invasive tumors, 77.2% were classified as Grade II and above. 23.4% of these patients had nodal involvement and the most common stages of presentation were Stage 1 (32.9%) and Stage 2 (35.7%). Majority of the tumors were oestrogen (95.5%) and progesterone (81%) receptor positive and 27.9% and 18.6% were cerbB2 score 3+ and 2+ respectively. Where treatment data was available, 90.2% patients with ER positive tumors received tamoxifen. 18.2% received adjuvant chemotherapy and 40.3% received radiation therapy. The mean follow up time was 55.4 (2–178) months. The 2-year vs. 5-year disease free and overall survival were 93.2% and 85.9% vs. 73.8% and 74.2% respectively. Interestingly 15 patients also had a second primary cancer not of breast origin. These patients had a significantly worse overall survival ($p = 0.07$).

Conclusions: Male breast cancer in Chinese men is rare and present at an old age but at an early stage (Stage 1 and 2). Although a majority of our cohort did not have family history of breast cancer, there was a high incidence of second primary cancer not of breast origin. Further investigation with genetic study in this group of patients is likely to be of relevance.

103 Poster

Body weight and the risk of breast cancer in BRCA1/2 families – the GEO-HEBON study

P. Manders[1], A. Pijpe[1], F. van Leeuwen[1], M. Rookus[1]. [1]*Netherlands Cancer Institute – Antoni van Leeuwenhoek Ziekenhuis, Epidemiology, Amsterdam, The Netherlands*

In the general population, an inverse association has been observed between both body weight and body mass index (BMI) and the risk of premenopausal breast cancer, whereas body weight and BMI increase the risk of postmenopausal breast cancer. So far, association between body weight and BMI and breast cancer risk in BRCA1/2 families is unknown.

We assessed the association between body weight and breast cancer in a large series of 485 BRCA1/2 families, consisting of 918 BRCA1/2 carriers and 142 obligate carriers from the GEO-HEBON study, a retrospective nationwide cohort study. Information on hormonal/lifestyle factors was obtained from a self-administered questionnaire. Information on breast and ovarian cancer and on preventive surgical measures was verified via the PALGA database (Pathological Anatomy National Automated Archive) and the Netherlands Cancer Registry until August 2007.

Participants were asked to report current body weight and height and body weight from age 18 years onwards in 10-year age groups (ages ranging from 20−29, 30−39, 40−49, 50−59 and 60−69 years), excluding pregnancy in these periods. Current body weight and height were used to compute current BMI in kilograms per squared meters. Analyses will be preformed to examine the effect of body weight and BMI at age 18 years and censoring, changes in body weight (20 years of age till censoring), and height on breast cancer risk in BRCA1/2 families. All analyses will be stratified according to menopausal status. Hazard ratios will be estimated using a Cox-regression approach stratified for gene and birth cohort. Results will be presented.

Wednesday, 16 April 2008 12:30–14:30

POSTER SESSION

Molecular biology, markers

104 Poster

Proteomics in mammary cancer research

A. Fink-Retter[1], D. Gschwantler-Kaulich[1], G. Hudelist[1], C.F. Singer[1], K. Pischinger[2], M. Manavi[1], K. Czerwenka[2]. [1]*University of Vienna, Special Gynecology, Vienna, Austria;* [2]*University of Vienna, Clinical Departement of Pathology Division of Gynecopathology, Vienna, Austria*

Background: This study combines a summary of proteomics techniques and protein analysis (in mammary cancer) with a report of expressed and up-regulated proteins in benign and malignant mammary tissues.

Till now, only few reports of proteomic research for mammary cancer could be found, including the techniques of two-dimensional gel electrophoresis (2-DE), MALDI/ESI/TOF and ESI/MS, browsing the PubMed database. Human carcinoma cell lines, mouse material or human serum were the most exercised materials for these studies. Only a few of them used native tissues from patients with mammary carcinomas.

The aim of this study was to search for more, not well-established (up-regulated) proteins in mammary cancer in the mean and low molecular weight (MW) range, to figure out the role of post-translational modification in biologic processes and to recognize newer pathways.

Material and Methods: Tissue samples ($n = 26$), originated from 10 healthy female donors (benign mammary tissue; K01–K10; control group) and 16 donors who had developed mammary carcinomas of a ductal type (P01–P16), were snap-frozen in liquid nitrogen and stored at −70ºC till analysis. High resolution 2-DE was performed, according to the literature, using a pH gradient from 2−11. The most abundant spots representing the selected variant spot groups were manually picked in a clean bench to provide sufficient material for MALDI-MS, as well as nano-liquid chromatography-electro spray ionization-mass spectrometry (nano-LC-ESI-MS) based protein identification.

Results: Beside hypothetical proteins a number of transcription factors, such as zinc finger proteins (ZNFs), and not well-investigated (high significant) proteins, e.g., elongation factor 1-alpha 1 (eEF1A1), were identified by mass spectrometry (MS). eEF1A1, expressed in the membrane of mammary carcinomas, is involved in gene expression/translational elongation and has a GTPase activity and an oncogenic potency.

Another protein, for example, calgizzarin (S100A11; S10AB human), which is involved in carcinoma invasion and tumor metastases, could be determined as over-expressed in the cytosol of mammary cancer tissues. It is also concerned with the regulation of numerous cellular processes such as cell cycle progression and differentiation.

Conclusion: With this study, we want to demonstrate that proteome analyses provide a powerful tool for detecting potential and new biomarkers, which could be validated for diagnostic and clinical features of mammary carcinomas.

105 Poster

Approaching molecular classification of breast cancer by using a panel of molecular tumor markers

P. Sinn[1], S. Aulmann[1], P. Schirmacher[1]. [1]*University of Heidelberg, Gynecopathology, Heidelberg, Germany*

Background: Gene expression profiling has resulted in the definition of distinct and robust clusters of distinct types of breast cancer (luminal A and B, erbB2-like, basal-like, normal breast-like). However, the question how to transform this classification into clinical practice is quite uncertain.

Materials and Methods: We have used a panel of 6 immunohistological markers on primary invasive breast cancers and collected data from 3733 tumors. The panel includes ER (1D5), PgR (PgR636), HER2 (A0485), Ki-67 (MIB1), bcl-2 (124), and p53 (DO7, all antibodies by Dako). Data were clustered with the aim of creating groups similar to those obtained by gene expression classification.

Results: 75% of all breast cancers could be clustered using this panel of 6 immunohistological tumor markers. 30.2% were clusted as Luminal A, 18.0% as Luminal B, 11.3% as erbB2-like, 5.4% as basal-like, and 10.1% as normal-breast like.

Conclusions: While phenotypic clustering is very well possible for hormone receptor positive tumor into Luminal A and B subgroups, the markers are not sufficient to predict basal phenotype. With the addition of basal cytokeratins to this panel, a good immunohistological classification should be possible.

106 Poster

Basal- and non-basal phenotypes in triple-negative breast cancers

P. Sinn[1], Z. Sawaf[1], P. Schirmacher[1]. [1]*University of Heidelberg, Pathology, Heidelberg, Germany*

Background: Triple negative breast cancers are characterized by lack of expression of oestrogen, and progesterone hormone receptors, and lack of HER2 overexpression. Frequently they are associated with a basal phenotype, but there is a distinct subgroup of “quadruple-negative” cancers which not basal-like, and are yet ill defined yet. Therefore, in the present study, we have analysed the expression of basal and other markers the triple negative breast cancers.

Materials and Methods: 158 triple-negative invasive breast carcinoma were selected from the archives and used for construction of tissue microarrays. A panel of immunohistochemical markers, which included ER, PgR, HER2, CK5/6, CK14, CK18, EGFR, p53, c-KIT, MKI-67, bcl-2, and p16 was used to further characterize these tumours.

Results: 102 tumours (66%) showed a basal phenotype by being positive for either CK5/6 or CK14 using a cutoff value of 10%. The non-basal triple-negative cancers differed from the carcinomas with a basal phenotype by having a lower proliferative rate ($p = 0.04$), and were less frequently CD117 positive (14% vs. 32%, $p = 0.01$) and less frequently overexpressed p16 (31% vs. 52%, $p = 0.01$). No differences were seen for bcl-2 (9% vs. 10%) and p53 overexpression (37% vs. 36%).