Genetic Landscape of Breast Cancer in Southwestern Nigeria

Of all ethnic/racial groups, age-standardized mortality rate from breast cancer is highest for African American women in the US for reasons that remain understudied. To gain a better understanding of the genomic landscape of breast cancer in women of African ancestry, we developed a cross-continental translational research infrastructure to examine the spectrum of genetic alterations in breast tumors from West Africa compared to the spectrum of alterations observed in tumors from African-American and other women (predominantly Caucasian) in The Cancer Genome Atlas (TCGA) dataset.

Global Disparities in Breast Cancer

Median Age at Diagnosis:
- U.S.: 64 years old
- Sub-Saharan Africa: 45 years

Age-Adjusted 5-year survival:
- Developed Countries: 71%
- Developing Countries: 57%
- Sub-Saharan Africa: 12%

Studying the Genomic Landscape in Nigerian Breast Cancer Samples

- Peripheral blood and breast cancer tissue biopsies were collected from 214 patients enrolled in the West Africa Breast Cancer Study (WABCS) at the University College Hospital (UCH) and at Lagos State University Teaching Hospital (LASUTH).
- Blood DNA as well as breast cancer tissue DNA and RNA were extracted locally at the Nigerian sites using a modified protocol of PAXgene Tissue DNA and RNA extraction methods. IHC was performed to determine ER, PR and HER2 status.
- Samples were shipped to Novartis’ Next Generation Diagnostics (NGDx) group to perform whole exome (WES) and transcriptome (RNAseq) sequencing.
- Results were compared to the TCGA breast cancer data to identify both known and novel genomic events to uncover potential differences between African, African-American, and non-African-American breast cancer cases. The data presented here will focus on the initial WES data from 95 WABCS samples.

Conclusions and Future Directions

- Initial results show that TP53, MYC, and MCL1 are altered at significantly higher frequencies in both WABCS and African American breast cancer patients. However, ERBB2, GATA3 and AURKA alteration frequencies seem to be higher only in WABCS samples when compared to TCGA. PIK3CA, CDH1 and MAP3K1 are less frequently altered in the WABCS cohort.
- In triple negative samples, MDM4 is more frequently altered in both African American and WABCS patients when compared to other TCGA triple negative samples.
- Analysis of additional samples by WES and RNAseq will lead to a more complete understanding of the landscape of genetic alterations in breast cancer patients of African ancestry.