**[BIOINFO 2023]**

# Site-specific transcriptomic analysis reveals novel insights into pterygium pathogenesis

Hanseul Cho[1,2], Ye-Ah Kim[2,3], Chaerim Song[2,4], Tae Gi Kim[5], and Man S Kim[2]

[1] *College of Medicine, Kyung Hee University, Seoul, Republic of Korea*
[2] *Translational-Transdisciplinary Research Center, Clinical Research Institute, Kyung Hee University Hospital at Gangdong, College of Medicine, Kyung Hee University, Seoul, Republic of Korea*
[3] *Department of Biomedical Science and Technology, Graduate School, Kyung Hee University, Seoul, Republic of Korea*
[4] *Department of Biology, University of Pennsylvania, Pennsylvania, United States of America*
[5] *Department of Ophthalmology, Kyung Hee University College of Medicine, Kyung Hee University Hospital at Gangdong, Seoul, Republic of Korea*

Pterygium is a non-cancerous triangular-shaped fibrovascular tissue growth invading the cornea, potentially impairing vision and causing aesthetic concerns. The pathogenesis of pterygium is not fully understood, with debates regarding the primary site of proliferation. We analyzed RNA seq data from 18 surgically removed pterygium tissue samples from 6 patients, specifically comparing the head and neck of pterygium (MAIN), the body of pterygium (ACC), and adjacent conjunctiva removed together (NORMAL). Gene set enrichment analysis revealed that genes related to mitotic nuclear division were upregulated in MAIN, while downregulated in ACC compared to NORMAL. Additionally, pathways related to the development and differentiation of skin and epidermis were enriched in MAIN but not in ACC. These results indicate that the increase in epithelial cells takes place mainly in the head and neck region. In contrast, gene sets relevant to the development and regulation of blood vessels, muscle, and connective tissue, detection and response to stimulus, and extracellular matrix and cell adhesion organization were upregulated in ACC compared to MAIN and NORMAL. This suggests that neovascularization and fibrosis are the most prominent in the body. Furthermore, the transcriptome changes in ACC compared to MAIN and NORMAL, analyzed using Mitocarta 3.0, showed a systematic downregulation of mitochondrial energy metabolism including OXPHOS, mitochondrial central dogma, mitochondrial dynamics, protein homeostasis, and signaling. In conclusion, epithelial proliferative capacity is primarily derived from the pterygium head and neck, whereas angiogenesis, fibrosis, and mitochondrial dysfunction occur within the body. This site-specific distinction sheds light on pterygium's pathogenesis, potentially guiding targeted interventions.