SYSTEMS BIOLOGY AND SYSTEMS PHYSIOLOGY: REGULATION OF BIOLOGICAL NETWORKS

THE MEETING IS DEDICATED TO 75TH ANIVERSARY OF FAZLY ATAULLAKHANOV

HYBRID CONFERENCE 2021 ABSTRACTS

EDITED BY: MIKHAIL A. PANTELEEV AND ALEXANDRA A. FILKOVA

Aims: The aim of this work is to evaluate the effect of the AED peptide on gene expression and protein synthesis of early (PDGFR α , Engrailed1) and late (Twist2 and Spry4) differentiation of human stem cells into dermal fibroblasts.

Methods: Human embryonic bone marrow mesenchymal stem cells (line FetMSC) were grown up to the 3rd passage, and the AED peptide (100 ng/ml) or saline solution (control) was added. Quantitative PCR was performed using a qPCRmix-HS SYBR + ROX kit and a DT322 detection amplifier. The concentration of the internal standard (GAPDH mRNA) was taken as a 1. Visual assessment of the synthesis of PDGFR α , Engrailed1, Twist2, Spry4 proteins was performed via immunocytochemistry and immunofluorescence microscopy. The results were statistically processed using the Statistica 10.0 software (Statsoft Inc., Tulsa, USA). Comparison of the mean values of the studied parameter in groups was carried out according to the Student's t-test at a statistical significance level of p <0.01.

Results: The AED peptide significantly increased the expression of the PDGFR α , ENGRAILED1, TWIST2, SPRY4 genes in the FetMSC culture by 2.9, 3.8, 1.4, 1.9 times, respectively, compared to the control. The AED peptide stimulated the synthesis of PDGFR α , Engrailed1, Twist2, Spry4 proteins in the FetMSC culture. After the addition of the AED peptide, 60% of the cells acquired a stellate shape characteristic of fibroblasts, but this was not revealed in the control.

Conclusions: The AED peptide stimulates the expression of genes and synthesis of proteins involved in the differentiation of human skin fibroblasts.

KE and KED peptides regulate PARP and SIRT gene expression during replicative and stationary human mesenchymal stem cells ageing

Vladimir Khavinson^{1,2}, Natalia Linkova¹, Vasily Ashapkin³, Gregory Shilovsky³, Boris Vanuyshin³

1. Saint Petersburg Institute of Bioregulation and Gerontology, Saint Petersburg, Russia. 2. Pavlov Institute of Physiology, Russian Academy of Sciences, Saint Petersburg, Russia. 3. Belozersky Institute of Physical and Chemical Biology, Lomonosov Moscow State University, Moscow, Russia.

Background: Short peptides are involved in the epigenetic regulation of gene expression during cellular ageing. KE peptide has an immunoprotective effect, regulates telomere length of blood lymphocytes and increases animal lifespan. KED peptide possesses vaso- and neuroprotective properties.

Aims: The aim of this work is to study the effect of KE and KED peptides on the expression of PARP-1, PARP-2, PARG, SIRT1 gerontogens in stationary and replicative ageing models of human mesenchymal stem cells of the FetMSC line.

Methods: FetMSC ageing was studied using the Schweigert method with modifications. To simulate replicative senescence, cells were grown up to 7th and 14th passages with the addition of peptides at a concentration of 20 ng/ml. An appropriate volume of saline was added to the control cultures. Quantitative PCR using SYBR Green I dye was performed by means of the QuantiFast SYBR Green PCR Kit (Qiagen, FRG) and a CFX96 Real-Time PCR Detection System (BioRad Laboratories, USA). The results were statistically processed in CFX Manager Software. The GAPDH mRNA was taken as the internal standard; its concentration was taken as a unit. Statistical data analysis was performed according to the two-tailed Student's t test at p <0.05.

Results: KE peptide changed the expression of PARP-1, PARP-2, PARG, SIRT1 genes during replicative and stationary ageing of FetMSC by 1.9-5.5 times. KED peptide changed the expression of PARP-1, PARP-2, PARG, SIRT1 genes during replicative and stationary ageing of FetMSC by 1.9-26.7 times.

Conclusions: KE and KED peptides manifest geroprotective effect in the FetMSC models of replicative and stationary ageing through modulation of the expression of the PARP-1, PARP-2, PARG, SITR1 genes, involved in the regulation of cell repair, differentiation, and apoptosis.