

Expression and Promoter Methylation Analysis of DACH1 Gene in Tumor and Normal Breast Tissue in Breast Cancer

Mohammad Nasirpour Panahifarshad ¹, Mahdieh Salimi ^{2,*}, Hossein Mozdarani ³

¹ Research and Technology Department, Islamic Azad University, Iran

² Department of Medical Genetics, Institute of Medical Biotechnology, National Institute of Genetic Engineering and Biotechnology (NIGEB), Tehran, Iran

³ Department of Medical Genetics, Tarbiat Modares University, Tehran, Iran

* Corresponding author: Mahdieh Salimi, Department of Medical Genetics, Institute of Medical Biotechnology, National Institute of Genetic Engineering and Biotechnology (NIGEB), Tehran, Iran. E-mail: salimi@nigeb.ac.ir

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Abstract

Introduction: Breast cancer is common malignancy and ranked as a second cause of death in women population. DACH1 is a major key member of the retinal genes network, the retinal determination gene network (RDGN) plays crucial role in the basically mechanism of cells such as differentiation and proliferation. The DACH1 gene acts as a suppressor tumor, and its expression has decreased in several cancer cell lines. This study focuses on DACH1 expression and its promoter methylation pattern in tumoral and normal breast tissues.

Materials and Methods: The expression of DACH1 in tumor and normal adjacent tissue samples was assessed using comparative Real Time RT-PCR by SYBR green dye at the presence of beta-actin housekeeping gene as internal control in 60 samples. The DNA methylation pattern in the promoter region of DACH1 was analyzed using the methylation specific PCR method. The proper statistical method was used for significance evaluation using SPSS software.

Results: Our data indicated that DACH1 gene expression in tumor tissues was down regulated compared with normal adjacent tissues. Methylation pattern of promoter region of this gene in tumoral breast tissues was hyper methylation.

Conclusions: DACH1 down regulation and its promoter hypermethylation as its epigenetics cause may be considered as a possible biomarker associated with breast cancer. More study in this field would be promising and have great importance in cancer management.