

Prognostic Impact of HER2-Low Expression in Hormone Receptor Positive Early Breast Cancer

Raz Mutai^{1,} Tamar Barkan¹, Assaf Moore^{1,2}, Michal Sarfaty^{1,2}, Tzippy Shochat³, Rinat Yerushalmi^{1,2}, Salomon M. Stemmer^{1,2}, Hadar Goldvaser^{4,5} ¹Davidoff Cancer Center, Rabin Medical Center, Petah Tikva, Israel, ² Sackler Faculty of Medicine, Tel Aviv University, Israel, ³ Statistical consulting unit, Rabin Medical Center, Petah Tikva, Israel. ⁴The Oncology Institute, Shaare Zedek Medical Center, Jerusalem, Israel . ⁵ Faculty of Medicine, Hebrew University, Jerusalem, Israel.

Background

- Recent data suggest that human epidermal growth factor receptor 2 (HER2)-low breast cancer may represent a distinct entity.
- We aimed to compare disease characteristics and outcomes between HER2-low and HER2-0 in estrogen receptor (ER) positive, early-stage breast cancer.

Methods

- A single center retrospective study comprising all women with ER positive, HER2 negative early breast cancer, for whom an Oncotype DX test was performed between 2005-2012.
- Women were grouped to HER2-low (immunohistochemistry +1 or +2 and in situ hybridization not amplified) or HER2-0.
- Clinico-pathological features and Oncotype recurrence score (RS) were collected.
- Data on overall-survival (OS), disease-free survival (DFS) and distant disease-free survival (DDFS) were evaluated according to HER2 expression status.

Results

- 608 women were included, of which 304 women had HER2-0 and 304 had HER2-low disease.
- Lobular subtype was significantly more common in HER-0 compared to HER2-low disease (17% vs. 8%, p=0.005).
- The prevalence of other clinic-pathological characteristics were comparable between both groups (Table 1).
- HER2 expression was not associated with long-term prognosis in whole population (Fig 1)
- For high genomic risk (RS>25), HER2-low expression was associated with significantly favorable OS (HR=0.31, 95% CI 0.11-0.78, p=0.01), DFS (HR= 0.40, 95% CI 0.20-0.82, p=0.01) and DDFS (HR=0.26, 95% CI 0.11-0.63, P=0.002) compared to women with HER2-0 (Fig 3).
- For genomic risk (RS≤25) HER2 expression did not affect longterm prognosis (Fig 2)

Corresponding author: Hadar Goldvaser, hadar7g@gmail.com

Table 1- Patients Clir	nicopathologi	c Characteristi	cs at Baseli	ne F	ig. 1: /	A-Overall Survival B- Di
Characteristic	HER2-0	HER2-Low	P-Value	Product-Limit Survival Estim		
	(n=304)	(n=304)		1.0 -		With Number of Subjects at Ris
Median age (range)-yr	. 61 (34-84)	60 (35-85)	0.36	0.8 -		
Ethnicity			0.58	- 9.0		
Ashkenazi Jews	151 (52%)	133 (47%)		val Prot		
Sephardi Jews	119 (40%)	120 (43%)		ivins		
Arab	5 (2%)	6 (2%)		0.2 -		
Other	17 (6%)	23 (8%)		0.0 – 0	304	291
Postmenopausal	234 (80%)	220 (76%)	0.32	>0	304 I O	293 I 5
T ≤2 cm	226 (74%)	242 (80%)	0.12	A		FUDeathYears
T >2 cm	78 (26%)	61 (20%)				
Node negative	257 (85%)	245 (81%)	0.23	Fig.	2: A-C	Overall Survival B- Dise
Grade 1	43 (18%)	42 (16%)	0.83			Product-Limit Survival Estin
Grade 2	154 (64%)	174 (66%)		1.0	-	With Number of Subjects at Ri
Grade 3	43 (18%)	46 (18%)		0.8	-	
Ki67% < 20%	150 (70%)	161 (71%)	0.36	o.6	_	
Histologic type ²			0.005	val Prot		
IDC	232 (76%)	259 (86%)		Surv.		
ILC	51 (17%)	25 (8%)		0.2	Log	Rank <i>P</i> =0.77
Other	21 (7%)	19 (6%)		0.0	- 252	245
ER intensityw	4 (1%)	6 (2%)	0.103		0	5 T ime (means)
ER intensity	76 (25%)	55 (18%)		A		HER2 Status: 0
iintermediate						
ER intensity strong	224 (74%)	243 (80%)		Fig. 3	: A-Ov	erall Survival B- Diseas
PR positive	260 (86%)	262 (86%)	0.90			Product-Limit Survival Esti
LVI present	20 (7%)	14 (5%)	0.37	1.0	-	With Number of Subjects at R
Oncotype DX RS ≤ 25	252(83%)	245 (81%)	0.52	0.8		┙╹╽ <mark>╘────────────────────────────────────</mark>
25>Oncotype DX RS	52 (17%)	59 (19%)		ability		Ϋ́

Conclusions

- The prognostic impact of HER2-low expression in early-stage luminal disease varies across the genomic risk.
- Significant favorable outcomes of HER2-low expression compared to HER2-0 in women with high genomic risk were observed.





isease Free Survival - All Study population



ase Free Survival - Low Genomic Risk- RS 0-25



se Free Survival High Genomic Risk- RS >25