FLIP, BCL-2, BCL-XL and cIAP1. Also GSCs stimulate tumor angiogenesis by expressing elevated levels of VEGF and contribute to tumor growth. On the other hand, hypoxic condition induced VEGF expression, which has been translated into a useful therapeutic strategy in the treatment of recurrent or progressive GBMs.

Results: Hypoxia may enhance tumor progression and therapeutic resistance through its promotion of a cancer stem cell phenotype and induction of VEGF and other proangiogenic factors. Cancer cells in each tumor has greater potential of cancer initiation and repopulation. GSCs are relatively resistant to radiation due to preferential response of the DNA damage checkpoint and the enhanced DNA repair capacity and likely are responsible for GBM tumor recurrence.

Conclusion: In this review, we summarize the current understanding and advances in glioma stem cell research, and discuss potential targeting strategies for future development of antiGSC therapies.

Keywords: GBM, Radiation, Resistance, Cancer, Stem Cell

Ps-58: Expression Level of Transforming Growth Factor-β1 Is Reduced by Increasing The Passage Number of Equine Mesenchymal Stem cells

Shojaee A[1], Parham A[1, 2*], Ejeian F[3], Masaeli E[3, 4], Nasr Esfahani MH[3]

1. Division of Physiology, Department of Basic Sciences, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran
2. Embryonic and Stem Cell Biology and Biotechnology Research Group, Institute of Biotechnology, Ferdowsi University of Mashhad, Mashhad, Iran
3. Department of Reproductive Biotechnology, Reproductive Biomedicine Research Center, Royan Institute for Biotechnology, ACECR, Isfahan, Iran
4. Department of Textile Engineering, Isfahan University of Technology, Isfahan, Iran
Email: parham@um.ac.ir

Background: It is widely accepted that growth factors (GFs) powerfully regulate the biological responses of mesenchymal stem cells (MSCs). TGF-β has been attracting attention in the tenogenic regenerative field as it participates in all phases of tendon healing process. Moreover, TGF-β involves in tendon differentiation of MSCs. Since passage number influence function and behavior of the cells as well as gene expression profile, this study was aimed to investigate mRNA expression of TGF-β1 in equine MSCs at different passages.

Materials and Methods: Equine MSCs were isolated from the fat tissue of gluteal region and expanded. The cells at passages 5 and 8 were seeded and maintained in basic culture medium. 75 % confluency of cels was considered as day 0 and cells were harvested at days 1 and 3. Then, total RNA was extracted and transcribed into cDNA using commercially available kits. Primers for GAPDH (as internal control) and TGF-β1 were designed. Quantitative RT-PCR (qPCR) was performed using a SYBR green master mix and data was analyzed using Student t test.

Results: The mRNA expression of TGF-β1 at P5 and P8 of equine MSCs were compared at 1 and 3 days after 75% confluency. Our data revealed that TGF-β1 expression was significantly higher at P5 compared with P8 in day 1, but there was no significant difference at day 3.

Conclusion: Based on the results, the expression level of TGF-β1 is significantly affected by the cell passage number of equine MSCs. So, tenogenic differentiation capability of quine MSCs can be affected by passage number which should be considered in tenogenic differentiation experiments.

Keywords: Mesenchymal Stem Cells, TGF-B1 Expression, Passage Number, Equine

Ps-59: Identification of Transcription Factors Involved in Conversion of PC12 Cells into Neuron-Like Cells by Staurosporine

Soleimani T*, Fallahi H, Azadbakht M

Department of Biology, School of Sciences, Razi University, Kermanshah, Iran
Email: h.fallahi@razi.ac.ir

Background: Neurogenesis is an important process occurs during embryogenesis in all animals. Neurons are generated from neural stem cells and progenitor cells. Stem cells exhibit two characteristics, selfrenewal and capacity for generating almost any types of differentiated cells. In adult mammals, neurogenesis occurs in three places in the brain, including dentate gyrus, the subventricular zone (SVZ) and the olfactory bulb. Impaired adult neurogenesis was demonstrated in many degenerative diseases, such as Alzheimer. Neural cells can be generated from somatic cells through somatic cell reprogramming or via direct conversion. There are a variety of cell lines, which are used as models for the study of neural differentiation. Induced cell differentiation has been studied in retinal ganglion cells (RGCs), PC12 and SH-SY5Y. PC12 cell line derived from a pheochromocytoma of the rat adrenal medulla, have been widely used as a preferable model for neural differentiation because this cell line has advantages beyond others including showed no recognizable changes in properties for the first 70 passages in culture. This cell line can be differentiated by several chemicals and transcription factors such as nerve growth factor (NGF), epidermal growth factor (EGF), Rapamycin, Staurosporine (STS), trimetyltin (TMT), Ginsenoside-Rd and pituitary adenylate cyclaseactivating polypeptide (PACAP). Staurosporine is a protein kinase inhibitor, which induces neurite outgrowth in PC12 cell lines within a few hours in comparison other materials. Many studies showed that transcription factors could convert somatic cells into neuron-like cells. However, the complete molecular significance of these factors on this cell line has not been uncovered.

Materials and Methods: In this study, the impact of the staurosporine as an inducer of neural differentiation in PC12 cell line was investigated. PC12 cells were grown in RPMI 1640 culture medium, supplemented with 10 % fetal bovine serum (FBS). After treatment with staurosporine we have extracted total RNA from cells. Following RNA-seq analysis, we have identified differentially expressed genes (DEGs). We then constructed and analyzed regulatory networks for transcription factors involved and their genes using JActivemadule, MCODE and Network Analyzer apps from the Cytoscape software environment.

Results: By analysis of RNA-seq data and using online tools and freely available software, we have identified the most important transcription factors (TFs). Network analyses showed integration of these TFs into core differentiation regulatory network.

Conclusion: Such studies would be useful in clarifying the molecular pathways of neural differentiation. We hope our analysis can facilitate the generation of neurons for *in vitro* disease mod-