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ORIGINAL ARTICLE

MiR-22 alleviates the proliferation and metastasis of melanoma by targeting FASN

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Summary

Purpose: *To explore the role of MicroRNA-22 (miR-22) in the development of malignant melanoma and the underlying mechanism.*

Methods: *Potential miRNAs binding FASN (fatty acid synthetase) were predicted by bioinformatics analysis and miR-22 was selected. Their binding relationship was confirmed by dual-luciferase reporter assay. MiR-22 and FASN levels in 40 clinical samples of melanoma were detected. Expression correlation between miR-22 and FASN was assessed by Pearson correlation test. To uncover the role of miR-22 in regulating cell phenotypes of malignant melanoma, M21 and A375 cells were transfected with miRNA-NC, miR-22 mimics or miR-22 mimics+FASN-OE, respectively. Proliferative and metastatic abilities in each group were determined by cell counting kit-8 (CCK-8), 5-Ethynyl-2'- deoxyuridine (EdU) and Transwell assay, respectively.*

Results: *MiR-22 was the target gene binding the oncogene FASN. Downregulated miR-22 and upregulated FASN were observed in melanoma tissues, showing a negative correlation between them. Overexpression of miR-22 inhibited proliferative, migratory and invasive abilities in M21 and A375 cells. Notably, overexpression of FASN abolished the inhibitory effects of miR-22 on proliferative and metastatic abilities in melanoma.*

Conclusions: *MiR-22 is lowly expressed in the malignant melanoma samples. Overexpression of miR-22 inhibits proliferative and metastatic abilities in melanoma by targeting FASN and negatively regulating its level. MiR-22 may be a promising therapeutic target of melanoma.*

Key words: *malignant melanoma, MiR-22, FASN, proliferation, metastasis*

Introduction

Melanoma is caused by the malignant deterioration of melanocytes distributed in the stroma, most of which are formed by the canceration of normal moles and pigmented plaques [1]. Although the incidence of malignant melanoma accounts for only 1% of skin tumors, its mortality is extremely high [2]. Melanoma rapidly progresses, leading to local or distant metastasis in a short period. Therefore, clarifying potential mechanisms of proliferation and metastasis in melanoma contributes to improve its prognosis.

MicroRNAs (miRNAs/miRs) are a kind of short, single-stranded non-coding RNAs with a length of about 22nt. They mainly regulate target gene expressions at the post-transcriptional level. In recent years, miRNAs have been considered to be closely related to tumorigenesis and tumor progression [3]. Increasing evidences have indicated that dysregu-

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