Dan Li et al., J Cancer Sci Ther, 3:7
doi: http://dx.doi.org/10.4172/1948-5956.S1.12

OMICS Group Conferences
Accelerating Scientific Discovery

International Conference & Exhibition on
Cancer Science & Therapy
15-17 August 2011 Las Vegas, USA

Analysis of miR-195 and miR-497 expression, regulation and role in breast cancer

Dan Li[1], Yulan Zhao[1], Changxing Liu[3], Xiaona Chen[1], Yanting Qi[2], Yue Jiang[2,1], Chao Zou[1], Xiaolong Zhang[1], Shunying Liu[1], Xuejing Wang[4], Chuan-Xiu Bian[2], Dan Zhao[1], Qiang Sun[4], Zhenbing Zeng[7], Andreas Dress[7], Marie C. Lin[6,1], Hsiang-Fu Kung[5,1], Feng Mao[4], Bing-Hua Jiang[2,1] and Lihui Lai[1]

[1]Institute of Molecular and Chemical Biology, East China Normal University, Shanghai, China
[2]Department of Pathology, Anatomy and Cell Biology, Thomas Jefferson University, Philadelphia, PA 19107, USA
[3]Department of General Surgery, Huashan Hospital, Shanghai Medical College, Fudan University, Shanghai, China
[4]Department of Breast Surgery, Peking Union Medical College Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China
[5]Faculty of Medicine, The Chinese University of Hong Kong, HK, SAR, China
[6]Brain Tumor Center, Neurosurgery Division, Faculty of Medicine, PWH, The Chinese University of Hong Kong, Shatin, Hong Kong, China
[7]CAS-MPG Partner Institute and Key Lab for Computational Biology, SIBS, CAS, Shanghai, China

Purpose: To investigate expression, regulation, potential role and targets of miR-195 and miR-497 in breast cancer.

Experimental design: The expression patterns of miR-195 and miR-497 were initially examined in breast cancer tissues and cell lines by Deep sequencing: Northern blotting and quantitative real-time PCR. Combined bisulfite restriction analysis and bisulfite sequencing were carried out to study the DNA methylation status of miR-195 and miR-497 genes. Breast cancer cells stably expressing miR-195 and miR-497 were established to study their role and targets. Finally, normal, fibroadenoma and breast cancer tissues were employed to analyze the correlation between miR-195/497 levels and malignant stages of breast tumor samples.

Results: MiR-195 and miR-497 were significantly down-regulated in breast cancer. The methylation state of CpG islands upstream of the miR-195/497 gene was found to be responsible for the down-regulation of both miRNAs. Forced expression of miR-195 or miR-497 suppressed breast cancer cell proliferation and invasion. Raf-1 was identified as a novel direct target of miR-195 and miR-497. miR-195/497 expression levels in clinical specimens were found to be correlated inversely with malignancy of breast cancer.

Conclusion: Our data imply that both miR-195 and miR-497 play important inhibitory roles in breast cancer malignancy and may be the potential therapeutic and diagnostic targets.