ERBB2 - A Potential Breast Cancer Marker: An Integrated Bioinformatics Strategy

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ABSTRACT

INTRODUCTION

Breast cancer is one of the most common malignant cancers in women around the world. Until now, despite great improvements in treatment the high incidence rate and mortality worldwide are exponential. Thus identification of novel molecular cancer drivers and evaluation of existing breast cancer biomarkers is a critical step.

OBJECTIVE

This study aims to explore one of the driven genes-ERBB2 receptor- a good predictive cancer biomarker, its specific TK receptor domain mutations, biological pathways, and oncoproteins challenging the apoptotic process, involved in the progression of breast cancer using the *in-silico* approach.

METHODOLOGY

We used the multiple advanced bioinformatics tools performing structure-based Domain architecture analysis with predicted functional protein association of ERBB2 gene and the role of posttranslational modification--in instigating TK receptor domain mutations providing an understanding of the underlying mechanism of tumor invasion and metastasis.

RESULTS

Considering all approaches as complementary the TK inhibitors and the role of the ERBB2 gene can improve drug targeting prediction strategy highlighting the importance of driver genes. Our results suggest that functional validation is a positive prediction and we provided answers to some of the imperative questions although important concerns in the field remain unresolved like the implications for therapeutics etc. for future biological and clinical accomplishments.

CONCLUSION

The evaluation of the existing cancer candidate gene and the interacting proteins and pathways particularly ERBB2- downstream signaling pathway has the potential to generate novel hypotheses in oncology. Thus provide a baseline to identify target protein-based pathways involved through wet experiments.

KEYWORDS

Breast Cancer, ERBB2, Protein-Protein Interaction, Post Translational Modification, Tyrosine Kinase Receptor.

REFERENCE

Afshan Zeeshan Wasti, Rabya Saleh Alotaibi, Anjuman Gul Memon, and Nikhat Ahmed (2020); Proteomic analysis of ERBB2 - a potential breast cancer marker: an integrated bioinformatics strategy. *Int. J. of Adv. Res*. **8** (Jun). 1451-1461] (ISSN 2320-5407).