OP 06 - Genetic variants detected by comparative genomic hybridization in a cohort of BRCAX hereditary breast cancer patients in Sri Lanka

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Introduction: Breast cancer is one of the most common cancers among women in the world. However for a substantial fraction of women having family history of cancer, the genetic changes contributing, remains undetermined. These cases are grouped as a separated "*BRCAX*" category. The discovery of gene variants to explain this "missing heritability" is of clinical relevance. Hence this study was aimed at identifying the presence of genomic alterations that could explain the missing heritable risk of breast cancer in women with family history strongly suggestive of hereditary breast cancer in Sri Lanka.

Methods: A cohort of ten patients affected with breast cancer who tested negative for pathogenic variants in next generation sequencing studies was investigated using *Sure Print G3 Human CGH 4x180K* microarray platform. *Agilent Genomic-Workbench-v7.0.4.0* software was used to identify the Copy Number Variants (CNV). Four healthy individuals (>55years) were used as controls. Annotations of the CNV regions which were observed were done using the *database of Genomic Variants*.

Results: We identified 104 CNVs including regions of both genomic gains and losses in this cohort. CNVs were residing on the positions of 1p36.13, 2q37.3, 4q34.3, 6p12.3, 7q31.33, 7p14.1, 7p22.2, 8q24.23, 8p23.1, 12q15, 14q11.2, 15q11.1-q11.2 in genes that were assessed by the array platform used in the study. Several CNVs were identified in similar locations (4q13.2, 4q31.21, 8p23.1, 11q11) where Genome Wide Association Studies (GWAS) have previously been identified as having association for hereditary breast cancer predisposition.

Conclusion: This study shows that CNVs are likely contributors to the breast cancer predisposition in a small but significant proportion of patients affected with breast cancer in this cohort. Further studies have to perform to get a better understanding on the contribution of CNVs to the breast cancer predisposition in the Sri Lankan population.

Keywords: Comparative Genomic Hybridization, Copy Number Variants, Genome Wide Association Studies, hereditary breast cancer.

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