Next-Generation Sequencing (NGS) based analysis of *BRCA1/2* genes in breast cancer patients in Georgia – a small population study

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Abbreviation

BRCA - Breast Cancer gene

CNA – Copy number alterations

CNVs – Copy number variations

DNA - Deoxyribonucleic acid

ER - Estrogen receptor

HER2 - Human epidermal growth factor receptor 2

IHC - Immunohistochemistry

NCDC – National Center for Disease Control

NGS - Next-Generation Sequencing

PR - Progesterone receptor

TN – Triple-negative

TP – Triple-positive

FFPE - Formalin-fixed paraffin-embedded (tissue)

Abstract

The growing number of breast cancer patients in Georgia indicates the need for implementing timely risk assessment practices. According to statistical data, which was collected in Georgia from 2015-to 2018 years by the National Center for Disease Control (NCDC), out of the total number of cancer cases, 17.4% belonged to breast cancer. Noteworthy, one of the clinically important genetic associated alterations is widely regarded to be loss-of-function mutations in *BRCA1/BRCA2* genes, small insertions/deletions, and/or copy number variation. Whereas, the most recent approach for their identification is next-generation sequencing (NGS) techniques.

The stated technology was also applied within the given study to detect *BRCA1/BRCA2* gene mutations. Within which DNA was extracted from the blood and FFPE of 110 breast cancer patients, who have been going through the treatment in three oncology clinics located in the capital city – Tbilisi. *BRCA1* and *BRCA2* gene exons were amplified using the Devyser BRCA kit and sequenced on the Illumina MiSeq platform.

The findings of the below study revealed that 9% of the study population were carriers of clinically significant mutations of *BRCA1/BRCA2*. Out of these patients, CNVs were detected in 90%. For all of the participants of the study total number of detected CNVs was 18(16%), out of which not all were clinically significant.

To our knowledge, these mutations have not been reported yet in the Georgian population. The use of the NGS technique increases the possibility of detecting mutational changes in patients with breast cancer. Furthermore, the findings of this paper bring additional benefits treatment-wise or for the screening purposes since the quick determination of pathogenic variants is important to facilitate specific therapy, in addition to the identification of familial predisposition to cancer.