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POSTERS

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Abstracts submitted to the 41st FEBS Congress, which was planned for Kuşadası, Turkey from 3rd to 8th September 2016, and accepted by the Congress Organizing Committee are published in this Special Issue of The FEBS Journal. Unfortunately, the Congress was cancelled by FEBS after the excellent scientific programme was compromised by an insufficient number of confirmed speakers, and so the authors of these abstracts were not able to present their work at the event*. Late-breaking abstracts and abstracts withdrawn after Congress cancellation are not included in this issue.

About these abstracts

Abstracts submitted to the Congress are not peer-reviewed. In addition, abstracts are published as submitted and are not copyedited prior to publication.

We are unable to make corrections of any kind to the abstracts once they are published.

Indexing

Abstracts published in The FEBS Journal Special Issue for the 41st FEBS Congress will be included individually in the Conference Proceedings Citation Index published by Web of Science.

How to cite these abstracts

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* An optional closed online presentation opportunity of short duration on the Congress website was offered after Congress cancellation and may be taken up by some abstract authors.

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** Each poster has been given a unique number beginning with the letter P; the next part relates to the session in which the poster will be presented.

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09.02	Mechanism of neurodegenerative diseases
09.03	Aging
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EDU	Education, Training, and Career Planning in Molecular Life Sciences
MISC	Miscellaneous

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respond differently to treatment thus supporting the idea of personalized therapy need for individuals.

Renin angiotensin system (RAS) have key roles in AML and ALL progression and it has been shown by many studies suggests that these system's genes might be good biomarkers for AML and ALL personalized therapy.

We aimed to identify RAS gene based homogeneous subgroups of acute leukemia and determine the most effective chemotherapoetic agent for each subgroup. After validation and verication of the results, more effective drugs can be recommended for the use in clinics for chemotherapy of AML and ALL.

Results of our preliminary studies showed that we are able to identify subgroups of AML and ALL as well as correlating each existing subgroup with FDA approved drugs. Considering the long and highly cost process of developing new drugs for cancer treatment makes the present study all the more valuable. In addition, there is a serious need for change in AML and ALL therapy since there is no highly effective chemotherapy protocol available for their treatment.

Welcome Trust Sanger (WTS) and Cancer Cell Line Encyclopedia (CCLE) databases will be used to determine subgroups of AML and ALL based on RAS genes or whole genome expression using standard deviation and hierarchical clustering analysis. The most effective drugs for each subgroup will be identired using Pearson's r correlation analysis with drug sensitivity data (IC50, IC50, Amax, Aare, etc.) available in same databases. Further validation tests will be performed by in vitro validation using AML and ALL cell lines: drug sensitivity prorles will be determined and gene expression will be shown by Q-RT-PCR.

P-08.02.5-003
Functional polymorphisms of EPHX2 in a Turkish population

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Soluble epoxide hydrolase (sEH; EC 3.3.3.2) is encoded by EPHX2 and catalyses the degradation of endogenous fatty acid epoxides generated by CYP450 epoxygenases. These fatty acid epoxides such as epoxyeicosatrienoic acids (EETs) have been shown to posses vasodilator, anti-insammatory, anti-platelet, anti-hypertensive, anti-apoptotic, anti-thrombotic and natriuretic effects. It has been reported that EET levels are associated with hypertension, stroke and cardiovascular diseases. Individual differences in the EPHX2 gene that affect the sEH activity may alter the circulating levels of EETs. K55R and R287Q polymorphisms have been known to cause increased and decreased sEH activity, respectively. Therefore we aimed to determine the genotype frequencies of these two polymorphisms in a Turkish population. K55R and R287Q polymorphisms were determined by the real time PCR using double-dye hydrolysis probes or PCR-RFLP method. The observed genotype frequencies for K55R polymorphism were 80.8% wild type (AA) and 19.2% polymorphic genotype (AG+GG) and for R287Q polymorphism 81.4% wild type and 18.6% polymorphic genotype (GA+AA). The genotype distributions for both polymorphisms were in Hardy-Weinberg equilibrium.

P-08.02.5-004
Frequencies of alleles and polymorphic variations of genes for folate cycle in women of Kazakh ethnic group with complicated pregnancy

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Pregnancy is one of manifestations for thrombophilia factors, which in its turn leads to various complications of its course. One of the markers of hereditary thrombophilia is mutations in the folate cycle MTR, MTRR and MTHFR genes. Insufricient intake of folate during pregnancy disrupts the functioning of the genome, leading to miscarriage, violation of embryogenesis and various fetal malformations. However, results of studies on the role of hereditary thrombophilia in the occurrence of complications during pregnancy are rather contradictory.

Aim of this study was to determine the frequency of alleles and polymorphic variants of folate cycle genes MTR A2756G, MTRR A66G and MTHFR C677T in women of Kazakh ethnic group with pregnancy complications. We used Real-time PCR. Blood samples for DNA isolation were obtained from 129 pregnant women. The main group consisted of women (n = 90) which had a history of two or more pregnancy complications in the form of pre-eclampsia, eclampsia, missed abortion, miscarriage, and etc. Control group consisted of women (n = 39) with two or more normal pregnancy outcomes, and had no complications during pregnancy in history. Average age of women in experimental group was 32.0 ± 0.50 years compared with control of the age 33.6 ± 0.33.

The analysis of the frequency distribution of alleles of genes in experimental group of women with complications of pregnancy revealed no signircant differences relative to the control group. Analysis of the distribution of polymorphic variants of folate cycle genes showed signircant difference between the study and control groups in the occurrence frequency of heterozygotes for the mutant allele G in the gene MTRR A66G (OR = 2.89, CI 95% = 1.25–6.71; v^2 = 6.376, p < 0, 05). No signircant differences in alleles between homozygous wild-type and homozygous mutant alleles were observed.

This work was funded by the MES Kazakhstan (GR 0115RK00287 project number).

P-08.02.5-005
A study on the association between rs6918698 polymorphism in connective tissue growth factor gene and pseudoexfoliation syndrome

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Pseudoexfoliation syndrome (PES) is a disorder of the extracellular matrix characterized by the production and progressive accumulation of an abnormal rbrillary material in many ocular tissues. PES prevalence is 11.3% above the age 40 in Turkey. Since PES is characterized by excessive synthesis of elastic microrbrillar components throughout the body, growth factors can have important roles in the pathophysiology of PES. Human Connective Tissue Growth Factor (CTGF) is a protein expressed

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