Abstract of Presentation

Note: This paper should be typed in "Times New Roman" of 12pt.

Presentation Title(Should be no more than 20 words):

High-resolution analysis of somatic alterations in the genome and transcriptome of breast cancer tumors from Mexican patients.

Abstract : Breast cancer is the leading cause of cancer related deaths among the Mexican female population and an increase in the incidence of the disease is expected in the following years. Specific patterns of genomic alterations related to particular clinical behaviors have been reported in breast cancer. However, these findings have been described in samples from mainly Caucasian origin, and there is very limited information about the prevalence of these alterations in tumors from Hispanic ancestry. We analyzed a set of 63 normal/tumor pairs obtained from Mexican breast cancer patients with the genome wide SNP 6.0 array to describe the patterns of DNA copy number aberrations. RNA from a subset of these same samples was analyzed with the human gene ST 1.0 expression array and with a taqman low-density array to evaluate the correlation between changes in messenger RNA and changes in the expression of 670 microRNAs. Immunohistochemical analysis was also performed in these samples to determine the expression of hormone receptors and HER2. Copy number analysis detected amplifications in chromosomes 1p, 8q, 11q, 15, 17 and 22. The use of a high-resolution array allowed the identification of genes in these amplicons whose role in breast cancer pathogenesis has not been explored. Correlation between DNA copy number and changes in gene expression also allowed the identification of genes with similar behavior of known breast cancer clinical targets. Micro RNA analysis identified over-epxression of mir21, mir155 and mir206, as well as down-regulation of mir125a, mir125b, mir10a and the let7 family. We also explored the influence in the detection of DNA copy number changes of using different populations as normal diploid differences, compared to the use of paired normal tissue from the same patient. Our analysis identified several genomic regions where population-dependent copy number changes were detected. Our results constitute one of the firsts high-resolution, genome-wide analysis of somatic alterations in breast tumors from Hispanic

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women, and has allowed the detection of novel genes whose role in breast cancer deserves further investigation.