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Transcriptional activity of epigenetic remodelling genes in human skin and regenerative capacity

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Epigenetic regulation determines the development of organisms, cell differentiation as well as the differentiation potential DNA methylation/demethylation processes, histone modifications and other regulators of chromatin remodelling could be considered as the markers of epigenetic remodelling and their transcriptional activity can be regarded as an estimate of cellular plasticity and regenerative potential. Surgical skin wounds of patients receiving neoadjuvant therapy prior to abdominal surgery are known to show delayed healing, which complicates further therapy. The aim of this study was to investigate the transcriptional activity of genes involved in epigenetic remodelling in the skin samples collected from neoadjuvant patients. We performed qPCR quantification of transcript levels for a selection of genes involved in different epigenetic mechanisms including DNA methylation, histone modifications and chromatin structure regulation. In the predominant part of examined genes, we observed statistically significant 2-5-fold decreases in expression in the skin of neoadjuvant patients in comparison to other oncological patients who received no neoadjuvant treatment prior to surgery. In addition, we found that the expression levels of the same epigenetic markers in in vitro expanded human epidermal progenitor were markedly, 2-16-fold lower than in the skin samples and non-cultured epidermal cells collected from the patients. Significant reduction in the activity of epigenetic markers in the skin after neoadjuvant therapy indicates the importance of epigenetic remodelling in wound healing and suggests novel therapeutic directions for skin wound treatment.

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