World Academy of Science, Engineering and Technology International Journal of Biomedical and Biological Engineering Vol:18, No:08, 2024

Correlating Lactoferrin Expression Profiling of Cancer Cell, Proliferation and Metastasis, With Clinical Features, as Well as Early Stages of Breast Cancer

Authors: Azar Heidarizadi, Mahdieh Salimi, Hossein Mozdarani

Abstract: Introduction: As a complex disease, breast cancer results from several genetic and epigenetic changes. Lactoferrin, a member of the transferrin family, is reported to have a number of biological functions, including DNA synthesis, immune responses, iron transport, etc., any of which could play a role in tumor progression. The aim of this study was to investigate the bioinformatics data and experimental assay to find the pattern of promoter methylation and gene expression of LTF in breast cancer in order to study its potential role in cancer management. Material and Methods: In order to evaluate the methylation status of the LTF promoter, we studied the MS-PCR and Real-Time PCR on samples from patients with breast cancer and normal cases. 67 patient samples were conducted for this study, including tumoral, plasma and normal tissue adjacent samples, as well as 30 plasmas from normal cases and 10 tissue breast reduction cases. Subsequently, bioinformatics analyses such as cBioPortal databases, string, and genomatix were conducted to disclose the prognostic value of LTF in breast cancer progression. Results: The analysis of LTF expression showed an inverse relationship between the expression level of LTF and the stages of tissues of breast cancer patients (p<0.01). In fact, stages 1 and 2 had a high expression in LTF, while, in stages 3 and 4, a significant reduction was observable (p < 0.0001). LTF expression frequently alters with a decrease in the expression in ER+, PR+, and HER2+ patients (P < 0.01) and an increase in the expression in the TNBC, LN $^{-}$, ER $^{-}$, and PR- patients (P < 0.001). Also, LTF expression is significantly associated with metastasis and lymph node involvement factors (P < 0.0001). The sensitivity and specificity of LTF were detected, respectively. A negative correlation was detected between the results of level expression and methylation of the LTF promoter. Conclusions: The altered expression of LTF observed in breast cancer patients could be considered as a promotion in cell proliferation and metastasis even in the early stages of cancer.

Keywords: LTF, expression, methylation, Breast Cancer

Conference Title: ICCST 2024: International Conference on Cancer Science and Therapy

Conference Location : Toronto, Canada **Conference Dates :** August 08-09, 2024