FREQUENCY OF *BRCA1/2* AND OTHER GENE VARIATIONS IN PATIENTS WITH BREAST CANCER IN OUR CENTER

Erdal Fırat Çaralan[1,2], Serhat Seyhan[1], Akif Ayaz[1], Dilek Alpsar Budak[1], Zeynep Doğru[1,2], Abdullah Hüseyin Köseoğlu[1], Çağrı Çakıcı[2], Türkan Yiğitbaşı[1,2]

1-Istanbul Medipol University, Genetic Diagnosis Center
2-Istanbul Medipol University, Department Of Biochemistry

2nd International Cancer & Ion Channels Congress, Turkey on September 22-24, 2019

OBJECTIVES

One of the major risk factor of developing Hereditary Breast and Ovarian Cancer Syndrome (HBOC) is, occurance mutation in *BRCA1* and *BRCA2* genes. The risk for breast cancer in the general population is about 12%, but for women with a *BRCA1* gene variation it can be between 46%-87% and between 38%-84% for women with a *BRCA2* variation. The risk for ovarian cancer in the general population is about 1%-2%, but about 39%-63% with *BRCA1* gene variations and 16.5%-27% with *BRCA2* variations. In addition to *BRCA1* and *BRCA2*, other genes, such as *TP53*, *PTEN*, *CDH1*, *ATM*, *CHEK2* or *PALB2*, can play an important role of developing HBOC Syndrome.

Clinical/Date	Prediagnosis HBOC / From 1 January 2019 to 1 August 2019
Sample / Age	43 sample/ between 22 and 60
Target	23 gene, exon specific*
Sequencing	illumina MiSeq
Center	Istanbul Medipol University, Genetic Diagnosis Center (MEDIGEN), Turkey

***Gene List:** *ATM, BLM, BRCA1, BRCA2, BRIP1, CDH1, CHEK2, EPCAM, FANCC, MEN1, MLH1, MSH2, MSH6, MUTYH, NBN, PALB2, PMS2, PTEN, RAD51C, RAD51D, STK11, TP53, XRCC2.*

METHODS

MiSeq Output
(obtain FastQ file)

Aligment - hg19
(obtain SAM/BAM file)

Variant calling
(obtain vcf file)

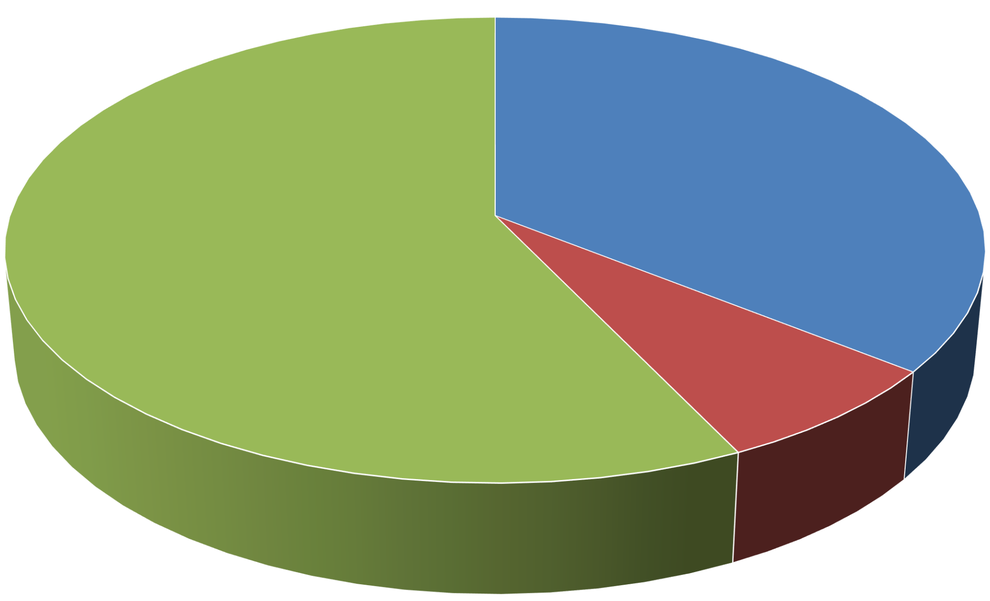
Variant annotation
(obtain annote vcf file)

Variant filter
(MAF < 0,01, Exclude benign)

Variant Classification
(ClinVar, HGMD, ACMG, ExAC, *in silico* tools, pedigree vb.)

RESULT

Distrubition of variants
(in MEDIGEN, totaly 14 variants)



Distributions of variants

Clinical significance	Variants
Pathogenic	5
Likely pathogenic	1
Uncertain significance	8

All *BRCA1* and *BRCA2* mutations were classified as pathogenic in 6 patients while other HBOC related gene variants classified as likely pathogenic in one patient and variant of uncertain significance (VUS) in 8 patients.

CONCLUSIONS

In conclusion, the possibility of variation in other genes should be kept in mind in addition to *BRCA1* and *BRCA2* genes in cases with HBOC. However, more data sharing and functional studies are needed to determine the pathogenicity of variants of unknown clinical significance.

REFERANCES

1- Hoang LN, Gilks BC. Hereditary Breast and Ovarian Cancer Syndrome: Moving Beyond BRCA1 and BRCA2. Adv Anat Pathol. 2018 Mar;25(2):85-95. doi: 10.1097/PAP.0000000000000177. Review. PubMed PMID: 28914618.

2- https://rarediseases.org/rare-diseases/hereditary-breast-ovarian-cancer-syndrome/