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Identification of Common Differentially Expressed Genes in Human Breast Cancer and Developing Bovine Mammary Tissues

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Abstract:

Accelerated cell proliferation in breast cancer is a coordinated process that comprises cell cycle dysregulation and a specific gene expression program to determine tissue identity. Many studies have provided knowledge about the molecules involved in the cell proliferation and key regulatory transcription factors that control tissue specific gene expression. In most cancer tissues the rate of cell proliferation exceeds the rate of cell death. In the first lactation of cows there is an incredible growth and development rate in mammary glands. This phenomenon is very similar to developing a tumor tissue. Therefore, pathways involved in breast cancer and bovine mammary gland may share common genes. In this study, three datasets (GSE21422, GSE29431, and GSE19055) from Gene Expression Omnibus (GEO) were analyzed. Differential expression genes between breast cancer and normal tissue were recognized through LIMMA package of R. Also, DEG between lactation and dry period in bovine were identified using this package. The P-values of DEGs were adjusted to FDR (false discovery rates) and the threshold adj-P.value <0.01 were used to recognize significant DEGs. After that, common DEGs between breast cancer samples and bovine mammary gland samples were found using R. A total of 327 shared DEGs were identified. Among these genes, BUB1, ANLN, KIF14, BUB1 and NDC80 were reported as candidate genes in breast cancer. Our results suggest that the developing bovine mammary tissue could be used as an animal model in order to investigate breast cancer.

Keywords: Breast Cancer, Differentially Expression Gene, Bovine Mammary Gland