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POSTERS

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Abstracts submitted for the main call for abstracts to the 42nd FEBS Congress (Jerusalem, Israel; September 10–14, 2017) and accepted by the Congress Organizing Committee, as well as abstracts from invited speakers for the event, are published in this Supplement to *The FEBS Journal*. Late-breaking abstracts are not included in this supplement.

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Abstracts submitted to the Congress are **not peer-reviewed**.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.

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Indexing

Abstracts published in *The FEBS Journal* Supplement for the 42nd FEBS Congress will be included individually in the Conference Proceedings Citation Index published by Web of Science.

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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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differentiation, paracrine secretion and anti-inflammatory effects. However, signaling pathways which regulates cell suvirval and function after transplantation are not investigated in detail. Here we investigated the role of Notch pathway in the regulation of CPC function *in vitro* and after epicardial implantation in scaffold free cell sheet. After coronary artery ligation in rats syngeneic c-kit+Lin CPC marked with CM-DIL were grafted by epicardial placement of cell sheet generated using temperature-responsive dishes. Cell sheets integration, neovascularization, Notch signalling activation state, proliferation and differentiation were assessed by immunofluorescence analysis of myocardial frozen sections harvested 14 days after transplantation. For Notch signalling activation NICD overexpression and cultivation of CPC on Jagged 1-coated dishes were used. Histological analyses revealed that CPC sheet grafts produced thick, well vascularized tissues on the epicardial surface of the heart. Part of transplanted CPC migrated into myocardium, showed signs of Notch signaling activation (NICD in nucleus) and differentiation to cardiomyocytes and endothelial cells. Cultivation of CPC *in vitro* on dishes coated with Jagged 1 released NICD and activated expression of Notch target genes (Hes and Hey). Activation of Notch signaling upregulated expression of vascular cell transcription factors in CPCs and γ-secretase inhibitor prevented Notch signaling activation and CPCs commitment to endothelial lineage. Notch activation in CPC increased their ability for tube formation in Matrigel angiogenesis assay. These findings suggest that targeted modulation of Notch1 signalling may be useful for upregulation of cardiac progenitor cell sheets functionality and vacularization.

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P.5.4-053
Protective effect of betaine against paraquat-induced oxidative stress and pulmonary fibrosis in rats

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Betaine is a methyl donor utilized in remethylation of homocysteine to methionine, which is mediated by betaine-homocysteine methyltransferase (BHMT) mostly localized in the liver. However, our recent study revealed that the metabolism of sulfur-containing substances in extrahepatic tissues was also influenced significantly by betaine intake, probably due to a change in supply of sulfur-containing amino acids in blood. In this study we determined the effect of betaine against paraquat (PQ)-induced pulmonary injury in rats. Rats received betaine in drinking water (1%) for 2 wk prior to PQ challenge (0.3 mg/kg, it). In 2 wk after PQ instillation, 4-hydroxyproline levels in the lung and oxidative DNA damage measured by the Comet assay were increased significantly. Similar results were shown in histopathological assessment of lung tissues. Betaine supplementation effectively inhibited the fibrogenic changes in the rats treated with PQ. PQ instillation decreased methionine levels in the lung, but betaine supplementation elevated methionine and *S*-adenosylmethione (SAM) levels significantly. Putrescine and spermidine levels were also elevated by betaine supplementation. On day 4 after PQ instillation, the metabolomics of sulfur-containing substances was disturbed markedly, but glutathione (GSH) and its metabolic substrates, including methionine, *S*-adenosylhomocysteine (SAH), homocysteine and cysteine, were all elevated in the lung by betaine supplementation. Elevation of proinflammatory cytokines was also inhibited. Taken together, the results suggest that betaine may protect the lung from PQ-induced oxidative stress and pulmonary fibrosis most probably via enhancement of antioxidant capacity and polyamine synthesis.

P.5.4-054
Serotonergic signaling system in granulosa cells of the developing ovarian follicle

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Granulosa are the somatic component of the ovarian follicle, through which the interaction of the maturing egg with the mother's organism occurs. Serotonin is one of the important factors regulating both functional activity of granulosa cells and processes of oogenesis. The expression and functional activity of the components of the serotonergic system in postovulatory cumulus cells were shown earlier, but little is known on the composition of the serotonergic system in granulosa cells at the initial stages of folliculogenesis. We performed a RT-PCR screening of mRNA expression of all known components of the serotonergic system in granulosa cells obtained from mouse primary, secondary (antral) and preovulational ovarian follicles. Although tryptophan hydroxylase *tph1* is expressed at all stages, the aromatic L-amino acid decarboxylase *ddc* is not, hence the synthesis of serotonin in granulosa cells is impossible. Both the serotonin membrane transporter *sert* and the vesicular monomamine transporter *vmat2* are expressed in granulosa cells, suggesting the possibility of serotonin uptake from the intercellular medium and its accumulation into vesicles. mRNA of several serotonin receptors are expressed in granulosa cells – *htr1b*, *htr1d*, *htr2a* and *htr7*. In addition, the main serotonin degradation enzyme monoamine oxidase A *maoa* is expressed at all stages of folliculogenesis. Thus, all major components of the serotoninergic system that are necessary for the implementation of all the steps of the signaling process, with the exception of serotonin synthesis, are expressed in granulosa cells during all stages of folliculogenesis.

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P.5.4-055
Genetically encoded fluorescent probe to visualize phosphatidylinositol

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Phosphatidylinositol (PI) is an important lipid that serves as a membrane constituent and also participates in cell signaling as a precursor for phosphoinositides made by phosphorylation of one or more hydroxyl groups in positions 3, 4 or 5 of the inositol ring. However, the temporal and spatial distribution of PI remains unclear owing to the lack of a specific biosensor to visualize PI. Here we derive a new PI optical probe using phosphatidylinositol-dependent phospholipase C, an enzyme secreted by *Bacillus cereus* specifically cleaving PI into diacylglycerol and inositol 1-phosphate. Unlike eukaryotic isoforms bacterial inositol-dependent phospholipase C (PI_PLC) cannot use either PtdIns4P or PtdIns(4,5)P2 as a substrate, what makes it an ideal candidate for construction of genetically encodable fluorescent PI-specific biosensor. To potentially increase the affinity and specifity towards PI, we designed several mutant forms of PI_PLC. Further, we structurally characterized these mutants using protein crystallography. We performed lipid binding assay using phospholipid vesicles with and without PI, which showed that PI_PLC binding to membranes is PI-dependent. To asses *in vitro* PI-binding properties of each PI-PLC mutant GUVs recruitement assay using fluorescently labeled PI_PLCs was carried out. Our results revealed no binding to other phospholipids tested. Overall our findings indicate that our PI_PLC probe