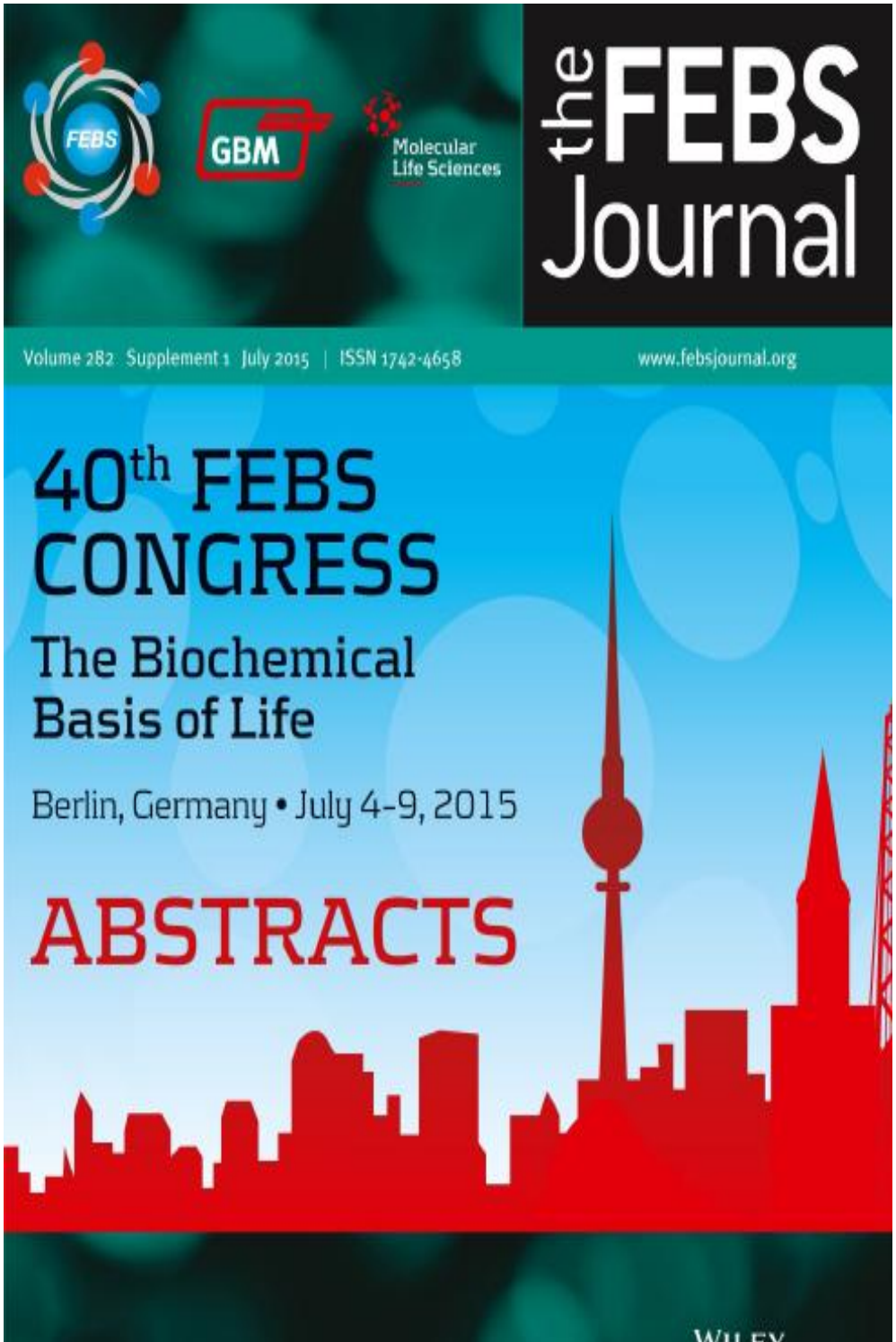

the FEBS Journal

the FEBS Journal

Volume 282 Supplement 1 July 2015

Poster Sessions

Table of Contents

Poster Session 1

Sunday 5 July & Monday 6 July
08:30-19:30, Foyer Convention Center

Poster Session 2

Tuesday 7 July & Wednesday 8 July
08:30-19:30, Foyer Convention Center

Each poster has been given a unique number and the first part of the poster number relates to the session in which the poster was

tional mechanisms which underlying these responses. This is due to the capacity of sugars to act as nutrients, osmotic regulators and signalling molecules. *Cis*-acting sugar regulatory elements are important molecular switches involved in the temporal and spatial expression of a dynamic network of gene activities. This network controls hormone and abiotic stress responses, and developmental events such as juvenility and floral induction. In this study, we have examined expression levels and promoter features of different genes encoding proteins that have been implicated as targets of glucose signal transduction pathways, and might participate in juvenility and floral induction. Identifying the functionally active sugar response elements in the predicted promoter regions of genes that undergo glucose induced transcriptional regulation will lead us closer to understanding these signal transduction mechanisms.

P28-026
Study of *Brachypodium distachyon* and local breed soft wheat varieties tolerance to adverse environmental factor

N. Z. Omirbekova, A. I. Zhussupova, Z. K. Zhunusbayeva, B. N. Askanbayeva
Al-Farabi Kazakh National University, Almaty, Kazakhstan

The Republic of Kazakhstan is one of the world leading countries in production of trade wheat grain, and the problem of lands salinity here is quite acute. Proline is one of the most widely distributed natural osmolytes, which is accumulated in plants during their protection against various abiotic factors. *Brachypodium distachyon* is a widely recognized model plant, closely related to wheat. The aim of our study was to evaluate the content of proline and soluble protein in *Brachypodium* and local breed soft wheat varieties (Shagala and Kazakhstanskaya 3) under standard 2% NaCl salinity. Experimental data on Shagala variety have shown 3 times increase in proline content under salinity for seedlings (namely, 126.53±0.011 mg/g from 45.21±0.02), and 5 times increase in such for roots; thus leading to a conclusion that under salinity prolin is mostly accumulated in seedlings, rather than in roots. However, we got an opposite picture for Kazakhstanskaya 3: 9 times proline increase in seedlings (169.00±0.03 mg/g), with only 3 times increase in roots (16.65±0.05 mg/g). In *Brachypodium* proline content under salinity in seedlings raised up to 101.00±0.03 mg/g, in roots 16.90±0.05 mg/g; absence of change in proline content in seedlings and roots has been observed. Content of soluble protein in *Brachypodium* is higher (0.460±0.002 mg/ml) in comparison with such of Kazakhstanskaya 3 and Shagala (0.179±0.01 and 0.188±0.01 mg/ml, correspondingly), using microbiurete method by *Bailey*. Experimental data allowed to place them in the following order of salt tolerance *Brachypodium* < Shagala < Kazakhstanskaya 3.

P28-027
Collagen I induces TNF-α production and down-regulation of IRF4 to regulate the activation of dendritic cells

H.-H. Ki[1], B. Poudel[1,2], Y.-M. Lee[2], D.-K. Kim[1]
[1]*Department of Immunology, Medical School, Chonbuk National University, Jeonju, Korea,* [2]*Department of Oriental Pharmacy, College of Pharmacy, Wonkwang University, Iksan, Korea*

The activation of dendritic cells (DCs) play a role to regulate the immune response. Inflammatory mediators such as tumour necrosis factor (TNF)-α, interleukin (IL)-1β and lipopolysaccharide (LPS) are also known to activate DCs. We have previously shown that collagen I enhances the maturation and function of DCs. Here we investigated the involvement of TNF-α on the collagen I-induced DCs activation. The of neutralization of TNF-α inhibited collagen I-induced IL-12 secretions by DCs. Additionally, we observed suppression of collagen I-induced co-stimulatory molecules expression along with down-regulation of genes involved in DCs activation pathway. Furthermore, TNF-α inhibition upon collagen I stimulation up-regulated the expression of interferon regulatory transcription factor IRF4, when compared to collagen I only treated cells. Collectively, our data demonstrate that collagen I induce TNF-α production, which is crucial for the activation and function of DCs, through down-regulation of IRF4, and implicates the importance in development of anti-TNF-α therapeutics for several inflammatory diseases.

P28-028
Luteolin attenuates adipocyte-derived inflammatory responses via suppression of NF-κB/MAPK pathway

S. Nepali[1], J.-H. Lee[1], D.-K. Kim[1], Y.-M. Lee[2]
[1]*Department of Immunology, Chonbuk National University, Jeonju, Korea,* [2]*Department of Oriental Pharmacy, Wonkwang University, Iksan, Korea*

Inflammation of adipocytes has been a therapeutic target for treatment of obesity and metabolic disorders which cause insulin resistance and hence lead to type II diabetes. Luteolin is a bioflavonoid with many beneficial properties like antioxidant, antiproliferative and anti-cancer. To elucidate the potential anti-inflammatory response and the underlying mechanism of luteolin in 3T3-L1 adipocytes we stimulated 3T3-L1 adipocytes with the mixture of TNF-α, LPS and IFN-γ (TLI) in the presence or absence of luteolin. Luteolin opposed the stimulation of inducible nitric oxide synthase (iNOS) mRNA and protein expressions and NO production by simultaneous treatment of adipocytes with TLI. Also, it reduced the mRNA expression of pro-inflammatory genes like COX-2, IL-6, and resistin and also the chemokine, MCP-1. This inhibition was associated with suppression of IκB-α degradation and subsequent inhibition of NF-κB p65 translocation to the nucleus. In addition, luteolin blocked the phosphorylation of ERK1/2, JNK and also p38 MAPKs. These results illustrate that luteolin attenuates inflammatory responses in the adipocytes through suppression of NF-κB and MAPKs activation, suggesting that luteolin may represent a therapeutic agent to prevent obesity-associated inflammation and insulin resistance.

P28-029
CrossHub: cross-analysis of TCGA RNA-Seq, miRNA-Seq, methylation and mutation data

G. S. Krasnov[1,2,3], A. A. Dmitriev[1,4], N. V. Melnikova[1], V. N. Senchenko[1], A. V. Kudryavtseva[1,4]
[1]*Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, Russian Federation*

[2]Orekhovich Institute of Biomedical Chemistry, Russian Academy of Medical Sciences, Moscow, Russian Federation

[3]Mechnikov Institute of Vaccines and Sera, Russian Academy of Medical Sciences, Moscow, Russian Federation

[4]P.A. Herzen Moscow Cancer Research Institute, Ministry of Healthcare of the Russian Federation, Moscow, Russian Federation

The Cancer Genome Atlas Project (TCGA) is the largest resource in the field of molecular oncology. It accumulates genomic, transcriptomic and methylomic data for more than 15 cancers. We developed the CrossHub software (available at https://