ABSTRACT BOOK ABSTRACTS



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SKIN CANCER (OTHER THAN MELANOMA)

COMPUTATIONAL DISCOVERY AND EXPERIMENTAL VALIDATION OF THE GENE ALPHA-ENOLASE PROMOTING TUMORIGENESIS IN CUTANEOUS SQUAMOUS CELL CARCINOMA

 $Lm Song^{(1)} - Wx Fan^{(2)} - Zx Ying^{(1)} - X Wang^{(2)} - Sb Wang^{(3)} - N Wang^{(3)} - Y Zheng^{(3)}$

Department Of Dermatology, The Second Affiliated Hospital Of Xi'an Jiaotong University, Xi'an, China⁽¹⁾ - Department Of Dermatology, The Second Affiliated Hospital Of Xi'an Jiaotong University, Xi'an, China⁽²⁾ - Department Of Dermatology, The Second Affiliated Hospital Of Xi'an Jiaotong University, Xi'an, China⁽³⁾

Introduction: α-enolase (ENO1) is a conserved glycolytic enzyme which plays pivotal roles in tumorigenesis. The overexpression of glycolytic genes has been found in more than 20 human cancer types, including oral squamous cell carcinoma, but its function in cutaneous squamous cell carcinoma(cSCC) has remained unclear.

Objective: Integrate chip-based high-throughput and KEGG analysis to identify cell signals involved in glucose metabolism and then validated the gene expression and functional role of hub gene ENO1 in cSCC.

Materials and Methods: The gene expression profiles GSE45216, GSE42677 were downloaded from Gene Expression Omnibus. Then we performed differentially gene expression analysis, protein-protein interaction network and selected the hub gene ENO1 for in-depth research. Western blot, qRT-PCR and immunohistochemistry were carried out to examine the expression of ENO1 in human cSCC patients and cell lines. The effects of ENO1 on cell growth were investigated by CCK-8. The impacts of ENO1 on cell migration and invasion were explored by Transwell assays.

Results: The expression level of ENO1 was significantly elevated in cSCC tissues and A431 and SCL-1 cell lines. Ablation of ENO1 in A431 and SCL-1 cell lines inhabited cell proliferation, migration and invasion in vitro.

Conclusions: ENO1 may be a potent promoter to the occurrence and development of cutaneous squamous cell carcinoma. The ENO1 gene can be used as therapeutic targets for treating ENO1-overexpressing cSCC.





