Results: A total 43 patients were enrolled (isolated mediastinal LN:13 patients, isolated pulmonary nodule: 30 patients). Eighteen patients (42%) were confirmed to have benign lesion (group A) and 25 patients (58%) confirmed to have metastasis (group B). The disease free interval (median duration from initial operation of breast cancer to the detection of mediastinal LN or lung nodules) was similar between two groups (7.8 months (A) vs 9.5 months (B), p = 0.386). Between two groups, initial T stage (p = 0.145) and N stage (p = 0.749) was not different. Hormone receptor positivity was more prevalent in group A (72.2% vs 40.9%, p = 0.048) and triple-negativity was more prevalent in group B (16.7% vs 40%, p = 0.113). The mean size of the largest lesion was bigger in group B than in group A (20.8 mm vs 14.4 mm, p = 0.024). There was no difference in the number of lesions between two groups (2.17 (A) vs 2.76 (B), p = 0.361). PET was performed in 29 patients (67%). Metastatic lesions had significantly higher maximal SUV than that of benign lesions (6.42 vs 3.41, p = 0.021). mSUV more than 6.0 could define the lesion to be metastasis with the sensitivity of 50% and the specificity of 92% by ROC curve.
Conclusions: The biologic subtype, size of lesion and maximal SUV on PET could help physician to differentiate metastasis from benign lesion in breast cancer patients who present new isolated mediastinal LN or pulmonary nodule during surveillance.

5088 POSTER

Analysis of factors predicting response to second-line trastuzumab-based therapy in patients (pts) with Her2-positive advanced breast cancer (ABC)

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Background: Upfront use of trastuzumab (T), either alone or in combination with chemotherapy or aromatase inhibitors, is well established in Her2-positive ABC. Upon disease progression, pts may be switched to lapatinib plus capecitabine. Others however may be candidates for continued antibody therapy. Finding the optimal treatment approach therefore is pertinent. We tried to identify factors predicting efficacy of second-line T-based therapy.
Methods: 97 pts treated with >1 line of T-based therapy were identified from a breast cancer database. Her2-status was determined by immunohistochemistry and re-analyzed by FISH if a score of 2+ was gained. Time to progression (TTP) on second-line therapy was defined as primary study endpoint. Secondary endpoints consisted of response rate (RR), clinical benefit rate (CBR; CR+PR+SD >6 months), overall survival (OS), development of brain metastases, and cardiac toxicity.
Response was evaluated every three months (m) using UICC criteria. TTP and OS were estimated using the Kaplan-Meier product limit method. Multivariate analyses (Cox proportional hazards model, multinomial logistic regression) were applied in order to identify factors associated with TTP and RR.
The following variables were included: age, initial tumor stage, grading, endocrine receptor status, prior non T-containing palliative chemotherapy, metastatic sites, and clinical benefit from T-based first-line therapy. *p* values <0.05 were considered to indicate statistical significance.
Results: Second-line TTP was median 7 m (95% CI 5.74−8.26) and first-line 8 m (95% CI 6.25−9.74) (n.s.). RR on second-line was 30.9% (44.3% first-line). In the multivariate models, none of the factors included could independently predict for activity of second-line treatment. OS was 43 months (95% CI 37.92−48.09).
A significant deterioration of cardiac function was observed in three patients; 40.2% developed brain metastases on second-line T or during follow-up after a median 21 m (95% CI 13.86−28.14).
Conclusions: Trastuzumab in multiple lines showed considerable activity. None of the variables investigated correlated with activity of second-line therapy. In order to predict for activity of second-line T, evaluation of other factors known to confer trastuzumab-resistance (p95Her2, PTEN-loss) appears necessary.

5089 POSTER

Shorter Overall Survival (OS) in HER2-positive (HER2+) metastatic breast cancer (MBC) patients (pts) treated with trastuzumab (T) ± chemotherapy (CT) and overexpressing HER3 by immunohistochemistry (IHC)

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Background: Mechanisms of resistance to T in HER2+ MBC pts are still poorly understood. Both EGFR and HER3 form heterodimers with HER2. We investigated the role of HER3 protein expression by IHC in HER2+ MBC pts treated with T ± CT.
Material and Methods: From 04/99 and 03/06, 76 consecutive HER2+ MBC pts were treated at our institution but tumor tissue was available, for this analysis, from 42 pts. HER2 was evaluated by IHC (MoAb CB11) and scored according to DAKO Herceptest. HER3 status was evaluated by IHC on 3.5 μm section of formalin-fixed, paraffin embedded tissue using a mouse MoAb (clone RTJ1; Novocastra United Kingdom; used at 1:20). The immunostaining reactivity was citoplasmatic. Tumors were considered HER3+ if >50% of tumor cells were positive.
Results: At median follow up of 26.5 months (3.7−99.6) from the start of T, 42 pts were evaluable for OS and incidence of CNS metastases and 40 for response to T and TTP. Median age of pts was 53 years (23−77). We observed 25/40 responses (CR+PR) to T ± CT (62.5%) and CNS metastases in 20/42 pts (47.6%); median TTP from the start of T was 9.6 months (1.3−80+). Median OS from the start of T was 29.6 months (3.7−99.6+). Twenty-one pts were HER3+ with a cut-off of 50%. HER3 overexpression was not significantly correlated with response to T, TTP, incidence of CNS metastases; OS from start of T was shorter in HER3+ tumors compared to HER3 tumors (28.2 vs 42.7 months; p = 0.152). These data confirm the notion that HER2/HER3 heterodimer is the major oncogenic unit in HER2+ MBC.
Conclusions: In this limited series of pts, a worse OS was observed in HER2+ MBC with HER3+ status by IHC. Approaches to target HER2/HER3 signaling may be warranted.

5090 POSTER

Micrometastatic tumor cells in blood and bone marrow of patients with primary breast cancer: extended surrogate marker-panel for multi-gene expression analysis

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Background: We have validated a new preanalytical enrichment and molecular detection method using embedded tumor cell calibrators (ETC) for quantitative gene expression analysis of circulating tumor cells (CTC) and bone marrow tumor cells (DTC). Here we present results of an extended surrogate marker panel.
Methods: Samples from patients were divided in native probes and matched calibrator probes containing either 2 or 10 breast carcinoma tumor cells (ETC). The high affinity antibodies BM7 (MUC-1) and VU1D9 (EpCAM) coupled to 4 μm dynabeads (Invitrogen®) were used for immunomagnetic tumor cell enrichment from $1x10^7$ bone marrow (BM) cells and 10 ml peripheral EDTA-blood of patients with primary breast cancer and metastatic disease. Separated cells were lysed and used for mRNA isolation and c-DNA synthesis. We used end point RT-PCR (Adnagen®) and real-time quantitative RT-PCR approaches with the epithelial markers cytokeratin19 (CK19), mammaglobin1 (MG1), MUC1 and EpCAM for tumor cell identification. The phenotype of micrometastatic cells was determined by expression analysis of the markers ALDH1, TKTL1, Survivin, CXCR4, HIF-1, HER2 and CD276 (B7-H3).
Results: Positivity rate of ETC controlled RT-PCR on the basis of CK19, MG1, and EpCAM was 8.6% in 16/187 patients with primary breast cancer, 24% for DTC analysis in BM and 61.1% in patients with metastatic disease. During a 12 to 24 months follow-up of 114 patients of the primary breast cancer group CTC positivity was determined in 9.6% of the patients, however only one of these had been positive before operation. In three patients with multimarker expression early metastasis was clinically confirmed later. Progressive disease in metastatic breast cancer patients was characterized by elevated marker levels of CXCR4 (86%), survivin (58%) and CD276 (50%).

Conclusion: We have used embedded tumor cells (ETC) as internal calibrators for accurate process control and normalization of the immunobead quantitative RT-PCR technique. The specificity and detection rate of tumor cells in blood and bone marrow was significantly increased by molecular analysis of a multi-marker gene panel. The newly introduced surrogate markers from the networks of apoptosis, invasion, angiogenesis and stem cell phenotype should improve early detection of metastasis, monitoring of therapy response and efficacy and selection of tailored therapy regimes.

5091 POSTER

Predictive role of Her-2 receptors on primary tumour in patients with liver metastases from breast cancer treated by surgery

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Introduction: Hepatic resection is a well-established therapy for patients with liver metastases (LM) from colorectal or neuroendocrine carcinoma. However, for patients with LM from breast cancer, the role of surgery in management of metastases from breast cancer is not well-defined and still controversial.
The objective of this retrospective study is to evaluate outcomes after surgical treatment of breast LM and to identify factors associated with longterm survival.
Material and Methods: Tumour characteristics, treatments, and outcomes of patients undergoing resection for hepatic metastases from breast cancer from June 1995 to Augustus 2005 were analyzed. Patient demographics, tumor characteristics, treatment, and postoperative outcome were analyzed. The start date for follow-up and survival analyses was the date of surgery for LM.
Results: After median follow-up of 25.5 months (range: 5−80) from hepatic surgery, the median cancer specific survival and median disease-free survival (DFS) was 50 months and 16.6 months respectively. There was no postoperative mortality. Univariate analysis suggests that prechemotherapeutic number of HM (single vs multiple) was associated with CSS; estrogen and progesterone receptors on primary tumour were associated with improved DFS. Furthermore, positive Herceptine receptor (HerR) on primary tumour was associated with worse CSS ($p < 0.0102$).
Conclusions: In selected patients, resection of breast LM can be done safely. HerR on primary tumour could be representing an unfavourable predictive factor for CSS.

5092 POSTER

Molecular predictive factors of response to taxanes and anthracyclines in breast cancer: toward a targeted perspective for cytotoxic therapy

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Background: Anthracyclines and Taxanes are among the most active drugs in the treatment of breast cancer. Acute and long-term side effects are mainly cardiotoxicity for anthracyclines and neuropathy for taxanes. The objective of the study is to identify markers of response to anthracyclines and to taxanes in the aim of tailoring a treatment plan. Topoisomerase IIa (TopoIIa) is the anthracyclines target and MAPtau regulates the microtubules dynamic instability, target of taxanes. Some studies have shown a positive correlation between TopoIIa overexpression and MAPtau underexpression and responsiveness to Anthracyclines or Taxanes.
Material and Methods: TopoIIa and MAPtau protein expression were evaluated by IHC using monoclonal antibodies (Ki-S1 and A0024) in 36 breast tissues from women with advanced breast cancer, treated with anthracyclines and taxanes. The protein expression was related to response, as well as to other prognostic fatcors such as age, hormone receptors (HRs), c-erb, p53, ki67 and bcl-2. Response was assessed using RECIST criteria.
Results: Our early data suggest that TopoIIa overexpression (cut-off$\geqslant$12%) and MAPtau underexpression (cut-off <30%) correlate with objective response to anthracyclines (p 0.004) and to taxanes (p 0.007). HRs is related to probability of response to both drugs ($p < 0.005$), even in the subgroups TopoIIa negative and MAPtau positive. Bcl-2 overexpression seems to be related to response in the subgroup MAPtau positive (p 0.006). Other prognostic factors (age, c-erbB2, p53 and Ki67) are not related with response either to anthracyclines and taxanes ($p > 0.01$), in particular HER-2 gene amplification did not alter neither the response to anthracyclines (p 0.86) nor TopoIIa expression (p 0.4).
Conclusion: These preliminary data suggest that TopoIIa overexpression and MAPtau underexpression are related to response to anthacyclines and taxanes, respectively. The presence of HRs favourably affects response to treatment with both drugs; Bcl-2 overexpression is related to response only in the subgroup MAPtau positive, while HER-2 gene amplification is not related to response to anthracyclines or to TopoIIa expression. These results should be considered in a larger cohort of patients, also to identify the role of other factors in the subgroup of responders which are TopoIIa negative and MAPtau positive and the mechanism of resistance in non-responders which are TopoIIa positive and MAPtau negative.

5093 POSTER

Beta-catenin stability, frizzled and cyclin D1 proteins expression in human breast cancer and its relation with their prognosis

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Background: Development and progression of breast cancer is associated with a number of genetic events, including changes in proto-oncogene and tumor suppressor gene expressions. Defects in components of Wnt signaling pathway including Adenomatosis Poliposis Coli (APC) tumor suppressor protein and β-catenin are known to cause colon and melanoma tumors. Beta-catenin is a central element in Wnt signaling pathway. Post-transcriptional accumulation of β-catenin in cytoplasm and subsequent translocation into the nucleus is thought to be the cause of its tumorigenic potential. Genes which have a definitive role on cell cycle control such as MYC and Cyclin D1 have important roles in development of tumors. Accordingly we have examined β-catenin stability, which is known to have the transcriptional activation affect on such genes mentioned above, in tissues from 118 primary breast cancer patients. Since there is no data on the inactivation of APC in breast cancers, we decided to focus on two other factors which could be the cause of β-catenin stability; 1) β-catenin mutations and 2) Wnt pathway.
Materials and Methods: We used immunocytochemical staining to investigate the stability and location of β-catenin, expression of FRP-1 and FRP-2 proteins as Wnt signaling inhibitors and the expression of Cyclin D1 as one of the genes controlled by β-catenin.
Results: β-catenin, Cyclin D1, FRP1 and FRP2 expression percentages were 53.5±32, 41.8±33, 25.0±26.9 and 31.6±28.3 respectively. When these results were correlated with factors including menopausal status, progesterone receptor positivity, Cerb2 positivity, lymph node involvement and staging no statistical significance was found. On the other hand in patients with Estrogen receptor positivity ($p = 0.0005$) and Ki67 positivity ($p = 0.037$) Cyclin D1 and in Ki67 positive patients FRP1 ($p = 0.024$) expression percentages were significantly high. β-catenin expression was increased only in p53 posivite patients ($p = 0.039$). Disease free and overall survival rates were not found to be correlated with β-eta catenin, Cycln D1, FRP1 ve FRP2 expression percentages. β-catenin localization and disease free and overall survival relation was also assessed 64 patients and existence of cytoplasmic localization of β-catenin was not found to affect survival rates.
Conclusion: β-catenin, Cyclin D1, FRP1 ve FRP2 expressions were not found to influence disease free and overall survivals.

5094 POSTER

Clinical and biological metastatic breast cancer (MBC) outcomes after discontinuation of treatment with bevacizumab plus metronomic capecitabine and cyclophosphamide: a retrospective analysis

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Background: Angiogenesis plays an important role in breast cancer development and progression. Bevacizumab is a humanized monoclonal antibody against VEGF, which showed activity in monotherapy or in combination with chemotherapy in MBC. We recently reported results of a phase II trial evaluating the association of bevacizumab plus oral metronomic capecitabine and cyclophosphamide in MBC, showing efficacy