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# Influence of blue light irradiation on endothelial cells and weighted gene co-expression network analysis in the development of abdominal aortic aneurysm

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This doctoral thesis includes two independent projects which are not thematically related. Therefore, all sections of this thesis have been divided into two separate independent parts.
Part 1. Influence of blue light irradiation on endothelial cells
In this study, we systematically investigated the impact of LED blue light with a wavelength of 453 nm on human umbilical vein endothelial cells. We demonstrated firstly that blue light irradiation regulates the biological activities of HUVECs in a biphasic manner. At a low fluence (10 mW/cm2 * 12 min), blue light promoted cell viability, migration and angiogenic function of HUVECs. However, at high fluence (40 mW/cm2 * 12 min), blue light irradiation inhibited all the above-mentioned cell activities. Furthermore, blue light increased the intercellular ROS production in a fluence-dependent manner. The mechanisms of the observed biphasic effect were revealed from RNA sequencing. Several pathways, e.g., MAPK, JAK-STAT, PI3K-Akt and VEGF - known to improve cell viability, migration and angiogenesis - were upregulated in the low fluence group, while Ferroptosis, Necroptosis and the p53 signaling pathways - which are known to negatively regulate above cell activities - were activated after higher fluences of light irradiation. This study would provide an underlying insight into photobiomodulation by blue light and may help to implement potential treatment strategies for treating angiogenesis-dependent diseases.
Part 2. Weighted gene co-expression network analysis in the development of abdominal aortic aneurysm
In this study, we undertook a bioinformatic approach to find the key genes and predict drug candidates for the prevention of aneurysm progression. With the weighted gene co-expression network analysis, which provides more biologically meaningful correlations between gene expression and sample features, hub genes and key modules were identified from the public database of mouse abdominal aortic aneurysm progression. Furthermore, we performed a functional enrichment analysis of the key modules, which revealed mitotic cell cycle, GTPase activity, and metabolic processes involved in the disease development. Key genes like ACACB, validated both in mouse and human abdominal aortic aneurysm datasets, provide new directions for further studies. Potential drugs or compounds targeting key genes were predicted in the Drug–Gene Interaction Database. Of these candidates, five drugs (PF-05175157, firsocostat, and metformin targeting ACACB; maraviroc targeting CCR5; rosiglitazone targeting LPIN1) have been already registered in clinical trials related to abdominal aortic aneurysms.