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BRCA1 and *BRCA2* Mutation Analysis in Breast Cancer Patients in Brunei Darussalam

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OBJECTIVE

This study investigates mutational analysis of *BRCA1* and *BRCA2* genes in breast cancer patients in Brunei Darussalam.

MATERIAL AND METHODS

Blood samples are taken from consented breast cancer patients from The Brunei Cancer Centre (TBCC) diagnosed from 2001 to 2015. Mutational analyses of *BRCA1* and *BRCA2* coding region are conducted using polymerase chain reaction (PCR) and Sanger dideoxy sequencing using forward and reverse primers on an 8 capillary 3500 Genetic Analyzer (Applied Biosystems). Variant Reporter Version 1.0 is used to perform variant analysis. Experiments are conducted twice as a validation method.

RESULTS

Preliminary analysis of thirty index cases shows the majority of breast cancer patients in Brunei Darussalam were Malays (n=23, 76.7%), Chinese (n=3, 10%) and others (n=4, 13.3%), reflecting the population. The mean age of diagnosis was 48.5±9.00 years. Ten index cases (33.3%) had family history of breast or ovarian or other cancers in first-degree relatives, and six (20%) had them in second-degree relatives. Ten deleterious insertion/deletion (indel) mutations in *BRCA2* gene were detected in ten different cases (0.33%). Various missense, synonymous and variants of unknown significance (VUS) were identified in all the cases. Nine of the indel mutations have not been validated yet.

CONCLUSIONS

Ten deleterious indel mutations in *BRCA2* were detected in ten breast cancer cases. Large rearrangement analysis and mutational analyses of *TP53* and *PALB2* genes would provide more comprehensive mutational findings in the studied index cases. Strong family history is an indicator for breast cancer risk.

Back to Table of Contents