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Sequence analysis of mutations pattern among breast cancer patients in Pakistan

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Breast cancer is the causes of female mortality across the world. Among Asian countries, Pakistan has the highest rate of breast cancer. NGS analysis of cancer provides a platform to identify the novel drugs for human breast cancer. The regulatory mechanisms of critical cancer-associated genes involved in the progression of tumors help us to develop future therapeutics. Human breast cancer shows a diversity of histological types of mammary tumors compared to other types of cancer. Hereditary breast cancer is due to an inherited mutation in the BRCA1 and BRCA2 genes. Comparative analysis of Next-generation sequencing (NGS) technologies offer higher throughput and lower per-base cost as compared to legacy approaches such as Sanger sequencing. Several laboratories have recently reported applying an NGS approach for diagnostic testing of mutations in the BRCA1/2 genes or can help us to scan the Pakistani population and we can save many lives.

In our study, Whole-genome sequences of Pakistani patients are used to find the mutational processes generating somatic mutations in human breast cancer. Proteincoding cancer genes are carried exonic mutations. Mutational profiles (TCGA data) of the Pakistani population with different populations revealed the PIK3CA gene mutation among all populations. In this study, the conservation for amino acid substitutions H1047R and H1047L will be identified which may suggest that this mutation plays a functional role in developing breast cancer in a diverse population range. Additionally, the role of germline and somatic variants on protein structure and interactions has been explored in detail. Through structure-based virtual screening, we identified inhibitors against target breast cancer protein mutations. Our proposed inhibitors may be used as therapeutic agents in cancer cells and will largely benefit the community in terms of cancer treatment within a short period. Collectively, this study suggests the somatic genetic changes and germline in breast cancer demonstrate the tumorigenesis is quite similar and very different. This area of research needs more care to explore the complete image of breast cancer in Pakistan.

Biography

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