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Influence of blue, green, and yellow light irradiation on HaCaT, NHDF, and HUVECs and weighted gene co-expression network analysis in the development of abdominal aortic aneurysm

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The healing process of wounds and scrapes on the skin is one of the most vital processes that occur during the lifetime of an organism. In this thesis, we investigate the influence of light on HaCaT, NHDF, and HUVECs. It is common knowledge that the efficacy of light therapy depends on a number of variables, including the wavelength of the light, timing of the treatment, quantity of energy employed, and distribution of the light. Using a novel experimental set up we were able to compare the influence of blue, green and yellow constant illumination on HaCaT, NHDF, and HUVECs. We found that an energy output at 10 mW/cm^2 was feasible, while higher light energy output led to high temperatures toxic to the cells. Blue light irradiation at 507 nm, green light irradiation at 533 nm, and yellow light irradiation at 592 nm regulated the viability and proliferation of HaCaT, NHDF, and HUVECs. For 507 nm, a peak in metabolic activity and proliferation of HaCaT was observed with 10 minutes of irradiation at 10 mW/cm^2, corresponding to an energy density of 6 J/cm^2. Meanwhile, a peak in metabolic activity and proliferation of NHDF and HUVECs was observed after 12 minutes of irradiation at 10 mW/cm^2, corresponding to an energy density of 7.2 J/cm^2. For 533 nm, a peak in the metabolic activity of HaCaT, NHDF, and HUVECs was observed with 12 minutes of irradiation at 10 mW/cm^2, corresponding to an energy density of 7.2 J/cm^2. A peak in the proliferation of HaCaT and HUVECs was observed after 12 minutes of irradiation at 10 mW/cm^2, corresponding to an energy density of 7.2 J/cm^2. A peak in the proliferation of NHDF was observed after 10 minutes of irradiation at 10 mW/cm^2, corresponding to an energy density of 6 J/cm^2. For 592 nm, a peak in metabolic activity and proliferation of HUVECs was observed with 10 minutes of irradiation at 10 mW/cm^2, corresponding to an energy density of 6 J/cm^2. A peak in metabolic activity and proliferation of HaCaT was observed after 12 minutes of irradiation at 10 mW/cm^2, corresponding to an energy density of 7.2 J/cm^2. A peak in metabolic activity and proliferation of NHDF was observed after 12 minutes and 10 minutes of irradiation at 10 mW/cm^2, corresponding to an energy density of 7.2 J/cm^2 and 6 J/cm^2, respectively. Based on these data, we conclude that blue light irradiation at 507 nm, green light irradiation at 533 nm, and yellow light irradiation at 592 nm have potential therapeutic value in wound healing.

There is still an unmet need for therapeutic drugs for patients with an abdominal aortic aneurysm (AAA), especially for candidates unsuitable for surgical or interventional repair. Therefore, the purpose of this in silico study is to identify significant genes and regulatory mechanisms in AAA patients to predicate the potential therapeutic compounds for significant genes. GSE57691 dataset was obtained from Gene Expression Omnibus (GEO) and used to identify the Differentially expressed genes (DEGs) by Weighted Correlation Network Analysis (WGCNA). The biological function of DEGs was determined using Gene Ontology (GO) and the Kyoto Ency-clopedia of Genes and Genomes (KEGG). AAA-related genes were obtained from Comparative Toxicogenomics Database (CTD) using the keywords Aortic Aneurysm, Abdominal, and the hub genes in AAA were obtained by overlapping DEGs, WGCNA-based hub genes, and CTD-based genes. The diagnostic values of hub genes were determined using ROC curve analysis. Hereby, a TF-miRNA-hub gene network was constructed based on the miRnet database. Using these data, potential therapeutic compounds for the therapy of AAA were predicted based on the Drug Gene Interaction Database (DGIdb). A total of 218 DEGs (17 upregulated and 201 downregulated) and their biological function were explored. 4093 AAA-related genes were derived by text mining. Three hub modules and 144 hub genes were identified by WGCNA. Asparagin Synthetase (*ASNS*), the axin related protein 2 (*AXIN2*), Melanoma cell adhesion Molecule (*MCAM*), and the Testis-specific Y-encoded-like protein 1 (*TSPYL1*) were obtained as intersecting hub genes and the diagnostic values were con-firmed with ROC curves. As potential compounds targeting the hub genes, Asparaginase was identified as

target compound for *ASNS*. Prednisolone and Abiraterone were identified as com-pounds targeting *TSPYL1*. For *MCAM* and *AXIN2* no compound could be predicted.