The FEBS Journal

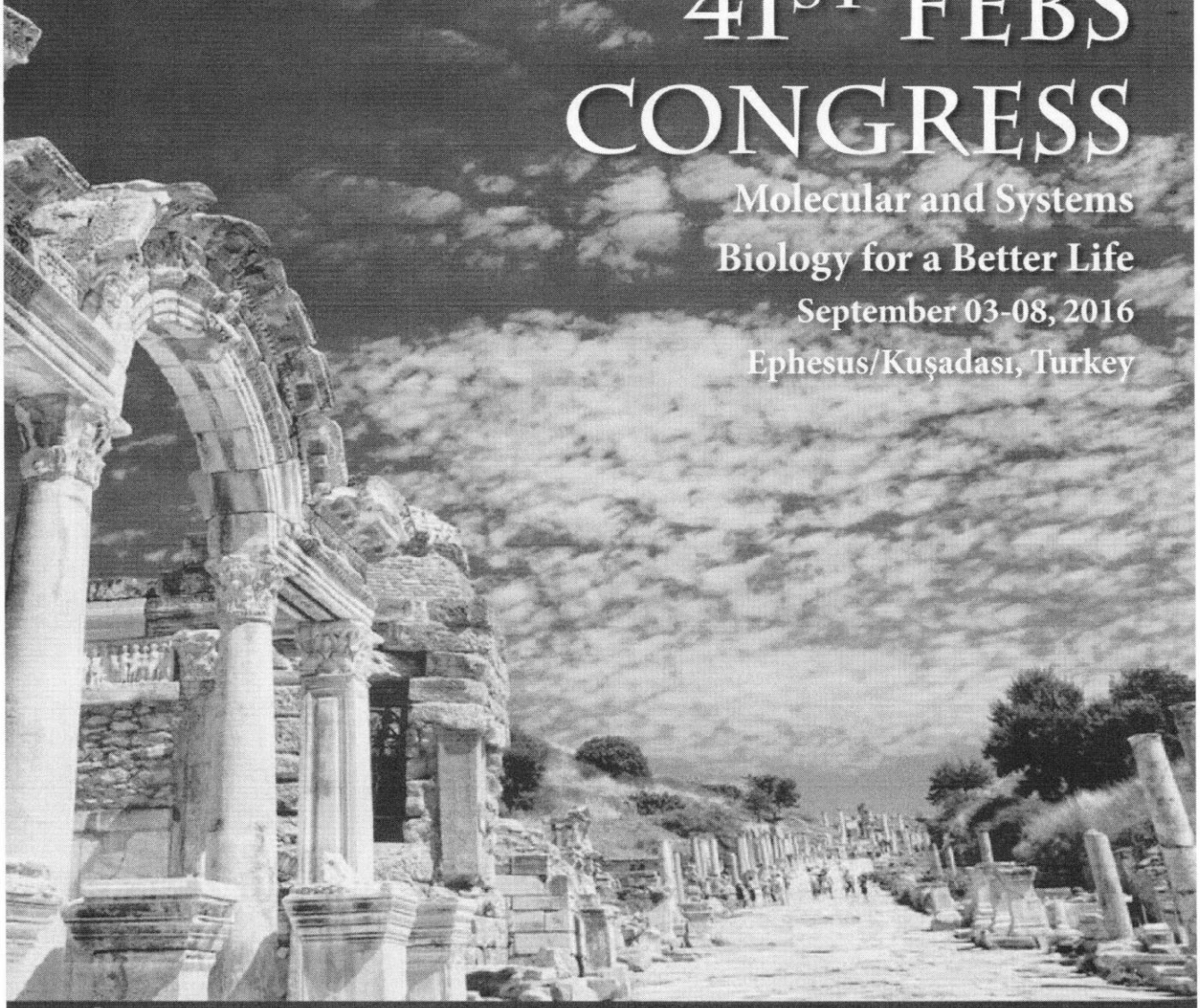
Volume 283 Supplement 1 September 2016 | ISSN 1742-464X www.febsjournal.org

41ST FEBS CONGRESS

Molecular and Systems Biology for a Better Life

September 03-08, 2016

Ephesus/Kuşadası, Turkey



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Volume 283 Supplement 1 September 2016

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 Late-breaking abstracts and abstracts withdrawn after Congress cancellation are not included in this issue.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Abstracts submitted to the Congress are **not peer-reviewed**.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

AuthorOne, A., AuthorTwo, B. (2016). Abstract title. FEBS J, 283: Abstract number**. doi:10.1111/febs.13808

* 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.

cultivation. To identify alternative oxidase encoding genes in *N. alba*, we performed transcriptome analysis. By using transcriptome analysis data, *AOX* gene sequences, subcellular localization of AOX proteins and structural modelling of AOX proteins were predicted. In 272934 transcripts, database search with Trinotate tool revealed 77 transcripts with AOX domains characterized in known alternative oxidases. Blast analysis of these 77 sequences with known AOX proteins revealed three distinct *AOX* genes (*Nalba-AOX1*, *Nalba-AOX2* and *Nalba-AOX4*). After subcellular localization analysis of three identified AOX proteins by using TargetP server tool, *Nalba-AOX1*, *Nalba-AOX2 are predicted as mitochondrial while Nalba-AOX4 is localized in chloroplasts*. Template based structural modelling results showed that all identifed proteins are statistically similar to known structure models of corresponding AOXs.

P-02.08.5-013
Antioxidant and antimutagenic activity of *Limonium gmelinii* (fam. Plumbaginaceae) and *Inula britannica* (fam. Compositae)

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Most environmental contaminants have toxic and mutagenic effects on living organisms as a result of the activation of free radical formation and inhibition of reparation activity. It is becoming relevant to search for protectors of natural origin from the effects of xenobiotics. Many biologically active substances (BAS) of inartificial origin are found to be antioxidants and can increase the body's resistance to the toxic and mutagenic effects of a wide range of pollutants.

The aim of the study was to investigate the antioxidant and antimutagenic properties of BAS from medicinal plants *Limonium gmelinii (Plumbaginaceae)* and *Inula britannica (Compositae)*.

The antioxidant potential of plant extracts was determined by the activity of superoxide dismutase (SOD), catalase, and the content of malonic dialdehyde. Mutagenic and anti-mutagenic properties of the extracts were determined in the test by counting chromosomal aberrations in root meristem of barley seeds. Barley seeds were treated with an aqueous solution of unsymmetrical dimethyl hydrazine (UDMH), which is highly toxic I class hazardous material, well known pro-oxidant.

The results showed that UDMH enhanced the process of lipid peroxidation and decreased the mitotic activity. Treatment of barley seeds with extracts from *I. britannica* and *L. gmelinii* and their germination in the presence of stress factors stimulated antioxidant defenses in the primary roots of barley seeds. Increase of the activity of SOD and catalase, and reduction of peroxidation level of lipids were observed. Cytogenetic study showed no mutagenic activity in plant extracts. When effects of plant extracts and UDMH were combined there was a significant reduction in the frequency of structural mutations, induced by the toxicant.

Conclusion about the presence of the antioxidant and antimutagenic activity in the studied plant extracts is made.

The work done within the framework of the MES project (No. GR 0115RK00378).

P-02.08.5-014
Comparative analysis of cytokinin dehydrogenase inhibition and trans-zeatin treatment in Arabidopsis seedlings

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Cytokinins are plant hormones regulating many processes during plant life ranging from germination to senescence. Manipulation of cytokinin levels and their impact on plant vitality, production and ability to defend against stresses is in great interest of agriculture. In this work we focused on comparison of inhibitor of the cytokinin degradation INCYDE (2-chloro-6-(3-methoxyphenyl)aminopurine) and exogenous application of *trans*-zeatin on *Arabidopsis thaliana* seedlings. Transcripts of genes regulating cytokinin metabolism were analysed by RT-qPCR analysis. Classical cytokinin root essay revealed that INCYDE effect is comparable to that of *trans*-zeatin in a similar concentration-dependent manner. Besides a negative effect on the primary root length, both substances induce flavonoid accumulation and an increase in the root hairs formation. Histochemical staining of transgenic plants expressing glucuronidase (GUS) under cytokinin-responsive promoter of *ARR5* gene revealed increased GUS activity in cotyledons following INCYDE treatment suggesting diverse localization of cytokinin modulation upon *trans*-zeatin and INCYDE treatment, respectively. Possible molecular differences originating in different cytokinin population and distribution following *trans*-zeatin or INCYDE treatments were monitored on the level of gene expression and via an LC-MS proteome analysis in roots and shoots of 14-day-old plantlets. RT-qPCR analysis revealed an alteration in cytokinin metabolism that could explain observed differences on the proteome level between INCYDE and *trans*-zeatin treated seedlings. Pharmacologically inhibited cytokinin degradation could be very efficient tool for modulation of cytokinin levels. Interestingly, the application of INCYDE and *trans*-zeatin shows a contrasting spatial and temporal pattern on molecular levels. INCYDE represents potent growth regulator with interesting properties useful for agriculture.

P-02.08.5-015
The expression yield of prokaryotic alpha-amylase is significantly magnified by molecular cloning techniques

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Randomly hydrolyzing glycosidic bond alpha-amylase has been traditionally employed in bread and similar industries. In that regard, increasing the overall expression level of the enzyme is a crucial concern in biotechnology.

To reach the goal, appropriate alpha-amylase producing species and expression vector were carefully selected. Therefore, genome of *Bacillus subtilis* was extracted and amplified by polymerase chain reaction (PCR) using specifically designed primers. Subsequently, the extracted gene was inserted in expression vector pHT43 and transferred to *E. coli* as intermediate host followed by *Bacillus subtilis* host replacement. The recombinant vector was expressed in *Bacillus subtilis* and the expression was evaluated by agarose gel electrophoresis. Relative purification of the recombinant enzyme was performed by 50 kDa filtration to remove impurities. To identify the biochemical characteristics, starch was used as specific substrate to measure enzyme activity