P6. **Histone acetylation regulates endothelial differentiation of fetal stem cells**

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Introduction. Epigenetic changes in the genome include DNA methylation, histone modifications (acetylation, methylation, phosphorylation, ubiquitination, sumoylation, ADP-ribosylation), and recently discovered miRNAs, three mechanisms that are often tightly linked in the regulation of gene expression and involved in many cellular processes. Histone acetylation was seen as a phenomenon correlated with an open chromatin conformation that allowed the expression of different genes involved in differentiation. Currently it has been observed that in acetylated state many genes are repressed and thus differentiation to a specific cell line is blocked, maintaining the pluripotent state.
Our aim was to investigate the role of histone acetylation in differentiation of endothelial progenitor cells.

Materials and methods. Characterization of EPCs was performed by flow cytometry and neovascularisation potential was achieved by western blot, qRT-PCR, wound-healing assay, matrigel assay.

Results. Flow cytometry analysis showed that histone acetylation reduces the expression of endothelial markers such as CD31, CD105, CD117, CD133, CD144, and VEGFR2. Furthermore, histone acetylation inhibited neovascularization *in vitro*, acting in the processes of proliferation, adherence, migration and in the formation of vascular network structures.

In conclusion, the discovering of acetylation patterns involved in the differentiation of stem cells to different cell types open new opportunities at the interface between chemistry and stem cell biology and can improve applications of stem cells in tissue engineering and regenerative medicine.