S14. DNA methylation changes in GABAergic and glutamatergic markers in early schizophrenia.

FACHIM, Helene, LOUREIRO, Camila, CORSI-ZUELI, Fabiana, MENEZES, Paulo Rossi, LOUZADA JR, Paulo, DALTON, Caroline <http://orcid.org/0000-0002-1404-873X>, DEL-BEN, Cristina Marta and REYNOLDS, Gavin <http://orcid.org/0000-0001-9026-7726>

from ROD. In classification, a 65% sensitivity and specificity are found. Data will also be presented on the CHR group and their alignment, together with VBM analysis for structural MRI examining correlates with highly weighted classifying symptoms in and across all three groups.
Discussion: When given early in the course of illness, interventions have the greatest potential impact, and characterization and accurate diagnosis of depression in emerging mental disorders is an important goal. This study suggests it may be possible to accurately identify depression in different diagnostic categories, including major depressive disorder, psychosis and clinical high risk, and that neuroimaging holds potential to add to diagnostic accuracy in complex co-morbid disorders.

S14. DNA METHYLATION CHANGES IN GABAERGIC AND GLUTAMATERGIC MARKERS IN EARLY SCHIZOPHRENIA

Helene Fachim*[,1], Camila Loureiro[2], Fabiana Corsi-Zueli[2], Paulo Rossi Menezes[2], Paulo Louzada Jr[2], Caroline Dalton[1], Cristina Marta Del-Ben[2], Gavin Reynolds[1]
[1]Sheffield Hallam University; [2]University of Sao Paulo

Background: GABAergic and glutamatergic systems play an important role in the neurobiology of schizophrenia, and changes in their markers are reported in both postmortem human brain and in animal models. Recent studies have demonstrated that abnormalities in DNA methylation may underlie the alterations in various indicators of GABAergic and glutamatergic functions in schizophrenia. As our group previously found decreased NR2 protein plasma levels and downregulation of parvalbumin (PVALB) mRNA in first episode of psychosis (FEP) patients, we hypothesised that changes in DNA methylation may be responsible for these indicators of glutamatergic and GABAergic deficits in FEP patients.
Methods: Blood samples were collected from patients in FEP (n = 35) after their first contact with the mental health assistance, siblings (n = 21) and population-based controls (n = 35). Bisulfite conversion and pyrosequencing were used to determine methylation levels in 4 CpG sites in promoter sequence of PVALB and 5 CpG sites at GRIN2B (gene which encodes NR2).
Results: We found hypermethylation at a CpG site within the PVALB promoter sequence in patients and their siblings compared to population-based control group ($p< 0.001$) while overall hypomethylation was found in the 5 CpGs analysed within GRIN2B promoter sequence ($p < 0.01$).
Discussion: Our PVALB findings are consistent with our previous studies showing that PVALB promoter methylation is elevated in schizophrenia and, additionally this is the first evidence showing changes in GRIN2B promoter methylation in psychosis. These results together suggest that these epigenetic findings may relate to the reduction of protein expression of indicators of glutamate and GABA systems seen in this disease.

S15. ABNORMAL EYE TRACKING IN PATIENTS WITH SCHIZOPHRENIA UNDER THE SOCIAL SCENE

Qijing Bo*[,1], Xianbin Li[1], Wenlong Jiang[1], Changming Wang[1], Chuanyue Wang[1]
[1]Beijing Anding Hospital, Capital Medical University

Background: To investigate whether the eye movement pattern is different between facial emotion recognition and real social scene emotion recognition, and which can better reflect the social function and the clinical symptoms using a novel theme identification task.
Methods: Total 29 patients with schizophrenia and 31 healthy controls completed the theme identification task, in which subjects selected which word, out of positive, neutral and negative, described the theme of a picture under facial emotion recognition and real social scene emotion recognition. Positive and negative syndrome scale (PANSS) and social function in psychosis inpatients (SSPI) were used to assess the symptom and social function.
Results: The schizophrenia's eye movement paradigms under both facial emotion and social scene show decreased number of fixation ($t=-3.49$, $P=0.00$; $t=-3.62$, $P=0.00$), decreased number of saccades ($t=-3.15$, $P=0.00$; $t=-3.72$, $P=0.00$), decreased scan path length ($t=-2.23$, $P=0.03$; $t=-4.18$, $P=0.03$), decreased fixation number in interest area ($t=3.01$, $P=0.00$; $t=-3.24$, $P=0.00$). Different from facial emotion cognition, the eye movement under social scene cognition showed lower percentage of fixation number in interest area than that in healthy subjects ($P=0.01$), furthermore, the length of scan path under the negative social scene pictures was associated with the total score of SSPI ($r=-0.38$, $P=0.04$), the PANSS total score ($r=-0.46$, $P=0.01$), the positive symptoms score ($r=-0.39$, $P=0.04$), the general score ($r=-0.50$, $P=0.01$).
Discussion: The patients showed more abnormal eye tracking indicators under social scene than facial emotion. Under negative emotion social scene, the length of scan path related to social function and clinical symptoms, it may be a potential indicator to evaluate social function and degree of disease.

S16. GLUTAMATERGIC NEUROMETABOLITE LEVELS IN PATIENTS WITH TREATMENT-RESISTANT SCHIZOPHRENIA: A CROSS-SECTIONAL 3T PROTON MRS STUDY

Yusuke Iwata*[,1], Shinichiro Nakajima[2], Eric Plitman[2], Jun Ku Chung[2], Fernando Caravaggio[2], Julia Kim[1], Eric Brown[1], Nathan Chan[1], Parita Shah[1], Sofia Chavez[1], Philip Gerretsen[2], Masaru Mimura[3], Gary Remington[1], Ariel Graff-Guerrero[2]
[1]Centre for Addiction and Mental Health; [2]Centre for Addiction and Mental Health, University of Toronto; [3]Keio University School of Medicine

Background: In terms of response to antipsychotic treatment, patients with schizophrenia can be classified into three groups; (1) treatment-resistant patients who are clozapine (CLZ)-resistant (ultra treatment-resistant schizophrenia [UTRS]), (2) treatment-resistant patients who are CLZ-responsive (TRS), and (3) patients who respond to non-CLZ antipsychotics (treatment non-resistant schizophrenia [TnRS]). The aim of this study was to examine glutamatergic neurometabolite levels in these three patient groups, along with healthy controls (HCs), using proton magnetic resonance spectroscopy (1H-MRS).
Methods: Glutamate (Glu) and glutamate+glutamine (Glx) levels were assessed in the associative striatum (Str), anterior cingulate cortex (ACC), and dorsolateral prefrontal cortex (DLPFC) using 3T 1H-MRS (PRESS, TE=35ms). Neurometabolite levels were corrected for cerebrospinal fluid proportion.
Results: A total of 100 participants (26 UTRS, 27 TRS, 21 TnRS, and 26 HCs) were included in this study. Patients with UTRS showed higher Glx levels in the ACC compared to HCs ($p=0.038$). When patients with UTRS and TRS were combined into one group, this subset of patients showed higher Glu and Glx levels in the ACC compared to HCs ($p=0.028$ and $p=0.023$, respectively). There were no significant group differences in the Str or DLPFC.
Discussion: Previous findings reporting higher glutamatergic levels in the ACC of patients with TRS may be mainly influenced by patients with CLZ non-responder. Higher ACC glutamatergic neurometabolite level may be a biological trait of resistance to the first-line antipsychotic treatment that is retained even after CLZ administration.