Parallel Session 2: Implementing Research Findings in Clinical Practice

T2c - Risk Assessment of Hereditary Breast and Ovarian Cancer Syndrome in Chinese Population by Multiple-gene Sequencing

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Differences in the mutation spectrum across ethnicities suggest that it is important to identify genes in addition to common high penetrant genes to estimate the associated breast cancer risk in Chinese. A total of 1,338 high-risk breast cancer patients who tested negative for germline BRCA1, BRCA2, TP53 and PTEN mutations between 2007-2017 were selected from the Hong Kong Hereditary Breast Cancer Family Registry. Patient samples were subjected to next-generation DNA sequencing using a multigene panel. All detected pathogenic variants were validated by bi-directional DNA sequencing. The sequencing data was co-analyzed by our in-house developed bioinformatics pipeline. Sixty-one pathogenic variants (4.6%) were identified in 11 cancer predisposition genes. The majority of the carriers (77.1%) had early-onset of breast cancer (age <45), 32.8% had family members with breast cancer and 11.5% had triple-negative breast cancer (TNBC). The most common mutated genes were PALB2 (1.4%), RAD51D (0.8%) and ATM (0.8%). A total of 612 variants of unknown significance (VUS) were identified in 494 patients, and 87.4% of the VUS were missense mutations. An additional 4.6% of the patients were identified in patients who tested negative for germline BRCA1, BRCA2, TP53 and PTEN mutations using the multigene test panel.

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