Conclusions The present data suggest that the psychosocial stress response is a multidimensional physiological event that is affected by a variety of factors as diverse as 5-HTTLPR genotype, personality profile, BMI, and age.
Disclosure of interest The authors have not supplied their declaration of competing interest.

http://dx.doi.org/10.1016/j.eurpsy.2017.01.2049

EW0181

Skin conductance response to emotional stimuli and injury location in patients with single right hemisphere damage

S. Álvarez[1], G. Lahera[2,3,*]
[1] *Foundation Alicia Koplowitz Research Fellow, New York University Child Study Center, Child Psychiatry, NY, USA*
[2] *Psychiatry, University of Alcalá, Alcalá de Henares, Madrid, Spain*
[3] *Cibersam, Mental Health, Madrid, Spain*
[*] *Corresponding author.*

Introduction Right hemisphere damage (RHD) has been related to alterations in emotion processing. However, results regarding physiological responses are limited and inconsistent. More research regarding specific brain areas involved in emotional physiological responses is needed.
Objectives To examine the skin conductance response (SCR) to emotion eliciting images in patients with single RHD. To explore the relationship between SCR and brain injury location in patients with single RHD.
Aims To examine the relationship between SCR and cortical and subcortical damage in RH regarding emotional processing.
Method Forty-one individuals with RHD due to stroke were assessed (mean age 68.5, SD 12.2, 51.1 males). The amplitude of event-related SCR was registered through a biofeedback system while observing 54 photographs from the international affective picture system (IAPS). Emotional images were classified using two different approaches: emotional valence (pleasant, unpleasant, neutral) and social vs. non-social content. Brain damage location, determined through medical records, included cortical (frontal, parietal, temporal and occipital lobes) as well as sub-cortical (caudate nucleus, thalamus, lenticular nucleus, insular cortex, basal ganglia and limbic system) structures.
Results Amplitude of SCR to emotional images was significantly lower in individuals with occipital cortex injury compared to those with damage in other brain locations ($P < 0.05$). These results were consistent through all stimuli categories but non-social pictures, which presented the same pattern though, did not reach statistical significance.
Conclusions Results show a relationship between occipital areas in HD and SCR to emotional eliciting stimuli, suggesting occipital right lobe involvement in physiological emotional processing.
Disclosure of interest The authors have not supplied their declaration of competing interest.

http://dx.doi.org/10.1016/j.eurpsy.2017.01.2050

EW0182

The use of polygenic risk scores to inform aetiology of mood and psychotic disorders

J. Harrison[*], S. Mistry
Cardiff University School of Medicine, MRC Centre for Neuropsychiatric Genetics and Genomics, Cardiff, Wales, United Kingdom
[*] *Corresponding author.*

Introduction Polygenic risk scores (PRS) incorporate many small genetic markers that are associated with conditions. This technique was first used to investigate mental illnesses in 2009. Since then, it has been widely used.
Objectives We wanted to explore how PRS have been used to the study the aetiology of psychosis, schizophrenia, bipolar disorder and depression.
Aims We aimed to conduct a systematic review, identifying studies that have examined associations between PRS for bipolar disorder, schizophrenia/psychosis and depression and psychopathology-related outcome measures.
Methods We searched EMBASE, Medline and PsychInfo from 06/08/2009 to 14/03/2016. We hand-searched the reference lists of related papers.
Results After removing duplicates, the search yielded 1043 publications. When irrelevant articles were excluded, 33 articles remained. We found 24 studies using schizophrenia PRS, three using bipolar PRS and nine using depression PRS. Many studies successfully used PRS to predict case/control status. Some studies showed associations between PRS and diagnostic sub-categories. A range of clinical phenotypes and symptoms has been explored. For example, specific PRS are associated with cognitive performance in schizophrenia, psychotic symptoms in bipolar disorder, and frequency of episodes of depression. PRS have also demonstrated genetic overlap between mental illnesses. It was difficult to assess the quality of some studies as not all reported sufficient methodological detail.
Conclusions PRS have enabled us to explore the polygenic architecture of mental illness and demonstrate a genetic basis for some observed features. However, they have yet to give insights into the biology, which underpin mental illnesses.
Disclosure of interest The authors have not supplied their declaration of competing interest.

http://dx.doi.org/10.1016/j.eurpsy.2017.01.2051

EW0183

Identification of biological pathways to Alzheimer's disease using polygenic scores

J. Harrison[*], E. Baker, L. Hubbard, D. Linden, J. Williams, V. Escott-Price, P. Holmans
Cardiff University School of Medicine, MRC Centre for Neuropsychiatric Genetics and Genomics, Cardiff, Wales, United Kingdom
[*] *Corresponding author.*

Introduction Single nucleotide polymorphisms (SNPs) contribute small increases in risk for late-onset Alzheimer's disease (LOAD). LOAD SNPs cluster around genes with similar biological functions (pathways). Polygenic risk scores (PRS) aggregate the effect of SNPs genome-wide. However, this approach has not been widely used for SNPs within specific pathways.
Objectives We investigated whether pathway-specific PRS were significant predictors of LOAD case/control status.
Methods We mapped SNPs to genes within 8 pathways implicated in LOAD. For our polygenic analysis, the discovery sample comprised 13,831 LOAD cases and 29,877 controls. LOAD risk alleles for SNPs in our 8 pathways were identified at a *P*-value threshold of 0.5. Pathway-specific PRS were calculated in a target sample of 3332 cases and 9832 controls. The genetic data were pruned with $R^2 > 0.2$ while retaining the SNPs most significantly associated with AD. We tested whether pathway-specific PRS were associated with LOAD using logistic regression, adjusting for age, sex, country, and principal components. We report the proportion of variance in liability explained by each pathway.
Results The most strongly associated pathways were the immune response (NSNPs = 9304, $= 5.63 \times 10^{-19}$, $R^2 = 0.04$) and hemostasis (NSNPs = 7832, $P = 5.47 \times 10^{-7}$, $R^2 = 0.015$). Regulation of endocytosis, hematopoietic cell lineage, cholesterol transport, clathrin and

https://doi.org/10.1016/j.eurpsy.2017.01.2052 Published online by Cambridge University Press

protein folding were also significantly associated but accounted for less than 1% of the variance. With APOE excluded, all pathways remained significant except proteasome-ubiquitin activity and protein folding.
Conclusions Genetic risk for LOAD can be split into contributions from different biological pathways. These offer a means to explore disease mechanisms and to stratify patients.
Disclosure of interest The authors have not supplied their declaration of competing interest.

http://dx.doi.org/10.1016/j.eurpsy.2017.01.2052

EW0184

Peripheral levels of the micro-RNA miR-1202 are correlated with changes in brain activity and connectivity during an antidepressant treatment

J.P. Lopez[1,2], F. Pereira[3], S. Richard-Devantoy[4], Y. Ding[4], L.M. Fiori[4], P. Niola[5], G. Turecki[4], F. Jollant[4,6,*]
[1] *Max Plank Institute, Stress Neurobiology and Neurogenetics, Munich, Germany*
[2] *Human genetics department, McGill University, Montreal, Canada*
[3] *Radiology department, Nîmes Academic Hospital, Nîmes, France*
[4] *Psychiatry department, McGill University, Montreal, Canada*
[5] *Biomedical Science department, Università degli studi Di Cagliar, Cagliari, Italy*
[6] *Psychiatry department, Nîmes Academic Hospital, Nîmes, France*
* *Corresponding author.*

Introduction Micro-RNAs are short non-coding sequences playing a major role in regulating gene expression. Peripheral levels of the micro-RNA miR-1202 have been shown to predict antidepressant response and to change during treatment. However, it is not clear to what extent these peripheral measures reflect central neural changes in vivo.
Objectives We aimed at investigating a potential link between peripheral micro-RNA and neuroimaging measures.
Methods At baseline and after 8 weeks of desvenlafaxine (50–100 mg die), twenty depressed patients were scanned with 3 T magnetic resonance imaging, first at rest then during the Go/NoGo task, a classical test of response inhibition. Blood samples were taken for RNA extraction.
Results During resting state, baseline miR-1202 levels were predictive of decreased connectivity between the posterior cingulate and the prefrontal, occipital and parietal cortices. Changes in miR-1202 levels were correlated with changes in activity in right precuneus within the default-mode network, and with decreased connectivity between the posterior cingulate and the temporal and prefrontal cortices, and the precuneus. During the Go/NoGo task, baseline levels and changes in these levels were correlated with activity changes in different regions, including bilateral prefrontal, insular, cingulate, and temporal cortices. Finally, secondary analyses suggest an association between miR-1202 levels and glutamate levels measured by spectroscopy in dorsomedial prefrontal cortex.
Conclusions This is the first study showing that baseline and changes in peripheral levels of one micro-RNA were associated with changes in brain activity and connectivity during an antidepressant treatment. MiR-1202 may act through the modulation of the glutamatergic system.
Disclosure of interest The authors have not supplied their declaration of competing interest.

http://dx.doi.org/10.1016/j.eurpsy.2017.01.2053

EW0185

Concomitant 3q13.31 microdeletion and ring chromosome 22 in a patient with severe developmental delay, ventriculomegaly, and Dandy-walker malformation

A. Kashevarova[1,2,*], E. Belyaeva[3], N. Skryabin[1,2], S. Vasilyev[1,2], M. Lopatkina[1], L. Nazarenko[3], A. Nikonov[4], I. Lebedev[1,2]
[1] *Research Institute of Medical Genetics- Tomsk National Research Medical Center- Russian Academy of Sciences, Laboratory of Cytogenetics, Tomsk, Russia*
[2] *Tomsk State University, Laboratory of Human Ontogenetics, Tomsk, Russia*
[3] *Research Institute of Medical Genetics, Tomsk National Research Medical Center, Russian Academy of Sciences, Laboratory of Hereditary Pathology, Tomsk, Russia*
[4] *Diagnostic Center of Altai Region, Medical and Genetic Clinic, Barnaul, Russia*
* *Corresponding author.*

Introduction Over 20% of patients with developmental delay (DD) has copy number variations (CNV) of unknown significance. Some CNV may be associated with disease in a patient and also present in their apparently healthy parents. According to the two-hit model another CNV may contribute to phenotypic variation of such genomic disorders.
Objectives DD diagnostics improvement.
Aims Understanding the pathogenic significance of concomitant 3q13.31 and 22q13.32-q13.33 microdeletions.
Methods Ring chromosome 22 was first detected by conventional cytogenetics. Microdeletions at 3q13.31 and 22q13.32–q13.33 were revealed by agilent technologies 60 K microarray and confirmed by qPCR. Ring chromosome was confirmed by FISH.
Results We present a four-year-old girl with del22q13.32-q13.33 resulted in a ring chromosome 22 and a single TUSC7 gene microdeletion at 3q13.31. The del22q13.32-q13.33 originated de novo, whereas del3q13.31 was inherited from healthy mother. The 22q13.32-q13.33 locus is associated with Phelan-McDermid syndrome (PHMDS, OMIM 606232). The patient demonstrated features both typical for the syndrome (psychomotor and speech development delay, autistic signs, aggression, sleep alteration, seizures) and atypical – attention deficit-hyperactivity disorder (ADHD), ventriculomegaly, and reduced size of cerebella hemispheres (Dandy-Walker variant). ADHD and ventriculomegaly were previously described in patients with del3q13.31 (OMIM 615433) but Dandy-Walker variant was observed in our patient for the first time. Possibly, atypical for PHMDS features, may result from transepistasis of microdeletions.
Conclusions Multiple CNVs in one patient complicate genotype-phenotype correlations due to possible overlapping phenotypes and/or modifying effect of variants. This study was supported by Russian Science Foundation, grant no. 16-15-10231.
Disclosure of interest The authors have not supplied their declaration of competing interest.

http://dx.doi.org/10.1016/j.eurpsy.2017.01.2054

EW0186

CYP450 enzymes genetic polymorphism influence on treatment of affective disorders

A. Lengvenytė[1,*], R. Strumila[2], E. Dlugauskas[3], A. Utkus[4]
[1] *Clinic of Psychiatry, Vilnius University, Faculty of Medicine, Vilnius, Lithuania*
[2] *Vilnius University, Faculty of Medicine, Vilnius, Lithuania*
[3] *Clinic of Psychiatry, Department of Psychiatry, Center of Neurology, Vilnius University, Vilnius, Lithuania*
[4] *Department of Human and Medical Genetics, Vilnius University, Center for Medical Genetics, Vilnius, Lithuania*
* *Corresponding author.*

Introduction Individualized treatment decisions in psychiatry may be important, since substantial part of first choice drugs are