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Fatty acid synthase expression in breast carcinoma patients. Correlation with hormone receptors

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Purpose: Recent studies have demonstrated that high expression of fatty acid synthase (FAS) occurs in a variety of cancers including the breast cancer. The aim of this study was to compare FAS expression with the clinicopathologic and clinical outcome in breast cancer.

Methods: We evaluated 243 primary breast cancer in the period between 1989 and 1994. Immunohistochemical staining for FAS was performed on formaline-fixed, paraffin-embedded sections. FAS staining was graded for intensity as low or high.

Results: The expression of FAS was high in 145 (60%), low in 98 cases (40%). High FAS was associated with positive estrogen receptor (ER) ($p = 0.0022$) and positive progesterone receptor (PgR) ($p = 0.0085$) status. Furthermore, these finding were significantly shown in premenopausal cases than postmenopausal ones. The survival analysis showed that FAS staining intensity was not significantly associated with a high risk of recurrence in overall cases. However, we found that high FAS expression significantly related to shorter disease-free survival in ER positive cases ($p = 0.018$) and also in PgR positive cases with a borderline significance ($p = 0.057$). There was no significant association with FAS expression in both receptor negative cases ($n = 89$), while the low FAS was associated with longer disease-free survival in remaining 154 cases ($p = 0.012$).

Conclusions: This study showed close correlations between FAS expression and ER and PgR. FAS expression can be a useful tool for assessing hormonal responsiveness. It might be a possible predictor of response to endocrine therapy, especially in steroid hormone receptor positive breast cancers.

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Altered expression of E-cadherin in breast cancer: Patterns, mechanisms and clinical significance

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Altered E-cadherin expression has been associated with increased invasiveness, metastatis formation and poor prognosis in various malignancies. In the present study, the primary tumours from 120 breast cancer patients were evaluated by immunohistochemistry using the monoclonal antibody 5H9. Possible mechanisms of altered expression were looked at by PCR. Evaluation for LOH was possible on 90 samples using two markers close to the E-cadherin gene. Finally, the clinical outcome was ascertained with a mean follow-up of 49.7 months for 109 patients. Our results show that 18 out of 97 (18.5%) of infiltrating ductal carcinomas showed complete loss of E-cadherin expression compared with with 9 out of 14 (64.3%) infiltrating lobular carcinomas. LOH was detected in 21 out of 50 (42%) infiltrating ductal carcinomas and 6 out of 8 (75%) infiltrating lobular carcinomas. LOH was associated with complete loss of E-cadherin expression in the infiltrating lobular carcinomas but not in the infiltrating ductal carcinomas. In the infiltrating lobular carcinomas, complete loss of surface E-cadherin expression and LOH was accompanied by cytoplasmic expression for E-cadherin. Univariate and multivariate analysis showed that loss of E-cadherin expression was associated with a shorter disease-free survival in node-negative breast cancer patients ($p = 0.05$ and 0.035). We conclude that different mechanisms are involved in the altered E-cadherin expression seen in different subtypes of breast carcinomas. The results implicate E-cadherin as a possible independent prognostic marker for disease recurrence in node-negative breast cancer patients, irrespective of histological type.

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Plasminogen activator inhibitor type 2: Expression and prognostic value in primary breast cancer

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Objective: The aim of this study was to assess the association of plasminogen activator inhibitor 2 with etablished prognostic factors and survival in tumor extracts of primary breast cancer.

Material and Methods: The study was performed on patients ($n = 252$) with operable breast cancer. Tissue from benign breast lesions ($n = 20$) served as control.

Results: The PAI-2 median value (2.43 ng/mg protein) was significantly higher ($p < 0.001$) in the cancer samples than in the extracts of the control group (0.19 ng/mg protein). Tissue extracts from invasive ductal breast cancer showed higher levels of PAI-2 (2.64 ng/mg) than invasive lobular breast cancer ($p = 0.037$). Patients without lymph-node involvement had significant higher levels of PAI-2 (2.82 ng/mg) than patients with lymph-node metastasis (2.30 ng/mg) at the time of the surgery ($p = 0.015$). After a follow-up of 44 months (range 11–57 months) we found that patients with low levels of PAI-2 had a shorter overall survival ($p = 0.140$).

Conclussion: Measurment of PAI-2 is prognosticator for breast cancer and high levels of PAI-2 antigen exercise a protective function in tumor metastasis.

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Quantitative analysis of circulating tumour cells in breast cancer patients using reverse transcriptase polymerase chain reaction

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Purpose: The major cause of morbidity and mortality in cancer patients is metastatic spread of the tumour to secondary sites. To monitor the dissemination of tumour cells, we study the feasibility of detecting tumour cells in the peripheral blood of breast cancer patients by reverse transcriptase polymerase chain reaction (RT-PCR) using cytokeratin 19 (CK19) and carcinoembryonic antigen (CEA) mRNAs as molecular markers. We aim to develop a semiquantitative method for distinguishing levels of the mRNA markers between breast cancer patients and healthy subjects.

Methods: We have analyzed peripheral blood samples from 36 female breast cancer patients and 29 healthy subjects. The levels of CK19 and CEA mRNAs were quantified by semiquantitative RT-PCR with reference to a breast cancer cell line.

Results: We detected variable CK19 mRNA levels in the peripheral blood from 6 of 29 healthy subjects and 11 of 36 breast cancer patients. The normal upper reference range was found exceeded by 7 breast cancer patients. Different CEA mRNA levels were also detected in 28 of 29 healthy subjects and 33 of 36 breast cancer patients and The normal upper reference range for CEA mRNA was found exceeded by 3 breast cancer patients.

Conclusion: We have developed semi-quantitative RT-PCR for distinguishing the CK19 and CEA mRNA levels in the peripheral blood between breast cancer patients and healthy subjects. Much higher CK19 and CEA mRNA levels concomitantly detected in the seven breast cancer patients appeared to originate from circulating tumour cells. Low CK19 and CEA mRNA levels detected in healthy subjects were possibly attributed to skin contamination in the peripheral blood caused by needle aspiration and/or "illegitimate" transcription. This suggests the importance of our quantitative approach in monitoring the levels of mRNA markers for risk assessment and prognostic indication.

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Breast cancer: Does tumour location influence survival and cosmesis? Experience from 644 patients (1984–1995)

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Purpose: The authors demonstrate the unfavourable survival rate in patients with medially and centrally located breast tumours (m/c) compared to patients with cancer in the lateral quadrants (lat).

Methods: From 1984 to 1995 644 patients with 649 T1–2 tumours were treated. 429 presented with lat and 220 with m/c. Treatment method included breast conserving surgery and radiotherapy (45 to 50 Gy) and one interstitial 10 Gy boost. All axillary nodal positive patients underwent systemic therapy (6 × CMF or tamoxifen). Mean follow up of survivors: 77 months (25 to 158). From the first 216 patients the cosmetic results were evaluated using a 4 grade scoring system.