Staging for de novo Metastatic Breast Cancer:
Can genomic data make it better?

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Poster C6

Building Interdisciplinary Research Careers in Women's Health

BACKGROUND & METHODS

Background: A staging system was recently developed for *de novo* metastatic breast cancer (dnMBC) that stratifies patients into subgroups (IVA, IVB, IVC, IVD) based on overall survival (OS) and select disease characteristics.

Objective: To evaluate if somatic mutations are associated with prognosis in these subgroups.

Methods: Patients (N=92) with dnMBC and genomic test results from one academic institution were assigned to subgroups based on published criteria defined by T-category, grade, ER, PR, HER2, histology, site of metastases, and number of organs involved). Subgroup's unadjusted OS (estimated by Kaplan-Meier) were compared (log-rank tests). The association of genomic mutations with adjusted OS was estimated using Cox Proportional hazards models.

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RESULTS

Table 1. Patient characteristics

Overall Cohort, N=92	N (%), or specified
Age (Years) – Median (IQR)	52 (43.5 - 61)
Race/Ethnicity	
Non-Hispanic White	58 (63%)
Non-Hispanic Black	23 (25%)
Hispanic	0 (0%)
Other	4 (4.3%)
Gender	
Female	90 (97.8%)
Male	1 (1.1%)
Bone Only Metastasis	18 (19.6%)
Brain Only Metastasis	0 (0%)
Visceral Metastasis	53 (57.6%)
# Metastatic Sites	
1	54 (58.7%)
2	24 (26.1%)
3	12 (13%)
4+	2 (2.2%)
Grade	
1	3 (3.3%)
2	31 (33.7%)
3	39 (42.4%)
Subtype	
HR+/HER2+	12 (13%)
HR+/HER2-	48 (52.2%)
HR-/HER2+	6 (6.5%)
HR-/HER2-	18 (19.6%)
Clinical T-Stage	
T0	0 (0%)
T1	15 (16.3%)
T2	19 (20.7%)
T3	18 (19.6%)
T4	4 (4.3%)
Clinical N-Stage	
N0	13 (14.1%)
N1	28 (30.4%)
N2	4 (4.3%)
N3	6 (6.5%)
Metastatic Stage	
A	7 (7.6%)
B	40 (43.5%)
C	28 (30.4%)
D	17 (18.5%)
Histology	
Ductal	68 (73.9%)
Lobular	2 (2.2%)
Other	22 (23.9%)

Figure 1. OS stratified by stage group (A/B/C/D)

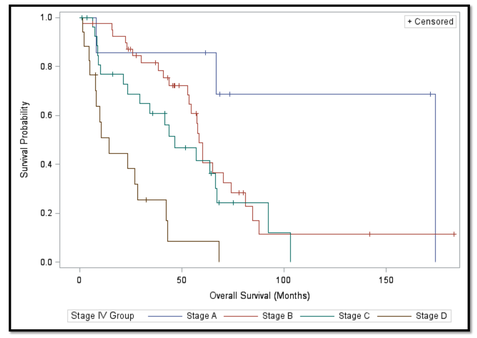

Table 2. Most common genes with somatic mutations

Overall Cohort N=92	N (%)
TP53	57 (62%)
PIK3CA	28 (30.4%)
ESR1	23 (25%)
CCND1	23 (25%)
MYC	20 (21.7%)
FGFR1	20 (21.7%)
FGF19	17 (18.5%)
FGF3	17 (18.5%)
FGF4	17 (18.5%)
ZNF703	13 (14.1%)

Table 3. Adjusted OS with gene, age, race, treatments, and stage

	Hazard Ratio (95% CI)	P-Value	Overall P-Value
TP53 Mutation	1.52 (0.7-3.27)	0.29	0.29
Stage Group			0.04
A	REF		
B	2.08 (0.45-9.68)	0.35	
C	3.36 (0.7-16.09)	0.13	
D	10.04 (1.54-65.42)	0.02	

DATA HIGHLIGHTS

- Median age 52, median follow-up 75.3 months
- 90.2% received chemotherapy (n=83)
- Assigned stage-subgroups
  - 7.6% IVA (n=7)
  - 43.5% IVB (n=40)
  - 30.4% IVC (n=28)
  - 18.5% IVD (n=17)
- Most common genes with mutations
  - *TP53* (62%, n=57), *PIK3CA* (30.4%, n=28), *ESR1* (25%, n=23), *CCND1* (25%, n=23), *MYC* (21.7%, n=20), *FGFR1* (21.7%, n=20).
- After adjusting for subgroup, demographics, and treatments, none of these mutations were individually associated with OS (all p>0.05).

CONCLUSION

Our findings suggest that adding the somatic mutation status of the most commonly mutated genes in patients with dnMBC may not improve the prognostic estimates beyond already identified variables, including those related to extent of disease and tumor biomarkers.

This work was in part supported by Duke Cancer Institute through NIH grant P30CA014236 (PI: Kastan) for the Biostatistics Core, and Dr. Plichta is supported in part through NIH grant *K12AR084231* (PI: Amundsen).