O-31 ACCURACY OF UNIDIMENSIONAL AND VOLUMETRIC ULTRASOUND MEASUREMENTS IN PREDICTING GOOD PATHOLOGICAL RESPONSE TO NEOADJUVANT CHEMOTHERAPY IN BREAST CANCER PATIENT

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Background: Pathologic complete response (pCR) is an important predictor of long term survival in patients with breast cancer receiving neoadjuvant chemotherapy.

Methods: Unidimensional and volumetric ultrasound measurements prior to, after 4 cycles (mid-treatment), and at the end of 8 cycles (end-treatment) of chemotherapy were available from a subset of 55 patients enrolled in Neo-tAnGo, a phase III neoadjuvant chemotherapy trial. Changes in proportional longest diameter (LD) and volume as well as absolute residual size thresholds were examined for their ability to predict pCR or pCR plus minimal residual disease (pCR/MRD). Sensitivity, specificity, positive (PPV) and negative predictive values (NPV) and likelihood ratios (LRs) were calculated. Receiver–operator characteristic (ROC) curves and logistic regression models were constructed.

Results: At mid-treatment, neither complete radiological response, nor proportional LD or volume changes were found predictive of final pCR. Residual tumour volume $\leqslant 1\ cm^3$ was associated with pCR/MRD ($p = 0.014$). Sensitivity, specificity, PPV, NPV, LR+ and LR– values were 61%, 77%, 61%, 77%, 2.62 and 0.51 respectively. The area under the ROC curve (AUC) was 0.689 ($p = 0.03$). Volume $\leqslant 1\ cm^3$ was found significant in a univariate logistic regression ($p = 0.011$), but not in multivariate analysis. At end-treatment, no ultrasound measurements were found predictive of pCR or pCR/MRD.

Conclusions: Proportional tumour size changes were not found predictive of good pathologic response, yet residual volume $\leqslant 1\ cm^3$ after 4 cycles of chemotherapy was found predictive. Multiple volume and LD thresholds were examined and uncorrected *p*-values presented, increasing the possibility of type I errors. Replication in an independent dataset is required.

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O-32 D-DIMER AS A MARKER FOR EARLY PROGRESSION IN PATIENTS COMMENCING NEOADJUVANT CHEMOTHERAPY

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Objective: D-dimer, the end product of coagulation, is increased pre-operatively in abdominal cancers with poor prognosis, and in early breast cancer is associated with lymph node positivity. However, d-dimer as a marker of response to treatment has not been investigated.

Methods: In early breast cancer patients receiving neoadjuvant chemotherapy ($n = 11$), d-dimer was measured prior to commencement of chemotherapy and at 6 months following commencement of treatment. Clinical and radiological follow-up of breast cancer was at 3, 6, 12 and 24 months. We compared baseline d-dimer, d-dimer at 6 months, and change in d-dimer in response to treatment in patient with relapse compared to those remaining disease free at 2 years.

Results:

	Relapse at 2 years	Disease free at 2 years	*P*-value
D-dimer pre-chemotherapy, ng/ml (SD) (*n*)	1328 (1183) (3)	259 (91) (7)	0.03
D-dimer at 6 months, ng/ml (SD) (*n*)	1364 (221) (2)	454 (224) (5)	0.005
Change in d-dimer in response to chemotherapy, ng/ml (SD) (*n*)	717 (345) (2)	177 (188) (5)	0.04

(Upper limit of normal 500 ng/ml).
No patients had clinical evidence of relapse at 6 months.

Conclusions: Despite no clinical evidence of disease, d-dimer remains elevated at 6 months following breast cancer treatment in patients with early relapse. D-dimer, prior to treatment and following treatment, may act as a marker for early relapse in breast cancer.

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O-33 AN ARTIFICIAL NEURAL NETWORK BASED ALGORITHM FOR PREDICTING CONTINUOUS TIME TO EVENT DATA IN BREAST CANCER

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Introduction: Development of gene signatures usually focuses on changing time dependent data into binary categories, for example 5 year survival. Predicting actual time to an event has the potential to be much more powerful. Here we introduce a novel algorithm termed Risk Distiller that aims to overcome the splitting of data into arbitrary categories by using artificial neural networks to predict a continuous response variable describing the actual time to event.

Methods: Time to recurrence data (0–14 years) for a series of breast cancer patients was made available in a study described by Van de Vijver et al. We applied our method to those cases with known events to identify an optimal panel of genes with the ability to predict the actual time to recurrence. The gene signature started as a single gene and was grown upwards until the optimal model was determined.