ineffective or cause side effects. Polymorphic variants of genes that code CYP450 enzymes cause differences in their activity and therefore in efficacy and safety of drugs that are metabolized by them.
Aim of the study Determine whether pharmacogenetic testing of CYP2D6, CYP2C19 and CYP2C9 polymorphism would have had influence on selected patients' treatment courses.
Methods Five patients that were diagnosed for treament-resistant mood disorders in Vilnius university hospital Santariskiu clinics centre of neurology, department of psychiatry were invited to give blood samples for genetic testing retrospectively. Patients' CYP2C19, CYP2D6 and CYP2C9 enzymes genetic polymorphism results were compared with previous empirical pharmacological treatment courses of these patients.
Results In four out of five cases significant polymorphism of CYP2C19 enzyme allele was detected. In all of these cases 1*/2* variant, that conditions intermediate metabolizer phenotype, was identified. Alterations in CYP2D6 and CYP2C19 regions were not found. In three cases the presence of varied genetic variant could have been clinically relevant. In two of these cases Sertraline and valproates, that are both metabolized by CYP2C19 enzyme, were taken by patients and side effects were observed. Unsuccessful treatment was repeated without effect, both in clinical and outpatient environment. Continuous rehospitalization took place until appropriate empirical treatments were established.
Conclusions Pharmacogenetic testing could have had influence on treatment choices for three out of five selected patients leading to less side effects and rehospitalizations.
Disclosure of interest The authors have not supplied their declaration of competing interest.

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EW0187

Mthfr Allele distribution in Romanian schizophrenia patients

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Introduction Currently available data on the aetiology of schizophrenia suggests a major involvement of epigenetic mechanisms. One such mechanism could be the alteration of activation and silencing of genes, which involves DNA methylation and de-methylation. The main limiting enzyme involved in the methyl-donor cycle is methylene-tetra-hydro-folate-reductase (MTHFR), and the most frequently observed mutation in the MTHFR gene, altering its activity, is the C677 T mutation.
Aim In the present study, we investigated the frequency of MTHFR C677 T mutation and total plasma homocysteine (tHcy) concentrations in a sample of Romanian schizophrenia patients as compared to healthy controls.
Methods Seventy schizophrenia patients (35% females) with a mean age of 38.8 ± 20.5 years and 50 healthy controls (50% females) with a mean age of 36.3 ± 11.6 years were included. MTHFR genotype was determined through polymerase chain reaction and tHcy levels were determined through reversed phase high-pressure liquid chromatography.
Results Schizophrenia patients, registered higher frequency of the T allele, with the CC genotype observed in 39.4% of them, as compared to a frequency of 60.6% in the control group ($P = 0.002$–Fisher's exact test). tHcy concentrations did not differ between the two groups (10.7 ± 4.2 vs. 11.2 ± 4.1, $P > 0.005$–Mann–Whitney U test).
Conclusions Romanian schizophrenia patients have a significantly higher frequency of the MTHFR C677 T mutation, but without significant effect on tHcy concentrations.
Disclosure of interest The authors have not supplied their declaration of competing interest.

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EW0188

Influence of 5-HTR2C polymorphisms on metabolic syndromes in Thai schizophrenia patients

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Introduction Metabolic syndrome is a significant problem in the schizophrenia patients. Previous research demonstrated that single nucleotide polymorphisms in the serotonin 2C receptor (5HTR2C) genes are associated with metabolic syndrome related to schizophrenia patients taking atypical anti-psychotic drugs. This study aimed to investigate whether the effect of 3 SNPs in 5HTR2C gene on the presence of the metabolic syndrome in Thai schizophrenia patients.
Method We conducted a cross-sectional study and 154 patients were recruited. The schizophrenia patients were identified from a diagnostic and statistical manual of mental disorders, 4th edition, (DSM-IV) and criterion and determined the metabolic syndrome according to the 2005 international diabetes federation (IDF) Asia criteria. Patients were genotyped for the 5HTR2C rs51,8147, rs126,881,02, rs128,367,71 polymorphisms.
Results The preliminary analysis from 154 patients showed the metabolic syndrome prevalence was 38.73%, with 46.50% in male and 53.48% in female patients. The results showed that the patients who have heterozygous and homozygous variant on 5HTR2C gene (rs518,147 and rs126,881,02) showed a significant difference in the presence of metabolic syndrome when compare with patients who carry homozygous wild type ($P = 0.007$), especially in male patients ($P = 0.002$). The association between 5HTR2C polymorphisms and metabolic syndrome was found in male patients but not found in female patients.
Conclusion These findings suggest that 5HTR2C genotypes are associated with the metabolic syndrome in patients taking atypical anti-psychotics. However, the metabolic syndrome results from the multigenetic effects. The further studies should focus on the other genes, which were involved in metabolic syndrome.
Disclosure of interest The authors have not supplied their declaration of competing interest.

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EW0189

Prevalence of the CYP2D6*10 (C100 T) polymorphism in psycho-neurological patients in North-Western and Siberian regions of the Russia

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Introduction The gene CYP2D6 is of great interest also due to its highly polymorphic nature, and involvement in a high number of medication metabolisms. The presence of polymorphisms in the CYP2D6 gene may modulate enzyme level and activity, thereby affecting individual responses to pharmacological treatment.
Materials and methods Allele and genotype frequency distributions of CYP2D6*10 variants and predicted phenotypes were analyzed in blood samples of 123 patients (53 patients from north-western region and 69 patients from Siberian region) using polymerase chain reaction (PCR)-restriction fragment length polymorphism, PCR-single-strand conformation polymorphism.
Results The T/T, C/T, and C/C genotype frequencies of the CYP2D6*10 allele were significantly different ($P < 0.01$) in regional groups. The frequency of the wild homozygous variant C/C of the CYP2D6*10 allele (extensive metabolizers) in the Siberian region was the highest, while the north-western region of Russia had the lowest frequency ($P < 0.001$), which are 82.6% and 64.2%, respectively. The frequency of the heterozygous variant C/T of the CYP2D6*10 allele (intermediate metabolizers) was significantly a bit high in the north-western region, while the Siberian region of Russia had the lowest frequency ($P < 0.001$), which are 35.8% and 17.4%, respectively. The homozygous variant T/T of theCYP2D6*10 allele (poor metabolizers) was not identified.
Conclusion The C100T polymorphism of the CYP2D6 gene may be associated with several drug-induced reactions in patients with depression, schizophrenia, epilepsy etc. The differences in the prevalence of intermediate metabolizers in north-western and Siberian regions of Russia may be due to genetic drift and accumulation of alleles typical of European and Asian populations.
Disclosure of interest The authors have not supplied their declaration of competing interest.

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EW0190

Symptoms of anxiety during pregnancy and metabolism: A pilot metabolomics study

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Introduction Anxiety symptoms are frequent during pregnancy, and they adversely affect pregnancy outcomes and offspring development. The underlying biological mechanisms are not known, but may in part be explained by alterations in certain maternal metabolic pathways. No metabolomic studies have investigated possible metabolic alterations in anxious pregnant women.
Objective This pilot study compared the metabolic profiles of anxious and non-anxious pregnant women using a mass spectrometry-based quantitative metabolomics system.
Methods Cases were 20 participants of the Kuopio birth cohort study (www.kubico.fi) with first and third trimester symptoms of anxiety (Edinburgh postnatal depression scale, anxiety subscale – EPDS-3A ≥ 4), but no depression (EPDS ≤ 12). Controls were 20 participants with low anxiety (EPDS–3A ≤ 3) and depression (total EPDS ≤ 9) in both the first and third trimester. Maternal metabolic profiles were analyzed from serum samples drawn when the mothers arrived at the delivery hospital.
Results Metabolic pathway analyses revealed significant enrichment in the glycine, serine and threonine metabolism ($P = 0.046$), as well as in the betaine ($P = 0.048$) metabolism pathways. Homocysteine was the only metabolite to significantly differentiate between cases and controls (VIP score 3.3), with lower concentrations in cases ($P = 0.003$) even when excluding non-users of folic acid supplementation ($n = 5$; $P = 0.002$), C-sections ($n = 5$; $P = 0.013$), or samples taken immediately postpartum ($n = 2$; $P = 0.004$). No other metabolites significantly differed between the groups.
Conclusions Physiological adaptation induced by pregnancy, which may have homogenized the study populations, could explain the only minor metabolic differences between the two groups. Further research in larger samples, comparing metabolic alterations in umbilical cord blood and maternal blood is warranted.
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