SKIN CANCER (OTHER THAN MELANOMA)

DOWN-EXPRESSION OF HSA_CIRC_0001360 ENHANCED THE PROLIFERATION AND MIGRATION OF CUTANEOUS SQUAMOUS CELL CARCINOGENESIS

Jingyao Liang [1] - Pingjiao Chen [2] - Changxing Li [2] - Jianqin Wang [1] - Sanquan Zhang [1] - Xibao Zhang [1]

Guangzhou Institute Of Dermatology, Department Of Dermatology, Guangzhou, China [1] - Nanfang Hospital, Southern Medical University, Department Of Dermatology, Guangzhou, China [2]

Background: Circular RNAs (circRNAs) as important sponges of ncRNA-mediated regulatory networks have been implicated in many pathophysiological processes, including tumor development and progression. However, their roles in cutaneous squamous cell carcinoma (cSCC) are not yet well-understood.

Objective: To identify the differentially expressed circRNAs and further explore their potential functions in cutaneous squamous cell carcinogenesis.

Methods: The expression profile of circRNAs in 3 paired cSCC and adjacent normal tissues were detected with RNA sequencing and bioinformatics analysis. The candidate circRNAs were validated by PCR, Sanger sequencing, and qRT-PCR in another 5 matched samples. The biological functions of circRNAs were assessed using circRNAs silencing and overexpression, MTs, flow cytometry, transwell and colony formation assays. In addition, the circRNA-miRNA-mRNA interaction networks were predicted by bioinformatics.

Results: 1115 circRNAs including 457 up- and 658 down-regulated circRNAs (fold change ≥ 2 and $p < 0.05$) were differentially expressed in cSCC compared with adjacent normal tissues. Of 4 selected circRNAs, 2 circRNAs (hsa_circ_0000932 and hsa_circ_0001360) were further validated to have significant decreased in cSCC, in agreement with the results from RNA-Seq data analysis. Furthermore, hsa_circ_0001360 but not hsa_circ_0000932 silencing was found to result in a significant increase of the proliferation, apoptosis, migration and invasion of SCL-1 cells, whereas hsa_circ_0001360 overexpression showed the opposite regulatory effects. Hsa_circ_0001360 was predicted to interact with top 5 miRNAs and their corresponding genes.

Conclusion: CircRNAs dysregulation may play critical roles in carcinogenesis of cSCC, and hsa_circ_0001360 could be developed as a promising biomarker used for the therapeutic

targets of cSCC.