Concordance Between 21-gene Recurrence Score (RS) and the 70-gene Profile (MP) in Breast Cancer (BC) Patients (pts)

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BACKGROUND: Genomic assays are increasingly incorporated into treatment planning for pts with early stage BC to provide prognostic and/or predictive information. MP is a validated predictor of recurrence risk (RR) in pts without any treatment and RS is a validated predictor of RR in pts treated with 5 years of hormonal therapy (HT). Because concordance between RS and MP is largely unknown, we analyzed concordance in untreated pts that had both tests performed.

METHODS: Data are from 50 early stage BC pts treated at 4 US Oncology practices and the University of California, San Francisco. We used linear regression to test whether clinical features were related to discordance, measured as part of the gamma statistic.

RESULTS: Median age was 52.5 years, 16% (8 pts) had micro or macroscopic nodal involvement, and 66%, 30%, and 4% of pts had Stage I, II, and III disease, respectively. All pts had estrogen receptor positive disease and 2 pts had HER2 overexpression by IHC or FISH. Concordance of MP and RS is shown below. Clinical features, including tumor size, grade, and HER2 were not significantly related to discordance. Gamma concordance was 0.64 (95% CI 0.28 to 0.98, p=0.0013).

	MP Low (n=22, 44%)	MP High (n=28, 56%)
21 gene RS		
Low (n= 28, 56%)	17	11
Intermediate (n= 16, 32%)	4	12
High (n= 6, 12%)	1	5

CONCLUSION: Concordance is high, mostly due to agreement in low risk scores. Five cases are truly discordant (MP low/RS intermediate or high) based on predicted outcomes. The 11 cases with high-risk MP with low risk RS may reflect endocrine sensitivity to 5 years of HT, or true discordance. Our identification of discordance should stimulate research to further clarify biology and elucidate the drivers of different types of risk. Large studies are underway to refine risk definition and treatment recommendations.