A3. THE USE OF MICROARRAY ANALYSES IN THE ADJUVANT SETTING FOR BREAST CANCER

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In the treatment of breast cancer, patient-tailored therapy is becoming increasingly important. Decisions on optimal treatment include the choice between mastectomy and breast-conserving treatment; dose of radiotherapy; and decisions on adjuvant chemotherapy and hormonal therapy.
Gene expression profiling by micro-array analysis allows the study of the level of expression of large numbers of mRNA's in a single experiment. Gene expression analysis can be used to subclassify tumours on the basis of hierarchical cluster analysis in specific subgroups; supervised cluster analysis can be used to directly link gene expression profiles to clinical characteristics, including prognosis and response to various forms of treatment.
We have used micro-array analysis, first on a series of 117 breast carcinomas and, more recently, on a series of 295 breast carcinomas.
We have defined a gene expression profile of 70 genes that is predictive for a short interval to distant metastases (<5 years) in lymph node-negative (LN0) patients. We have validated the prognostic value of this gene expression profile in lymph node-negative patients; and also in premenopausal lymph node-positive patients. The profile outperforms all currently used clinical parameters in predicting outcome of disease.
At present, we are exploring the possibilities to use the prognostic expression profile in guiding adjuvant systemic treatment in lymph node-negative breast cancer patients younger than 60 years.

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A4. UPDATE ON THE WORLDWIDE EVIDENCE ON THE ADJUVANT TREATMENT OF BREAST CANCER

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In early breast cancer, all clinically apparent disease can be removed surgically. Following such surgery, adjuvant systemic treatments involving various cytotoxic, hormonal or other therapies may be considered. Before the 1980's, despite many trials of different adjuvant therapies, there was substantial uncertainty as to the net effects of such treatments, particularly on survival, because none of the trials was large enough individually to provide reliable answers. In 1983, the Clinical Trail Service Unit (CTSU) established the Early Breast Cancer Trialists' Collaborative Group (EBCTCG) to bring together updated data on each woman randomised into all trials on the treatment of early breast cancer, in an overview or series of systematic reviews. These reviews provide definitive evidence on the effects of treatments on recurrence, second cancer and mortality, which could not be obtained by other means. The fourth cycle of data collection (involving 200 000 women in 400 randomised trials, done by 250 trial groups) was presented to the EBCTCG for discussion in September 2000. Analyses were available for 10 000 women who were randomised in trials directly comparing different types of surgery; 10 000 in trials of ovarian ablation or suppression; 20 000 in trials of radiotherapy; 50 000 in trials of chemotherapy (including trials of chemotherapy versus control and direct comparisons of different regimens) and 80 000 in trials of tamoxifen (50 000 in trials of tamoxifen versus control, and 30 000 in trials of different durations of tamoxifen). The main results will be presented.

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