Abstract: 69O

Transciptome analysis of the effects of polarized photobiomodulation on human dermal fibroblasts

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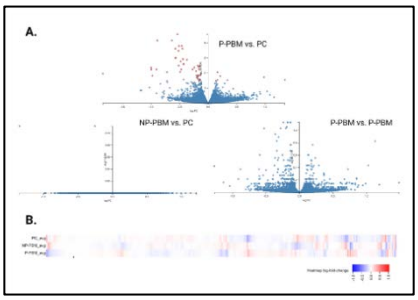
Introduction and Aims: Photobiomodulation (PBM), the therapeutic use of light, is used to treat a myriad of conditions in clinical practice—from wound healing to neonatal jaundice. Despite the presence of clinical evidence surrounding PBM, the fundamental mechanisms underpinning its efficacy remain unclear. There are many variables that can be altered in the application of PBM, including: wavelength, power, irradiation time, beam area, fluence, polarization, pulse parameters and treatment cycles, all of which influence treatment outcomes. Of these, polarization—the filtering of light into specified plane(s)—is an attractive variable to investigate. Therefore, the aim of this work is to evaluate transcriptomic changes in human dermal fibroblasts in response to polarized PBM, to uncover key mechanisms driving its clinical outcomes.

Methods: All experiments were completed using the human caucasian foetal foreskin fibroblast cell line. 24 hours after plating, the cells were exposed to 0.5 µM of H_2O_2 to induce oxidative stress. Immediately after H_2O_2 exposure, cells were irradiated by PBM at a fluence of 1 J/cm^2. There were three experimental groups, all conducted in quadruplicate: 1: linearly polarized light + H_2O_2 (P-PBM); 2: non-polarized light + H_2O_2 (NP-PBM); 3. no-light + H_2O_2 (positive control - PC). RNA was subsequently extracted, and underwent RNA-sequencing. The resulting data underwent analysis for differentially expressed genes (DEGs), ontological enrichment, and pathway analysis through STRING-db and SR plot. DEGs were obtained with a False Discovery Rate (FDR) ≤ 0.05 and enrichment groups were considered significant at $p<0.05$.

Results: There were a total of 71 (from a total of 16280) DEGs when each experimental group was compared only to the control group (FDR <0.05). All of these DEGs were found in the PPBM group, relative to the PC group (Fig x). Of the 71 DEGs, 10 genes were upregulated and 61 one were downregulated. Most DEGs were either mitochondrial or extracellular matrix (ECM)-related. Gene Ontology (GO) analysis was then performed using the DEGs from the P-PBM vs. PC group. Within biological processes there were 95 terms found ($p<0.05$); in the molecular function there were 18 terms found ($p<0.05$); while in the cellular component there were 32 terms enriched ($p<0.05$). A KEGG pathways analysis was performed for the DEGs found in the P-PBM vs. PC group. This revealed 21 significantly enriched pathways ($p<0.05$). Finally, there were 24 significantly enriched reactome pathways found when comparing the DEGs of the P-PBM vs. PC groups ($p<0.05$).



Discussion and Conclusions: The P-PBM DEGs were almost always down regulated compared to the comparator groups, conflicting with analogous research. This may be explained by the P-PBM treatment conditions decreasing the amount of cellular stress, hence causing a decreased mitochondria and ECM protective response. Alternatively, it could point to an alternate mechanism, outside the mitochondria, by which PBM exerts its effects. Overall, further research is needed to elucidate the fundamental mechanisms of PBM.