranes from striatum tissues of LRRK2-associated PD mouse model (control and mutated LRRK2 G2019S) were injected in *X. laevis* oocytes. The activity of AMPA and $GABA_A$ receptors from the mouse specimen, inserted in the oocytes membrane, was characterized using the two-electrode voltage clamp.
The results show a significant increase in the current amplitudes of the glutamate receptors in oocytes injected with mouse striatum LRRK2 G2019S, compared to LRRK2 wild type striatum membranes.
Interestingly, the data demonstrate a significant reduction of the amplitude of the GABA evoked current in the LRRK2 G2019S condition than in the LRRK2 wild-type striatum.
The ratio of Glutamatergic and GABAergic currents confirms the impact of the mutated LRRK2 on excitatory/inhibitory imbalance in this pathological tissue.
To better investigate GABAergic transmission, we tested whether the chloride homeostasis was altered in oocytes injected with LRRK2 G2019S membranes. We find that the reduction of GABA current amplitude was not associated with a change in GABA reversal potential (E_{GABA}). Moreover, $GABA_A$ receptors exhibit a higher EC_{50} in LRRK2 G2019S tissues, compared to the wild-type counterpart.
In conclusion, our preliminary data show a reduced GABAergic transmission in LRRK2 G2019S mouse tissues requiring further investigation to clarify underlying mechanisms better.

Showcase of two analytical workflows for omic data analysis.

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As a scientific discipline, biology has always been data-driven, but after the advent of genomic sequencing in the '90s, it began shifting into the field of data science. Now the application of the so-called omic technologies is becoming widespread, and the large datasets produced as output are freely accessible to anyone. With the term omics, we refer to the technologies (like Genomics, Transcriptomics, Proteomics, Metabolomics and Metagenomics, to name the most cited ones) that exploit high-throughput assays to comprehensively measure molecules of the same type from a biological sample. The result is generally a comprehensive (non-targeted) picture of the samples, and because of that, these technologies allow us to provide holistic views of the biological system.
The constant cost reduction for data generation and the scientific impact on advancing the fields has produced a constant increase in deposited datasets. Moreover, the guidelines provided by funding agencies and scientific journals are nowadays mandating to have data publicly available, making the scientific finding reproducible and open to peer review.
This phenomenon is becoming even more interesting now, with the recent development of single-cell approaches. Cellular diversity, especially in the brain, is a critical component that is not accounted for using a bulk approach. The availability of single-cells datasets allows us to digitally dissect and explore the contribution of any individual cell or cell type in the context of the condition of interest (even if it was initially outside the scope of the investigators who produced the data). The need to generate new data might come from the absence of a specific model or experimental design, but public databases are growing as an excellent source to explore and generate hypothesis effectively or as a benchmark.
This short presentation will show two case examples where Omic studies have been processed to generate or test a new hypothesis.
The first case study applied a shotgun proteomic approach to the primary skin fibroblasts of patients with ALS. ALS patients were characterized by having the C9orf72 mutation, the sporadic form of the disease or some other causal genetic factor. The study aimed to identify how the proteome changes between ALS patients with or without the C9orf72 mutation (same clinical phenotype but different genotype) and perform a systems biology analysis to identify significantly altered pathways between the different conditions.
The second case study will show how data produced by different labs and deposited in a publicly available repository (GEO) can be used to generate and test new hypotheses out of the scope of the original authors.
Briefly, we downloaded two independent scRNA-seq datasets from two mice models of Alzheimer. Based on the authors' QC and imputation, we extracted the contribution of pure microglia from mice brains. We then focus our analysis on the contribution of the cannabinoid pathway in both models.

Inflammatory biomarkers and antidepressant response in Major Depressive Disorder: the role of C-Reactive Protein.

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Inadequate response to antidepressant treatment, in a significant proportion of patients diagnosed with Major Depressive Disorder, contributes to the large burden of disability associated with the disease; thus, predicting treatment response is one of the most important challenge for clinicians who deal with depressed patients. The cytokine hypothesis of depression suggests that altered peripheral cytokine levels are involved in the pathophysiology of depressive disorder and in modulating response to treatment. Authors performed a meta-analysis aims to investigate the association between cytokine levels at baseline and response to antidepressant therapies, in order to identify those markers implicating in antidepressant response. Patients who failed to respond to antidepressant had aberrant inflammatory process, namely higher baseline levels of C-Reactive Protein, which is associated with treatment outcome in Major Depressive Disorder. Despite these promising results, further investigations are needed. In light of the above, authors are evaluating CPR levels in depressed patient referring to the Psychiatry ward of Ospedale di Circolo – Fondazione Macchi, in order to examine the potential role of this inflammatory marker as a novel predictive tool for pharmacological treatment of depressive disorder. From December 2019 to day, 27 patients diagnosed with Major Depressive Disorder were recruited. Blood samples were collected at the moment of admission (T0) in all enrolled patients. Severity of depression was evaluated trough the Hamilton Depression Rating Scale – 21 items at T0 and after 4 weeks (T1); response to treatment was defined as a reduction in HDRS score above 75% after one month of treatment. From available data analysis, CRP levels are significantly higher in those patients who failed to respond after 4-weeks of antidepressant treatment ($p = 0.013$). Despite these encouraging results, the study is still ongoing: authors plan to enlarge the sample and to evaluate the role of CRP in modulating treatment response according to antidepressants' class used.

A longitudinal evaluation of the peripheral immune phenotype in a cohort of Parkinson's disease patients

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Background - Parkinson's disease (PD) represents a common neurodegenerative disorder caused by the loss of dopaminergic neurons in the pars compacta of the substantia nigra. The pathophysiological process is complex and multifactorial but in the last years the role of immune system has been identified as crucial. Indeed, PD patients display a pro-inflammatory peripheral immune phenotype but less is known about the trend of immunological parameters during disease decourse.
Aim - The object of our work is to evaluate the suitable modifications of immunological parameters in a thorough characterized population of Italian PD patients
Subjects and methods - Starting from 2014, drug naïve PD patients were enrolled and underwent a peripheral blood withdrawal annually, evaluating the different lymphocytes sub-populations with the flow cytometry and the lymphocytes transcription factors with the RT-PCR. Patients were excluded in presence of active or past immune disease or immunomodulant/depressant treatment. A complete blood cell (CBC) analysis, including C-Reactive Protein (CRP) and erythrocyte sedimentation rate (ESR), was performed in order to exclude abnormal immune system activation. Subjects were also evaluated clinically by movement disorders experts and demographic and clinical parameters were monitored.
Results - 49 PD patients (33 male) with a mean age of 68±8.4 years and with at least one follow-up visit were included. 16 of them (32.6%) completed a 4-year follow-up visit. Regarding peripheral immune phenotype, Th1 lymphocytes (as % of CD4+ cells) were significantly higher after 2 and 4 years (V0: 15.91±6.61; V2:17.93±9.4; V4:20.88±11.6; p=0.03 and p=0.0006, respectively) while Th2 (as total count) were persistently reduced (V0:0.06*10^3±0.02; V3: 0.04*10^3±0.01; p=0.003). Furthermore, Th17 lymphocytes were significantly reduced both as percentage (V0: 8.13±4; V1:7.43±3.75; V4:7.84±0.84; p=0.04 and p=0.02, respectively) and total count (V0:0.07*10^3±0.02; V1: 0.05*10^3±0.03; V4: 0.05*10^3±0.0; respectively p=0.01 and p=0.01). These data are in line with the mRNA expression of lymphocytes transcription factors. Accordingly, STAT1 (which drives the Th1 differentiation) presented constantly increased levels (V0: 1.61*10^{-4}±0.0001; V1 2.39*10^{-4}±0.0001; V2: 2.38*10^{-4}±5*10^{-5}; V3: 2.86*10^{-4}±0.0001; respectively p=0.01; p=0.006; p<0.0001) while STAT6 (leading to Th2 phenotype) levels were reduced (V0:6.96*10^{-6}±9.6*10^{-6} ; V1: 9.01*10^{-7}±8.72*10^{-8} ; V2: 1.51*10^{-6}±2.8*10^{-6} respectively p<0.0001 and p=0.0001). Moving to the Treg compartment, total number of Treg was significantly reduced in V3 and V4 (0.06*10^3±0.02; V1: 0.05*10^3±0.01; V4: 0.05*10^3±0.01, respectively p=0.008

and p=0.0004) as well as the activated and resting subsets. These data were also supported by the analysis of the correspondent transcription factors: FOXP3 levels were significantly reduced at V4 compared to baseline (V0: $7.55*10^{-5}\pm6.4*10^{-5}$; V4: $4.55*10^{-5}\pm5.01*10^{-5}$)

Conclusions - To the best of our knowledge, this is the first longitudinal study evaluating the modification of peripheral immune system in PD. Our data, though preliminary, support the concept that the move toward a pro-inflammatory phenotype represents an early phenomenon in the disease decourse which tends to persist in the years. These data have important clinical impact since several immunotherapies in PD are under investigation and, accordingly, they should be started soon in the disease history in order to best act as disease modifiers.

EFFECT OF DOPAMINERGIC AGENTS ON HUMAN PERIPHERAL CD4+T LYMPHOCYTES: RELEVANCE FOR PARKINSON'S DISEASE.

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Background: Parkinson's disease (PD) is the second most common chronic neurodegenerative disease, affecting up to 10 million people worldwide. Hallmarks of PD are the progressive loss of dopaminergic neurons in substantia nigra, which lead to a complex burden of motor and non-motor symptoms. The pathological mechanisms involved in the disease remain unknown, but increasing evidence points to the peripheral immune system as a key player in PD. In particular, CD4+ T lymphocytes may promote neurodegeneration by means of proinflammatory cytokines such as tumour necrosis factor (TNF)-α, interferon (IFN)-γ and interleukin (IL)-17A as well as neuroprotection through the activity of interleukin (IL)-4-producing T cells and T regulatory cells. Dopamine substitution therapy is currently the only available strategy to treat symptoms. Dopaminergic modulation of the immune response is nowadays well established, but the possible effects of dopaminergic agents in PD have never been assessed so far. Therefore, the aim of this study was to assess the effect of dopaminergic antiparkinsonian drugs pramipexole (PPX), ropinirole (ROP) and rotigotine (ROT) on human peripheral CD4+T cells of healthy subjects and PD patients.

Methods: Peripheral blood mononuclear cells (PBMCs) were isolated from buffy coats of healthy donors and from peripheral blood of drug-naive PD patients by Ficoll-Paque™ Plus density-gradient centrifugation. Isolated PBMCs were then stimulated with anti-CD3/anti-CD28 Abs (2/2 μg/ml) and cultured alone or in the presence of one of the following dopaminergic agonists: PPX, ROP and ROT, all at the concentration of 0.1 μM at 37°C under a 95% O_2/5% CO_2 atmosphere. Cell pellets and supernatants were collected after 48 h and TNF-α, IFN-γ and IL-17A were assayed by RT-PCR and by ELISA. Cell proliferation of both PBMCs and isolated CD4+ T effector cells alone or in presence of T regulatory cells (separated by means of MACS® Cell Separation) was assessed after 120 h incubation by flow cytometry. The percentage of IFNγ-, IL17A- and IL4-producing CD4+ T cells from PBMCs was assessed after a short-time incubation of 5 h with PMA/Ionomycin (0.01/1 μg/ml) in the presence of each dopaminergic agonist.

Results: Stimulation of PBMCs with anti-CD3/anti-CD28 Abs increased TNF-α, IFN-γ and IL-17A mRNA levels (by 4-, 8- and 4-folds, respectively), and TNF-α, IFN-γ and IL-17A secretion (from 61.4 to 1304.7 pg/mL, from 5.9 to 176.9 pg/mL and from 7.4 to 84.8 pg/mL). In preliminary experiments incubation of stimulated PBMCs with either PPX, ROP or ROT reduced mRNA levels of TNF-α (by 24%, 27% and 32%, respectively), IFN-γ (by 36%, 37% and 40%) and IL-17A (by 22%, 30% and 21%). Extracellular secretion of TNF-α was significantly reduced by ROP and PPX (by 32% and 10% respectively), while only ROP significantly reduced IFN-γ by 42%. ROT did not affect IFN-γ secretion, while

slightly decreased TNF-α and significantly increased IL-17A secretion (29%). Proliferation of PBMCs as well as proliferation of isolated CD4+T effector cells, alone or co-incubated with T regulatory cells, were unaffected by dopaminergic agonists. No major results were obtained by dopaminergic agents on percentage of IFNγ-, IL17A- and IL4-producing CD4+T cells compared to untreated controls. In PBMCs of PD patients, all dopaminergic agonists exhibited patterns of effects similar to those reported in buffy coats from healthy subjects.
Conclusions: All the dopaminergic agonists tested reduced TNF-α, IFN-γ and IL-17A mRNA levels in healthy donors and PD patients. However, only ROP and PPX, but not ROT, also resulted in reduction of TNF-α and IFN-γ production at least in healthy subjects. Results suggest that antiparkinsonian dopaminergic agents may affects CD4+ T cell function, and further studies are urgently needed to evaluate whether this pattern of effects occurs also in vivo and to what extent it may be relevant for PD development and progression.

Pilot study aimed to identify the role of peripheral adaptive immunity in the mechanism of Alzheimer's disease Neuroinflammation

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BACKGROUND AND AIMS - Alzheimer's disease (AD) is a condition characterized by a progressive cognitive decline, resulting from a cerebral neurodegenerative process. There are many macro and microscopic modifications linked to protein misfolding and accumulation. Early involvement of other mechanisms is increasingly evident. These include processes of chronic neuroinflammation with activation of peripheral-adaptive-immunity. However, the study of peripheral immunity in AD received less attention than in Parkinson Disease and only few studies investigated the dysregulation of peripheral adaptive immune pattern.
Based on these assumptions, we've designed a case-control pilot-study, with the aim of analyzing the pattern of expression of CD4+T cells transcription-factors and identifying an immune profile in the peripheral blood of AD and Mild Cognitive Impairment (MCI) patients, compared with Healthy Subjects (HS).
METHODS - Between December 2019 and June 2021, we recruited 48 patients, selected with inclusion and exclusion criteria, established by the study. We selected 2 different groups age-and-sex-matched: HS group and MCI-AD group, this last enrolled according to National-Institute-on-Aging-and-the-Alzheimer's-Association criteria and previously selected with Amyloid-Pet-Cerebral-Scan. All patients performed an enrollment-visit, 20 patients performed a follow-up after 6 months, 12 patients performed also a follow-up visit after 12 motnhs. During each visit we collected demographic, clinical, instrumental, pharmacological variables and blood samples for isolation of PBMC, followed by identification of CD4+T cells. Furthermore, in the first 16 patients, CD4+T cells were processed, using real-time-PCR for identification of specific transcriptional-factors-mRNA levels (Nurr1/RORyC/GATA3/Tbet1/FoxP3/STAT1/STAT3/STAT4/STAT6). We performed a transversal statistical analysis of the main demographic, clinical and laboratoristic data of the first 24 enrolled subjects. Statistical significance of the difference among groups was analyzed by means of two-tailed Student's t-test and chi-q test for continuous variables.
RESULTS - Despite the small size of the population currently analyzed in the study, a preliminary statistical analysis was performed to assess any differences in clinical, anamnestic and pharmacological variables, within the two groups NCI and MCI/AD at the time of enrollment (T0). In order to compare the two groups, a second preliminary analysis was conducted, in terms of immune "gene pattern" of CD4+ T lymphocytes both at T0 and at the first follow-up performed by patients after 6 months (T1). As shown in Table 1, the comparison between the two groups showed a statistically significant difference with regard to positive family history for cognitive impairment in the group of MCI/AD cases, compared

to the group of NCI controls (p=0.036), confirming the data already present in the literature. A preliminary analysis was carried out in the first 16 subjects enrolled at T0, and in 7 subjects evaluated at T1. In addition, the mRNA values of the transcription factors of TCD4+ lymphocytes, analyzed by real-time PCR, were analyzed in the two groups, thus comparing the immune gene pattern, in order to evaluate the presence of statistically significant differences between the groups at T0 and at T1 (Table 2). From this analysis, remembering the limits of the small sample size available, no statistically significant difference emerged, in terms of "gene pattern" of TCD4+ lymphocytes, between the two groups, as shown in Table 2. No statistically significant difference emerged, moreover, when analyzing over time the variations of transcription factors, within the two groups.
CONCLUSIONS - Further data are necessary to evaluate the possibility of being able to identify an immune profile of CD4+ T lymphocytes, pro- and anti-inflammatory cytokines in the peripheral blood of subjects with AD and MCI, and compare them with healthy individuals, in order to be able to characterize the mechanism of neurodegeneration in Alzheimer's disease. It will also be important to assess, even during the follow-up of enrolled subjects, any changes in the expression pattern of these transcription factors over time and examine, therefore, the possible correlation with the clinical profile.

Table 1: Clinical-anamnestic variables at the time of enrollment of the two groups (T0 visit)

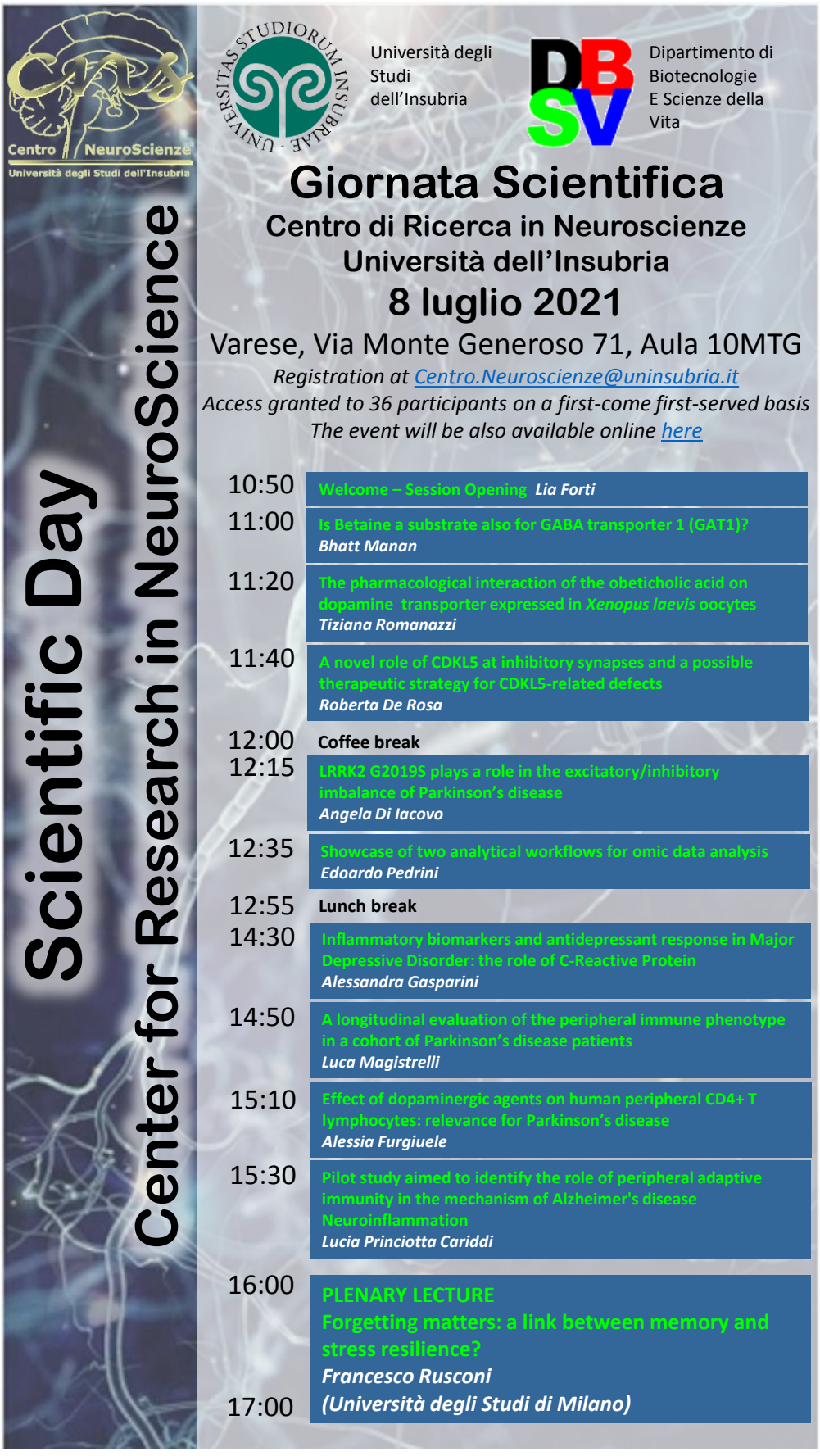
	NCI Group (Healthy Subject) ***n=12***	**MCI/AD Group (cases)** ***n=12***	**P value**
Age	72.95 ±9.19	73.08±9.0.1	p= 0.22
Sex	6F-6M	6F-6M	p=1
Family history of dementia	2	8	**p= 0.036**
Years of schooling	9.78±2.87	9.3±2.07	p=0.30
Hypertension	8	6	p= 0.48
Diabetes	2	3	p= 0.61
Oncologic Pathologies	1	1	p= 1
Immune Disorders	1	2	p= 0.53
Heart Disease	3	3	p= 1
Sleep Disorders	2	2	p= 1
Dyslipidemia	6	5	p= 0.68

Table 2: Comparison of mean values of the "gene pattern" of CD4+ T lymphocytes in the two groups NCI and MCI/AD

	NCI Group (Healthy Subject) T0 ***n=8***	**MCI/AD Group (cases) T0** ***n=8***	**P value**	**NCI Group (Healthy Subject) T1** ***n=3***	**MCI/AD Group (cases) T1** ***n=4***	**P value**
NR4A2	1,88E-04±1,88E-04	1,80E-04±1,84E-04	*p=0.9*	2,18E-04± 2,26E-04	1,93E-04±2,11E-04	*p=0.49*
RORyC	1,04E-05±3,11E-05	9,71E-06±3,01843E-05	*p=0.47*	2,30E-05± 4,97E-05	1,92E-05±4,54E-05	*p=0.44*
GATA3	1,44E-04± 1,96E-04	1,36E-04±1,92E-04	*p=0.89*	1,94E-04± 2,10E-04	1,57E-04±2,05E-04	*p=0.63*
Tbet1	5,09E-07±2,27E-07	5,05E-07±2,2E-07	*P=0.69*	5,07E-07± 2,23E-07	4,66E-07±2,25E-07	*p=0.59*
FoxP3	8,01E-05±7,11E-05	7,54E-05±7,13E-05	*p=0.90*	1,00E-04± 9,60E-05	9,35E-05±8,75E-05	*p=0.43*
STAT1	2,75E-04±1,69E-04	2,76E-04 ±1,63E-04	*p=0.82*	1,87E-04± 1,94E-04	2,23E-04±1,74E-04	*p=0.18*
STAT3	8,88E-05±8,45E-05	8,71E-05±8,2E-05	*p=0.35*	5,29E-05± 8,19E-06	6,93E-05±4,48E-05	*p=0.57*
STAT4	1,43E-05± 6,00E-06	1,60E-05±8,9E-06	*P=0.25*	1,34E-05± 1,88E-06	1,48E-05±3,72E-06	*p=0.80*
STAT6	9,06E-07±7,31E-08	9,03E-07±7,18E-08	*P=0.6*	9,04E-07± 1,43E-07	9,16E-07± 1,24E-07	*p=0.24*

Appunti

Appunti


Centro NeuroScienze
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Dipartimento di Biotecnologie E Scienze della Vita
Scientific Day
Center for Research in NeuroScience
Giornata Scientifica
Centro di Ricerca in Neuroscienze
Università dell'Insubria
8 luglio 2021
Varese, Via Monte Generoso 71, Aula 10MTG
Registration at Centro.Neuroscienze@uninsubria.it
Access granted to 36 participants on a first-come first-served basis
The event will be also available online here
10:50 Welcome – Session Opening Lia Forti
11:00 Is Betaine a substrate also for GABA transporter 1 (GAT1)? Bhatt Manan
11:20 The pharmacological interaction of the obeticholic acid on dopamine transporter expressed in Xenopus laevis oocytes Tiziana Romanazzi
11:40 A novel role of CDKL5 at inhibitory synapses and a possible therapeutic strategy for CDKL5-related defects Roberta De Rosa
12:00 Coffee break
12:15 LRRK2 G2019S plays a role in the excitatory/inhibitory imbalance of Parkinson's disease Angela Di Iacovo
12:35 Showcase of two analytical workflows for omic data analysis Edoardo Pedrini
12:55 Lunch break
14:30 Inflammatory biomarkers and antidepressant response in Major Depressive Disorder: the role of C-Reactive Protein Alessandra Gasparini
14:50 A longitudinal evaluation of the peripheral immune phenotype in a cohort of Parkinson's disease patients Luca Magistrelli
15:10 Effect of dopaminergic agents on human peripheral CD4+ T lymphocytes: relevance for Parkinson's disease Alessia Furgiuele
15:30 Pilot study aimed to identify the role of peripheral adaptive immunity in the mechanism of Alzheimer's disease Neuroinflammation Lucia Princiotta Cariddi
16:00 PLENARY LECTURE
Forgetting matters: a link between memory and stress resilience?
Francesco Rusconi
(Università degli Studi di Milano)
17:00