Real-World Data Explores New Gene Expression Profiles in Breast Cancer

BY SARAH LACORTE

Researchers at the SABCS 2020 Annual Meeting gave an update on the FLEX registry, a large-scale, population-based registry that links comprehensive clinical data with full genome expression data to elucidate new prognostic and predictive gene associations in a real-world setting (Poster OT-12-01).

“Gene expression profiles have enabled the classification of breast cancers into molecular subtypes with distinct clinical outcomes, which has significant implications for patient stratification and treatment strategy,” said Laura Lee, MD, a specialist in breast surgery, general surgery, and oncology surgery at the Comprehensive Cancer Center at Desert Regional Medical Center in Palm Springs.

“However, there are several challenges in implementing gene signatures into clinical practice. One of the challenges is excision of full genomic expression data that is annotated with comprehensive clinical data. This is the foundation of the FLEX study protocol.”

Study Details

According to the poster session presented as SABCS, the FLEX Registry (NCT03053193) is a multi-center, prospective, observational trial for patients with stage I-III breast cancer whose primary tumor is analyzed by MammaPrint, with or without BluePrint. The FLEX Registry uses a shared study infrastructure to develop and investigate hypotheses for targeted subset analyses and clinical trials based on full genome expression data.

“The FLEX registry is generating a large, real-world dataset which will enable discovery of novel genomic profiles that will improve personalized treatment for breast cancer.”

—Laura Lee, MD, at the Comprehensive Cancer Center at Desert Regional Medical Center

These sub-studies cover topics like identifying novel gene expression signatures associated with response to neoadjuvant therapy, optimization of therapeutic strategies, and refining the heterogeneity of breast cancer sub-groups,” Lee said.

“Enough data has already been collected to study patient subsets previously poorly represented in traditional clinical trials, including male breast cancer, metaplastic breast cancer, breast cancer in the elderly, and breast cancer in patients of African-American ancestry.

“The FLEX registry is generating a large, real-world dataset which will enable discovery of novel genomic profiles that will improve personalized treatment for breast cancer,” Lee concluded.

Sarah LaCorte is associate editor.