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Introduction It is widely recognized that parents and peers play a critical role in the adolescent's introduction to alcohol.
Objectives The aim of the study was to examine the relationship of parental and peers drinking to adolescent drinking behavior.
Methods A cross-sectional study was carried out in four colleges and schools in Sfax in Tunisia, in May and June 2016. The sample consisted of 317 pupils, and was determined through a simple randomized sampling. These adolescents were asked to answer a self-administered questionnaire, after their consent. Alcohol use disorders identification test (AUDIT) was used to evaluate alcohol dependence.
Results The mean age was 16 years, with a sex-ratio of 1.07. The participants reported having drunk alcohol at least once in 18.9% of cases and 41.66% of them still consume. According to AUDIT, 1.6% of alcohol users presented an alcohol misuse and 21.6% presented dependence. They reported that parents' attitude toward their alcohol use was favorable in 27.11% of cases. Among dependent adolescents, the prevalence of fathers' alcohol consumption was 20% while that of friends was 70%. Adolescent drinking was significantly correlated to fathers, mothers and peers drinking ($P < 0.001$, $P = 0.004$, $P < 0.001$ respectively), mothers and peers smoking ($P = 0.05$, $P < 0.001$ respectively), fathers and peer's cannabis use ($P < 0.001$, $P < 0.001$ respectively).
Conclusion Findings suggest that negative family and peers influence increased risk of alcohol consumption in adolescents. Understanding the influences on parents' beliefs about their children's drinking and the functions of social networks in preventing alcohol consumption may be necessary to address adolescent risky drinking.
Disclosure of interest The authors have not supplied their declaration of competing interest.

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EW0582

Drug metabolizing enzyme and transporter genes associated with plasma risperidone level in Thai autism spectrum disorder

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Background The associations between genetic variants of drug metabolizing enzyme and transporter (DMET) genes and steady-state plasma concentrations of risperidone, 9-hydroxyrisperidone, total active-moiety, and metabolic ratio remain unclear.
Objective The objective of the present study was to present the results of the association between genetic variants of DMET gene and steady-state plasma concentration risperidone and its metabolite using Affymetrix DMET Plus genotyping microarray.
Methods Subjects eligible for this study included male and female adolescents with ASD diagnosed according to the Diagnostic and Statistical Manual of Mental Disorders, Fourth Edition (DSM-IV) criteria and being treated with risperidone for at least 4 weeks prior to the blood sample collection. Blood samples were drawn prior to the next dose of risperidone intake to determine the steady-state plasma trough concentrations of risperidone and 9-hydroxyrisperidone. Genotyping profile was obtained using the microarray. Steady-state plasma risperidone and 9-hydroxyrisperidone were measured using liquid chromatography/tandem mass spectrometry (LC-MS/MS) assay.
Results The polymorphisms of UGT2B4, CYP2D6 were highly associated with metabolic ratio. Of all the DMET analysis, ABCB11 (3084A > G, 420A > G, 368G > A, and 236G > A) and ADH7 (690G > A and −5360G > A) were found to be associated with plasma concentrations of risperidone ($P < 0.01$). In addition, 6 genetic variations among the SLC transporter family were associated with the plasma concentration of 9-hydroxyrisperidone.
Discussions This study provides a pharmacogenomic approach to investigate further among the DMET genetic variants which influence plasma concentration of risperidone. The treatment of ASD should be based on genetic factors making the challenge of psychopharmacological treatment more efficacious with lesser adverse events.
Disclosure of interest The author has not supplied his/her declaration of competing interest.

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EW0583

Exome sequencing detection of genetic markers for Thai autism spectrum disorder

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Background Autism spectrum disorders (ASD) are neurodevelopmental disorders characterized by abnormalities in 3 domains; social interaction, communication/language, and restricted and repetitive behavior. The study of ASD prevalence in Thailand showed that it is approximately 9.9 children per 10,000 population for children 1–5 years old. ASD has a strong genetic basis, although the genetics of autism are complex and it is unclear. The objective of this study was to identify the genetic markers of Thai ASD.
Methods Exome sequencing was performed with twelve unrelated ASD affected individuals from twelve families. Each sample was sequenced on SOLiD 5500xl genetic analyzer, and the resulting data was processed and analyzed on LifeScope Genomic Analysis software. Exome sequencing with two additional samples was performed Ion Proton System and the data was processed on Ion Reporter server. Tertiary data analysis with all fourteen exome sequencing data were performed by using Golden Helix software. In filtering process, data were annotated to various databases including UCSC KnownGenes for non-coding and synonymous variants filter, 1000 Genomes Project for high frequency variants filter, and dbNSFP for functional prediction.
Results The genetic markers were identified for Thai ASD associated variants (c.2014G > A in EIF2AK3, c.2951G > A in FGD6, and c.6119A > G in CHD8).
Conclusions these genetic markers were the most possible of causing variants Thai. We also demonstrated a potential of exome sequencing and bioinformatics pipeline to identify the possible causative variants of ASD, which could by applied in the case that unable to identified variants by other technique.
Disclosure of interest The author has not supplied his/her declaration of competing interest.

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EW0584

Hyperuricemia and metabolic adverse effect in children and adolescents with autism spectrum disorder treated with risperidone

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Background Atypical anti-psychotics have been found to be associated with hyperuricemia. The aims of this study were to determine the prevalence of hyperuricemia and metabolic adverse events in children and adolescents with ASD treated with risperidone.
Methods In this cross-sectional study, we recruited 127 Thai ASD children and adolescents aged 3–20 years receiving risperidone for more than 4 weeks. The clinical data and laboratory data were obtained and analyzed. Hyperuricemia was defined as serum uric acid > 5.5 mg/dL.
Results Hyperuricemia was present in 57.48% of total ASD patients treated with risperidone. Uric acid levels were significantly higher in adolescents as compared to children. Uric acid levels correlated with risperidone dose ($P = 0.01$), duration of treatment ($P < 0.0001$), BMI ($P < 0.0001$), waist circumference ($P = 0.003$), triglyceride (TG; $P < 0.0001$), triglycerides/high-density lipoprotein cholesterol ratio (TG/HDL-C; $P < 0.0001$), insulin ($P = 0.04$), homeostatic model assessment index (HOMA-IR; $P = 0.03$), high-sensitivity CRP (hs-CRP; $P < 0.0001$), and leptin levels ($P < 0.0001$). HDL-C and adiponectin levels were negatively correlated with uric acid levels ($P < 0.0001$). In multiple regressions analysis, age, BMI, TG/HDL-C, and adiponectin level remained significantly associated with uric acid levels ($P < 0.0001$).
Conclusion Hyperuricemia may play a role in metabolic adverse effects in children and adolescents with ASD receiving high dose and/or long-term treatment with risperidone.
Disclosure of interest The author has not supplied his/her declaration of competing interest.

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EW0585

Effects of executive function stimulation in the language improvement of children with ASD

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The Autism Spectrum Disorder (ASD) is a neurobiological disorder that involves deficits currently classified into two areas:.
– social communication and interaction across multiple contexts;
– restricted, repetitive patterns of behavior, interests or activities.
Although, these disorders do not have any causal relationship, both are always present. It has increasingly been sought methods aiming at the effectiveness of intervention for this population seeking to include all aspects. A promising research field is the one that considers the interdependence of the language and cognition areas, specifically regarding executive functions. This study was designed to verify the effectiveness of an executive functions stimulation program (EFS) during the regular speech-language therapy sessions and its impact in language development, specifically in the pragmatic aspects, through the evaluation of the functional profile of communication (FPC) in 14 children with ASD. During a 12-week period of regular speech-language therapy, the following areas were focused: working memory, cognitive flexibility, central coherence, inhibitory control and specific language aspects. Data were registered and analyzed statistically. The average performance of children in the stimulation was 85%, ensuring the effectiveness of EFS. The association analysis between pre- and post-EFS performance with FCP a significant improvement was observed in the occupation of the communicative space and the percentage of interactivity. These results are consistent with the hypothesis of the study, which believes in strong association between communication aspects and executive functions skills.
Disclosure of interest The authors have not supplied their declaration of competing interest.

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EW0586

Cytogenetic characteristic the patients of both sexes with phobic-anxiety disorders

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Background and aims Anxiety-phobic disorders are caused both by environmental and hereditary factors. The study was designed to determine the level of chromosomal aberrations in the peripheral blood lymphocytes (PBL) of children and adolescents of both sexes with phobic-anxiety disorders (PAD).
Patients and methods Cytogenetic analysis was performed in 27 children and adolescents of both sexes with PAD, aged 9–15 years; the control group consisted of 50 healthy peers of both genders. Statistical analysis-Excel and SPSS statistics 17.0.
Results Cytogenetic analysis of patients with PAD and in healthy age-matched individuals has established normal female (46,XX) and male (46,XY) karyotypes. The frequency of the chromosomal aberrations (CA) spontaneous level in the PBL is 4.6 times higher than the CA frequency in healthy persons. In children and adolescents with the disease, the spontaneous frequency of aberrations of chromatid and chromosome types is also significantly higher than the same in healthy children and adolescents. Single acentric fragments and exchanges prevail among the chromatid–type aberrations; pair acentric fragments prevail among the chromosome–type aberrations. An increase in the frequency of the chromosome-type aberrations has been revealed in boys with PAD (1.72 vs.0.55 per100 cells in healthy boys, $P < 0.001$ by pair acentric fragments), in comparison with healthy boys; and the chromatid–type aberrations have been observed in girls with PAD (3.22 vs.0.94 per 100 cells in healthy girls, $P < 0.001$ by single acentric fragments), in comparison with healthy girls. A pronounced individual variability of CA frequency, which ranges in our patients from 2.0 to18.0 per 100 metaphase plates, has been found along with an increase in the CA level in patients with PAD.
Conclusion Children and adolescents with PAD require a careful cytogenetic analysis and the consequent therapeutic measures for genome stabilization.
Disclosure of interest The authors have not supplied their declaration of competing interest.

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EW0587

Effect of adenotonsillectomy on attention-deficit/hyperactivity disorder symptoms, sleep disturbance symptoms, and quality of life of children with adenotonsillar hypertrophy and sleep-disordered breathing

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