Feasibility of using core-needle biopsies for the 70-gene prognosis signature

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Background

A 70-gene microarray prognosis signature was previously discovered to improve the selection of patients with breast cancer for adjuvant therapy. This diagnostic test known as “MammaPrint” was recently validated in an independent cohort and implementation was shown to be feasible in community hospitals. MammaPrint was originally established on surgical resection specimens. Since most breast cancer patients will undergo core needle biopsies, we investigated whether the MammaPrint prognosis signature could be assessed in core needle biopsies.

Chemotherapy response

All but one patient (received TEC) received AT, usually 6 cycles. Most therapies ended late 2007, beginning 2008. Tumor diameter was assessed by physical examination and mammography.

Results

Thirty five signatures were obtained in this study. In this neo-adjuvant data set four of the 35 cases were assigned low risk for recurrence and thirty-one cases were predicted to be high risk. The high percentage of high risk MammaPrint outcome can be ascribed to the inclusion criteria of the trial, including breast cancer patients with stages III and IV. MammaPrint is originally designed for early stage breast cancer patients (stage I and II).

Twelve samples were rejected on the grounds of low tumor percentage, three samples because of insufficient RNA quality. Ninety two percent (92%) of samples with sufficient tumor cell percentage received a MammaPrint result.

Conclusion

The MammaPrint assay was originally designed for tumor tissue from surgical specimens. We show here that MammaPrint prognosis signatures can be obtained in the majority of core needle biopsies. In addition the same biopsy can be used for ER, PR and HER2 gene expression read-out. The results of this study have broadened the clinical applicability of the MammaPrint prognosis signature.

References

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Diagnostic Microarray

A diagnostic ‘8-pack’ is a single 1”x3” slide with eight subarrays each containing ER, PR and HER2 probes and normalization features. This allows simultaneous analysis of up to 8 samples.

Microarray based receptor read-out

Roepman et al. recently showed microarray read-out of hormone and HER2 receptor status to be strongly correlated with IHC assessment, especially for ER and HER2. Here we show the ER data for the current study: