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