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Making Cancer History®

The I-SPY Trials

Introduction

The SET2.3 index combines an accurate measure of transcription related to both estrogen and progesterone receptors (SETER/PR index) with a baseline prognostic index (BPI) derived from c-T Stage c-N status and molecular subtype by RNA4 (ESR1, PGR, ERBB2, and AURKA). SET2.3 index was translated from a microarray-based signature to a customized hybridization assay that yields highly reproducible results from routine pathology tissue sections.

Study Goal

To evaluate the SET2.3 index of predicted sensitivity to endocrine therapy in the context of molecular prognosis and response to negadiuvant chemotherapy, i.e. residual cancer burden (RCB).

Methods

- · Prognostic risk from cT and cN Stage categories were estimated from the published results in the Oxford overview (Pan et al) and refined using subject-level clinical data from the control arms of two adjuvant trials of chemotherapy for Stage II-III HR+/HER2breast cancer (Project DataSphere).
- . The RNA4 classification was developed from published gene expression data sets, using ESR1, PGR, ERBB2 and AURKA.
- . The SET2.3 index was measured from pre-treatment biopsies in the MDACC cohort (N=307), and a cutpoint was defined
- Blinded independent validation of SET2.3 index in pre-treatment biopsies from the I-SPY2 trial, which evaluates novel therapies added to neoadiuvant taxane-anthracycline chemotherapy in breast cancers that have high-risk MammaPrint test result.
- Evaluation of SET2.3 in contexts of RCB-II and RCB-III, and in prognostic gene expression signatures from U133A microarrays at MDACC, and Agendia'a MammaPrint signature in I-SPY2 trial.

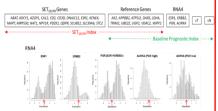


Figure 1. Schema of components of SET2.3 index

Increasing SET2.3 Index Was Associated with Decreased Risk of Distance Relapse in the MDACC Cohort

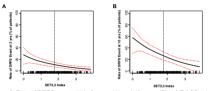


Figure 2. Rate of DRFS event within 3 years (A) and 10 years (B) in MDACC cohort The cutpoint for high SET2.3 was defined as SET2.3 index > 1.77 units.

SET2.3 Index in the Context of RCB and Genomic Subtype

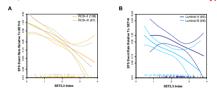


Figure 3. The prognosis (Log EFS event rate) of increasing SET2.3 index in patients with HR+/HER2- cancer who have significant residual disease (RCB-II/III) after neoadjuvant chemotherapy, stratified according to: A) RCB-II (vellow) or RCB-III (grev), and B) PAM50 subtype of Luminal A (dark blue) or Luminal A (light blue).

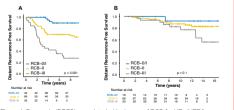


Figure 4. Prognosis (DRFS) associated with classes of RCB for HR+/HER2- cancers with Low (A) or High (B) predicted sensitivity to subsequent adjuvant endocrine therapy, defined from the cutpoint for SET2,3 index in this MDACC cohort.

Baseline Prognostic Index, SET2.3 Index and RCB Add Prognostic Information

Table 1. Multivariate Cox models for the components of residual prognostic risk (DRFS) after chemo-endocrine therapy

Results

	MDACC Coh	ort	I-SPY2 Trial		
Multivariate: Components of Residual Risk	HR (95%CI)	р	HR (95%CI)	р	
Baseline Prognostic Index (BPI)	0.55 (0.40, 0.76)	<0.001	1.02 (0.64, 1.63)	0.929	
Predicted Endocrine Sensitivity (SETER/PR Index)	0.56 (0.41, 0.75)	< 0.001	0.41 (0.27, 0.62)	<0.001	
Residual Cancer Burden after NAC (RCB Index)	2.03 (1.61, 2.54)	< 0.001	2.02 (1.57, 2.59)	<0.001	
Multivariate: SET2,3 versus RCB	HR (95%CI)	р	HR (95%CI)	р	
SET2,3 Index	0.23 (0.09, 0.62)	0.004	0.27 (0.08, 0.89)	0.031	
RCB Index	1.77 (1.25, 2.50)	< 0.001	1.68 (1.14, 2.45)	0.008	
SET2,3 Index * RCB Index	1.19 (0.87, 1.62)	0.257	1.17 (0.81, 1.68)	0.401	

SET2,3 Index was Independent from Microarray-derived Prognostic Signatures

Table 2. Prognostic signatures in neoadjuvant treatment cohorts (DRFS). Each signature was initially tested in univariate Cox model, then compared with SET2.3 index in a multivariate Cox model.

Prognostic Signatures	MDACC Cohort Study (N=307)					I-SPY2 Trial (N=268)						
Analyses of Continuous Scores	Univariate		Multivariate with SET2,3			Univari	ate	Multivariate with SET2,3				
	Signature Signa		Signatu	ignature SET2,3 Inde		ndex	Signature		Signature		SET2,3 Index	
	HR (95%CI)	р	HR (95%CI)	р	HR (95%CI)	р	HR (95%CI)	р	HR (95%CI)	р	HR (95%CI)	р
21-gene Recurrence Score (RS)	1.01 (1.00, 1.02)	0.030	0.99 (0.99, 1.00)	0.242	0.49 (0.35, 0.68)	<0.001	-		-		-	
11-gene EndoPredict (EP)	1.07 (1.02, 1.14)	0.012	0.94 (0.86, 1.01)	0.104	0.45 (0.32, 0.64)	<0.001	-		-		-	
70-gene Mammaprint (MP)	10.27 (2.65, 39.91)	0.001	1.34 (0.23, 7.68)	0.741	0.57 (0.42, 0.78)	<0.001	0.54 (0.17-1.72)	0.299	2.82 (0.65-12.74)	0.178	0.39 (0.22-0.71)	0.002

Blinded Independent Validation of SET2.3 Index in the I-SPY2 Trial

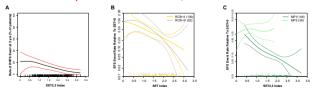
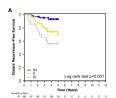


Figure 5. Prognostic association of SET2,3 index in patients with HR+/HER2- breast cancer from the I-SPY2 trial: A) the overall I-SPY2 trial HR+/HER2- population; B) patients with residual disease after negadiuvant chemotherapy. stratified by residual cancer burden classes RCB-II (yellow) and RCB-III (grey); and C) patients who have significant residual disease (RCB-II/III) after neoadjuvant chemotherapy, stratified by MammaPrint prognostic subgroups of highrisk (MP1, dark green) and very high-risk (MP2, light green).



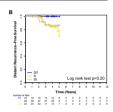


Figure 6. Prognosis (DRFS) associated with classes of RCB in patients with HR+/HER2- cancer with Low (A) or High (B) predicted sensitivity to subsequent adjuvant endocrine therapy defined from the SET2.3 index in the I-SPY2 trial.

Conclusions

- The prognostic performance of SET2,3 index was demonstrated in the MDACC cohort and independently validated in the I-SPY2 clinical trial.
- SET2,3 index added significant prognostic information that was independent from genomic subtype, prognostic score, and response to negadiuvant chemotherapy (RCB)
- Response to neoadiuvant chemotherapy (RCB class) was highly prognostic if low SET2.3, but not if high SET2.3 index.
- These results suggest that patients with high SET2,3 might be selected for endocrine-based neoadiuvant treatments in clinical trials.

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