J Cancer Sci Ther 2016, 8:6 (Suppl)
http://dx.doi.org/10.4172/1948-5956.C1.070

10th Global Annual Oncologists Meeting

July 11-13, 2016 Cologne, Germany

MiR-205 is a potent promoter thet enhance motility in ovarian cancer cells

Ke Niu and Yongxian Lu
First Affiliated Hospital, China

There are many molecular regulators in tumor EMT, such as miR-125a, the miR-200 family of microRNAs (miR-141, miR-200a, b, c, and miR-429), miR-34, miR-205, zinc finger E-box binding homeobox 1 (ZEB1) and zinc finger E-box binding homeobox. Our study investigated the clinical significance of microRNA-205 (miR-205) and zinc finger E-box binding homeobox 1 (ZEB1) in epithelial ovarian cancer (EOC) and the underlying mechanisms by which they are involved into tumorigenesis. In our research, we found miR-205 (P=0.0001) and ZEB1 mRNA (P b 0.0001) in clinical EOC tissues were significantly higher and lower than those in normal tissues, respectively. Interestingly, there was a negative correlation between miR-205 and ZEB1 mRNA expression in EOC tissues (P=0.01). Additionally, miR-205-upregulation and/or ZEB1-downregulation were significantly associated with high pathological grade and advanced clinical stage of EOC patients (all P b 0.05). Meantime, luciferase reporter assays identified ZEB1 as a direct target of miR-205 in EOC cells. Moreover, miR-205 blockage inhibited, whereas miR-205 mimics promoted the motility of EOC cells in vitro. Importantly, all the alterations of the above cellular phenotypes by blocking or enhancing of miR-205 could be alleviated by subsequent suppression or re-introduction of its target ZEB1, respectively. It is concluded that MiR-205, acting as an oncogenic miRNA, may promote the clinical progression of EOC patients and enhance the cellular motility in vitro by directly and negatively regulating ZEB1, providing a potential therapeutic strategy for suppression of EOC metastasis.

niuke304@163.com

Correlation between XRCC1 Arg194Trp Gene Polymorphism and Protein Expression Status in Breast Tumors: Evidence from a Kurdish Population

Abbas Ahmadi[1*], Mohammad Abdi[2], Hiresh Ayoubian[2], Mohammad Nazir Menbari[2], Farid Zandi[2] and **Shoaib Advai[2]**
[*1]PhD student of Molecular medicine, Cellular and Molecular Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran.
[2]Cellular and Molecular Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran.

Introduction: To evaluate the role of Arg194Trp polymorphism of X-ray repair cross-complementing group 1 (XRCC1) as a risk factor for breast cancer in Kurdish patients, and to investigate the possible association between Arg194Trp XRCC1 gene polymorphisms with clinical and histopathological outcomes of patients with breast cancer.

Methods: A total of 100 breast cancer patients and 200 cancer-free controls in Kurdish population were enrolled in this study. Tissue expression of ER, PR, Her2/neu and Ki67 were evaluated by immunohistochemistry (IHC). The Arg194Trp genotypes were determined by polymerase chain reaction- restriction fragment length polymorphism method (PCR-RFLP).

Results: Our data showed that the risk for breast cancer increased significantly among the Trp variant of XRCC1. Significant association was found between codon 194 polymorphisms and tissue expression of Ki67.

Conclusion: Our results demonstrated that the Trp allele of codon 194 XRCC1 is a potential risk factor for breast cancer in Kurdish ethnicity. Furthermore, this polymorphism showed a substantial effect on clinical and histological features of breast cancer in this ethnicity.

Keywords: Breast cancer, XRCC1 gene Polymorphism, Estrogen receptor, Progesterone receptor, Her2/neu, Ki67

abbasahmady1@gmail.com