

( $p = 0.41$ ), grading ( $p = 0.45$ ), hormonal status ( $p = 0.92$ ) or Her2-Status of the tumor ( $p = 0.59$ ).

In this patient group, 9.7% and 6.9% of pts had presented with >1CTC at primary diagnosis and after chemotherapy, respectively. We found no correlation of CTCs after chemotherapy with the results at primary diagnosis ( $p = 0.08$ ) or at two years ( $p = 0.23$ ). However, the presence of CTCs at diagnosis was associated with CTCs after two years ( $p = 0.03$ ). In 184 postmenopausal HR+ pts endocrine treatment data was analyzed. CTCs at two years were detected in 6.8% of pts on tamoxifen ( $n = 9$ ), while 1.9% of pts were positive on anastrozole treatment ( $n = 1$ ;  $p = 0.19$ ).

**Conclusions:** In the SUCCESS trial we observed persisting circulating tumor cells in a relevant number of recurrence-free breast cancer patients after cytostatic, endocrine and zoledronate treatment. Longer follow-up will deliver insight if these cells can identify patients with increased risk for recurrence who might benefit from additional treatment approaches.

5169

POSTER

#### Comparison and combination of gene-set classifiers for prediction of localized breast cancer survival

X. Zhao<sup>1</sup>, T. Sørli<sup>2</sup>, B. Naume<sup>3</sup>, A. Langerød<sup>2</sup>, A.L. Børresen-Dale<sup>1</sup>, O.C. Lingjærde<sup>4</sup>. <sup>1</sup>Faculty Division The Norwegian Radium Hospital, Faculty of Medicine, University of Oslo, Oslo, Norway; <sup>2</sup>Institute for Cancer Research, Norwegian Radium Hospital, Oslo University Hospital, Department of Genetics, Oslo, Norway; <sup>3</sup>Oslo University Hospital, Cancer Clinic, Oslo, Norway; <sup>4</sup>Biomedical Research Group, Faculty of Mathematics and Natural Sciences, University of Oslo, Department of Informatics, Oslo, Norway

**Background:** Genome-wide expression profiling has been used to identify gene sets and corresponding gene signatures associated with clinical end-points of breast cancer patients. Here, we assessed and compared the risk predictive ability of 13 published gene sets in localized breast cancer patients.

**Materials and Methods:** The training set was data from a recent microarray study of 123 early-stage breast cancer patients. A clinically similar cohort of 80 localized breast cancer patients was used as test set. As clinical end points both systemic recurrence status and breast cancer specific death were considered. A Cox model was used to model the relationship between survival and gene expression of selected genes. Penalized likelihood regression (using an L2 penalty) was used to estimate regression parameters. Cross-validation was used to determine the penalty parameter. A Cox model for specific gene set was developed from the training set; this model was further applied to test set to calculate a Prognostic Index (PI) for a patient. The derived PIs from individual gene set were then used for comparison of the predictive performance across gene sets, as well as for combination of multiple gene-set predictors. The performance of specific gene set for risk prediction was also compared with the Adjuvant! Online model.

**Results:** A Gene-Set expression prognostic model was developed for individual gene set from the training set and a PI as risk indicator for each patient in test set was predicted using the gene-set specific model. The patients were then classified into different prognostic groups based on the derived PIs. The survival probabilities among the patient-groups were found significantly different and various clinical indications were explored in these groups. Each gene set in our study was assessed for risk prediction performance using PIs both in the univariate setting and compared with clinical information added by Adjuvant! Online. The results showed that the overall predictive information added by multiple gene sets was significant and the model incorporated gene-set predictors outperformed Adjuvant! Online model.

**Conclusions:** The proposed method can be used to quantify the potential contribution of a predefined gene set for breast cancer risk prediction and multiple gene sets as well as clinical parameters can be integrated in a risk prediction model to improve the prediction performance.

5170

POSTER

#### Breast cancer - Clinical early disease Neoadjuvant versus adjuvant chemotherapy for women with operable breast cancer: a matched-pair analysis and prognostic factors on overall survival

A. Arnaud<sup>1</sup>, G. Crehange<sup>1</sup>, S. Dabakuyo<sup>2</sup>, B. Coudert<sup>3</sup>, K. Peignaux<sup>1</sup>, G. Truc<sup>1</sup>, P. Arveux<sup>4</sup>, F. Bonnetain<sup>2</sup>, P. Maingon<sup>2</sup>. <sup>1</sup>Centre Georges-François Leclerc, Radiotherapy, Dijon, France; <sup>2</sup>Centre Georges-François Leclerc, Biostatistics and Epidemiology Unit, Dijon, France; <sup>3</sup>Centre Georges-François Leclerc, Medical oncology, Dijon, France; <sup>4</sup>Centre Georges-François Leclerc, Breast and Gynecologic Cancer Registry of Côte d'Or, Dijon, France

**Background:** Neoadjuvant chemotherapy (NAC) for patients with localised breast carcinoma became a standard approach although several phase II

trials failed to demonstrate higher overall survival rates, when compared with the adjuvant chemotherapy (AC) while improving rates of breast-conserving surgery. Registry-base Study of potential prognostic factors on overall survival (OS) whether chemotherapy was delivered in the NAC or the AC setting are valuable for optimizing the therapeutic strategy.

**Methods & Materials:** From 1982 until 2005, 184 women with localised breast carcinoma were retrospectively selected: 92 patients were treated with NAC followed by surgery and then radiotherapy (RT) and 92 matched-pair patients were treated with surgery followed by AC and then RT. Criteria for matching were: clinical AJCC stage at baseline, age ( $\leq 50$  vs  $>50$  years), diagnosis period (1982–1999 vs 2000–2005) and oestrogen receptor status (OR). The Kaplan Meier methods were used to estimate OS and DFS. Cox multivariate model was applied to assess independent prognostic factors of NAC for OS and DFS.

**Results:** Patients' characteristics were similar between the two groups, especially for SBR. All women received RT. No difference was found between irradiated lymph node (LN) stations. Median follow-up were 7 years and 6 years for the NAC and AC groups, respectively. Rates of breast-conserving surgery (BCS) were 57.6% and 48.9% for AC and NAC groups, respectively ( $p = 0.24$ ). DFS rates at 1, 5 and 10 years were 91%, 73% and 53% for the NAC group and 96%, 70% and 52% for the AC group, respectively ( $p = 0.85$ ). OS rates at 1, 5 and 10 years were 96%, 82% and 64% for the NAC group and 97%, 72% and 62% for the AC group, respectively ( $p = 0.2$ ). With univariate analysis prognostic factors for OS were OR, SBR and post operative staging AJCC. With multivariate analysis, OR and SBR remained significant. Timing of chemotherapy did not impact on OS. If NAC, the pathological complete response rate was 13% with OS rates at 1, 5 and 10 years: 100%, 83%, 83%, respectively.

**Conclusion:** This first registry-based case-control study failed to demonstrate improvements in breast-conserving surgery, DFS and OS rates with NAC compared with AC for women with localised breast carcinoma. Although, patients with a pathological complete response had excellent survival rates at 10 years, new phase III trials testing NAC strategies should be done to definitely answer on its impact on quality of life and/or in a medico-economic perspective.

5171

POSTER

#### Neo-adjuvant anthracycline based chemotherapy in locally advanced breast cancer: assessment of topoisomerase IIA with response

J. Singer<sup>1</sup>, A. Dewdney<sup>2</sup>, L. Mapp<sup>3</sup>, H.A. Bradpiece<sup>4</sup>, S. Jenkins<sup>4</sup>, S. Jader<sup>3</sup>, A. Patel<sup>4</sup>. <sup>1</sup>St Margarets Hospital, Breast Oncology, Epping, United Kingdom; <sup>2</sup>Royal Free Hospital, Oncology, London, United Kingdom; <sup>3</sup>Princess Alexandra Hospital, Cellular Pathology, Harlow, United Kingdom; <sup>4</sup>St Margarets Hospital, Breast Surgery, Epping, United Kingdom

**Background:** The anthracycline group of chemotherapy drugs are reported to target DNA Topoisomerase IIA (TopoIIA), indicating that breast cancers which over express TopoIIA are more likely to respond to anthracycline based chemotherapy. We sought to test this hypothesis by studying a number of biomarkers, including TopoIIA, in biopsies taken from patients with locally advanced breast cancer treated with neo-adjuvant anthracycline based chemotherapy.

**Method:** Between July 2001 and November 2006, thirty seven consecutive breast cancer patients with locally advanced inoperable (T2-T3) or locally advanced inoperable (T4) were treated with primary neo-adjuvant chemotherapy.

Analysis was carried out to assess response using the following methods: clinical measurement, mammogram, ultrasound, magnetic resonance imaging and histopathology. Chemotherapy treatment was according to protocol: 2000–2002 Six cycles Fluorouracil, Epirubicin, Cyclophosphamide (FEC).

2002–2006: Four cycles (FEC); followed by four cycles taxotere. Pre and post operatively, specimens were analysed for size, type, nodal status, oestrogen receptor, progesterone receptor, HER2 status. Patients were asked, with informed consent, for retrospective analysis biopsy specimen for TopoIIA using fluorescent in situ Hybridisation (FISH).

**Results:** Of 37 patients, 28 consented for retrospective Topo IIA specimen testing. All those that were Topo IIA amplified were also HER2 amplified. Histological complete response (CR) rates were 9/37 (24%). Of 7/28 patients that were TopoIIA positive, 2 had histological CR (29%). Of 14/28 patients that were Topo IIA negative, 4 had Histological CR (29%).

**Conclusion:** In this small neoadjuvant study, Topo IIA tumour testing did not predict for likelihood of complete histological response to anthracycline based chemotherapy.