Advances in Therapy

OPEN ACCESS

PEER-REVIEWED SUMMARY SLIDE

Why carry out this study?

- The use of genomic assays in early breast cancer is increasing with several commercial assays currently available; these assays differ in the technological platforms, development, analytical/clinical validation and the gene sets included in the algorithm.
- Increasingly, there is a misconception that all the risk-stratifying assays provide similar information that can be used interchangeably for prognostication and treatment decisions.
- We hypothesized that genomic assays risk-stratify patients differently and compared results obtained using the 21-gene Recurrence Score® and the Prosigna® assays on the same tumor samples from patients with estrogen receptor positive early breast cancer.

What was learned from the study?

- The Recurrence Score and the Prosigna assays stratify patients differently; agreement between risk classifications based on these assays was 54%.
- Furthermore, luminal A and luminal B subtypes (as determined by the Prosigna assay) include patients with a wide range of Recurrence Score results; of the luminal B samples, 83% had a low Recurrence Score result.
- Consistent with prior comparisons between the 21-gene and other genomic assays, our findings suggest that different genomic assays cannot be used interchangeably.

This summary slide represents the opinions of the authors. Sponsorship for this study was funded by Genomic Health, Inc. Medical writing assistance for this study was provided by Dr. Avital Bareket-Samish of BioInsight Ltd.