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Topic of Research: Integrative analysis of genomic alteration profiles in breast cancer and proposing drug targets

Findings

Breast cancer remains a global health challenge, with increasing incidence rates due to aging, lifestyle changes, and healthcare disparities. Despite advances in detection and treatment, novel therapeutic targets are needed. This study aimed to identify differentially expressed genes (DEGs) in breast cancer and explore their therapeutic potential. Using in-silico analysis, four gene expression datasets (GSE29044, GSE42568, GSE89116, GSE109169) were examined, identifying nine key DEGs. COL11A1, MMP11, and COL10A1 were up-regulated, while PCOLCE2, LAMA2, TMTC1, ADAMTS5, TIMP4, and RSPO3 were down-regulated. Expression patterns were validated in MCF-7 and MDA-MB-231 cell lines. LAMA2, TMTC1, and TIMP4 were significantly associated with age-related breast cancer occurrence and poor survival. Structural analysis of LAMA2 revealed 11 deleterious mutations disrupting integrity and increasing flexibility. Virtual screening of FDA-approved drugs, metabolome molecules, and natural compounds identified cyanuric acid as a promising modulator of LAMA2. Molecular docking showed strong binding affinity (-5.4 kcal/mol), while MD simulations confirmed complex stability. These findings provide insights into LAMA2-associated cancer progression and highlight cyanuric acid's therapeutic potential. Further experimental validation is warranted to establish LAMA2 as a viable target for breast cancer treatment.

Keywords: Breast cancer, differentially expressed genes, protein–protein interaction network, single nucleotide polymorphisms, molecular dynamics simulations