

Molecular Portraits: The Role of Posttranslational Modification in Cancer Metastasis

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Abstract : Aim: Breast cancer is the most common cancer in women worldwide, and resistance to the current therapeutics, often concurrently, is an increasing clinical challenge. Glycosylation of proteins is one of the most important post-translational modifications. It is widely known that aberrant glycosylation has been implicated in many different diseases due to changes associated with biological function and protein folding. Alterations in cell surface glycosylation, can promote invasive behavior of tumor cells that ultimately lead to the progression of cancer. In breast cancer, there is an increasing evidence pertaining to the role of glycosylation in tumor formation and metastasis. In the present study, an attempt has been made to study the disease associated sialoglycoproteins in breast cancer by using bioinformatics tools. The sequence will be retrieved from UniProt database. A database in the form of a word document was made by a collection of FASTA sequences of breast cancer gene sequence. Glycosylation was studied using yinOyang tool on ExPASy and Differential genes expression and protein analysis was done in context of breast cancer metastasis. The number of residues predicted O-glc NAc threshold containing 50 aberrant glycosylation sites or more was detected and recorded for individual sequence. We found that there is a significant change in the expression profiling of glycosylation patterns of various proteins associated with breast cancer. Differential aberrant glycosylated proteins in breast cancer cells with respect to non-neoplastic cells are an important factor for the overall progression and development of cancer.

Keywords : breast cancer, bioinformatics, cancer, metastasis, glycosylation

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