**POSTER SYMPOSIUM – P10**

**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**