bility of the Nottingham Prognostic Index (NPI) as a prognostic instrument was investigated. The incidence of early-onset breast cancer has increased very moderately and ten-year survival rate has not improved during the last 35 years. 52%, 49% and 55% of patients diagnosed 1960, 1975 and 1988 respectively were alive at ten years. The 5-year survival increased by a factor of 1.004 per year 1960–1992. 64% had grade 3 tumours, 67% were node positive. Lymph node status was the strongest sole prognostic indicator but the use of NPI gave a more accurate prognostic information than node status alone.

O-119. AGE IS NOT AN INDEPENDENT PROGNOSTIC FACTOR

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In 3959 women with primary (<5 cm clinically) breast cancer, treated at one centre between 1974 and 1999, 1372 < 50 years of age and 2237 50+, breast cancer specific actuarial survival (OS) was a little lower in the <50's.

Divided into five groups according to the Nottingham Prognostic Index (NPI) the figures were:

	<50				50+			
NPI	n	%	10 yr OS	20 yr OS	n	%	10 yr OS	20 yr OS
EPG	144	10.5	94	88	333	14.8	95	87
GPG	229	16.7	87	75	516	23.1	84	81
MPGI	349	25.4	76	71	455	20.3	75	66
MPGII	362	26.4	56	41	574	25.7	58	43
PPG	288	21.0	28	20	362	16.2	22	8

OS is remarkably constant within all NPI groups independent of age. OS for the whole sets is better in 50+ because more lie in EPG and GPG.

Difference in adjuvant therapy (<50 more CMF, 50+ more Tamoxifen) gave no survival differences between corresponding NPI groups for the ages.

Conclusion: Survival depends on features at diagnosis (grade is higher in young women, particularly <35) and age is not an independent prognostic factor.

O-120. COMPARATIVE GENOMIC HYBRIDISATION ANALYSIS OF 40 BREAST CANCERS WITH LONG TERM PATIENT SURVIVAL DATA

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The aim of this study was to perform comparative genomic hybridisation (CGH) analysis on 40 primary breast tumours for which 7 year disease recurrence and survival data were available.

Using CGH, the mean number of aberrations per cancer was 9 with an average of 5.5 amplifications and 3.5 deletions per tumour. The most common regions of amplification were 1q (67%), 8q (47.5%), 17q (32.5%) and 20q (22.5%). Most frequently deleted areas included 17p (30%), 8p (27.5%) and 19p (25%). The CGH data are consistent with an underlying molecular pathology such as activation of myc (8q24), erb B2 amplification (17q12), cyclin D1 over-expression (11q13) and inactivation of tumour suppressors p53 (17p13) and E-cadherin (16q22). In other instances, such as amplification of 1q and 17q23 and deletion of 8p and 19p, strong candidate genes have yet to be identified.

A higher mean number of deletions was seen in cancers from patients who died during the follow-up period than in those from the survivors. Three tumours showed no copy number changes and these patients did not suffer disease recurrence. These results are consistent with acquisition of distinctive patterns of large scale (karyotypic) genetic change in malignant breast disease.

O-121. DETECTION OF ISOLATED TUMOR CELLS IN BONE MARROW IN EARLY STAGE BREAST CANCER. FINAL LABORATORY RESULTS FROM THE OSLO STUDY

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Large clinical studies are still needed to substantiate the detection of micrometastases bone marrow (BM) as an independent prognostic marker. With support from The Norwegian Cancer Society bone marrow aspirates have been collected from 917 patients with early stage breast cancer during primary surgery at 5 hospitals. BM was aspirated from anterior and posterior iliac crest bilaterally. Mononuclear cells (MNC) were prepared and analysed for tumor cells by direct immuncytochemical analysis (ICC) of 2×10^6 MNC using anti-cytokeratin mAb (AE1/AE3) and APAAP, negative controls and standardized morphological criteria (all samples). In addition, negative immunomagnetic enrichment (negative IMS) followed by ICC was performed on 615 of the patient samples (10×10^6 MNC analysed) for comparison with the standard ICC technique (2×10^6 MNC analysed). Analyses of the primary tumor specimen have been performed, including histomorphology, TNM staging, grading, immunohistochemical analysis for ER, PgR, mutant p53, CathepsinD and c-erbB2.

The basic micrometastasis analysis and primary tumor characteristics have been completed on all patients (exept for c-erbB2). Of the patients with infiltrating carcinoma, 63% were node negative (NO), 33% node positive (N+), 13% had >3 affected nodes and 62% had T1 tumors. The results show the presence of tumor cells in 13.5% of the evaluable patients after direct ICC analysis of 2×10^6 cells. The presence of tumor cells have been related to tumor-size and nodal status, showing BM-positivity in 10% of the NO cases, whereas 21% were positive in the N+ group. Of the patients with T1 tumors 10.5% were positive, increasing

to 14.1% in T2 tumors. No correlation between detection of micrometaststasis and p53- or CatepsinD-expression were detected. Patients with ER+ and/or PgR+ tumors had lower frequency of micrometastasis than ER−/PgR−. The standard direct ICC detection of tumor cells seems to correlate with primary tumor stage and ER/PgR status. The use of negative IMS increased the frequency of positive BMs by 62%, and the most prominent increase was detected in the NO group.

The implication of this and other studies of micrometastasis in bone marrow for future clinical trials will be discussed.