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Breast Cancer Gene Expression Profile Analysis in terms of Genes Specific to Non-breast tissues

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Investigation of cancer gene expression profile in context of tissue-specific genes has not been studied in detail, although it provides important signatures for cancer. In this study, we aim to understand genetic alteration of tumors in context of tissue-specific genes.

Specific genes for various healthy tissues were determined using extended tau which is a robust and rigorous method generated in our previous study. Tissue-specific genes for all tissues were joined with breast cancer expression data downloaded from TCGA. Utilizing a statistical approach, we identified genes which are specific to a tissue other than breast but having high expression in cancerous breast, not in normal breast. After applying all criteria, we pinpointed 34 genes specifically expressed in breast cancer, although they are specific to ovary, placenta or testis. This unsuspected phenomenon was also observed in different cancers.

Some of cancer-testis genes which are only specific to testis but expressed in various tumors shown in literature such as MAGE, TEX and PAGE family members have been confirmed by our study and we observed additional cancer-testis genes such as CT83, SPANX family members. Some placenta-specific genes CRISP2, DKKL1 and CST9L had been identified as cancer-testis genes before. Several placenta and testis-specific genes are highly expressed in only breast cancer, while some of them are expressed in breast, lung and liver cancer.

As conclusion, detected genes have potential to be adopted as early diagnostic markers and immunogenic therapeutics. Germline and placental genes should be studied in detail to reveal cancer cells characteristic features.

Biography:

Hatice Büşra Konuk has completed her undergraduate and graduate studies in Yildiz Technical University, Bioengineering Department, Turkey in 2015 and 2018, respectively. Her master thesis was about calculation of tissue-specific genes and investigation of intra-tumoralheterogeneity to understand cancer cell molecular mechanisms to reveal biomarkers for diagnosis and targeted therapy in solid tumors using computational approaches. She is now a PhD student and Research Assistant in Gebze Technical University Bioengineering Department/Bioinformatics and System Biology Program. Her keywords are data analysis, human genome, cancer genetics and computational approaches.

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