respectively ($p < 0.001$). Kohen-kappa homogeneity test revealed that breast cancers in each patient differed as regards histological type (MBC $p = 0.85$, SBC $p = 0.83$) but not as regards histological grade (MBC $p < 0.01$, SBC $p' < 0.001$). BRCA1 mutation was detected in 12 out of 120 patients (10%). In 8 of them Ins C was revealed. Patients with BRCA1 mutation were younger (43 vs 48 years), more often had MBC (8/12 pts) and had family history of breast cancer (55%). Eleven out of 12 patients with BRCA1 mutation live without any symptoms of the disease. BRCA2 mutation was detected in 1 (0.8%) out of 120 pts and CHEK2 mutation – in 7 (6%) out of 120 pts.
Conclusions: Cancers in two breasts of the same patient differ as regard histological type. Overall survival of bilateral breast cancer is good, but there is a significant difference between SBC and MBS. Patients with BRCA1 and BRCA2 mutation have a good prognosis. Other mutations should be searched, especially in older patients and with SBC.

304 POSTER

Prognostic profiling of node negative untreated breast cancer patients based on outcome: genomic fine-tuning

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Background: Various prognostic molecular signatures for breast cancer patients have been recently published, some of which have been recently validated on independent series, with a good prognostic value on distant recurrences.
However, all existing signatures fail to provide useful information on the type of recurrence expected, which could have significant impact on clinical management. On behalf of the TRANSBIG Network which will be initiating a large prospective trial of the clinical usefulness of genomic profiling, we initiated a study aimed at defining molecular profiles for several subgroups of patients based on their outcome.
Materials and methods: Untreated consecutive node negative breast cancer patients with available tumour samples were selected based on their outcome in two different French cancer centres (Institut Gustave Roussy and Centre René Huguenin): patients who did not relapse (NR)after minimum 10 years of follow-up, patients with a local relapse (LR), 30 patients with distant metastais before 5 years after initial diagnosis (M1), and 23 patients with distant metastasis after 5years of initial diagnosis (M2). Gene expression profiling using the Agilent technology was performed at Institut Gustave Roussy. A specific prognostic gene signature was defined for each sub-group of patients.
Results: A total of 15O patients were included in the present analysis: 63 NR (IGR = 39, CRH = 24), 33 LR (IGR = 14, CRH = 19), 30 M1 (IGR = 17, CRH = 13) and 23 M2 (IGR = 11, CRH = 12).
Discussion: Results of the comparison of molecular profiles of each sub-group and their prognostic value will be presented. This approach should provide some insight into pathways of local and metastatic recurrence and allow more accurate prediction of outcome for node-negative breast cancer patients.

Publication
Breast cancer – basic science, molecular predictive assays, translational research

305 PUBLICATION

Expression pattern of E cadherin in invasive ductal breast carcinoma

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Introduction: E-cadherin (E-CD) is considered to be the most important cell adhesion molecule in mammary gland. Some studies suggest that downregulation of E-CD and subsequent loss of cellular adhesiveness correlate with poor prognosis and metastasis but this is not confirmed by other studies. Many investigations suggest that E-CD protein is not expressed in invasive lobular in comparison with invasive ductal carcinoma (IDC) of the breast. A few papers report that E-CD mediated cell adhesion system can be disrupted by oncoprotein c-erbB-2/HER-2/neu in c-erbB-2-positive breast carcinomas despite ductal or lobular type.
Purpose of study: To evaluate the expression patternt of E-CD and relationship with the status of HER-2/neu in IDC and analyze an association with lymph node positivity.
Methods: We reviewed 91 cases of IDC. All cases were examined in our laboratory for suspicion for c-erbB-2 overexpression. Nottingham histologic grade, immunohistochemical staining for estrogen and progesterone receptors (ER and PR), proliferating cell nuclear antigen (PCNA), E-CD; fluorescense in situ hybridization for HER-2/neu gene amplification; and lymph node positivity were evaluated.
Results: HER-2/neu gene amplification was observed in 60.5% of IDC and positively correlated with higher histological grade and lymph node positivity. Strong positivity for PCNA was observed in 84.2% of IDC and positively correlated with histological grade and HER-2/neu positivity. IDCs were negative for ER in 50%, and PR in 57.8% of cases. ER/PR-negativity was associated with histological grade, HER-2/neu gene amplification and lymph node positivity. E-CD expression was lost in 26.3% cases of IDCs and positively correlated with histological grade, HER-2/neu gene amplification and lymph node positivity.
Conclusion: The loss of E-CD expression can be a feature of some typical invasive ductal carcinomas of the breast. E-CD negativity seems to be associated with higher histological grade, HER-2/neu gene amplification and lymph node positivity suggesting that c-erbB-2 may act as a regulator of E-CD expression in most human breast carcinomas *in vivo*.
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306 PUBLICATION

The immunohistochemical expression of estrogen receptor beta in breast cancer and its correlation with selected clinicopathological parameters and with survival

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Background: The role of estrogen (ER) and progesterone receptors (PgR) in breast cancer is well established. Recently, another type of estrogen receptor, termed ERβ has been discovered. The "classical" ER is now called estrogen receptor α (ERα). While ERα and PgR assays have been routinely used for a number of years, the role of ERβ is still undefined. The aim of this work was to determine the extent of ERα, ERβ and PgR immunohistochemical expression in breast cancer and to determine if the ERβ expression is correlated with selected clinical parameters, biological markers and with survival.
Methods: Formalin-fixed, paraffin embedded breast cancer tissues used in our study came from 110 women who had undergone surgery at our department between 1998–1999. None of the patients had been treated pre-operatively with endocrine therapy. Immunostaining for ERα, ERβ and PgR was performed using monoclonal antibodies against ERα, PgR (DakoCytomation), and against ERβ (CHEMICON). The EnVision detection system was applied. The data were analyzed using a nonparametric Fisher-Freeman-Halton test and log-rang test for disease-free survival (DFS) and overall survival (OS). The statistical significance was considered when $p < 0.05$.
Results: 61% of tumors were ERα positive, 64% were PgR positive and 55% were ERβ positive. As many as 14% of ERβ positive tumors had no expression of ERα. In tumors expressing ERβ, the expression of p53 was less common and ERβ positive tumors were of a lower histological grade. There was no correlation between ERβ expression and tumor size and axillary node involvement. Patients with tumors expressing ERβ had better DFS (5 years follow-up), but there was no statistically significant difference in OS.
Conclusions: The expression of ERβ was significant in breast cancer and was also present in a noticeable proportion of ERα negative tumors. Future studies will be required to determine the clinical significance of ERβ in breast cancer.

307 PUBLICATION

The expression of CCR7 in breast cancer tissue and CCL21 in lymph node does not correlate with sentinel node metastasis

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Background: Lymph node metastasis is a major prognostic factor for breast cancer patients. Sentinel node (SN) is defined as the nearest lymph node(s) from primary tumor, however, the factor(s) that can affect on SN metastasis has not been elucidated yet. On the other hand, some types of chemokines have been known to correlate with breast cancer metastasis. Among them, CC chemokine receptor7 (CCR7) is expressed on breast cancer cells, and the CCR7 ligand CCL21 is expressed selectively in lymph nodes. The aim of the present study was to examine the relationship between CCR7 protein expression of primary breast cancer and CCL21 expression of lymph nodes, including SN, and to explore whether CCR7 and/or CCL21 expression in breast cancer patient correlate with SN metastasis.