

Evaluation of ANG/TIE/hypoxia pathway genes and signatures as predictors of response to trebananib (AMG 86) in the neoadjuvant I-SPY 2 TRIAL for Stage II-III high-risk breast cancer

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I-SPY2 Trial

Hypothesis: We hypothesized genes/signatures in the ANG/TIE signaling axis specifically predict response to angiogenesis (ANG1/2) inhibition, and that hypoxic tumors with a fragile blood supply are especially vulnerable to drugs in this class.

Biomarkers tested: 11 genes: TIE1/2, ANGPT1/2/4, AGNPTL1/3, VEGFA ICAM1, PECAM1 and MMP2; and 2 signatures: hypoxia [PMC1334226] and angiogenesis (GO:0001525).



2. THE PATIENTS: I-SPY 2 TRIAL Standing Platform



Match therapies with most responsive breast cancer subtypes
Defined by HR, HER2, and Mammaprint
High1/(ultra)High2 (MP1/2) status

Agents/combinations "graduate" for efficacy = reaching >85% predictive probability of success in a subsequent phase III trial in the most responsive patient subset

16% (10/62) HR-HER2- (TN) 20% (11/54) 43% (23/53) HR+HER2+(TP) 16% (3/19) 27% (4/15)

pCR table for AMG386 + controls

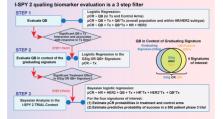
. Biomarker component: evaluate biomarkers associated with mechanism of action of each agent, along with the pre-defined subsets

3. DATA: Gene expression microarrays

Subtype	Control arm (n=132)	trebananib arm (n=134)	Total (n=266)
HR+HER2-	47	62	109
HR-HER2- (TN)	54	53	107
HR-HER2+	12	4	16
HR+HER2+(TP)	19	15	34

Data from 266 nationts (TR: 134 and concurrent controls: 132) were available. Pre treatment biopsies were assayed using Agilent 44K (32627) or 32K (15746) expression arrays, and these data were combined using ComPet

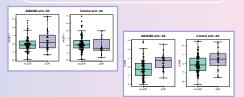
4. METHODS: Qualifying Biomarker **Evaluation (QBE)**



- · All I-SPY 2 qualifying biomarker analyses follow a pre-specified analysis plan.
- · We used logistic modeling to assess biomarker performance.
- treatment interaction is significant (likelihood ratio test, p<0.05).
- This analysis is also performed adjusting for HR and HER2 status as covariates, and within receptor subsets, sample size permitting.
- multiplicities of other biomarkers outside this study

5. RESULTS: Association between ANG/TIE pathway genes and hypoxia/angiogenesis signatures, and response to the ANG1/2 inhibitor trebananib (AMG386)

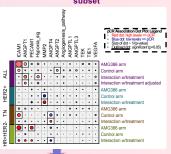




- C. Exploratory analysis: Immune signaling, not ANG1/2 pathway or hypoxia, predicts response in the TN subset
- In the TN subset, where pCR rates were highest in the TR arm relative to control, these mechanism-of-action biomarkers fail to predict response
 - associates with immune related genes and pathways (e.g. HLA's, IL21R



B. Association with response, by arm and receptor subset



- ANGPT1, a direct target of trebananib, associates with pCR in the TR arm but not the control arm, and shows a significant interaction with treatment that retains significance in a model adjusting for HR and HER2.
- . ICAM1, expressed on endothelial and immune cells, associates with response in the TR arm, but also in the control arm in the population as a whole.
- ❖ In the HR+HER2- subset, both ICAM1 and PECAM1 associate with pCR in the TR arm and not the control arm, with a trend toward treatment interaction.

6. CONCLUSION

Following our pre-specified analysis, ANGPT1 succeeds as a specific predictor of response to trebananib in I-SPY 2. In addition, ICAM1 and PECAM1 associate with response in the HR+HER2- subset; and in exploratory analysis immune signaling predicts response in the TN subset. These biomarkers may merit further