Cancer Genome Atlas Network. "Comprehensive molecular portraits of human breast cancer:ib, BRCA1, 50%; ERBB2, BRCA1, AKT1, 20%; IHC-EGFR, 10%; PIK3CA, cMET, 5%; TP53, 40%; ER, PR, AR, HER2 IHC results were similar in both age groups, BRCA2, 40%; 30%; PIK3CA, Jenkins IHC-RRM1, PIK3CA, ERBB2. The most frequently mutated genes were ERBB2, 5%; Triple Neg (n=149), and PIK3CA, 37%. Highest mutation rates were seen in PIK3CA (37%), carried mutations with frequencies ranging from 0.2% to 72%. Among 13 patients with ERBB2 mutation, 3 had it amplified. PD-1 expression on tumor cells was seen in 13% and PD-1 expression on tumor-infiltrating lymphocytes in 46%, with TNBC subtype showing the highest expression: 20% and 60%, respectively. In addition, TOP2A, TLE3, AR, TOPOA, SMRC were overexpressed in 61%, 58%, 55%, 51%, 37% of tumors, respectively, suggesting potential sensitivity to irinotecan, taxanes, anthracyclines and nab-paclitaxel. TS, RRM1 and ERCC1 were under-expressed in 65%, 60% and 53%, respectively, suggesting potential sensitivity to fluoropyrimidines, gemcitabine and platinum. A comparison with 7531 tumors from patients younger than 70, as well as description of abnormalities per molecular subtype of BC are presented.

Conclusion: Using multiple testing technologies, potentially targetable biomarker aberrations were identified in a large cohort of geriatric tumors. Our study provides key elements for the design of clinical trials focusing on geriatric patient population.

Results (updated to reflect female patients only)

Figure 1: Patient Characteristics

Figure 2: IHC and DH biomarker frequencies in the geriatric cohort. A and B show the IHC and DH markers in the complete geriatric cohort, while C shows selected IHC and DH markers in the subgroups.

Figure 3: Mutation rates in the geriatric cohort. A shows the genes with mutation rates <2% in the complete geriatric cohort, while B shows the Mutation rates in subgroups.

Figure 4: Comparison of the geriatric cohort with the younger cohort

Figure 5: Comparison of selected markers between geriatric and younger cohorts.

Figure 6: Comparison between geriatric (blue) and young (red) of selected markers by IHC or DH (upper panels) and sequencing (lower panels) in HR+ and HER2+ and Triple-negative cohorts. Stars indicate p<0.05 by Fisher-Exact test.

Conclusions

1. In this sample, the most frequently positive BC included ER, PR, AR, TOP2A, TLE3, BRC1, PTEN, P02/.
2. ER, PR, HER2 IHC results were similar in both age groups.
3. ER+ more often positive IHC in younger patients sampled.
4. AR+ more often positive in older patients in TNBC only. other subgroups had similar frequency results, regardless of age.
5. The most frequently mutated genes were PIK3CA and PTEN.
6. TOP2A was more frequently positive among younger patients; amplification is overall low in both age groups, and almost exclusive of HER2+ patients.
7. ERBB2 was mutated in 12 cases of geriatric breast cancer and in 38 cases among younger patients.
8. Only 1/69 geriatric TNBC samples (1%) had BRCA1 mutation, in comparison to 40/149 (27%) among younger patients with TNBC.
9. PD-L1 in tumor cells tested positive in 8% HR+, 20% HER2+ and 1% of TNBC geriatric patient samples.
10. TSLs were PD-1 positive in 39% HR, 44% HER2+ and in 60% of TNBC geriatric patient samples.

References