

Health Inequities related to biological and social determinants of health: An Update from SABCS

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DISCLOSURES

VMO- Oncology
T-Bio

Case Presentation

60-year AA female, *BRCA 2* mutation carrier, with a history of right breast cancer. She developed contralateral breast cancer while on AET

SOCIAL DETERMINANTS

- SDOH
- Food, financial, housing insecurities and other domains
- Delays in screening, advanced disease at diagnosis
- Treatment delays
- Treatment denials
- Survivorship issues

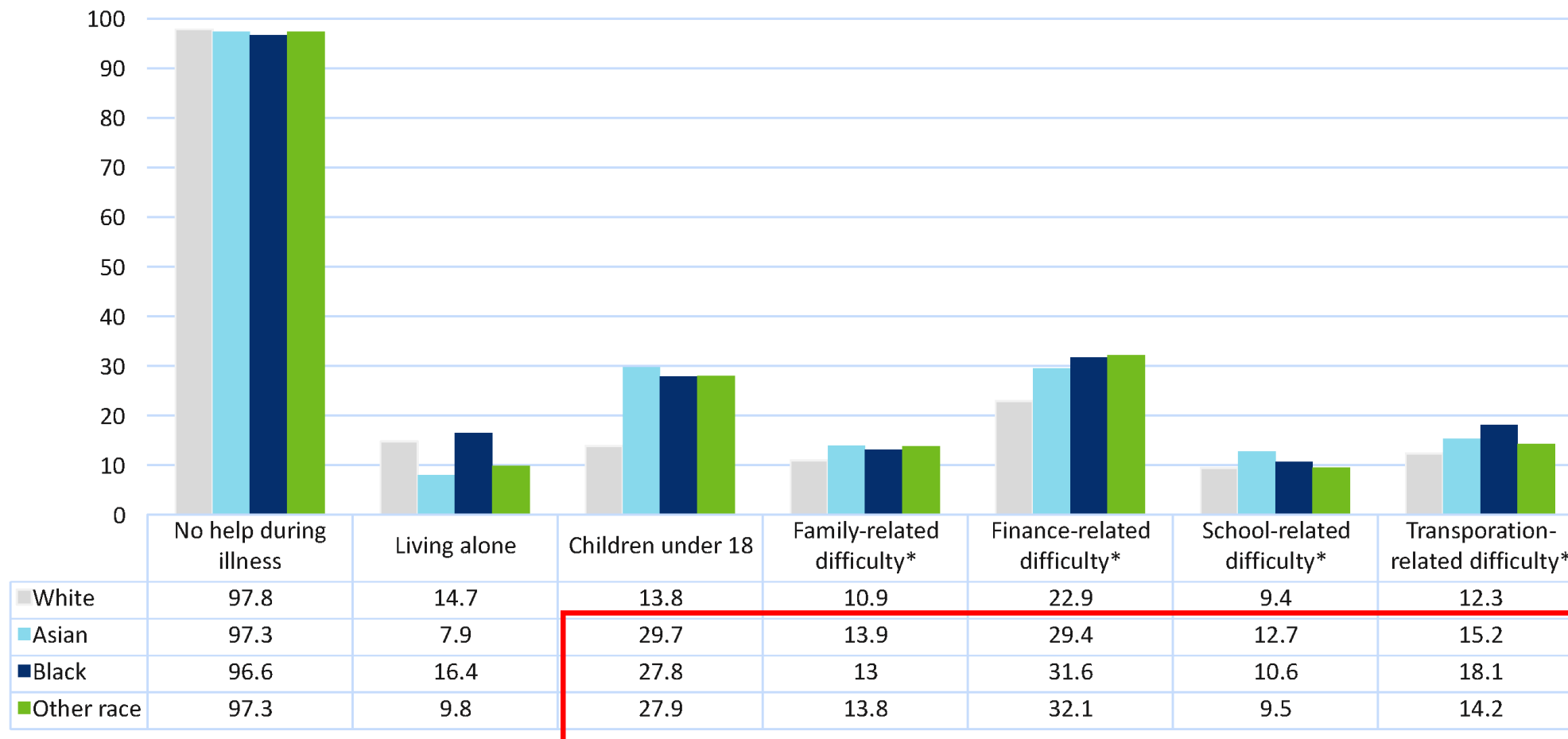
BIOLOGICAL DETERMINANTS

- Biology
- Aggressive biologies
- Tumor heterogeneity
- Germline vs. somatic alterations

Geographic area 53206, limited access to transportation, lives alone, morbidly obese

Prevalence of SDOH-Related Issues Stratified by Race

among 30,271 Cancer Registry patients who presented at Moffitt in 2008-2016



*Data related to item-specific difficulties were only available in EPQ versions 2 and 3 for patients who visit MCC between Jul 2008 and Aug 2016 (~27% of the total population).

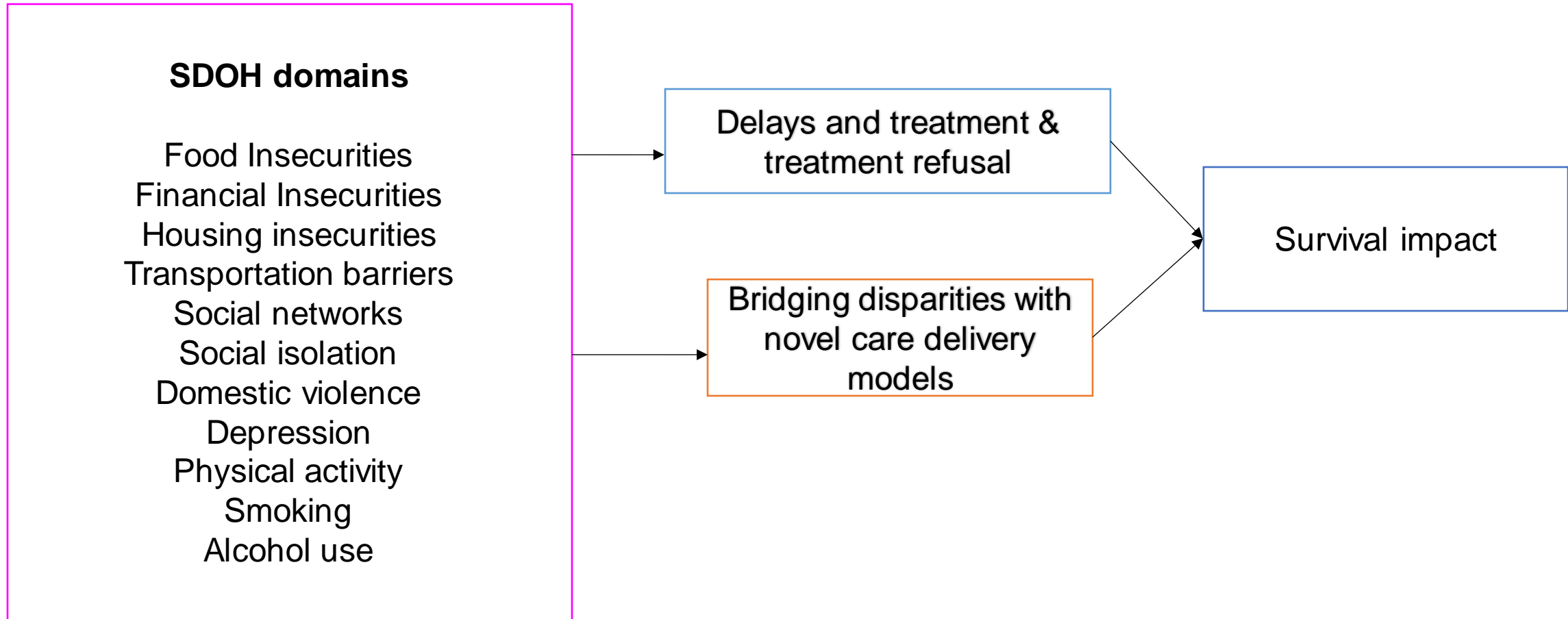


“The clinical care we provide only accounts for about 50% of the health factors that ultimately determine our health outcomes, the other 50% are determined by social determinants of health”

~ Margie Andreae, MD, Michigan Medicine’s chief medical officer of billing compliance

Vadaparampil S et al. SABCS, Tuesday [Special Session], 2023

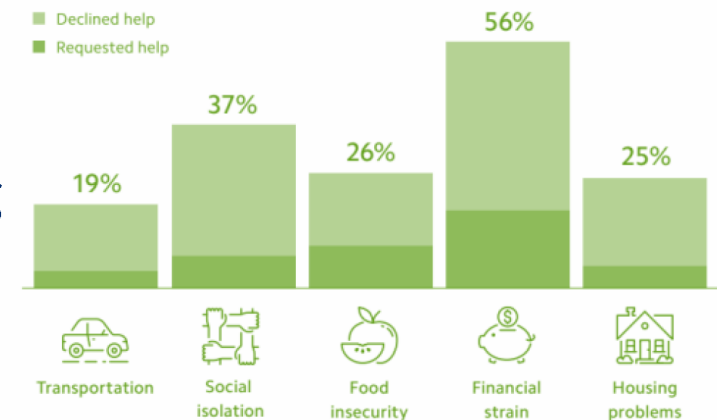
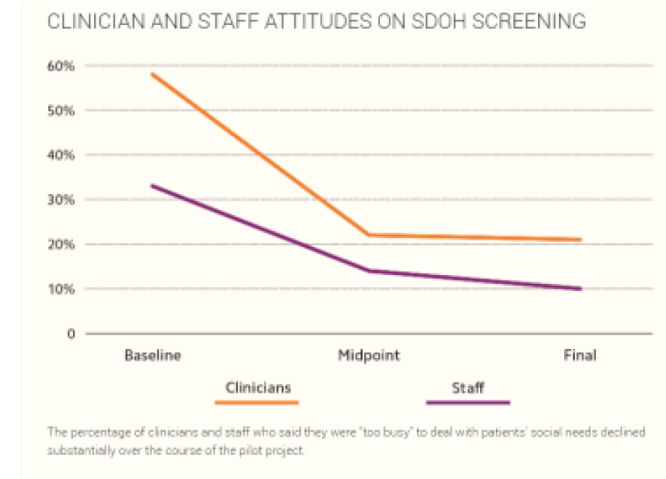
Time to Treatment Matters



Moving from Assessing to Addressing SDOH



- Leadership buy-in is essential
- Assessing clinician and staff barriers
 - Many find it overwhelming
 - Sharing clinic-wide progress can help increase staff engagement
- Identifying resources and referral systems ahead of time
- Navigators and Community Health Workers play a valuable role in screening and referral
- Not all patients who report social needs request help, but providing assistance to those who do, can change patient outcomes





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The Association between Food Deserts, Food Swamps, and Postmenopausal Breast Cancer Mortality in the United States

Malcolm S. Bevel, PhD, MSPH; Meng-Han Tsai, PhD, MPH; April Parham, BS; Sydney E. Andrzejak, MS; Samantha R. Jones, PhD; Justin Xavier Moore, PhD, MPH
Georgia Cancer Center, Augusta University, Augusta, GA
Center for Healthy Equity Transformation, Markey Cancer Center, University of Kentucky College of Medicine

Disclosure Information

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Hypothesis, Objectives and Methods

- Residing in geographical areas with no access to healthy foods (food deserts) or increased unhealthy food options (food swamps) reduces access to healthy foods and has been severely understudied regarding postmenopausal breast cancer (BRCA) mortality.
- Objective: examine the association between residing in food swamps and deserts with postmenopausal BRCA mortality.
- Methods:
 - Cross-sectional/Ecological analysis
 - 2010 – 2020 Center for Disease Control and Prevention Wonder (postmenopausal BRCA mortality data); aggregated 2012 – 2020 data from the U.S. Department of Agriculture Food Environment Atlas
 - Multilevel generalized mixed effects models

Results

- Among U.S. counties with high postmenopausal BRCA mortality rates:
 - Higher percentage of NH-black population (5.81% vs. 2.08%), poverty rates (17.2% vs. 14.2%), adult obesity rates (32.5% vs. 32.0%), and adult diabetes rates (11.8% vs. 10.5%) (p-value < 0.001).
- Among U.S. counties:
 - Age-adjusted odds of counties having high postmenopausal BrCa mortality was 53% higher among counties with high food desert scores (AOR = 1.53; 95% CI = 1.26 – 1.88) and over 2-fold times higher among high food swamp scores (AOR =2.09; 95% CI =1.69 – 2.58).
 - In fully adjusted models, the odds of counties having moderate postmenopausal BRCA mortality rates was 32% higher among counties with moderate food swamp scores (AOR = 1.32; 95% CI = 1.03 – 1.70).

Conclusions/Implications/Next Steps

- U.S. counties or county equivalents with poorer food swamp environments had a significantly greater odds of postmenopausal breast cancer mortality.
- Growing epidemic of food swamps could be due to systemic issues (e.g. gentrification/redlining, lack of true investment with chain grocery stores)
- Implement culturally tailored, sustainable community-garden based interventions for obesity and obesity-related cancer prevention including postmenopausal BRCA among underserved populations.



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Refusal of Recommended Cancer Treatments and Overall Survival Differences in Breast Cancer Patients: Analysis of the National Cancer Database

Jincong (Jason) Freeman, MPH, MS¹; James Li, BS^{1,2}; Susan Fisher, MS, PhD³; Katharine Yao, MD³; Sean David, MD, SM, DPhil^{2,3}; Dezheng Huo, MD, PhD^{1,4}

¹ The University of Chicago Department of Public Health Sciences, ² The University of Chicago Pritzker School of Medicine; ³ NorthShore University HealthSystem; ⁴ The University of Chicago Center for Clinical Cancer Genetics and Global Health

Disclosure Information: I have no financial relationships to disclose.

Acknowledgements: This study was supported in part by the Breast Cancer Research Foundation (BCRF-20-071), Susan G. Komen® (TREN21675016), and the NIH/NIA under grant award T32 AG000243 (PI: David Meltzer, MD, PhD). Its contents are solely the responsibility of the authors and do not necessarily represent the official views of the NIH/NIA.

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Objectives and Methods

Objectives

- ❑ To assess the prevalence of treatment refusals and correlated factors in breast cancer patients (pts).
- ❑ To examine the association between treatment refusal status and overall survival (OS) in breast cancer pts.

Methods

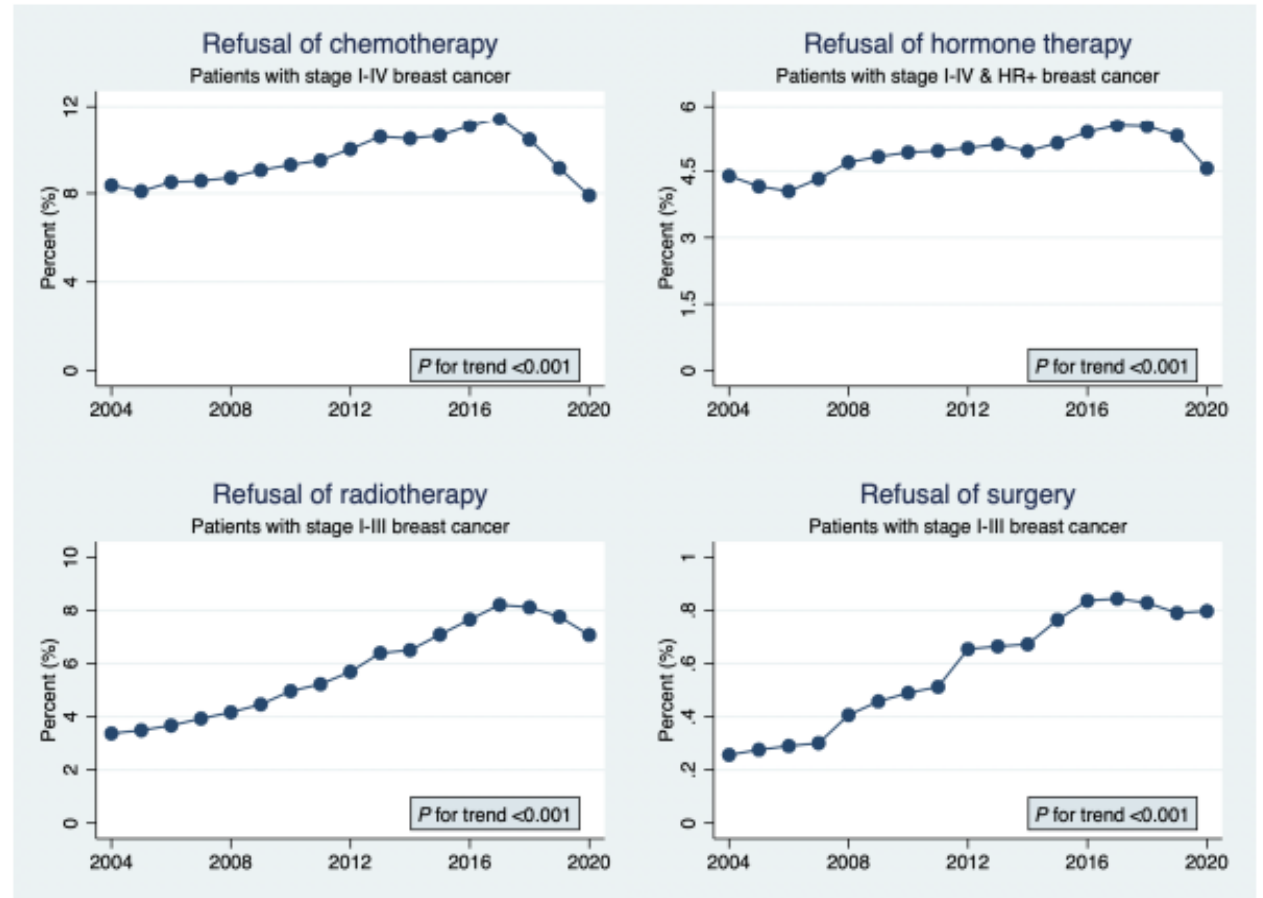
- ❑ Data were from the 2004-2020 National Cancer Database (NCDB).
- ❑ Four cancer treatment modalities were assessed:
 - ❑ **Chemotherapy (CT)**: included **stage I-IV** pts.
 - ❑ **Hormone therapy (HT)**: included **stage I-IV, HR+** pts.
 - ❑ **Radiotherapy (RT)**: limited to only **stage I-III** pts.
 - ❑ **Surgery**: limited to only **stage I-III** pts.
- ❑ Refusal status was categorized as "administered/refused" and modeled using multivariable logistic regression.
- ❑ The association between treatment refusal status and OS was examined using the log-rank test, followed by multivariable Cox proportional hazards regression.

Results

Overall Prevalence of Treatment Refusals

- ❑ In the CT cohort, 9.6% of 1,296,488 pts who were offered the treatment refused.
- ❑ In the RT cohort, 6.1% of 1,635,916 pts refused.
- ❑ In the HT cohort, 5.0% of 1,893,339 pts refused.
- ❑ In the surgery cohort, 0.6% of 2,590,963 pts refused.

Figure. Trends in Treatment Refusals, 2004-2020



Results, cont'd

Conclusions

Table. Differential OS by Treatment Refusal Status

	crude HR (95% CI)	adjusted HR (95% CI)
CT		
Administered	1.0 (ref.)	1.0 (ref.)
Refused	1.81 (1.79-1.83)	1.86 (1.83-1.90)^a
HT		
Administered	1.0 (ref.)	1.0 (ref.)
Refused	1.68 (1.66-1.70)	1.56 (1.53-1.59)^b
RT		
Administered	1.0 (ref.)	1.0 (ref.)
Refused	2.93 (2.89-2.96)	1.97 (1.93-2.01)^a
Surgery		
Administered	1.0 (ref.)	1.0 (ref.)
Refused	6.80 (6.65-6.96)	2.91 (2.82-3.01)^a

^a Adjusted for age, race/ethnicity, health insurance, median household income, type of cancer program, Charlson-Deyo comorbidity score, histology, AJCC stage, molecular subtype, tumor grade, and year of diagnosis.
^b Adjusted for age, race/ethnicity, health insurance, median household income, type of cancer program, Charlson-Deyo comorbidity score, histology, AJCC stage, HER2 status, tumor grade, and year of diagnosis.

- At the national level, the rate of treatment refusal was highest for CT and lowest for surgery, and there were significantly increased trends in treatment refusals from 2004 to 2020.
- Age, race/ethnicity, socioeconomic/care access indicators, AJCC stage, molecular subtype, and tumor grade were independently associated with treatment refusals, suggesting that differential refusals not only are affected by biological factors but also may reflect disparities in socioeconomic status.
- Furthermore, pts who refused treatment experienced worse OS, regardless of treatment modality.
- These findings suggest that stressing the importance of recommended treatment and interventions tailored for this patient population may be needed to improve their survival outcomes.

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Bridging Disparities in Survivorship Care: Leveraging Telehealth for Diverse Patients in Safety Net Hospital

Ivan Leung, MS

University of California, San Francisco

Zuckerberg San Francisco General Hospital

San Francisco, CA

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Background and Methods

- 67-88% of the 3.8 million breast cancer survivors report unmet needs in survivorship care
- Disparity exacerbated during COVID-19 pandemic
- Single-arm, pilot intervention trial of telehealth Group Medical Visits
 - Six cohorts (2 English, 2 Spanish, 2 Cantonese)
 - Four weekly, 2-hour-long sessions
 - Team-based approach (MD, RN, navigators, guest speakers)

Results

- 53 women with stage I-III breast cancer

	Total	English	Spanish	Cantonese
Participants	53	15 (28%)	18 (34%)	20 (38%)
Median Age	58	54	52	62.5
Foreign-born	43 (81%)	5 (33%)	18 (100%)	20 (100%)
Attendance	98%	97%	97%	100%

	Yes/Agree/Agree Strongly	No/Disagree/Disagree Strongly
Telehealth Format is acceptable	53 (100%)	0 (23%)
It was easy for me to login and stay connected	47 (89%)	3 (22%)
Telehealth group sessions are good use of my time	53 (100%)	0 (0%)

Lessons Learned & Next Steps

- Telehealth Group Visits are acceptable in a safety net setting in providing survivorship care
- Effective in bridging unmet survivorship care needs
- Fear of cancer recurrence is the biggest concern for patients

- Billing and financial sustainability
- Qualitative interview analysis
- Utilizing GMV for purposes (transitional from oncology to PCP, reducing oncology visits, etc.)



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Poster Spotlight Session 18: Disparate Care Calls for Desperate Measures: Understanding Gaps in Quality of Care and Opportunities to Improve it

- ctDNA genomic profiles
- Obesity/ Mammaprint
- Duffy-null and AA ancestry influence in the TNBC

Friday, December 8, 2023, 7:00 AM – 8:00 AM CT Location: Stars at Night Ballroom 1-2 CE: 1

Differences in ctDNA genomic profiles and outcomes in Black and White patients with metastatic breast cancer: results from a large multicenter consortium

Presenter: Emily L. Podany¹

Emily L. Podany¹, Lorenzo Foffano², Lorenzo Gerratana², Arielle J. Medford³, Katherine Clifton¹, Whitney L. Hensing⁴, Renee Morecroft¹, Marko Velimirovic⁵, Ami N. Shah⁶, Carolina Reduzzi⁷, Laura Munoz Arcos⁷, Charles S. Dai³, Jennifer Keenan³, Elyssa N. Denault³, Foluso O. Ademuyiwa¹, Fabio Puglisi², Cynthia X. Ma¹, Aditya Bardia³, Massimo Cristofanilli⁷, Andrew A. Davis¹

¹Washington University in St. Louis, St. Louis MO ²University of Udine, Udine, Italy ³Massachusetts General Hospital Cancer Center, Boston, MA ⁴Saint Luke's Hospital, Kansas City, MO ⁵Cleveland Clinic, Cleveland, OH ⁶Robert H. Lurie Comprehensive Cancer Center of Northwestern University, Chicago, IL ⁷Weill Cornell Medicine, New York, NY

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Hypothesis and Methods

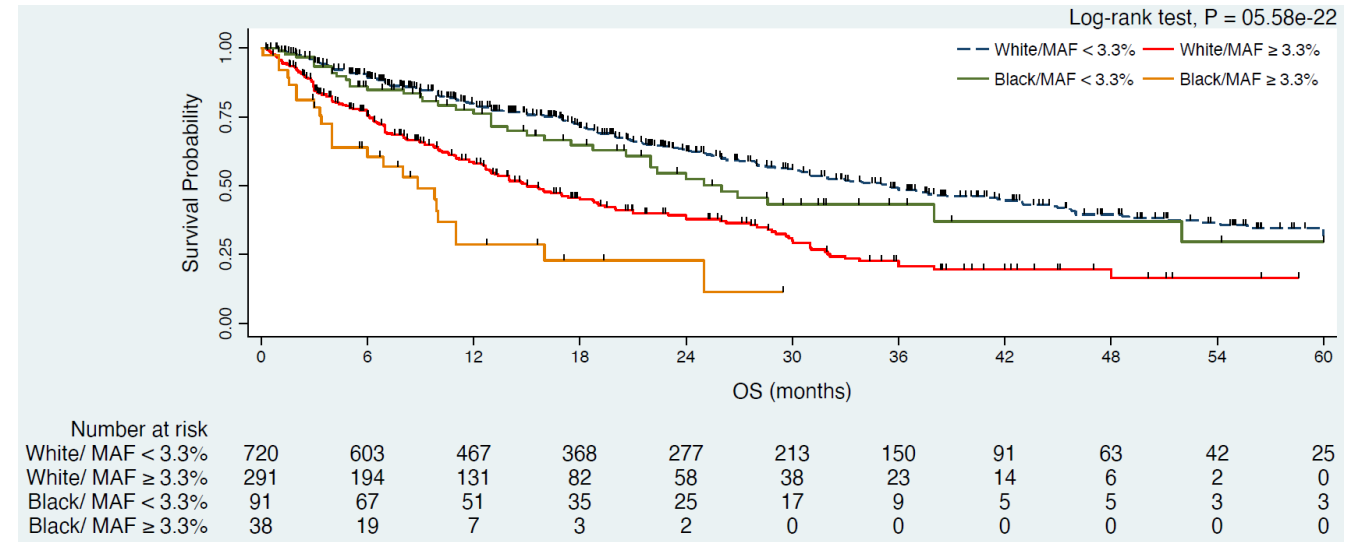
- **Hypothesis:** There may be racial differences in genetic profiles in metastatic breast cancer patients. These may impact treatment response and clinical outcomes.
- **Methods:**
 - Retrospective cohort study
 - 1327 patients treated at Washington University in St. Louis (n=474), Massachusetts General Hospital (n=412), and Northwestern University (n=441), all with ctDNA profiling from Guardant360. **Race was patient-reported.**
 - Univariate and multivariate analyses to evaluate single gene mutations and genetic pathways in both entire cohort and hormone-receptor positive, HER2 negative population
 - Prognostic impact evaluated through multivariate analysis in both White and Black patient populations

	<u>Number</u>	<u>Percentage</u>
<u>Race</u>		
White	1061	80.02%
Black	135	10.18%
<u>Histologic subtype</u>		
IDC	891	81.22%
ILC	152	13.86%
Other	54	4.92%
<u>HR status</u>		
Positive	1043	78.48%
<u>HER2 status</u>		
Positive	180	13.87%
Negative	1118	86.13%
<u>Metastatic disease sites</u>		
Lung	388	29.19%
Liver	468	35.21%
Bone	888	66.82%
Soft tissue	252	18.96%
CNS	107	8.13%
<u>Prior treatments</u>		
Chemotherapy	431	43.84%
Endocrine therapy	596	60.64%
CDK4/6i	401	40.79%
mTORi	128	13.02%
PI3Ki	43	4.37%
Immunotherapy	34	3.50%

Results

- Black patients had significantly higher rates of **GATA3 snv** and **CCND2 cnv**

Gene associations	Odds ratio	95% confidence interval	p-value
Black patients in overall population			
GATA3 snv	2.02	1.07-3.81	0.031
CCND2 cnv	3.42	1.39-8.43	0.008
Black patients in HR+/HER2- population			
GATA3 snv	2.04	1.02-4.08	0.042
PDGFRA cnv	3.95	1.33-11.72	0.013
CCND1 cnv	1.71	0.90-3.26	0.099
Prognostic associations	Hazard ratio	95% confidence interval	p-value
White patients in HR+/HER2- population			
Liver metastases	1.79	1.40-2.28	<0.001
Soft tissue metastases	1.63	1.19-2.23	0.002
CNS metastases	2.14	1.33-3.45	0.002
ESR1 snv	1.42	1.09-1.85	0.01
TP53 snv	1.53	1.20-1.94	0.001
NF1 snv	1.9	1.06-3.41	0.031
CCND1 cnv	1.54	1.03-2.30	0.037
MYC cnv	2.04	1.30-3.20	0.002
Black patients in HR+/HER2- population			
Liver metastases	3.9	2.02-7.54	<0.001
PI3Ksnvpathway	2.19	1.14-4.21	0.018



- Overall survival from time of ctDNA testing was significantly lower in Black patients after adjusting for other variables.
- Patients with higher mean allelic frequency had a worse prognosis regardless of race, though Black patients with MAF ≥ 3.3% had the poorest prognosis
- There was no difference in MAF between White and Black patients

Discussion and implications

- To our knowledge, this is the largest clinical genomic dataset examining ctDNA differences across Black and White patients
- GATA3 and CCND2 are not targetable by current treatments
- We will need to focus on both socioeconomic and genetic factors to explain shorter overall survival and early separation of the curves in Black patients
- We are working with Guardant Health to validate our findings in a large clinical genomic real-world dataset

Racial Disparities in Breast Cancer and Effect of Obesity: MammaPrint[®], BluePrint[®] and Whole Transcriptome Analyses of Tumors in Latin American Patients in the FLEX Trial

Marcela Mazo Canola¹,

Virginia Kaklamani¹, Pooja P. Advani², Sailaja Kamaraju³, Alfredo A. Santillan-Gomez⁴, Robert Maganini⁵, Julie L. Barone⁶, Sahra Uygun⁷, Lavanya Samraj⁷, William Audeh⁷, Joyce O'Shaughnessy⁸, FLEX Investigators Group

¹UT Health San Antonio, Mays MD Anderson Cancer Center, TX; ²Mayo Clinic, Jacksonville, FL; ³Medical College of Wisconsin, Milwaukee, WI; ⁴Texas Oncology Medical Center, San Antonio, TX; ⁵Ascension, Bartlett, IL; ⁶Vail Health, Vail, CO; ⁷Agendia Inc., Irvine, CA; ⁸Baylor University Medical Center, Texas Oncology and The US Oncology Network, Dallas, TX

Disclosure Information

This study is in collaboration with Agendia Inc.

Speaker: Gilead, Seagen and Menarini

Consulting: Lilly

Objectives

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- Latin Americans (LA) are more likely to be diagnosed with aggressive early-stage breast cancer compared to Non-Hispanic White (NHW) in the US¹.
- Studying genomic and transcriptomic differences between patient groups help understand disease biology and help tailor their treatment options.
- We compared clinically matched tumors from LA and NHW breast cancer patients enrolled in FLEX.
- FLEX (NCT03053193) is a prospective, observational trial including stage I-III breast cancer patients who receive MammaPrint (with or without Blueprint).

Matched tumors from Latin American and White patients

	LA	NHW	p-value
Diabetic status			
Type 2	68 (23.3%)	24 (8.5%)	< 0.001
Type 1	1 (0.3%)	3 (1.1%)	
Pre-diabetes	0 (0.0%)	1 (0.4%)	
No diabetes	223 (76.4%)	253 (90.0%)	
BMI category			
Obese	148 (49.0%)	119 (39.4%)	< 0.001
Overweight	106 (35.1%)	91 (30.1%)	
Normal	43 (14.2%)	85 (28.1%)	
Underweight	5 (1.7%)	7 (2.3%)	
BluePrint			
Luminal A (MP* Low)	141 (45.3%)	152 (48.9%)	0.190
Luminal B (MP High)	114 (36.7%)	122 (39.2%)	
Basal**	46 (14.8%)	29 (9.3%)	
HER2	10 (3.2%)	8 (2.6%)	
ImPrint HR+			
ImPrint+	30 (12.0%)	13 (5.1%)	0.005
ImPrint-	219 (88.0%)	242 (94.9%)	

Matching was done by age, T-stage, N-stage and hormone status

* MP: MammaPrint **Two-proportions z-test in Basal group, p-value = 0.049

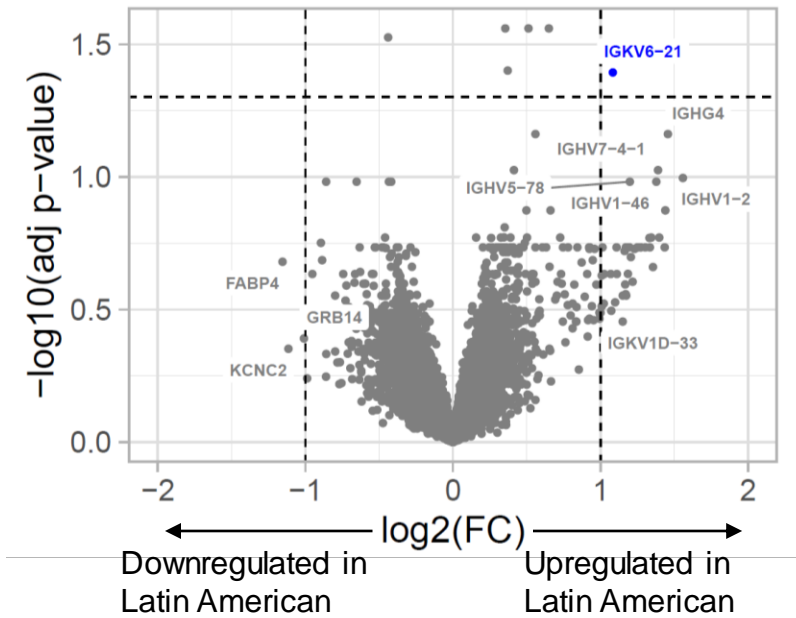
Results

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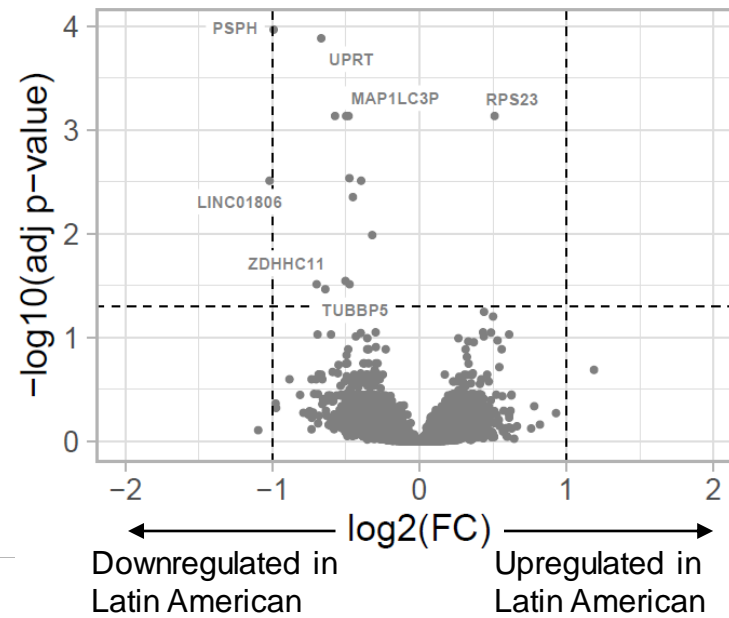
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Whole transcriptome comparison

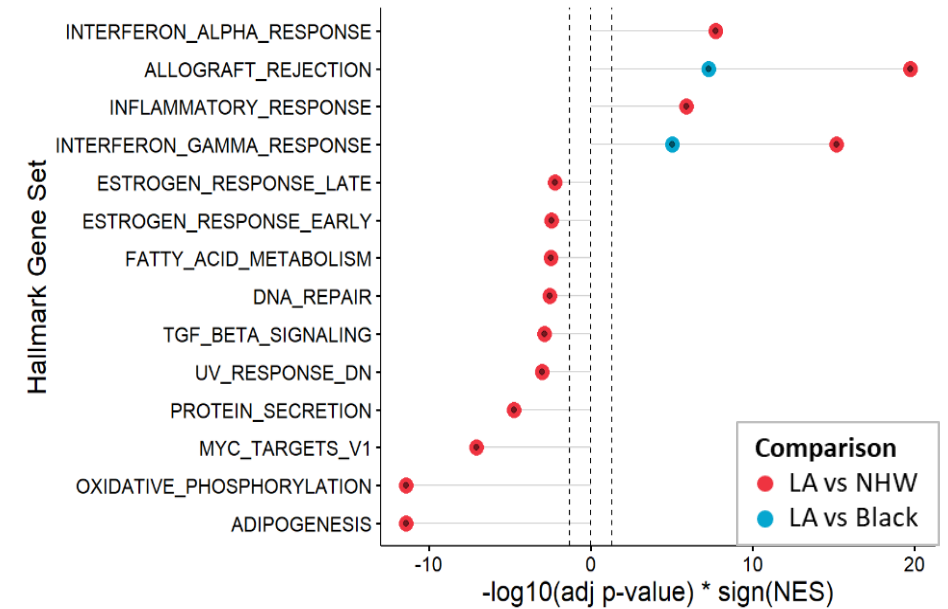
Luminal B obese LA vs NHW



Luminal B obese LA vs Black



Gene Set Enrichment Analysis



Gene expression differences between LA and NHW are associated with increased immune and inflammatory pathways in LA

Conclusions

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- When matched for age and tumor characteristics, LA patients had higher percentages of the following compared to NHW patients:
 - Type 2 diabetes (23.3% vs 8.5%)
 - BMI obese (49.0% vs 39.4%)
 - BluePrint Basal (14.8% vs 9.3%)
 - ImPrint positive in the HR+ subgroup (12.0% vs 5.1%)
- Transcriptomic differences between tumors from Luminal B obese LA and NHW showed immune response differences that may contribute to the aggressive tumor biology.
- Obesity seems to affect LA and Black breast cancer biology differently than NHW patients. Immune system differences derived from genetic ancestry may be involved.

This study shows the importance of including diverse patients in real world evidence cohorts such as FLEX to help reduce racial disparities in breast cancer outcome.



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The DARC side of Breast Cancer – DARC, Duffy-null and African ancestry influence in the Triple Negative Breast Cancer tumor microenvironment

Rachel Martini, PhD*, Stevens Patino, Emma Guyonnet, Brian Stonaker, Isra Elhussein, Julie Sahler, Avery August, Nancy Manley, Rick Kittles, Clayton Yates, Lisa Newman, Melissa Davis

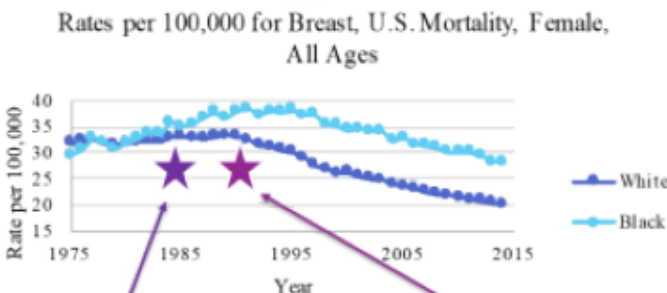
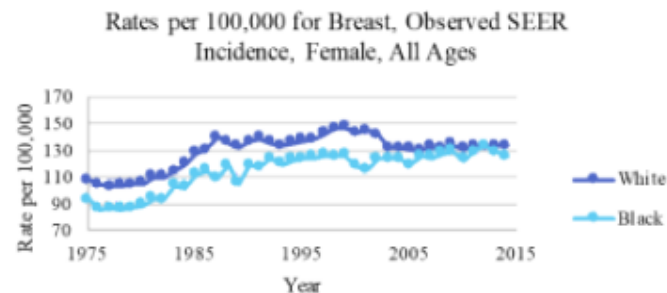
Morehouse School of Medicine, Atlanta, GA

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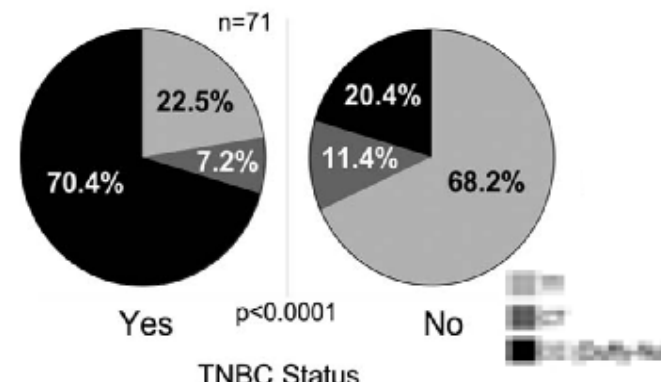
TNBC, African ancestry and the Duffy-null allele

Breast Cancer mortality remains 40% higher among African American women



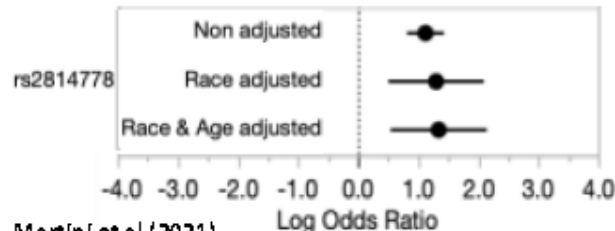
First Endocrine Targeted Trial (1985) | Targeted Therapy is Standard of Care (1995)

Duffy-null is a risk allele for a TNBC diagnosis



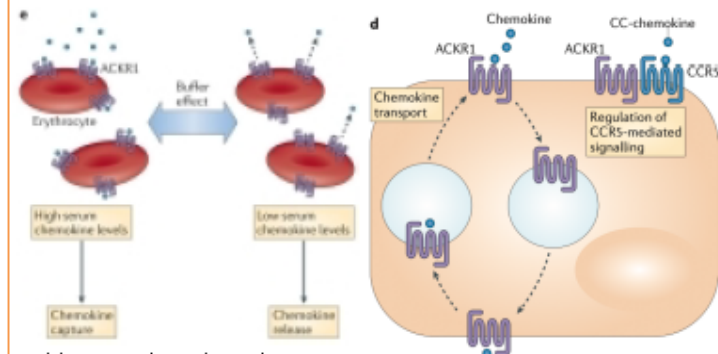
Newman et al (2019)

TNBC Case Series



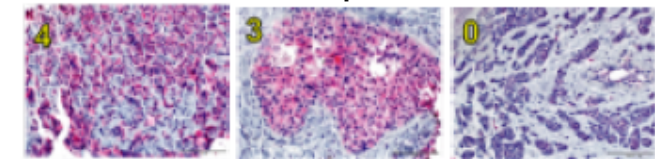
Martini et al (2021)

DARC/ACKR1 modulates chemokine levels in circulation and in tissues through expression on red blood cells and endothelial cells



Nihs & Graham (2013)

DARC/ACKR1 is expressed on breast tumor epithelial cells



Jenkins et al (2019)

What is the role of DARC in the triple negative breast tumor microenvironment?

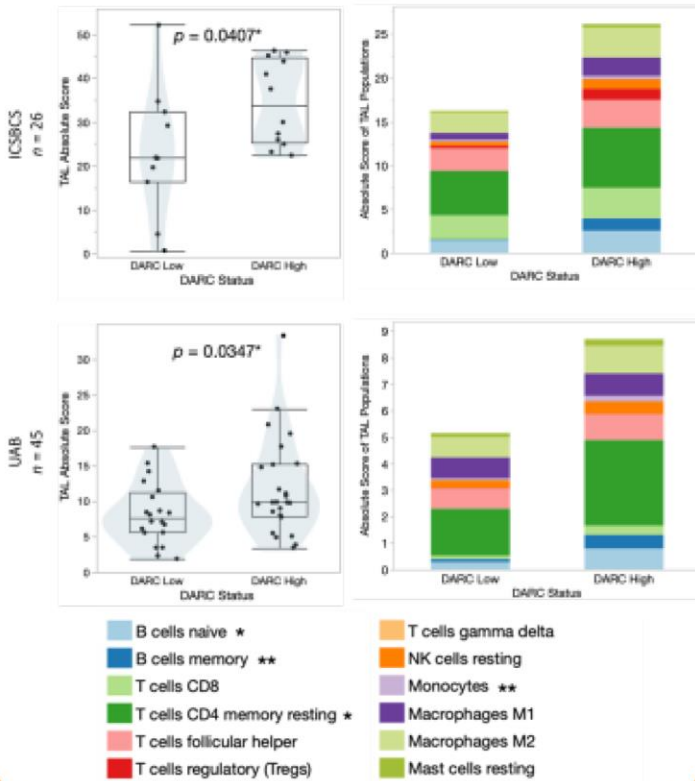
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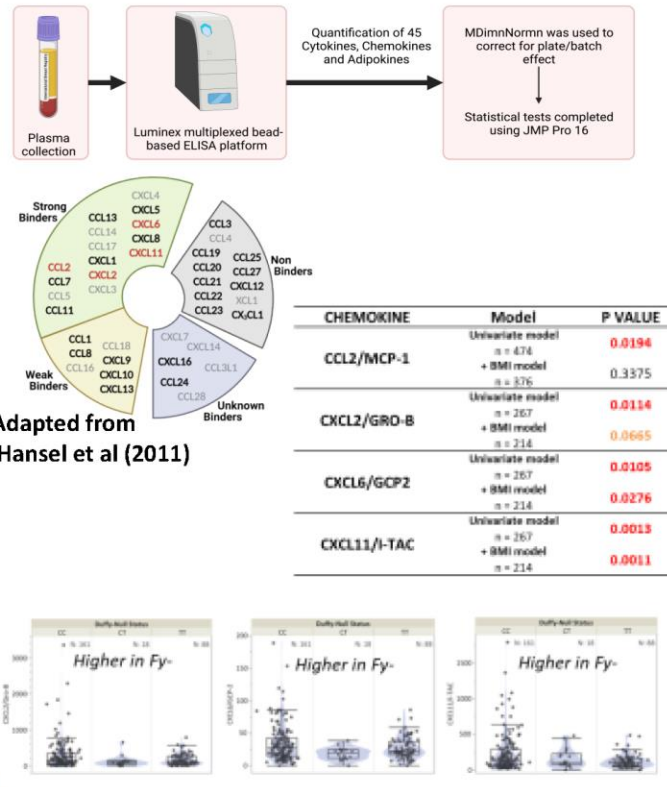
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Multi-omics approach to characterize influence of DARC in the TNBC tumor microenvironment

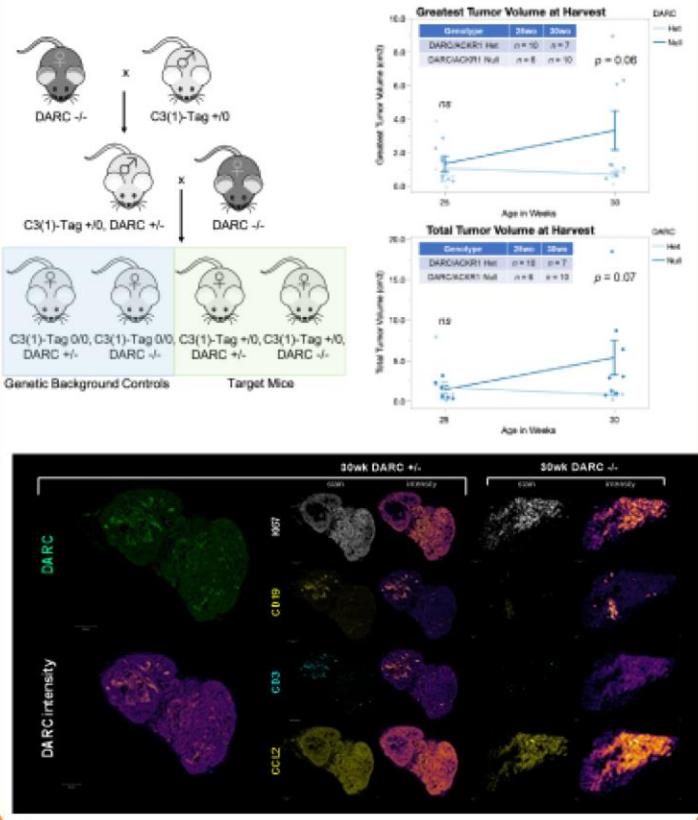
DARC/ACKR1 is highly correlated with deconvoluted immune cell abundance in TNBC cohorts of diverse ancestry groups



DARC strong binding chemokines are associated with Duffy-null status among breast cancer patients



DARC null breast cancer transgenic mice have increased tumor burden and volume



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Conclusions

- TNBC tumors have worse prognosis due to lack of targeted therapeutic options
- Increased immunogenicity of TNBC tumors may be driven by DARC expression, especially among women of African ancestry
- Characterization of Duffy-null status, and DARC among other cell types in the TNBC tumor microenvironment could present new opportunities for biomarker and/or therapeutic development to improve prognosis for these underserved populations
- Thank you!



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Tumor Infiltrating Lymphocytes and Breast Cancer-Specific Mortality in Racially and Ethnically Diverse Participants of the Northern California Breast Cancer Family Registry

Julia D. Ransohoff, MD, Iain Miller, MD, Jocelyn Koo, Vishal Joshi, Allison W. Kurian, MD, MSc, Kimberly H. Allison, MD, Esther M. John, PhD, MSPH*, Melinda L. Telli, MD* (*co-senior investigators)

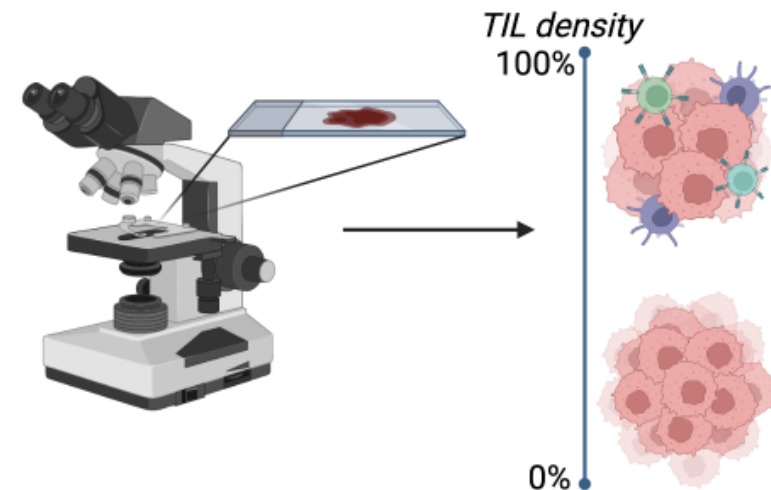
Stanford University School of Medicine
Stanford, California, United States

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Hypothesis, Objective, & Methods

- Hypothesis: Tumor infiltrating lymphocyte (TIL)-associated survival associations may vary by race and ethnicity, contributing to racial and ethnic disparities in breast cancer survival.
- Objective: To assess associations of TIL scores with baseline patient and tumor characteristics and survival outcomes of Northern California Breast Cancer Family Registry participants.
- Methods:
 - TILs scored in deciles by two independent pathologists; lymphocyte-predominant breast cancer defined as $\geq 50\%$ stromal TILs.
 - Associated stromal TIL scores with patient characteristics (regression analysis) and survival (Cox proportional hazards regression).

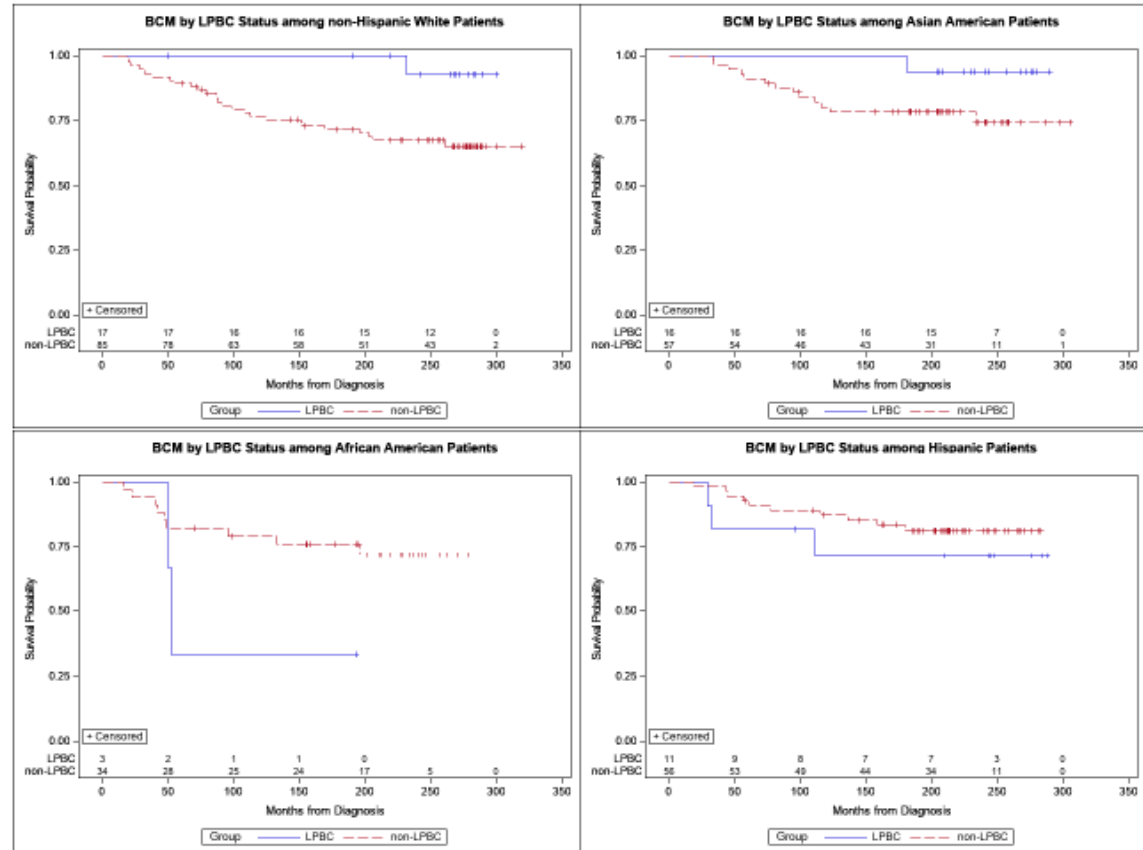


Results

Breast cancer-specific mortality varies by TIL score and by race and ethnicity

Group	Cases N	Deaths N	Breast Cancer-Specific Mortality	
			sTIL Per decile increase	LPBC vs non- LPBC
Overall	279	66	0.85 (0.74-0.99)	0.53 (0.24-1.18)
Race and ethnicity				
Non-Hispanic White	101	28	0.74 (0.58-0.94)	0.12 (0.02-0.91)
Asian American	73	14	0.59 (0.37-0.96)	0.25 (0.03-2.03)
African American	37	10	1.05 (0.72-1.53)	3.23 (0.49-21.3)
Hispanic	67	13	0.94 (0.66-1.32)	1.23 (0.29-5.2)
P heterogeneity by race and ethnicity	-	-	0.16	0.04

Models adjusted for age at diagnosis (continuous), stage (stage I, stage II, III, unknown), pre-diagnosis BMI (<30, ≥30 kg/m²), and germline *BRCA2* pathogenic variant status (positive, negative, not tested).



Conclusions, Implications, & Next Steps

- sTIL enrichment was not associated with a survival advantage among women from minoritized groups, who more often experience health disparities.
 - Suggesting complex factors influence sTIL phenotype.
- Key questions for future study:
 - Should immune biomarkers such as TILs be used to inform treatment de-escalation in African American and Hispanic women?
 - Does immunotherapy overcome survival disparities?
- Direct potential to inform future prospective investigations of TIL biology and TIL-guided treatment approaches.

THANK YOU