

# USE OF GENE SIGNATURES TO PREDICT BREAST CANCER OUTCOME

Craig W. Englund M.D.

Chemotherapy or hormone treatment after primary surgery for breast cancer contained in the breast and lymph nodes substantially decreases the risk for recurrence and increases the probability of survival. It is generally agreed that patients with poor prognostic features benefit the most from adjuvant treatment. In the past, the main prognostic indicators in breast cancer have been age, tumor size, status of axillary lymph nodes and hormone receptor status.

Using a sophisticated genetic test called microassays on breast cancer tissue, it has been shown these tests bear a significant potential for predicting the probability of recurrence.

Dr. Van de Vijver from the Netherlands looked at 295 patients with breast cancer younger than 53 years as having a gene expression signature associated with either a poor or good prognosis. The gene expression profile proved to be a more powerful predictor of outcome of disease in young patients with breast cancer than standard systems based on clinical and histopathological criteria. The ability to metastasize to distant sites is an early and inherent genetic property of breast cancer. Thus, the classification of patients into high-risk and low-risk subgroups on the basis of the prognosis profile may be a useful means of guiding adjuvant therapy in patients with lymph node positive breast cancer. This approach should also improve the selection of patients who benefit from adjuvant systemic treatment, thereby reducing the role of both overtreatment and undertreatment.